Table S2. DEGs between transgenic and wildtype fruits.

[a]Gene IDs and definitions according to Sol Genomics Networks ITAG3.2 annotation.
[b]Gene Ontology (GO), Enzyme Code (EC) and InterPro IDs annotated using Blast2GO software.
[c]Transcription factor family associated to Gene ID according to Plant Transcription Factor Database v.4.0 (http://planttfdb.cbi.pku.edu.cn/)
[d]Mean (n=4) of counts per million (CPM) mapped reads. Sample abbreviations: WT - wild-type; L1 - PPC2::$PHYB2^{OE}$ line #1; L6 - PPC2::$PHYB2^{Y252H}$ line #6; MG - mature green fruit stage; BK - breaker fruit stage.
[e]log2-fold change (logFC) values only for differentially expressed genes in each comparison.
[f]p-adjusted value (False Discovery Rate - FDR) values only for differentially expressed genes in each comparison.
[g]Up- or down-regulated differentially expressed genes in each comparison for Venn diagrams.

Solyc_ID_iTAG3.2[a]	Locus_definition_iTAG3.2[a]	Locus_symbol	GO_IDs[b]	GO_Names[b]	Enzyme_Code[b]	Enzyme_Name[b]	InterPro_IDs[b]	TF_IDs[c]	Mean_CPM_WT_MG[d]	Mean_CPM_L6_MG[d]	Mean_CPM_WT_BK[d]	Mean_CPM_L1_BK[d]	Mean_CPM_L6_BK[d]	logFC_L6MGxWTMG[e]	FDR_L6MGxWTMG[f]	logFC_L6BKxWTBK[e]	FDR_L6BKxWTBK[f]	logFC_L1BKxWTBK[e]	FDR_L1BKxWTBK[f]	Venn_L6MGxWTMG[g]	Venn_L6BKxWTBK[g]	Venn_L1BKxWTBK[g]
Solyc00g005000	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G20015.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM); IPR021109 (G3D		0,579	0,116	0,259	0,168	0,166									
Solyc00g005050	UPF0664 stress-induced protein C29B12.11c (AHRD V3.3 *** A0A151ST26_CAJCA)						PTHR31606:SF12 (PANTHER); PTHR:		46,679	42,349	95,870	88,965	89,652									
Solyc00g005080	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast			IPR008543 (PANTHER)		0,000	0,021	0,000	0,050	0,023									
Solyc00g005092	Serine/threonine phosphatase-like protein (AHRD V3.3 --* D5K8R0_9ASTR)						mobidb-lite (MOBIDB_LITE)		0,323	0,062	0,075	0,045	0,070									
Solyc00g005094	Glucose-6-phosphate 1-dehydrogenase 3, chloroplastic (AHRD V3.3 --* G6PD3_ARATH)								3,665	0,644	2,553	3,121	1,952	-2,450	0,000					down		
Solyc00g005283	Phytoene desaturase (AHRD V3.3 --* I0AXU6_NARTA)								0,301	0,170	0,176	0,099	0,164									
Solyc00g005285	O-methyltransferase (AHRD V3.3 *-* F6M2M1_VITPS)		F:GO:0008171	F:O-methyltransferase activity			IPR001077 (PFAM); G3DSA:3.40.50.1		0,658	0,466	0,370	0,296	0,565									
Solyc00g005287	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *-* W9S6R3_9ROSA)		F:GO:0004315; P:GO	F:3-oxoacyl-[acyl-ca	EC:2.3.1.41; EC:2.3.	Beta-ketoacyl-[acyl-c	mobidb-lite (MOBIDB_LITE)		0,727	0,675	0,440	0,196	0,374									
Solyc00g005430	UBX domain-containing protein (AHRD V3.3 --* AT1G14570.4)								0,160	0,036	0,050	0,000	0,046									
Solyc00g005440	40S ribosomal protein S9, putative (AHRD V3.3 *** Q60CZ2_SOLDE)		F:GO:0003735; F:GO	F:structural constituent of ribosome; F:rRNA binding; C:cytosoli			IPR022801 (PANTHER); PTHR11831:		0,105	0,036	0,044	0,123	0,093									
Solyc00g005445	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 --* AT3G23470.3)		F:GO:0008168; F:GO	F:methyltransferase activity; F:oxidoreductase activity; F:transferase activity; P:methylation; P:oxidatio					0,057	0,000	0,000	0,000	0,000									
Solyc00g005450	LOW QUALITY:Cysteine-rich repeat secretory protein 38 (AHRD V3.3 --* CRR38_ARATH)								0,000	0,043	0,022	0,000	0,000									
Solyc00g005840	Thioredoxin, putative (AHRD V3.3 *** B9RK57_RICCO)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D); IPR01:		16,264	19,844	5,720	6,506	10,349			0,849	0,006				up	
Solyc00g005850	LOW QUALITY:Protein TIC 214 (AHRD V3.3 --* TI214_EPIVI)								0,021	0,000	0,000	0,000	0,000									
Solyc00g006490	SIT4 phosphatase-associated family protein (AHRD V3.3 *** B9HQ89_POPTR)						IPR007587 (PFAM); mobidb-lite (MOB		37,842	40,924	47,389	47,016	45,293									
Solyc00g006530	LOW QUALITY:Calmodulin-binding protein (AHRD V3.3 --* AT4G31000.1)								0,000	0,057	0,000	0,000	0,072									
Solyc00g006540	LOW QUALITY:DNA ligase (AHRD V3.3 --* K4CCL3_SOLLC)						mobidb-lite (MOBIDB_LITE)		0,122	0,206	0,050	0,048	0,144									
Solyc00g006655	ABC transporter A family member 7 (AHRD V3.3 --* N1R5R8_AEGTA)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,000	0,000	0,000	0,024									
Solyc00g006680	LOW QUALITY:Senescence-associated protein (AHRD V3.3 *-* A0A072THV8_MEDTR)						PTHR33047 (PANTHER)		0,078	0,064	0,173	0,226	0,047									
Solyc00g006800	transaldolase	TALDO1	F:GO:0004801; C:GO	F:sedoheptulose-7-	EC:2.2.1.2	Transaldolase	IPR013785 (G3DSA:3.20.20.GENE3D		64,163	59,953	78,821	70,479	73,615									
Solyc00g006805	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT4G05160.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,040	0,136	0,097	0,025	0,000									
Solyc00g006810	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 *** AT5G13410.1)		P:GO:0000413; F:GO	P:protein peptidyl-pr	EC:5.2.1.8	Peptidylprolyl isomera	IPR001179 (PFAM); G3DSA:3.10.50.4		21,352	28,838	65,660	63,880	72,418									
Solyc00g006820	Major facilitator superfamily protein (AHRD V3.3 *** A0A097PNX1_SOLLC)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM); G3DSA:1.20.125		9,136	9,884	0,886	1,392	1,268									
Solyc00g006830	no exine formation 1 (AHRD V3.3 *** AT5G13390.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR353		39,221	38,300	43,067	44,165	42,036									
Solyc00g006867	DNA repair (Rad51) family protein (AHRD V3.3 --* AT2G28560.6)								0,059	0,000	0,094	0,186	0,000									
Solyc00g006900	LOW QUALITY:Phosphate transporter PHO1 like 3 (AHRD V3.3 --* A0A0B2RL68_GLYSO)		F:GO:0005525; C:GO	F:GTP binding; C:chloroplast outer membrane; F:hydrolase activ			mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,019	0,000	0,000	0,000									
Solyc00g007010	Phosphoinositide phosphatase family protein (AHRD V3.3 *** AT5G66020.1)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			IPR002013 (PFAM); IPR030069 (PTH		14,889	14,682	24,389	23,437	24,363									
Solyc00g007030	Glutathione S-transferase (AHRD V3.3 *** A0A096XCA4_BETPN)	GSTL6	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D); IPR00		0,882	0,569	0,025	0,094	0,000									
Solyc00g007040	Glutathione S-transferase family protein (AHRD V3.3 *** AT5G02790.1)	GSTL7	F:GO:0005515	F:protein binding			IPR004045 (PFAM); G3DSA:1.20.105		0,155	0,098	0,000	0,051	0,000									
Solyc00g007060	Kinase family protein (AHRD V3.3 *** U5GGQ9_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); IPR001245 (F		15,281	23,575	8,325	10,811	11,002	0,651	0,040					up		
Solyc00g007070	Heterogeneous nuclear ribonucleoprotein, putative (AHRD V3.3 *** B9S6U9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR000504 (PF		62,250	60,848	81,305	76,942	74,302									
Solyc00g007080	tail-anchored protein insertion receptor WRB-like protein (AHRD V3.3 *** AT4G16444.1)		P:GO:0071816	P:tail-anchored membrane protein insertion into ER membrane			IPR028945 (PFAM); PTHR11760 (PAN		1,717	1,589	0,699	0,791	0,891									
Solyc00g007090	GPI-GlcNAc transferase complex, PIG-H component (AHRD V3.3 *** A2Q4W7_MEDTR)		F:GO:0017176	F:phosphatidylinosit	EC:2.4.1.198	Phosphatidylinositol	IPR019328 (PFAM); PTHR15231 (PAN		8,000	8,866	9,834	10,300	9,956									
Solyc00g007100	Kinase family protein (AHRD V3.3 *** B9H679_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20		34,971	33,414	13,165	12,766	15,423									
Solyc00g007110	Calcium-binding EF-hand (AHRD V3.3 *-* A0A103XCL1_CYNCS)		F:GO:0005509; F:GO	F:calcium ion binding; F:protein binding			IPR002048 (SMART); IPR000261 (SM		11,094	8,535	8,259	6,835	6,755									
Solyc00g007120	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XCL1_CYNCS)		F:GO:0005509; F:GO	F:calcium ion binding; F:protein binding			G3DSA:1.10.238.10 (GENE3D); IPR0(		22,611	18,299	15,218	14,918	16,378									
Solyc00g007130	Amino acid transporter, putative (AHRD V3.3 *** B9S6V9_RICCO)		P:GO:0003333; F:GO	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM); PTHR22950:SF4		0,705	0,408	2,575	2,997	1,959									
Solyc00g007150	LOW QUALITY:WAT1-related protein (AHRD V3.3 --* R0HAL8_9BRAS)						mobidb-lite (MOBIDB_LITE)		11,525	8,917	1,905	2,731	3,335									
Solyc00g007160	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151SHE2_CAJCA)						IPR025312 (PFAM); PTHR33499 (PAN		1,329	1,412	0,682	0,887	0,726									
Solyc00g007170	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT5G46330.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,000	0,000	0,000	0,024									
Solyc00g007190	Phosphatase 2C family protein (AHRD V3.3 *-* U5G7W2_POPTR)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	mobidb-lite (MOBIDB_LITE); mobidb-lit		0,399	0,476	0,143	0,149	0,374									
Solyc00g007195	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G51470.2)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART); IPR001932 (PF		0,482	0,660	0,473	0,361	0,424									
Solyc00g007200	MLO-like protein (AHRD V3.3 *** A0A0V0IJD9_SOLCH)		P:GO:0006952; C:GO	P:defense response; C:integral component of membrane			IPR004326 (PFAM); mobidb-lite (MOB		0,463	0,473	0,267	0,200	0,260									
Solyc00g007220	RING/U-box superfamily protein (AHRD V3.3 *** AT1G20823.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART); IPR001841 (PF		7,098	4,401	38,773	34,890	29,738									
Solyc00g007260	Ulp1 protease family protein, putative (AHRD V3.3 *-* Q6L4B6_SOLDE)		P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM); G3DSA:3.40.395		12,807	11,397	14,334	12,681	12,614									
Solyc00g007270	Eukaryotic translation initiation factor 6 (AHRD V3.3 *** M1C4H3_SOLTU)		P:GO:0042256; F:GO	P:mature ribosome assembly; F:ribosome binding			IPR002769 (SMART); IPR002769 (TIG		162,547	146,014	180,219	158,111	156,373									
Solyc00g007300	Leucine-rich repeat-containing protein, putative (AHRD V3.3 *** B9T2K7_RICCO)		F:GO:0005515	F:protein binding			SM00365 (SMART); IPR003591 (SMA		23,433	17,227	67,610	97,491	59,248					0,531	0,008			up
Solyc00g007320	LOW QUALITY:Methyl-CpG-binding domain-containing protein 8 (AHRD V3.3 --* A0A199UGF7_ANACO)		F:GO:0003676; F:GO	F:nucleic acid binding; F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,018	0,000	0,000	0,024									
Solyc00g007550	LOW QUALITY:formin-like protein (DUF1421) (AHRD V3.3 --* AT4G28300.1)								0,000	0,041	0,000	0,025	0,023									
Solyc00g007555	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151RA30_CAJCA)						IPR019557 (PFAM); PTHR44194 (PAN		0,000	0,019	0,000	0,000	0,000									
Solyc00g007560	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151S6S1_CAJCA)						IPR019557 (PFAM); PTHR44194 (PAN		0,019	0,018	0,000	0,000	0,000									
Solyc00g007600	Meiotic recombination protein DMC1-like protein (AHRD V3.3 *-* W9RXM4_9ROSA)		F:GO:0000150; F:GO	F:recombinase acti	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:1.10.150.20 (GENE3D)		0,243	0,140	0,116	0,094	0,118									
Solyc00g008570	SPA1-related 2 (AHRD V3.3 --* AT4G11110.1)								7,623	10,093	9,644	20,623	11,988					1,105	0,005			up
Solyc00g008580	UDP-glucosyl transferase 73B5 (AHRD V3.3 --* AT2G15480.2)								55,589	72,364	54,734	124,917	74,570					1,198	0,001			up
Solyc00g008680	Calcium-binding EF hand family protein (AHRD V3.3 *** AT5G08580.2)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); IPR002048 (PF		63,282	58,648	95,536	98,121	88,045									
Solyc00g009020	MALE GAMETOPHYTE DEFECTIVE 1 (AHRD V3.3 *** AT2G21870.1)		P:GO:0009555	P:pollen development			IPR031432 (PFAM); IPR031432 (PAN		156,400	150,728	165,663	149,889	155,014									
Solyc00g009030	Sugar transporter protein 8	STP8	C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); IPR005828 (PF		0,102	0,165	0,146	0,164	0,071									
Solyc00g009040	Polyadenylate-binding protein (AHRD V3.3 *** M1CCI5_SOLTU)		F:GO:0003723	F:RNA binding			IPR003954 (SMART); IPR002004 (SM		2,327	1,935	0,097	0,226	0,095									
Solyc00g009050	UPF0544 protein C5orf45 isogeny (AHRD V3.3 *** A0A151T4T7_CAJCA)						IPR032739 (PFAM); mobidb-lite (MOB		0,474	0,316	0,174	0,000	0,047									
Solyc00g009060	Hypoxanthine-guanine phosphoribosyltransferase (AHRD V3.3 *** AT1G71750.1)		F:GO:0004422; P:GO	F:hypoxanthine pho	EC:2.4.2.8	Hypoxanthine phospl	IPR000836 (PFAM); G3DSA:3.40.50.2		11,788	11,377	17,637	18,470	19,060									
Solyc00g009080	Late embryogenesis abundant protein, putative (AHRD V3.3 *** A0A072VQC9_MEDTR)						PTHR35706 (PANTHER)		6,289	6,622	7,394	6,324	6,871									
Solyc00g009090	LRR receptor-like kinase (AHRD V3.3 *** A0A072VNN3_MEDTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS); IPR000719 (SMA		0,412	0,389	0,000	0,051	0,000									
Solyc00g009100	30S ribosomal protein S1 (AHRD V3.3 *** A0A072VPA0_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR022967 (SMART); IPR003029 (PF		14,864	14,118	32,745	29,779	30,815									
Solyc00g009110	inositol-1,4,5-triphosphate-5-phosphatase 2	5pt2	P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART); IPR005135 (PF		46,875	62,852	13,132	10,631	13,463									
Solyc00g009120	Short-chain dehydrogenase/reductase family protein (AHRD V3.3 *** D7LXC9_ARALL)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.720 (GENE3D); PTHF		14,739	23,793	4,421	2,988	4,624									
Solyc00g009140	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G09750.1)		C:GO:0016021	C:integral component of membrane			IPR002347 (PRINTS); G3DSA:3.40.50		8,210	10,585	38,037	37,339	45,957									
Solyc00g009141	Microsomal signal peptidase 25 kDa subunit (AHRD V3.3 *-* G7KBX4_MEDTR)		C:GO:0005787; P:GO	C:signal peptidase complex; P:signal peptide processing; F:pept			IPR009582 (PFAM); IPR009582 (PAN		15,686	16,185	17,903	18,632	16,864									
Solyc00g009540	PIF1 helicase (AHRD V3.3 *** G7J5Q6_MEDTR)		P:GO:0000723; F:GO	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR003840 (PFAM); IPR010285 (PFA		0,000	0,019	0,025	0,000	0,023									
Solyc00g009760	LOW QUALITY:Senescence-associated protein (AHRD V3.3 *-* A0A072THZ1_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit		17,824	24,709	20,634	49,810	26,257					1,279	0,003			up
Solyc00g010525	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT5G46400.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit		7,894	11,293	10,786	21,942	11,673					1,031	0,002			up
Solyc00g010530	protein FLOWERING locus D-like protein (AHRD V3.3 --* AT3G10390.4)						mobidb-lite (MOBIDB_LITE)		0,238	0,527	0,150	0,325	0,258									
Solyc00g010750	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924; F:GO	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D); IPR0		0,257	0,399	0,122	0,531	0,329									
Solyc00g010755	D-alanine-D-alanine ligase (AHRD V3.3 *-* G7KW01_MEDTR)		F:GO:0005524; F:GO	F:ATP binding; F:D-	EC:6.3.2.4	D-alanine--D-alanine	G3DSA:3.30.470.20 (GENE3D); PTHF		0,000	0,021	0,000	0,000	0,000									
Solyc00g010760	LOW QUALITY:DNA helicase homolog, putative (AHRD V3.3 *-* Q1EPC6_MUSAC)		P:GO:0000723; F:GO	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR010285 (PFAM); IPR003840 (PFA		0,000	0,000	0,025	0,000	0,024									
Solyc00g011150	LOW QUALITY:photosystem II stability/assembly factor, chloroplast (HCF136) (AHRD V3.3 --* AT5G23120.2)						mobidb-lite (MOBIDB_LITE)		13,033	20,625	15,000	28,746	18,729									
Solyc00g011160	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform (AHRD V3.3 --* E13B_HEVBR)								31,450	38,105	31,166	63,571	42,594					1,036	0,013			up
Solyc00g011170	LOW QUALITY:Senescence-associated protein, putative (AHRD V3.3 *-* A0A072TJH8_MEDTR)		C:GO:0005634; P:GO	C:nucleus; P:regulation of transcription, DNA-templated; F:sequ			PTHR33047 (PANTHER)		0,038	0,083	0,072	0,126	0,095									
Solyc00g011677	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)								0,000	0,000	0,000	0,000	0,023									
Solyc00g011870	LOW QUALITY:Protein phosphatase 2C family protein (AHRD V3.3 *-* AT4G31860.1)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM); IPR036457 (G3D		0,019	0,000	0,000	0,047	0,000									
Solyc00g011880	Protein AIG2-like protein (AHRD V3.3 *** A0A0B0P003_GOSAR)						G3DSA:3.10.490.10 (GENE3D); IPR0(		8,764	8,369	13,099	12,762	13,639									
Solyc00g011890	L-arabinokinase (AHRD V3.3 *** ARAK_ARATH)		F:GO:0005524; F:GO	F:ATP binding; F:galactose binding			PR00959 (PRINTS); G3DSA:3.40.50.2		116,338	108,945	329,238	357,740	336,732									
Solyc00g012430	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT5G27320.1)		F:GO:0004497; P:GO	F:monooxygenase activity; P:oxidation-reduction process			mobidb-lite (MOBIDB_LITE); PTHR341		6,027	8,345	6,940	18,527	10,364					1,424	0,000			up
Solyc00g012440	Senescence-associated protein (AHRD V3.3 *-* A0A072THH1_MEDTR)						PTHR33047 (PANTHER)		2,587	3,583	2,528	5,845	3,510					1,218	0,031			up
Solyc00g012702	S-acyltransferase (AHRD V3.3 --* A0A0Q3JEE4_BRADI)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,021	0,000	0,000	0,000									
Solyc00g013120	LOW protein: NADH-ubiquinone oxidoreductase chain-like protein (AHRD V3.3 *-* ATMG01330.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,040	0,141	0,072	0,073	0,095									
Solyc00g013133	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 --* CAMT_MESCR)		C:GO:0005739	C:mitochondrion					0,000	0,000	0,051	0,000	0,024									
Solyc00g013140	NADH-ubiquinone oxidoreductase chain 5 (AHRD V3.3 *** NU5M_WHEAT)		F:GO:0008137; P:GO	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	PR01434 (PRINTS); IPR001750 (PFA		0,361	0,472	0,497	0,933	0,449									
Solyc00g013150	LOW QUALITY:U-box domain-containing protein kinase family protein (AHRD V3.3 --* AT5G61550.4)								0,123	0,062	0,051	0,094	0,023									
Solyc00g013155	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* F8K8N5_BRANA)		F:GO:0003824; F:GO	F:catalytic activity; F:binding; C:mitochondrion; P:ion transport; C:membrane; P:ATP metabolic process:					0,059	0,105	0,122	0,148	0,093									
Solyc00g013160	NADH dehydrogenase subunit 4 (AHRD V3.3 *-* A0A142D7X4_ORYMI)		C:GO:0005739	C:mitochondrion			mobidb-lite (MOBIDB_LITE)		0,312	0,369	0,676	0,675	0,401									
Solyc00g013170	LOW QUALITY:myosin family protein with Dil (AHRD V3.3 --* AT5G20490.2)								0,140	0,439	0,698	0,627	0,399									
Solyc00g013180	NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 *-* A0A142I0Y7_NICSY)		F:GO:0008137; P:GO	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR003918 (PRINTS); IPR001750 (PF		0,160	0,229	0,100	0,324	0,142									
Solyc00g013181	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT1G08125.3)		C:GO:0005739; F:GO	C:mitochondrion; F:NADH dehydrogenase (ubiquinone) activity;			mobidb-lite (MOBIDB_LITE)		0,040	0,078	0,100	0,224	0,094									
Solyc00g014395	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G14730.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,000	0,090	0,022	0,047									
Solyc00g014790	LOW QUALITY:P-loop nucleoside triphosphate hydrolase superfamily protein (AHRD V3.3 --* AT5G37165.1)		C:GO:0005739	C:mitochondrion					0,038	0,021	0,050	0,098	0,047									
Solyc00g014810	LOW QUALITY:hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 --* AT3G48030.2)								0,000	0,000	0,000	0,025	0,000									
Solyc00g014820	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT5G65560.3)								0,000	0,000	0,000	0,047	0,000									
Solyc00g014830	NADH dehydrogenase subunit 7 (AHRD V3.3 *** A0A0C5B9X5_9SOLA)		F:GO:0016651; F:GO	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindin			IPR038290 (G3DSA:1.10.645.GENE3		0,178	0,339	0,226	0,643	0,327									
Solyc00g014840	LOW QUALITY:Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT2G31370.7)						mobidb-lite (MOBIDB_LITE)		0,063	0,103	0,049	0,149	0,117									
Solyc00g014850	LOW QUALITY:Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein (AHR		C:GO:0005739	C:mitochondrion					0,000	0,106	0,097	0,100	0,023									
Solyc00g014860	LOW QUALITY:Pectin lyase-like superfamily protein (AHRD V3.3 --* AT3G61490.5)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,000	0,047	0,000	0,000									
Solyc00g017540	Signal recognition particle subunit SRP72 (AHRD V3.3 *-* K4D938_SOLLC)		F:GO:0005515; P:GO	F:protein binding; P:SRP-dependent cotranslational protein targ			IPR011990 (G3DSA:1.25.40.GENE3D		0,040	0,080	0,025	0,000	0,023									
Solyc00g017550	Signal recognition particle subunit SRP72 (AHRD V3.3 *-* K4D938_SOLLC)		F:GO:0005515; P:GO	F:protein binding; P:SRP-dependent cotranslational protein targ			IPR011990 (G3DSA:1.25.40.GENE3D		0,040	0,021	0,000	0,000	0,000									
Solyc00g018970	LOW QUALITY:CYCLIN B2-4 (AHRD V3.3 --* AT1G76310.4)						PTHR33047:SF20 (PANTHER); PTHR:		0,038	0,126	0,075	0,147	0,093									
Solyc00g019730	Cytochrome c oxidase subunit 3 (AHRD V3.3 *** COX3_HELAN)		F:GO:0004129; C:GO	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR013833 (G3DSA:1.20.120.GENE3		0,261	0,250	0,221	0,621	0,398									
Solyc00g019740	ATPase subunit 8 (AHRD V3.3 *** A0A0K1ZF72_SOLCA)		C:GO:0005739; C:GO	C:mitochondrion; C:integral component of membrane			IPR009455 (PFAM); IPR003319 (PFA		0,342	0,596	0,318	1,038	0,470									
Solyc00g019750	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 --* AT2G28580.6)								0,059	0,126	0,093	0,322	0,093									
Solyc00g019950	NADH dehydrogenase subunit 9 (AHRD V3.3 *** ATMG00070.1)		F:GO:0008137; P:GO	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR037232 (G3DSA:3.30.460.GENE3		0,058	0,018	0,100	0,152	0,047									
Solyc00g019970	LOW QUALITY:protein kinase family protein (AHRD V3.3 --* AT4G12020.9)						mobidb-lite (MOBIDB_LITE)		0,021	0,209	0,096	0,596	0,116									
Solyc00g019980	LOW QUALITY:FAM91 carboxy-terminus protein (AHRD V3.3 --* AT1G35220.5)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; P:translation; C:chloroplast; C:large ribosomal subu					0,063	0,204	0,416	0,538	0,282									
Solyc00g019990	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT2G33170.2)								0,019	0,060	0,072	0,176	0,024									
Solyc00g020000	LOW QUALITY:Mitogen-activated protein kinase (AHRD V3.3 --* A0A0E0HQW2_ORYNI)								0,000	0,082	0,122	0,169	0,118									
Solyc00g020010	LOW QUALITY:Kinesin-like calmodulin-binding protein (AHRD V3.3 --* A0A199VU23_ANACO)						mobidb-lite (MOBIDB_LITE)		0,040	0,149	0,075	0,120	0,117									
Solyc00g020020	LOW QUALITY:DEAD-box ATP-dependent RNA helicase 49 (AHRD V3.3 --* RH49_ARATH)		C:GO:0005739	C:mitochondrion			mobidb-lite (MOBIDB_LITE); mobidb-lit		0,102	0,142	0,222	0,287	0,117									
Solyc00g020030	LOW QUALITY:TBP-associated factor 2 (AHRD V3.3 --* AT1G73960.3)								0,000	0,043	0,047	0,000	0,000									
Solyc00g020040	Cytochrome c biogenesis B (AHRD V3.3 *** A0A0C5ARM5_HYONI)		F:GO:0015232; P:GO	F:heme transporter activity; P:heme transport; C:membrane; P:(			mobidb-lite (MOBIDB_LITE); IPR0035		0,037	0,021	0,075	0,126	0,072									
Solyc00g020540	Aminotransferase-like protein (AHRD V3.3 *-* Q6EQM2_ORYSJ)						IPR019557 (PFAM); mobidb-lite (MOB		0,021	0,000	0,000	0,000	0,000									
Solyc00g020545	Ferric reductase oxidase (AHRD V3.3 *-* V9HYU8_MANES)		C:GO:0016021; F:GO	C:integral component of membrane; F:oxidoreductase activity; F			IPR013130 (PFAM); mobidb-lite (MOB		0,119	0,000	0,091	0,045	0,141									
Solyc00g021630	NADH-ubiquinone oxidoreductase chain 6 (AHRD V3.3 *** A0A075VXD0_CAPAN)		F:GO:0008137; P:GO	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001457 (PFAM); G3DSA:1.20.120		0,057	0,192	0,075	0,422	0,141									
Solyc00g021640	Ribosomal protein S4 (AHRD V3.3 *** A0A142I0Z6_NICSY)		F:GO:0003723	F:RNA binding			IPR002942 (SMART); IPR036986 (G3		0,233	0,471	0,368	1,043	0,680									
Solyc00g021650	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT5G09950.3)								0,037	0,000	0,025	0,101	0,023									
Solyc00g022070	beta glucosidase 8 (AHRD V3.3 --* AT3G62750.4)								0,000	0,018	0,022	0,000	0,000									
Solyc00g022080	30S ribosomal protein S4, chloroplastic (AHRD V3.3 --* RR4_EQUHY)								0,000	0,000	0,000	0,025	0,024									
Solyc00g022090	Formyltetrahydrofolate deformylase 1, mitochondrial (AHRD V3.3 --* PURU1_ARATH)								0,037	0,043	0,075	0,176	0,048									
Solyc00g022100	Ribosomal protein L10 (AHRD V3.3 *** E0D3E6_SOLLC)		C:GO:0005739; C:GO	C:mitochondrion; C:ribosome					0,415	1,050	0,791	1,751	0,853									
Solyc00g022103	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT5G43930.4)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,416	0,494	1,699	1,644	1,160									
Solyc00g022107	Ribosomal protein L2 (AHRD V3.3 *** A0A142I0Z9_NICSY)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002171 (SMART); IPR022666 (PF		0,333	0,880	0,967	2,001	1,013									
Solyc00g023570	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT1G75920.2)								0,019	0,021	0,000	0,025	0,046									
Solyc00g023580	Thioredoxin superfamily protein (AHRD V3.3 --* AT1G07700.4)								0,000	0,000	0,075	0,101	0,000									
Solyc00g023590	LOW QUALITY:Pectin lyase-like superfamily protein (AHRD V3.3 --* AT1G78400.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit		0,000	0,021	0,000	0,025	0,023									
Solyc00g023600	LOW QUALITY:SERINE CARBOXYPEPTIDASE-LIKE 49 (AHRD V3.3 --* AT3G10410.1)		C:GO:0005739	C:mitochondrion					0,000	0,021	0,000	0,050	0,000									

Solyc00g023700	Transcription elongation factor SPT5 (AHRD V3.3 --* M4C8W3_BRARP)					0,000	0,000	0,025	0,000	0,000									
Solyc00g023710	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_OPUQU)					0,000	0,043	0,000	0,022	0,000									
Solyc00g024150	Transcriptional coactivator/pterin dehydratase (AHRD V3.3 *** AT5G51110.1)		P:GO:0006729; F:G(	P:tetrahydrobiopteri EC:4.2.1.96 4a-hydroxytetrahydr(	IPR001533 (PFAM); IPR036428 (G3D	21,287	38,497	47,959	63,958	79,085	0,881	0,000	0,719	0,000	0,419	0,009	up	up	up
Solyc00g024160	LOW QUALITY:SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT4G17680.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;	PF13920 (PFAM); IPR013083 (G3DS/	0,098	0,018	0,125	0,119	0,072									
Solyc00g024570	LOW QUALITY:F-box protein, putative (AHRD V3.3 *-* A2Q1T0_MEDTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR032675 (G3	0,000	0,039	0,000	0,000	0,000									
Solyc00g025290	Alpha-1,4 glucan phosphorylase L-2 isozyme (AHRD V3.3 *-* W9S278_9ROSA)		C:GO:0005739	C:mitochondrion	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,119	0,284	0,297	0,372	0,356									
Solyc00g025300	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT2G07674.2)		C:GO:0005739; C:G(	C:mitochondrion; C:membrane	mobidb-lite (MOBIDB_LITE); PTHR352	0,021	0,000	0,000	0,000	0,000									
Solyc00g025400	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT2G42280.3)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,051	0,075	0,000									
Solyc00g026160	Ferric reductase oxidase (AHRD V3.3 *** V9HYU8_MANES)		C:GO:0016020; F:G(	C:membrane; F:oxidoreductase activity; P:oxidation-reduction p	IPR000778 (PRINTS); IPR013112 (PF	0,236	0,085	0,051	0,076	0,069									
Solyc00g027770	Pectinesterase (AHRD V3.3 *** A0A0V0I597_SOLCH)		F:GO:0030599; P:G(	F:pectinesterase ac EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR000070 (PFAM); IPR012334 (G3D	62,525	57,998	65,460	57,557	65,051									
Solyc00g030000	LOW QUALITY:Cellulose synthase (AHRD V3.3 *** A0A118J5T2_CYNCS)		C:GO:0016020; F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (U	IPR005150 (PFAM); IPR029044 (G3D	0,000	0,000	0,147	0,561	0,305									
Solyc00g030100	LOW QUALITY:Mitogen activated protein kinase kinase kinase-like protein (AHRD V3.3 --* AT2G42640.4)					0,040	0,059	0,050	0,069	0,071									
Solyc00g030215	Two-component response regulator ARR17 (AHRD V3.3 --* ARR17_ARATH)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc00g030510	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G07820.1)	PG38-1	F:GO:0004650; P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR006626 (SMART); IPR000743 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc00g030520	Endoplasmic reticulum vesicle transporter protein (AHRD V3.3 *-* AT3G22290.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:isomerase activity	IPR012936 (PFAM); PTHR10984 (PAN	4,577	4,485	5,453	6,246	4,890									
Solyc00g030820	LOW QUALITY:Maturase K (AHRD V3.3 --* U5YV62_9POAL)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,136	0,161	0,118	0,262	0,141									
Solyc00g031030	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS); IPR026992 (PFA	0,000	0,000	0,025	0,000	0,000									
Solyc00g032030	LOW QUALITY:E3 ubiquitin-protein ligase (AHRD V3.3 *-* K4BFX6_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR013083 (G3DSA:3.30.40.GENE3D	0,076	0,041	0,022	0,000	0,023									
Solyc00g032943	glutamate receptor 3.6 (AHRD V3.3 --* AT3G51480.4)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc00g032947	Salicylic acid carboxyl methyltransferase (AHRD V3.3 *-* A0A125QZJ1_9ROSI)		F:GO:0008168	F:methyltransferase activity	IPR005299 (PFAM); G3DSA:1.10.120	0,000	0,237	0,022	0,000	0,000									
Solyc00g036320	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *-* AT1G76510.4)		F:GO:0003677	F:DNA binding	IPR001606 (SMART); SM01014 (SMA	0,079	0,116	0,000	0,000	0,000									
Solyc00g036520	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT3G10845.1)					0,000	0,000	0,025	0,000	0,000									
Solyc00g036530	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)					0,000	0,000	0,000	0,025	0,000									
Solyc00g039990	LOW QUALITY:CCA tRNA nucleotidyltransferase (AHRD V3.3 *-* W9SEV9_9ROSA)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti	PTHR13734:SF5 (PANTHER); PTHR1:	0,059	0,021	0,047	0,049	0,071									
Solyc00g042640	LOW QUALITY:Helicase-like protein (AHRD V3.3 *-* Q9AYF0_ORYSJ)		P:GO:0000723; F:G(	P:telomere mainten EC:3.6.1.15 Nucleoside-triphosph	IPR010285 (PFAM); IPR025476 (PFA	0,124	0,124	0,025	0,025	0,047									
Solyc00g042840	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9H429_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART); G3DSA:1.20.12	0,258	0,512	0,193	0,231	0,235									
Solyc00g042850	GDSL esterase/lipase family (AHRD V3.3 *-* A0A151SCS9_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,025	0,000									
Solyc00g042854	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR036396 (G3DSA:1.10.630.GENE3	0,000	0,000	0,000	0,000	0,024									
Solyc00g044350	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *** AT5G10310.2),Pfam:PF17181		P:GO:0010374	P:stomatal complex development	PF17181 (PFAM); mobidb-lite (MOBID	0,139	1,010	0,075	0,075	0,188									
Solyc00g044750	RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:snRNA stem-loop binding	PTHR10501 (PANTHER); PTHR10501	0,782	0,801	0,000	0,000	0,000									
Solyc00g047180	LOW QUALITY:sucrose synthase 3 (AHRD V3.3 --* AT4G02280.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc00g047190	LOW QUALITY:Light-independent protochlorophyllide reductase subunit B (AHRD V3.3 --* A0A0G2UFA3_SELUN)					0,000	0,000	0,050	0,000	0,000									
Solyc00g047200	LOW QUALITY:cytochrome b (AHRD V3.3 *-* AT2G07727.1)		F:GO:0009055; C:G(	F:electron transfer activity; C:membrane	IPR027387 (G3DSA:1.20.810.GENE3	0,021	0,000	0,000	0,000	0,000									
Solyc00g047700	Nuclear RNA binding protein-like (AHRD V3.3 *** Q38M48_SOLTU)		F:GO:0003723	F:RNA binding	IPR006861 (SMART); IPR006861 (PF	141,903	165,428	147,768	130,325	131,942									
Solyc00g048510	Phloem protein 2 (AHRD V3.3 *** D0R6I7_MALDO)				IPR025886 (PFAM); PTHR32278 (PAN	0,040	0,064	0,194	0,264	0,120									
Solyc00g048515	TBP-ASSOCIATED FACTOR 6B (AHRD V3.3 --* AT1G54360.4)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc00g049210	Cytochrome c biogenesis FN (AHRD V3.3 *** A0A0C5ART5_HYONI)		F:GO:0015232; P:G(	F:heme transporter activity; P:heme transport; C:membrane; P:(	IPR003567 (PRINTS); IPR003569 (PF	0,096	0,163	0,220	0,569	0,210									
Solyc00g049220	LOW QUALITY:amino acid permease 7 (AHRD V3.3 --* AT5G23810.5)		C:GO:0005739	C:mitochondrion		0,019	0,041	0,025	0,025	0,000									
Solyc00g049520	LOW QUALITY:NAC domain protein 13 (AHRD V3.3 --* AT1G32870.2)				mobidb-lite (MOBIDB_LITE); mobidb-lit	12,388	10,103	1,214	1,286	1,060									
Solyc00g050130	Glycosyltransferase (AHRD V3.3 *** K4C6W0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR(	10,523	13,975	6,732	6,888	8,535									
Solyc00g050430	bHLH transcription factor 073		F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	0,375	0,587	0,770	0,076	0,238									
Solyc00g052430	Cytochrome c biogenesis FC (AHRD V3.3 *** A0A0C5B7H6_9SOLA)		C:GO:0005743; C:G(	C:mitochondrial inner membrane; C:integral component of memb	IPR032523 (PFAM); mobidb-lite (MOB	0,040	0,121	0,075	0,247	0,071									
Solyc00g052540	LOW QUALITY:RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT3G02890.4)					0,000	0,000	0,000	0,000	0,024									
Solyc00g052940	WAT1-related protein (AHRD V3.3 *** A0A068UX44_COFCA)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); mobidb-lite (MOB	0,000	0,043	0,000	0,025	0,000									
Solyc00g053440	Bax inhibitor (AHRD V3.3 *** A0A0K1ETI6_TECGR)		C:GO:0016021	C:integral component of membrane	IPR006214 (PFAM); PTHR23291:SF3	36,728	41,825	22,685	31,346	25,178									
Solyc00g056680	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GB30_THECC)		P:GO:0006629	P:lipid metabolic process	G3DSA:3.40.50.12520 (GENE3D); IPF	1,729	1,895	1,671	1,220	1,457									
Solyc00g057880	DELLA protein SLR1 (AHRD V3.3 --* SLR1_ORYSI)					0,139	0,186	0,124	0,075	0,163									
Solyc00g059100	Transducin/WD40 repeat protein (AHRD V3.3 *-* G7KD13_MEDTR)		F:GO:0005515	F:protein binding	IPR001680 (SMART); IPR001680 (PF	5,959	4,461	5,580	5,668	5,628									
Solyc00g059500	aminoalcoholphosphotransferase (AHRD V3.3 *-* AT3G25585.4)		F:GO:0004142; F:G(	F:diacylglycerol chc EC:2.7.8.1; EC:2.7.8 Ethanolaminephosph	IPR014472 (PANTHER); PTHR10414::	0,719	0,696	0,852	0,957	0,849									
Solyc00g060810	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response	IPR000916 (SMART); IPR023393 (G3	4,431	0,121	195,302	123,214	50,742			-1,945	0,000				down	
Solyc00g068970	Senescence-associated protein (AHRD V3.3 *-* A0A072THH1_MEDTR)				mobidb-lite (MOBIDB_LITE); mobidb-lit	44,001	59,648	49,610	113,649	68,577					1,203	0,001			up
Solyc00g068980	LOW QUALITY:Superoxide dismutase [Cu-Zn] 1 (AHRD V3.3 --* SODC1_ORYSI)					16,563	19,717	14,318	34,775	21,760					1,287	0,001			up
Solyc00g069880	LOW QUALITY:SET-domain containing protein lysine methyltransferase family protein (AHRD V3.3 --* AT5G43990.9)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,018	0,168	0,143	0,070									
Solyc00g071180	multicystatin	tmc	F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity	IPR000010 (SMART); G3DSA:3.10.45	0,000	0,079	0,025	0,000	0,000									
Solyc00g072100	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151S5P0_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid	PF14223 (PFAM); IPR039537 (PANTH	12,773	14,978	5,468	5,581	5,161									
Solyc00g072800	B-block binding subunit of TFIIIC (AHRD V3.3 --* AT1G17450.3)				IPR013210 (PFAM)	0,000	0,000	0,047	0,000	0,000									
Solyc00g074210	Mitochondrial import inner membrane translocase subunit tim16 (AHRD V3.3 *** A0A1D1XM35_9ARAE)		C:GO:0005744; P:G(	C:TIM23 mitochondrial import inner membrane translocase com	PF03656 (PFAM); IPR036869 (G3DS/	0,000	0,000	0,000	0,000	0,024									
Solyc00g075035	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *-* A0A103YFY3_CYNCS)		F:GO:0005199; P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz	PR01217 (PRINTS); IPR006706 (PFA	0,138	0,059	0,075	0,000	0,047									
Solyc00g080750	Plastid movement impaired protein (AHRD V3.3 *** A0A072VEV4_MEDTR)		C:GO:0005886	C:plasma membrane	IPR025322 (PFAM); PTHR33148 (PAN	0,118	0,443	0,025	0,123	0,070									
Solyc00g082150	kinesin light chain I2I isoform		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR011990 (G3	68,361	58,117	49,565	47,496	46,850									
Solyc00g090430	LOW QUALITY:DUF789 family protein (AHRD V3.3 *-* G7KKC4_MEDTR)				IPR008507 (PFAM); PTHR32010:SF8	1,030	0,733	0,025	0,025	0,047									
Solyc00g090870	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** A0A151TNE8_CAJCA)		F:GO:0005515; P:G(	F:protein binding; P:response to sucrose; P:cellular response to	IPR006828 (SMART); G3DSA:3.30.16	4,875	4,508	3,201	3,243	3,321									
Solyc00g091170	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A061DYZ4_THI		F:GO:0005525	F:GTP binding	G3DSA:3.40.50.300 (GENE3D); IPR0(	4,420	5,269	2,676	1,713	1,977									
Solyc00g094520	LOW QUALITY:NADH-ubiquinone oxidoreductase chain 6 (AHRD V3.3 *-* A0A151UEX6_CAJCA)		C:GO:0005739	C:mitochondrion		0,038	0,019	0,100	0,150	0,048									
Solyc00g094530	LOW QUALITY:NADH-ubiquinone oxidoreductase chain 1 (AHRD V3.3 *-* NU1M_PETHY)		C:GO:0016020; P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM); PTHR11432:SF3	0,057	0,149	0,072	0,122	0,118									
Solyc00g094540	Bestrophin-like protein (AHRD V3.3 --* AT3G61320.3)					0,058	0,245	0,147	0,297	0,235									
Solyc00g094550	LOW QUALITY:U-box domain-containing protein 14 (AHRD V3.3 --* PUB14_ARATH)					0,000	0,021	0,000	0,075	0,071									
Solyc00g096460	translation initiation factor (AHRD V3.3 *-* AT1G44780.2)				IPR037647 (PANTHER)	5,765	5,114	5,599	4,958	5,372									
Solyc00g097260	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT4G39140.5)					0,042	0,000	0,025	0,000	0,000									
Solyc00g097960	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 --* AT4G27590.1)					1,836	1,981	1,225	1,927	1,417									
Solyc00g098560	GDSL esterase/lipase (AHRD V3.3 *** A0A199UQJ3_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	9,658	10,491	7,508	8,578	7,949									
Solyc00g099580	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9GU68_POPTR)		F:GO:0003677	F:DNA binding	IPR000047 (PRINT HB-other	0,063	0,037	0,025	0,048	0,023									
Solyc00g104333	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 --* A0A0K9NHT4_ZOSMR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,021	0,000	0,000	0,000									
Solyc00g104940	BAX inhibitor 1 (AHRD V3.3 *-* AT5G47120.1)		C:GO:0016021	C:integral component of membrane	PTHR23291:SF34 (PANTHER); IPR00	0,393	0,202	0,173	0,220	0,093									
Solyc00g106650	basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 *-* AT4G06598.2)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc	mobidb-lite (MOBIDB_LITE); PTHR133	0,000	0,039	0,000	0,000	0,024									
Solyc00g107050	Nuclear transcription factor Y subunit C-4 (AHRD V3.3 *-* NFYC4_ARATH)		F:GO:0046982	F:protein heterodimerization activity	IPR009072 (G3DS NF-YC	0,000	0,018	0,000	0,000	0,000									
Solyc00g108550	LOW QUALITY:Homeodomain-like superfamily protein, putative isoform 1 (AHRD V3.3 *-* A0A061G387_THI		F:GO:0003677	F:DNA binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,057	0,061	0,268	0,415	0,142									
Solyc00g110370	LOW QUALITY:ZF-HD homeobox protein (AHRD V3.3 --* A0A0B2PG51_GLYSO)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 (GENE3D); PTHR3	0,040	0,124	0,000	0,000	0,000									
Solyc00g110870	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGR2_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001611 (PFAM); G3DSA:1.10.510	2,005	1,821	0,297	0,263	0,398									
Solyc00g112190	LOW QUALITY:Longifolia protein (AHRD V3.3 --* A0A072UUU5_MEDTR)		C:GO:0005739	C:mitochondrion	mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,025	0,000	0,000									
Solyc00g112930	Alpha-n-acetylglucosaminidase, putative (AHRD V3.3 *-* B9R8Y6_RICCO)				IPR024733 (PFAM); G3DSA:3.20.20.8	0,573	0,246	0,187	0,215	0,118									
Solyc00g117653	Glucose-6-phosphate isomerase, cytosolic 1 (AHRD V3.3 --* G6PI1_CLARO)				mobidb-lite (MOBIDB_LITE)	0,021	0,144	0,000	0,072	0,048									
Solyc00g117655	NADH-ubiquinone oxidoreductase chain 1 (AHRD V3.3 *-* NU1M_PETHY)		C:GO:0016020; P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM); PTHR11432:SF3	0,101	0,099	0,196	0,198	0,072									
Solyc00g118680	LOW QUALITY:pentatricopeptide (PPR) repeat-containing protein (AHRD V3.3 --* AT1G68930.2)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,042	0,190	0,050	0,348	0,116									
Solyc00g118690	NADH-ubiquinone oxidoreductase chain 1 (AHRD V3.3 *-* Q5MA12_TOBAC)		C:GO:0016020; P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM); PTHR11432:SF3	0,021	0,043	0,025	0,050	0,000									
Solyc00g125275	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	G3DSA:3.40.395.10 (GENE3D); IPR0(	0,112	0,134	0,000	0,000	0,000									
Solyc00g125990	NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A1C9I9Q6_9ROSI)		C:GO:0005739; F:G(	C:mitochondrion; F: EC:1.6.99.5; EC:1.6. Acting on NADH or N.	IPR001750 (PFAM); PTHR22773:SF1(	0,353	0,603	0,781	0,667	0,657									
Solyc00g126000	NADH-ubiquinone oxidoreductase chain 2 (AHRD V3.3 *-* NU2M_BETVU)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane		0,000	0,126	0,125	0,145	0,094									
Solyc00g126010	LOW protein: NADH-ubiquinone oxidoreductase chain-like protein (AHRD V3.3 *-* ATMG01330.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,041	0,047	0,097	0,257									
Solyc00g127670	membrane protein (AHRD V3.3 *** AT1G26180.1)		C:GO:0016021	C:integral component of membrane	IPR018710 (PFAM); PTHR37185 (PAN	2,736	1,946	2,007	1,874	2,159									
Solyc00g127870	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P (AHRD V3.3 *** A0A0B2SS56_GLYSO)		P:GO:0006506; F:G(	P:GPI anchor biosy EC:2.4.1.198 Phosphatidylinositol I	IPR016542 (PIRSF); IPR013717 (PFA	6,059	7,605	3,134	3,271	3,459									
Solyc00g128870	NUDIX hydrolase (AHRD V3.3 *** A0A118K334_CYNCS)		F:GO:0016787	F:hydrolase activity	IPR020476 (PRINTS); IPR000086 (PF	20,716	19,771	17,260	14,968	15,231									
Solyc00g133110	Transposon protein, putative, Mutator sub-class (AHRD V3.3 *-* Q7XE42_ORYSJ)		F:GO:0004180	F:carboxypeptidase activity	IPR029062 (G3DSA:3.40.50.GENE3D	0,123	0,039	0,198	0,000	0,164									
Solyc00g134620	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *-* A0A061G9X2_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR023213 (G3DSA:3.30.559.GENE3	0,201	0,187	0,000	0,000	0,000									
Solyc00g136260	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FKT7_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART); IPR013083 (G3	8,526	9,829	7,123	3,415	5,518					-1,060	0,002			down
Solyc00g136560	Alkyl transferase (AHRD V3.3 *** K7X479_SOLLC)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth	IPR001441 (PFAM); IPR036424 (G3D	2,244	3,357	15,003	19,315	20,203									
Solyc00g136565	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM); IPR026992 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc00g140060	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* W9SA17_9ROSA)		F:GO:0004252; P:G(	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	42,569	35,131	32,614	33,591	36,568									
Solyc00g141560	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A151SPC9_CAJCA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	G3DSA:2.40.50.140 (GENE3D); IPR0'	0,000	0,000	0,000	0,000	0,023									
Solyc00g142160	Mitovirus RNA-dependent RNA polymerase (AHRD V3.3 --* ATMG01110.1)		C:GO:0005739	C:mitochondrion		0,000	0,021	0,050	0,000	0,024									
Solyc00g142170	Mitovirus RNA-dependent RNA polymerase (AHRD V3.3 *** ATMG01110.1)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane	IPR008686 (PFAM); IPR008686 (PAN	0,019	0,043	0,166	0,200	0,047									
Solyc00g143770	ABC transporter family protein (AHRD V3.3 --* AT1G54350.1)					8,435	9,822	7,763	7,898	9,349									
Solyc00g144470	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)				IPR019557 (PFAM); mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc00g145170	Proteinase inhibitor II (AHRD V3.3 *** Q3S493_SOLTU)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity	G3DSA:3.30.60.30 (GENE3D); IPR00:	1,204	0,460	0,125	0,048	0,023									
Solyc00g147570	villin 2 (AHRD V3.3 *-* AT2G41740.2)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly	IPR007122 (PRINTS); IPR007122 (SM	0,037	0,060	0,000	0,000	0,000									
Solyc00g153680	Protein kinase (AHRD V3.3 *-* Q9FDV6_FAGSY)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); IPR001245 (PF	0,115	0,116	0,087	0,025	0,071									
Solyc00g154980	Ethylene insensitive 3 family protein (AHRD V3.3 *** AT5G10120.1),Pfam:PF04873		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus	IPR006957 (PFAM EIL	0,152	0,078	0,000	0,000	0,000									
Solyc00g156980	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *-* AT1G72970.2)		F:GO:0016614; F:G(	F:oxidoreductase activity, acting on CH-OH group of donors; F:	IPR000172 (PFAM); IPR036188 (G3D	5,348	3,333	0,000	0,025	0,000									
Solyc00g157087	Proteinase inhibitor II (AHRD V3.3 *-* B3F0C1_TOBAC)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity	IPR003465 (PFAM); G3DSA:3.30.60.3	0,019	0,191	0,075	0,574	0,000									
Solyc00g160780	LOW QUALITY:BnaA03g08910D protein (AHRD V3.3 --* A0A078DNF4_BRANA)					0,726	0,398	0,025	0,000	0,046									
Solyc00g164580	LOW QUALITY:phospholipase-like protein (PEARLI 4) family protein (AHRD V3.3 --* AT2G20950.9)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,043	0,047	0,050	0,000									
Solyc00g164680	ABC transporter G family member (AHRD V3.3 *-* A0A0K9NWI5_ZOSMR)	ABCG67	C:GO:0016020	C:membrane	IPR013525 (PFAM); mobidb-lite (MOB	17,211	20,055	44,375	40,123	48,355									
Solyc00g165195	UDP-glucose pyrophosphorylase 2 (AHRD V3.3 --* AT5G17310.6)		F:GO:0003824; P:G(	F:catalytic activity; P:nitrogen compound metabolic process; P:(	PTHR31470 (PANTHER); PTHR31470	0,000	0,000	0,025	0,000	0,000									
Solyc00g167290	LOW QUALITY:Single-stranded-DNA-specific exonuclease recJ, putative (AHRD V3.3 *** B9TGS8_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR003156 (PFAM); G3DSA:3.10.310	0,000	0,019	0,000	0,000	0,000									
Solyc00g167800	LOW QUALITY:NADPH-dependent codeinone reductase 1-1 (AHRD V3.3 --* COR11_PAPSO)				PTHR33095:SF23 (PANTHER); PTHR:	0,000	0,000	0,025	0,000	0,000									
Solyc00g170200	LOW QUALITY:Sigma factor sigB regulation protein rsbQ (AHRD V3.3 *** A0A0B2Q4V2_GLYSO)		C:GO:0005634; C:G(	C:nucleus; C:cytoplasm	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,025	0,022	0,046									
Solyc00g170210	SGNH hydrolase-type esterase superfamily protein (AHRD V3.3 --* AT5G37690.2)					16,296	15,864	18,538	16,884	17,765									
Solyc00g170510	Pectinesterase (AHRD V3.3 *** K4BAQ1_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR000070 (PFAM); IPR012334 (G3D	0,312	0,577	0,000	0,000	0,000									
Solyc00g171810	ATP synthase subunit a (AHRD V3.3 *** A0A075VV97_CAPAN)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP synthesis c	IPR000568 (PRINTS); IPR035908 (G3	2,043	1,505	2,132	1,601	1,058									
Solyc00g172410	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103XXH6_CYNCS)				G3DSA:2.40.50.140 (GENE3D); G3DS	0,019	0,019	0,000	0,022	0,000									
Solyc00g174330	Pathogenesis-related protein 1 (AHRD V3.3 *-* Q75QH2_CAPCH)		C:GO:0005615; P:G(	C:extracellular space; P:killing of cells of other organism; P:defe	IPR014044 (SMART); IPR014044 (PF	0,000	0,128	0,146	0,369	0,402									
Solyc00g174340	Pathogenesis-related protein 1 (AHRD V3.3 *** Q75QH2_CAPCH)		C:GO:0005615; P:G(	C:extracellular space; P:killing of cells of other organism; P:defe	IPR001283 (PRINTS); IPR014044 (SM	18,014	111,423	203,382	272,990	396,646	2,653	0,013					up		
Solyc00g178340	SlBCAT5	BCAT5	F:GO:0003824	F:catalytic activity	G3DSA:3.30.470.10 (GENE3D); PTHF	0,176	0,018	0,163	0,145	0,071									
Solyc00g180440	50S ribosomal protein L20, chloroplastic (AHRD V3.3 *** A0A0A1IRS6_9LAMI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR005813 (PRINTS); IPR005813 (PF	0,000	0,021	0,000	0,025	0,024									
Solyc00g180840	Transposon Ty3-I Gag-Pol polyprotein (AHRD V3.3 *-* A0A151SX41_CAJCA)				PF08284 (PFAM); IPR021109 (G3DS/	0,176	0,136	0,072	0,000	0,000									
Solyc00g181240	LOW QUALITY:Polygalacturonase inhibitor 1 (AHRD V3.3 --* PGIP1_ARATH)					0,019	0,000	0,025	0,000	0,023									
Solyc00g181250	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G09940.2)					0,000	0,021	0,025	0,050	0,000									
Solyc00g183050	Vacuolar sorting-associated protein 27 (AHRD V3.3 *-* A0A0B0NUH7_GOSAR)		C:GO:0009506; F:G(	C:plasmodesma; F:metal ion binding	PTHR22835:SF469 (PANTHER); PTHI	1,215	1,019	1,689	1,928	1,883									
Solyc00g184350	nuclear pore complex protein-like protein (AHRD V3.3 *-* AT5G05680.1)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:ribosomal sma	IPR019321 (PFAM); IPR037700 (PAN	11,938	11,218	13,185	14,444	15,963									
Solyc00g188850	Protein O-glucosyltransferase 1 (AHRD V3.3 *** A0A0B2R562_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:glucosyltransferase activ	IPR006598 (PFAM); PTHR12203:SF2:	0,000	0,041	0,000	0,000	0,000									
Solyc00g188857	Auxin response factor (AHRD V3.3 *-* E0AD21_SOLLC)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter	G3DSA:2.30.30.1040 (GENE3D); IPR(	58,725	53,149	50,134	50,983	51,001									
Solyc00g201160	Serine/threonine-protein kinase (AHRD V3.3 *-* K4BUH3_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR000719 (SMART); G3DSA:1.10.51	6,619	4,550	4,809	4,421	5,295									
Solyc00g203660	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_SOLBU)		F:GO:0000287	F:magnesium ion binding	IPR036376 (G3DSA:3.20.20.GENE3D	0,352	1,173	0,687	2,431	1,741			1,343	0,018				up	
Solyc00g207960	LOW QUALITY:ZF-HD homeobox protein (AHRD V3.3 --* A0A0B2PG51_GLYSO)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 (GENE3D); mobidb	0,338	0,346	0,100	0,123	0,024									
Solyc00g209460	GDSL esterase/lipase (AHRD V3.3 *-* A0A0B2QVH8_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,156	0,162	0,165	0,209	0,211									
Solyc00g210860	LOW QUALITY:disease resistance protein (TIR class) (AHRD V3.3 --* AT1G61100.1)		C:GO:0005739	C:mitochondrion	PTHR36344 (PANTHER)	0,000	0,000	0,000	0,025	0,000									
Solyc00g212260	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM); IPR004993 (PAN	1,209	1,042	0,000	0,000	0,000									
Solyc00g212265	cysteine-rich RLK (RECEPTOR-like protein kinase) 13 (AHRD V3.3 --* AT4G23210.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc00g215560	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein (AHRD V3.3 --* AT1G10050.3)					0,892	0,690	1,192	1,727	1,292									
Solyc00g217960	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT1G49200.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination; F:u	IPR001841 (SMART); IPR013083 (G3	9,390	4,754	6,217	12,174	8,208	-0,957	0,010			0,975	0,000	down		up
Solyc00g218560	LOW QUALITY:T-box transcription factor, putative (DUF863) (AHRD V3.3 --* AT1G69360.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,000	0,000	0,000	0,000									

Solyc00g226760	Sulfotransferase (AHRD V3.3 *** K4D8Q6_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D): IPR0(	0,817	0,573	0,000	0,000	0,000									
Solyc00g227860	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	59,277	52,401	10,478	10,123	11,998									
Solyc00g227960	Sulfotransferase (AHRD V3.3 *** K4D8Q6_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM): G3DSA:3.40.50.3	0,058	0,019	0,000	0,000	0,000									
Solyc00g230060	LOW QUALITY:Ribonuclease H protein (AHRD V3.3 --* A0A061DZ04_THECC)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.1.3: EC:3.1.26:	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3	0,000	0,000	0,025	0,000	0,024									
Solyc00g230070	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_CUSEX)		C:GO:0009521: P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM): PTHR33180:SF4	0,099	0,184	0,097	0,268	0,330									
Solyc00g230080	LOW QUALITY:Photosystem II D2 protein (AHRD V3.3 *-* PSBD_PLETE)		P:GO:0009772: F:G(	P:photosynthetic electron transport in photosystem II; F:electro			IPR000484 (PFAM): IPR000484 (PAN	0,099	0,472	0,173	0,446	0,330									
Solyc00g231680	(1-4)-beta-mannan endohydrolase	man1	F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001547 (PFAM): G3DSA:3.20.20.8	0,059	0,080	0,047	0,022	0,118									
Solyc00g231780	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 *-* NDHI_NANDO)		F:GO:0008137: C:G(	F:NADH dehydroge	EC:1.6.99.5: EC:1.6.	Acting on NADH or N	G3DSA:3.30.70.3270 (GENE3D): IPR(	0,063	0,062	0,093	0,152	0,046									
Solyc00g233480	ABC transporter (AHRD V3.3 *-* H1A8M9_DIOKA)	ABCG55	F:GO:0005524: F:G(	F:ATP binding; F:AT	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	0,000	0,306	0,025	0,025	0,000									
Solyc00g244280	LOW QUALITY:PAS domain-containing protein tyrosine kinase family protein (AHRD V3.3 --* AT1G67890.4)						mobidb-lite (MOBIDB_LITE)	0,042	0,018	0,122	0,025	0,047									
Solyc00g244290	LOW QUALITY:NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A1C9I9Q6_9ROSI)		C:GO:0005739: F:G(	C:mitochondrion; F:	EC:1.6.99.5: EC:1.6.	Acting on NADH or N	IPR001750 (PFAM): mobidb-lite (MOB	0,209	0,355	1,104	0,666	0,564									
Solyc00g244300	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* A		C:GO:0005739	C:mitochondrion			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,081	0,224	0,121	0,149	0,212									
Solyc00g244305	F-box protein (AHRD V3.3 *-* A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	0,000	0,019	0,000	0,000	0,000									
Solyc00g247300	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW6_POPTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	0,019	0,018	0,022	0,025	0,024									
Solyc00g247305	AT hook motif DNA-binding family protein (AHRD V3.3 *-* AT2G33620.4)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): mobidb-lite (MOB	0,000	0,000	0,022	0,000	0,000									
Solyc00g249900	AP-2 complex subunit alpha-1 (AHRD V3.3 *-* AP2A1_ARATH)		P:GO:0006886: C:G(	P:intracellular protein transport; C:AP-2 adaptor complex; F:clat			IPR011989 (G3DSA:1.25.10.GENE3D	0,340	0,391	0,314	0,161	0,143									
Solyc00g249910	AP-2 complex subunit alpha (AHRD V3.3 *-* A0A151RV94_CAJCA)		P:GO:0006886: C:G(	P:intracellular protein transport; C:AP-2 adaptor complex; F:clat			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,157	0,228	0,025	0,117	0,093									
Solyc00g256710	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT4G10840.2)		C:GO:0005737: C:G(	C:cytoplasm; C:microtubule; C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,564	7,352	4,903	3,968	3,796									
Solyc00g257110	Plasma membrane ATPase (AHRD V3.3 *** M1AUY5_SOLTU)		C:GO:0016021	C:integral component of membrane			PR00119 (PRINTS): IPR001757 (PRIN	0,021	0,041	0,025	0,000	0,024									
Solyc00g265110	RNA-binding Nova-1 (AHRD V3.3 *-* A0A0B0MMT7_GOSAR)		F:GO:0003723	F:RNA binding			IPR004088 (PFAM): IPR036612 (G3D	0,102	0,043	0,125	0,100	0,188									
Solyc00g265510	LOW QUALITY:Protein Ycf2 (AHRD V3.3 --* A0A0C5CHC0_ACTCH)							735,242	642,868	21,673	7,945	40,276									
Solyc00g270510	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS_NF-YB	0,021	0,000	0,000	0,000	0,000									
Solyc00g272810	Tyramine N-feruloyltransferase 4/11, putative (AHRD V3.3 *** B9T0B8_RICCO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): PTHR10545 (PAN	0,060	0,301	0,000	0,072	0,047									
Solyc00g273110	DNA ligase 4 (AHRD V3.3 --* H6URY6_NICBE)							24,427	18,451	10,432	9,411	12,721									
Solyc00g277510	Photosystem II protein D1 (AHRD V3.3 *-* PSBA_SOLNI)		P:GO:0009772: F:G(	P:photosynthetic electron transport in photosystem II; F:electro			G3DSA:3.10.10.10 (GENE3D): IPR00(	0,289	0,785	1,413	2,105	2,784									
Solyc00g278110	Fatty acid hydroxylase superfamily protein (AHRD V3.3 *-* A0A072TKE8_MEDTR)		P:GO:0000170: F:G(	P:sphingosine hydroxylase activity; F:iron ion binding; C:endopl			IPR021940 (PFAM)	0,021	0,122	0,815	0,956	0,400									
Solyc00g280110	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)		P:GO:0032502	P:developmental process			IPR006476 (TIGRFAM): IPR006476 (F	0,165	0,018	0,000	0,000	0,000									
Solyc00g281110	LOW QUALITY:inositol polyphosphate kinase 2 alpha (AHRD V3.3 --* AT5G07370.4)		C:GO:0005739	C:mitochondrion				0,000	0,019	0,000	0,000	0,000									
Solyc00g289230	Serine/threonine-protein kinase (AHRD V3.3 *** M1AFX4_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR003609 (SM	1,400	2,047	1,746	3,294	4,476			1,354	0,000	0,922	0,028		up	up
Solyc00g294237	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *-* AT5G18460.1)						IPR004314 (PFAM): PTHR31589 (PAN	0,019	0,115	0,072	0,000	0,023									
Solyc00g309530	LOW QUALITY:fatty acid desaturase 6 (AHRD V3.3 --* AT4G30950.1)							0,000	0,000	0,025	0,022	0,024									
Solyc00g311230	LOW QUALITY:LysM-domain containing receptor-like kinase (AHRD V3.3 --* A9DLL9_MEDTR)							0,019	0,000	0,000	0,000	0,024									
Solyc00g316530	LOW QUALITY:Glutaredoxin (AHRD V3.3 --* A0A0K9PD58_ZOSMR)		C:GO:0005739	C:mitochondrion			mobidb-lite (MOBIDB_LITE)	0,080	0,081	0,213	0,022	0,047									
Solyc00g318130	paired amphipathic helix Sin3-like protein (AHRD V3.3 *-* AT1G10450.3)		F:GO:0003714: P:G(	F:transcription corepressor activity; P:regulation of transcriptior			G3DSA:1.20.1160.11 (GENE3D): IPR(	0,903	1,183	0,050	0,050	0,000									
Solyc00g318830	XH/XS domain-containing family protein (AHRD V3.3 *-* B9HTH7_POPTR)		P:GO:0031047	P:gene silencing by RNA			PTHR21596:SF23 (PANTHER): PTHR:	0,019	0,000	0,025	0,000	0,000									
Solyc00g320430	LOW QUALITY:Vascular endothelial growth factor receptor 2 (AHRD V3.3 --* A0A1D1YH50_9ARAE)							0,115	0,062	0,121	0,050	0,071									
Solyc00g322635	MLP-like protein 28 (AHRD V3.3 *** AT1G70830.2)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	0,410	0,160	0,000	0,000	0,000									
Solyc01g005000	Glutamate decarboxylase (AHRD V3.3 *** B1Q3F2_SOLLC)		F:GO:0004351: P:G(	F:glutamate decarb	EC:4.1.1.15	Glutamate decarboxy	IPR010107 (TIGRFAM): IPR002129 (F	92,229	96,621	12,753	11,958	16,216									
Solyc01g005010	XRI1-like protein (AHRD V3.3 *** AT2G01990.2)		P:GO:0007140: P:G(	P:male meiotic nuclear division; P:female meiotic nuclear divisic			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,185	6,659	1,336	1,781	2,115									
Solyc01g005020	plasmalemma Na+/H+ antiporter	sos1	P:GO:0006812: F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR014710 (G3DSA:2.60.120.GENE3I	103,620	88,357	50,326	44,594	54,659									
Solyc01g005030	MAP kinase kinase kinase 1	MAPKKK1	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	70,429	57,425	96,917	105,076	102,660									
Solyc01g005070	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT1G68110.1)		F:GO:0005545: C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR008942 (G3DSA:1.25.40.GENE3D	0,000	0,081	0,000	0,022	0,000									
Solyc01g005080	microtubule-associated protein 65-7 (AHRD V3.3 *** AT1G14690.2)		P:GO:0000226: F:G(	P:microtubule cytoskeleton organization; F:microtubule binding			G3DSA:1.20.58.1520 (GENE3D): PF0	21,390	19,527	12,695	14,326	22,971			0,850	0,000				up	
Solyc01g005090	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** A0A0B2RAB0_GLYSO)		P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART): IPR005135 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc01g005100	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G68080.1)		P:GO:0032963	P:collagen metabolic process			G3DSA:2.60.120.620 (GENE3D): IPR(	15,270	12,230	10,612	11,715	12,839									
Solyc01g005110	dolichol-phosphate mannosyltransferase-like protein (AHRD V3.3 *** AT1G48140.1)		P:GO:0006486	P:protein glycosylation			IPR013174 (PFAM): IPR013174 (PAN	6,013	6,043	10,916	11,690	11,141									
Solyc01g005120	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4AS79_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR010713 (PFAM): G3DSA:2.60.120	4,709	4,149	4,737	7,989	9,206			0,956	0,000	0,757	0,019		up	up
Solyc01g005130	Zinc finger protein, putative (AHRD V3.3 *** B9SNH3_RICCO)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	8,347	8,604	6,753	9,138	8,638									
Solyc01g005140	Cytochrome b561 (AHRD V3.3 *** A0A151RHD6_CAJCA)		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR006593 (SMART): G3DSA:1.20.12	0,714	0,649	5,285	8,918	8,333									
Solyc01g005150	Cytochrome B561 family protein (AHRD V3.3 *** B9HJJ7_POPTR)		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR006593 (SMART): G3DSA:1.20.12	0,063	0,139	0,000	0,000	0,000									
Solyc01g005160	Avr9/Cf-9 rapidly elicited protein 1	CMPG1	F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR003613 (PF	0,582	11,395	0,330	1,712	1,104	4,277	0,000					up		
Solyc01g005170	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** G7LBJ2_MEDTR)		F:GO:0005545: C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART): IPR014712 (G3	0,473	0,207	0,629	0,417	0,470									
Solyc01g005180	Homeobox-leucine zipper protein HOX9, putative (AHRD V3.3 --* A0A061DUZ5_THECC)						mobidb-lite (MOBIDB_LITE): IPR0393'	2,997	1,074	0,625	1,176	0,921									
Solyc01g005190	Zinc finger family protein (AHRD V3.3 *** U7E2Y1_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	0,213	0,156	0,242	0,221	0,189									
Solyc01g005200	Zinc finger family protein (AHRD V3.3 *-* U7E1E1_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	0,038	0,021	0,094	0,025	0,024									
Solyc01g005210	Trehalose-phosphate synthase 6 (AHRD V3.3 *** W8Q024_CAMSI)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process			IPR003337 (PFAM): G3DSA:3.40.50.2	53,366	48,620	122,652	159,890	132,951									
Solyc01g005220	MACPF domain-containing protein (AHRD V3.3 *** A0A0B2Q4M6_GLYSO)		C:GO:0005886: P:G(	C:plasma membrane; P:plant-type hypersensitive response			IPR020864 (SMART): IPR020864 (PF	32,556	44,113	19,354	26,491	20,823									
Solyc01g005230	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *** AT5G37990.1)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM): G3DSA:3.40.50.1	0,240	0,419	0,068	0,075	0,071									
Solyc01g005240	Aspartokinase (AHRD V3.3 *** A0A0V0ILQ3_SOLCH)		F:GO:0004072: P:G(	F:aspartate kinase	EC:2.7.2.4	Aspartate kinase	IPR001048 (PFAM): G3DSA:3.30.70.2	70,279	72,270	70,699	69,834	67,257									
Solyc01g005250	Aspartate-semialdehyde dehydrogenase (AHRD V3.3 *** V5N8M5_PHAVU)		F:GO:0004073: P:G(	F:aspartate-semiak	EC:1.2.1.11	Aspartate-semialdehy	IPR000534 (SMART): IPR012280 (PF	45,699	51,743	54,050	51,324	50,843									
Solyc01g005260	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G14820.3)						IPR001251 (SMART): IPR001251 (PF	2,125	3,340	2,268	3,036	2,521									
Solyc01g005270	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G14820.3)						IPR001251 (SMART): IPR001251 (PF	4,810	3,625	6,121	6,515	6,961									
Solyc01g005280	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G14820.3)						IPR001251 (SMART): IPR001251 (PF	5,427	3,373	10,811	8,687	9,883									
Solyc01g005290	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *-* AT1G14820.3)						IPR001251 (PFAM): IPR036865 (G3D	0,583	0,408	26,173	21,923	21,156									
Solyc01g005295	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *-* AT1G14820.3)						PTHR10174:SF121 (PANTHER): PTHI	0,445	0,154	11,753	10,450	10,641									
Solyc01g005300	Flavin-binding kelch domain F box protein (AHRD V3.3 *** A0A088AWQ7_SOYBN)		F:GO:0005515	F:protein binding			PF13418 (PFAM): IPR000014 (TIGRF	10,294	15,980	15,006	9,878	16,341	0,662	0,040					up		
Solyc01g005310	Dynamin (AHRD V3.3 *** E5GB64_CUCME)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR003130 (SM	0,351	0,914	0,187	0,149	0,188									
Solyc01g005320	3-oxo-5-alpha-steroid 4-dehydrogenase (AHRD V3.3 *** G7ZZ33_MEDTR)		P:GO:0006629: F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t			IPR010721 (PFAM): G3DSA:1.20.120	0,155	0,236	0,101	0,022	0,047									
Solyc01g005330	Microtubule-associated protein 70-2 (AHRD V3.3 *** A0A0B2QPG9_GLYSO)		P:GO:0007010: F:G(	P:cytoskeleton organization; F:microtubule binding			IPR009768 (PFAM): mobidb-lite (MOB	101,311	77,849	42,869	40,006	46,661									
Solyc01g005340	Ankyrin repeat family protein (AHRD V3.3 *** B9HW17_POPTR)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	27,323	26,738	57,918	44,724	46,784					-0,369	0,018			down
Solyc01g005370	EF hand calcium-binding family protein (AHRD V3.3 *** G8A011_MEDTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	12,679	14,484	30,019	32,428	24,970									
Solyc01g005380	Unknown protein (AHRD V3.3)							0,200	0,073	0,140	0,218	0,070									
Solyc01g005390	Nudix hydrolase (AHRD V3.3 *** A0A061E9N4_THECC)		F:GO:0016787	F:hydrolase activity			IPR000086 (PFAM): G3DSA:3.90.79.1	0,237	0,634	0,533	1,988	1,174					1,878	0,000			up
Solyc01g005400	Caleosin-related family protein (AHRD V3.3 *** AT1G70670.1)		F:GO:0004497: F:G(	F:monooxygenase activity; F:calcium ion binding; C:integral cor			IPR007736 (PFAM): PTHR31495:SF1	2,305	1,637	2,938	4,902	4,271									
Solyc01g005410	Caleosin-related family protein (AHRD V3.3 *** AT1G70680.1)		F:GO:0004497: F:G(	F:monooxygenase activity; F:calcium ion binding; P:oxidation-re			IPR007736 (PFAM): G3DSA:1.10.238	9,269	12,068	0,623	0,867	1,198									
Solyc01g005420	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 --* AT4G15740.1		C:GO:0016020	C:membrane			IPR000008 (SMART): IPR035892 (G3	9,269	16,743	0,240	1,018	0,890	0,879	0,017					up		
Solyc01g005430	UBX domain-containing protein (AHRD V3.3 *** A0A0K9Q356_ZOSMR)		F:GO:0005515	F:protein binding			IPR018997 (SMART): G3DSA:3.10.20	13,410	13,835	9,956	11,898	12,147									
Solyc01g005440	Jasmonate ZIM-domain protein 3 (AHRD V3.3 *** B2XVS2_SOLLC)						IPR010399 (SMART): IPR010399 (PF	100,092	108,014	46,613	42,268	44,294									
Solyc01g005450	F-box protein SKIP28 (AHRD V3.3 *** A0A0B2QPD0_GLYSO)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	0,138	0,187	0,097	0,126	0,047									
Solyc01g005460	Dynein light chain (AHRD V3.3 *** W9T250_9ROSA)		P:GO:0007017: C:G(	P:microtubule-based process; C:dynein complex			IPR001372 (SMART): IPR001372 (PF	0,681	0,675	0,025	0,125	0,117									
Solyc01g005470	PLANT CADMIUM RESISTANCE 2 (AHRD V3.3 *** AT1G14870.1)		C:GO:0016021	C:integral component of membrane			IPR006461 (TIGRFAM): IPR006461 (F	0,102	0,915	1,177	0,684	0,710									
Solyc01g005480	UPF0496 protein (AHRD V3.3 *** A0A199VAF6_ANACO)		C:GO:0016021	C:integral component of membrane			IPR007749 (PFAM): IPR007749 (PAN	6,052	8,970	5,150	5,265	4,568									
Solyc01g005490	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9SWZ5_RICCO)		F:GO:0016787	F:hydrolase activity			G3DSA:3.40.630.10 (GENE3D): G3DS	25,703	24,399	43,154	35,730	37,048									
Solyc01g005500	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	0,000	0,000	0,149	0,339	0,213									
Solyc01g005510	L-ascorbate oxidase homolog (AHRD V3.3 *** ASOL_TOBAC)		F:GO:0005507: F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	0,040	0,000	0,022	0,000	0,023									
Solyc01g005520	Tetratricopeptide repeat containing protein (AHRD V3.3 *** M4Q9V8_TRIMO)		F:GO:0005515	F:protein binding			G3DSA:2.30.42.10 (GENE3D): IPR01'	20,225	33,822	20,414	19,943	33,105	0,769	0,004	0,694	0,000			up	up	
Solyc01g005530	nuclear polyadenylated RNA-binding protein (AHRD V3.3 *** AT3G13480.2)		P:GO:0009642	P:response to light intensity			IPR037492 (PANTHER): PTHR33401::	3,848	3,294	3,481	3,609	4,186									
Solyc01g005540	Lysine--tRNA ligase (AHRD V3.3 *** K4ASC0_SOLLC)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:6.1.1.6	Lysine--tRNA ligase	IPR018149 (PRINTS): G3DSA:2.40.5(	10,057	12,195	10,313	10,572	12,800									
Solyc01g005550	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity			IPR004314 (PFAM): IPR025521 (PFA	59,901	27,872	24,820	21,600	24,838	-1,075	0,000					down		
Solyc01g005560	Isocitrate dehydrogenase [NADP] (AHRD V3.3 *** IDHC_SOLTU)		F:GO:0004450: P:G(	F:isocitrate dehydrc	EC:1.1.1.42	Isocitrate dehydroge	IPR024084 (SMART): IPR024084 (PF	94,014	97,214	174,884	178,167	171,610									
Solyc01g005570	DUF1639 family protein (AHRD V3.3 *** A0A072U1E7_MEDTR)						IPR012438 (PFAM): mobidb-lite (MOB	23,163	17,795	21,945	18,731	18,129									
Solyc01g005575	DUF1639 family protein (AHRD V3.3 *** A0A072U1E7_MEDTR)						IPR012438 (PFAM): mobidb-lite (MOB	25,643	28,712	37,662	40,014	36,512									
Solyc01g005590	Arabinogalactan peptide 14 (AHRD V3.3 *** A0A151TQT2_CAJCA)		C:GO:0016021	C:integral component of membrane			PTHR34114:SF2 (PANTHER): IPR039	19,208	11,822	0,617	0,532	0,700									
Solyc01g005600	5'-adenylylsulfate reductase-like 5 (AHRD V3.3 *** APRL5_ARATH)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	46,085	35,890	75,826	70,704	67,640									
Solyc01g005610	GDSL esterase/lipase (AHRD V3.3 *** W9R6R2_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,021	0,060	0,025	0,075	0,047									
Solyc01g005620	oxoglutarate/malate translocator	aci36	F:GO:0022857	F:transmembrane transporter activity			IPR018108 (PFAM): IPR023395 (G3D	220,132	241,561	201,610	203,807	212,161									
Solyc01g005640	histidine-tRNA ligase (AHRD V3.3 *** AT3G10250.5)						IPR006476 (PFAM): IPR006476 (TIGF	17,717	16,447	24,631	30,840	25,857									
Solyc01g005660	R2R3MYB transcription factor 5	R2R3MYB5	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,329	0,256	0,072	0,092	0,188									
Solyc01g005665	MYB transcription factor (AHRD V3.3 --* A0A0A0R621_PAESU)		C:GO:0005634: P:G(	C:nucleus; P:cell differentiation; F:sequence-specific DNA bindi			mobidb-lite (MOBIDB_LITE)	0,383	0,409	0,091	0,147	0,326									
Solyc01g005670	BTB/POZ domain-containing protein (AHRD V3.3 *** W9S1B2_9ROSA)						IPR038920 (PANTHER): PTHR31060::	4,149	4,302	4,380	4,349	3,937									
Solyc01g005680	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** K4ASD4_SOLLC)		C:GO:0005634: C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): IPR0:	0,021	0,036	0,025	0,022	0,048									
Solyc01g005690	Calcium ion binding (AHRD V3.3 *** A0A061GR33_THECC)		F:GO:0005509: C:G(	F:calcium ion binding; C:Golgi apparatus; P:fucose metabolic pr			PTHR31469 (PANTHER): PTHR31469	82,785	66,423	46,170	43,524	47,686									
Solyc01g005700	Mutator-like transposase-like protein (AHRD V3.3 *** Q9FI74_ARATH)		F:GO:0008270	F:zinc ion binding			IPR006564 (SMART): IPR004332 (PF	15,593	14,146	15,195	13,532	14,113									
Solyc01g005710	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2		C:GO:0016021: F:G(	C:integral component of membrane; F:kinase activity; P:phosph			IPR013210 (PFAM): IPR032675 (G3D	0,063	0,064	0,000	0,000	0,000									
Solyc01g005715	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,080	0,043	0,022	0,025	0,000									
Solyc01g005720	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,095	0,226	0,025	0,000	0,118									
Solyc01g005730	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	1,671	2,238	1,956	4,061	3,872									
Solyc01g005760	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G26540.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	4,224	14,753	4,576	11,269	10,389	1,827	0,000			1,300	0,000	up		up
Solyc01g005770	Pentatricopeptide repeat-containing family protein (AHRD V3.3 --* B9NA20_POPTR)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane				0,000	0,019	0,025	0,025	0,000									
Solyc01g005775	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	1,095	7,788	0,990	0,887	1,344	2,847	0,000					up		
Solyc01g005790	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SFS4_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,502	1,459	1,552	1,549	1,486									
Solyc01g005795	AIG2-like (avirulence induced gene) family protein (AHRD V3.3 --* AT4G31310.2)							0,099	0,059	0,197	0,243	0,189									
Solyc01g005800	calmodulin-binding family protein (AHRD V3.3 *** AT3G13600.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,657	1,859	0,602	2,494	1,050					2,027	0,000			up
Solyc01g005810	MAK16 protein-like protein (AHRD V3.3 *** AT1G23280.1)		C:GO:0005730: C:G(	C:nucleolus; C:preribosome, large subunit precursor			IPR006958 (PIRSF): G3DSA:3.30.39(	106,164	99,007	69,037	70,347	60,356									
Solyc01g005820	Serine/arginine-rich-splicing factor SCL30A (AHRD V3.3 *-* A0A0M9UMR8_NICAT)		P:GO:0000381: P:G(	P:regulation of alternative mRNA splicing, via spliceosome; P:m			mobidb-lite (MOBIDB_LITE): mobidb-lit	149,440	171,108	146,028	127,434	132,090									
Solyc01g005825	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-containing protein (AHRD V3.3 --* AT3G10310.2)							0,000	0,018	0,000	0,000	0,023									
Solyc01g005830	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *-* B9T1E3_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR000490 (PF	15,186	13,109	4,181	3,552	5,195									
Solyc01g005840	ubiquitin-conjugating enzyme E2 -like protein		F:GO:0004553: C:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; C:nucle			SM00212 (SMART): IPR000608 (PFAI	8,003	7,553	16,566	13,928	16,020									
Solyc01g005850	LOW QUALITY:Extensin-like protein Dif54 (AHRD V3.3 *** Q43505_SOLLC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,198	0,202	0,074	0,075	0,071									
Solyc01g005860	LOW QUALITY:WD repeat protein (AHRD V3.3 --* Q84VB4_ORYSJ)							0,061	0,036	0,025	0,072	0,048									
Solyc01g005865	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT4G08850.2)		C:GO:0016021: P:G(	C:integral component of membrane; P:defense response to func			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,021	0,000	0,050	0,000									
Solyc01g005870	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT3G24240.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,827	0,638	0,660	0,967	0,492									
Solyc01g005890	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2 B, chloroplastic (AHRD V3.3 --* NU2C2_ILLOL)						PR01217 (PRINTS): mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc01g005900	HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT1G28680.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,059	0,061	0,000	0,000	0,094									
Solyc01g005910	Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** AT3G12685.1)						IPR003832 (PFAM): mobidb-lite (MOB	18,827	18,883	18,055	17,261	18,041									
Solyc01g005920	Amino acid transporter, putative (AHRD V3.3 *** B9SM54_RICCO)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmem			IPR002293 (PIRSF): IPR002293 (PFA	1,589	2,513	1,648	1,863	1,764									
Solyc01g005930	Lipase/lipooxygenase, PLAT/LH2 (AHRD V3.3 *** A0A118JU91_CYNCS)		F:GO:0005515	F:protein binding			G3DSA:2.60.60.20 (GENE3D): PTHR3	15,493	13,312	37,826	36,547	31,473									
Solyc01g005940	Phytoene synthase (AHRD V3.3 *** A0A0K1L5A0_MALDO)	PSY3	F:GO:0004310: P:G(	F:farnesyl-diphosph	EC:2.5.1.29: EC:2.5.	Geranylgeranyl diphc	IPR008949 (G3DSA:1.10.600.GENE3I	0,021	0,000	0,000	0,022	0,047									
Solyc01g005950	Serine/threonine-protein phosphatase (AHRD V3.3 *** B9GY91_POPTR)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	48,956	44,092	54,278	52,683	55,010									
Solyc01g005960	RNA helicase DEAD1	DEAD1	F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	51,282	45,895	73,390	68,257	68,954									
Solyc01g005970	F-box/kelch-repeat protein (AHRD V3.3 *** W9S3L7_9ROSA)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR006652 (PF	8,126	8,105	7,224	6,538	6,451									
Solyc01g005980	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT5G19860.1)		C:GO:0005773: C:G(	C:vacuole; C:integral component of membrane			IPR036758 (G3DSA:2.30.240.GENE3I	6,193	7,058	3,258	2,855	3,844									
Solyc01g005990	Lipid transfer protein (AHRD V3.3 *** A0A072TPI6_MEDTR)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding; C:integral component of membra			IPR016140 (SMART): G3DSA:1.10.11	14,692	10,925	0,745	0,126	0,258									
Solyc01g006000	GPI mannosyltransferase 2 (AHRD V3.3 *** W9S353_9ROSA)		F:GO:0004584: P:G(	F:dolichyl-phosphat	EC:2.4.1.13	Glycosyltransferases	IPR007315 (PFAM): mobidb-lite (MOB	24,568	20,913	18,980	20,609	19,462									
Solyc01g006010	RNA-binding KH domain protein (AHRD V3.3 *** G7JA56_MEDTR)		F:GO:0003723	F:RNA binding			IPR032570 (PFAM): IPR036612 (G3D	21,667	22,195	33,936	30,926	30,403									
Solyc01g006020	6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** AT3G32930.2)		C:GO:0009941	C:chloroplast envelope			PTHR37229 (PANTHER)	18,848	20,095	31,291	29,994	35,894									
Solyc01g006040	E3 ubiquitin-protein ligase BRE1-like 2 (AHRD V3.3 *** A0A0B0NKV7_GOSAR)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:histone monoubiquitina			mobidb-lite (MOBIDB_LITE): mobidb-lit	32,154	25,445	40,900	40,902	38,915									
Solyc01g006050	LOW QUALITY:Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR006904 (PFAM): IPR006904 (PAN	0,040	0,039	1,251	1,367	1,253									
Solyc01g006060	Dirigent protein (AHRD V3.3 *** K4ASH2_SOLLC)		C:GO:0016021: C:G(	C:integral component of membrane; C:apoplast			IPR004265 (PFAM): PTHR21495:SF1:	0,143	0,158	0,000	0,000	0,000									
Solyc01g006080	plant/protein (DUF789) (AHRD V3.3 *** AT1G03610.1)						IPR008507 (PFAM): PTHR31343:SF7	0,096	0,074	0,022	0,025	0,000									
Solyc01g006090	rRNA processing protein EBP2 (AHRD V3.3 *** B9ICW5_POPTR)						IPR008610 (PFAM): mobidb-lite (MOB	5,565	7,152	4,300	2,956	2,859									

Solyc01g006100	cytosine-5 DNA methyltransferase1L	MET1L	F:GO:0003682; F:GC	F:chromatin binding; F:methyltransferase activity			IPR001525 (PRINTS): IPR000953 (SM	6,288	4,357	2,601	1,184	1,415					-1,120	0,014			down
Solyc01g006110	PP2A regulatory subunit TAP46 (AHRD V3.3 *** TAP46_ARATH)		P:GO:0009966	P:regulation of signal transduction			IPR007304 (PFAM): IPR038511 (G3D	67,987	78,531	78,444	76,366	77,989									
Solyc01g006120	Protein kinase family protein (AHRD V3.3 *** AT3G13670.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	174,876	204,495	174,919	165,550	163,764									
Solyc01g006130	Chaperone protein dnaJ (AHRD V3.3 *** B9GLJ5_POPTR)						PTHR15852:SF29 (PANTHER): PTHR	48,953	64,420	30,670	28,239	41,555			0,435	0,010				up	
Solyc01g006140	CDT1-like protein a, chloroplastic (AHRD V3.3 *** A0A0B0P9Z8_GOSAR)		F:GO:0005488; P:GC	F:binding; P:DNA replication; P:cellular component organization;			IPR014939 (SMART): IPR032054 (PF.	1,275	1,495	1,694	0,791	1,603									
Solyc01g006150	Metal tolerance protein (AHRD V3.3 *** D7RJ71_CARPA)		P:GO:0006812; F:GC	P:cation transport; F:cation transmembrane transporter activity;			IPR027469 (G3DSA:1.20.1510.GENE	11,244	12,958	9,604	9,906	9,871									
Solyc01g006160	60S acidic ribosomal protein P1 (AHRD V3.3 *** B9IDH5_POPTR)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translationa			PF00428 (PFAM): IPR038716 (G3DSA	163,582	169,436	123,407	101,044	114,900									
Solyc01g006170	rRNA processing protein EBP2 (AHRD V3.3 *** B9ICW5_POPTR)						IPR008610 (PFAM): mobidb-lite (MOB	25,623	47,761	24,386	24,451	22,595	0,925	0,000					up		
Solyc01g006180	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G10620.1)		F:GO:0005525	F:GTP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	7,277	9,525	9,735	8,641	9,602									
Solyc01g006190	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4ASI5_SOLLC)		F:GO:0005515; C:GC	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal			IPR013083 (G3DSA:3.30.40.GENE3D	34,076	35,071	49,566	53,604	46,240									
Solyc01g006195	histidine kinase 3 (AHRD V3.3 --* AT1G27320.1)							3,261	3,437	4,460	5,181	4,057									
Solyc01g006200	Reticulon-like protein B14 (AHRD V3.3 --* RTNLN_ARATH)							3,844	5,458	6,804	7,127	6,837									
Solyc01g006210	Non-structural maintenance of chromosomes element 1 (AHRD V3.3 *** A0A118K055_CYNCS)		P:GO:0006281; C:GC	P:DNA repair; C:Smc5-Smc6 complex			IPR011513 (PFAM): IPR036388 (G3D	1,996	1,511	0,910	0,932	1,061									
Solyc01g006220	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A072UKT3_MEDTR)		F:GO:0005515; C:GC	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR001214 (SMART): IPR003616 (SM	5,246	4,729	2,816	2,479	2,868									
Solyc01g006230	Cysteine protease ATG4B, putative (AHRD V3.3 *** B9STA6_RICCO)		C:GO:0005737; P:GC	C:cytoplasm; P:proteolysis; P:autophagy; F:cysteine-type pepti			IPR005078 (PFAM): mobidb-lite (MOB	32,308	32,361	94,341	108,729	81,185									
Solyc01g006240	Mannose-binding lectin superfamily protein (AHRD V3.3 *** AT1G05760.2)		F:GO:0030246	F:carbohydrate binding			IPR001229 (SMART): IPR001229 (PF.	0,101	0,154	0,051	0,000	0,000									
Solyc01g006250	F-box family protein (AHRD V3.3 --* AT1G67390.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	2,337	2,207	2,876	2,852	2,548									
Solyc01g006260	Ribonuclease P/MRP protein subunit POP5 (AHRD V3.3 *** A0A068TLU2_COFCA)		F:GO:0004540; P:GC	F:ribonuclease activity; P:tRNA processing			IPR002759 (PFAM): IPR038085 (G3D	3,038	3,648	2,339	2,105	2,684									
Solyc01g006280	Formate--tetrahydrofolate ligase (AHRD V3.3 *** FTHS_SPIOL)		F:GO:0004329; F:GC	F:formate-tetrahydr	EC:6.3.4.3	Formate--tetrahydrof	IPR000559 (PFAM): G3DSA:1.10.8.77	133,685	138,862	177,635	185,666	172,870									
Solyc01g006290	Peroxidase (AHRD V3.3 *** K4ASJ5_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,019	0,043	3,712	8,667	5,692									
Solyc01g006300	LECEVI1A	cevi1	F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,000	0,050	0,022	0,070									
Solyc01g006320	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G20600.1)		C:GO:0009506; C:GC	C:plasmodesma; C:integral component of membrane; C:anchore			PTHR31415:SF22 (PANTHER): PTHR	0,241	1,992	0,121	0,176	0,238	3,028	0,000					up		
Solyc01g006330	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT1G51110.1)		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:chloroplast envelope			IPR006843 (PFAM): PTHR31906:SF1	1,303	4,565	1,191	1,009	2,140	1,827	0,002					up		
Solyc01g006340	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RGT5_RICCO)		F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	12,173	11,024	15,274	15,659	15,850									
Solyc01g006350	Callose synthase-like protein (AHRD V3.3 *-* A0A072VRY1_MEDTR)		C:GO:0000148; F:GC	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan syntl	IPR003440 (PFAM): PTHR12741 (PAN	93,177	79,389	86,929	95,445	90,741									
Solyc01g006360	glucan synthase-like 10 (AHRD V3.3 *** AT3G07160.3)		C:GO:0000148; F:GC	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan syntl	IPR026899 (SMART): IPR026899 (PF.	65,180	48,247	52,778	57,547	58,986									
Solyc01g006370	Callose synthase (AHRD V3.3 *** K7PRK8_MAIZE)		C:GO:0000148; F:GC	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan syntl	IPR026899 (SMART): IPR003440 (PF.	249,728	212,913	86,110	75,960	81,798									
Solyc01g006380	U-box domain-containing protein (AHRD V3.3 *** B6V8G2_HELAN)		F:GO:0003824	F:catalytic activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,281	0,101	0,140	0,072	0,072									
Solyc01g006390	LOW QUALITY:Extensin-like protein (AHRD V3.3 *** Q9XG52_SOLLC)							0,000	0,021	0,025	0,050	0,000									
Solyc01g006400	Extensin-like protein (AHRD V3.3 *** O49946_SOLTU)							3,706	11,795	3,347	1,939	1,191									
Solyc01g006420	LOW QUALITY:wall associated kinase-like 6 (AHRD V3.3 --* AT1G16110.1)							0,000	0,021	0,000	0,000	0,000									
Solyc01g006430	Fatty acid desaturase (AHRD V3.3 *** M4QSE6_9ERIC)		P:GO:0006629; F:GC	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR005804 (PFAM): IPR021863 (PFA	490,592	496,235	269,018	238,281	264,424									
Solyc01g006440	Major facilitator superfamily protein (AHRD V3.3 *** A0A061GSQ4_THECC)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	0,019	0,058	0,000	0,125	0,071									
Solyc01g006450	Enoyl reductase (AHRD V3.3 *** P93062_BRANA)		F:GO:0004318; F:GC	F:enoyl-[acyl-carrie	EC:2.3.1.85; EC:1.3.	Fatty-acid synthase;	IPR002347 (PRINTS): G3DSA:1.10.8.	21,967	27,719	29,186	30,900	29,058									
Solyc01g006460	Non-structural maintenance of chromosome element 4 (AHRD V3.3 *** A0A1D1XPL1_9ARAE)		C:GO:0005634; P:GC	C:nucleus; P:DNA repair; C:Smc5-Smc6 complex			IPR014854 (PFAM): PTHR16140:SF1	0,021	0,061	0,267	0,269	0,213									
Solyc01g006470	LOW QUALITY:DNA-binding bromodomain-containing protein (AHRD V3.3 *-* AT2G44430.1)		F:GO:0005515	F:protein binding			IPR001487 (SMART): IPR001487 (PF.	0,021	0,019	0,000	0,000	0,000									
Solyc01g006480	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G19630.1)		F:GO:0016787	F:hydrolase activity			IPR000073 (PFAM): IPR029058 (G3D	8,642	8,014	13,977	14,692	13,370									
Solyc01g006490	uncharacterized protein						IPR003846 (PFAM): IPR003846 (PAN	19,925	16,472	29,236	28,590	26,297									
Solyc01g006500	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061DV75_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 (C	8,376	8,514	11,765	11,929	12,675									
Solyc01g006510	sorbitol related enzyme	sdh	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.90.18	64,244	67,896	61,077	64,543	76,468									
Solyc01g006520	Serine/threonine-protein kinase (AHRD V3.3 *** K4ASL8_SOLLC)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	9,048	14,699	3,503	2,945	4,753	0,727	0,019					up		
Solyc01g006530	Serine/threonine-protein kinase (AHRD V3.3 *** K4ASL9_SOLLC)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	0,000	0,018	0,124	0,025	0,047									
Solyc01g006540	lipoxygenase C	LOX3	F:GO:0005515; F:GC	F:protein binding; F	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR001024 (SM	25,992	33,246	2462,591	2496,538	3094,840									
Solyc01g006550	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT2G33170.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	2,108	2,632	0,794	1,107	1,407									
Solyc01g006560	Lipoxygenase (AHRD V3.3 *** C0KKU8_SOLLC)	LOX12	F:GO:0016702; F:GC	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	1,688	8,943	0,121	0,174	0,212	2,423	0,000					up		
Solyc01g006565	Lipoxygenase (AHRD V3.3 *-* C0KKU8_SOLLC)		F:GO:0005515; F:GC	F:protein binding; F	EC:1.13.11	Acting on single donc	IPR001024 (SMART): IPR001024 (PF.	0,432	2,382	0,000	0,049	0,000	2,455	0,000					up		
Solyc01g006575	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc01g006580	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc01g006590	Serine/threonine-protein kinase (AHRD V3.3 *** K4ASL8_SOLLC)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): IPR036426 (G3D	0,000	0,000	0,000	0,025	0,023									
Solyc01g006600	Long-chain-fatty-acid--AMP ligase FadD28 (AHRD V3.3 *** W9QXF8_9ROSA)		F:GO:0004096; F:GC	F:catalase activity;	EC:1.11.1.7; EC:1.1	Peroxidase; Catalase	PR00419 (PRINTS): G3DSA:2.160.10	1,036	1,698	0,321	1,133	0,185									
Solyc01g006610	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	2,139	3,565	0,025	0,101	0,046									
Solyc01g006620	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072ULK6_MEDTR)		C:GO:0009506; C:GC	C:plasmodesma; C:integral component of membrane			IPR000008 (SMART): IPR013583 (PF.	0,058	0,183	0,512	0,631	0,727									
Solyc01g006630	Oxidoreductase, putative (AHRD V3.3 *** B9RI76_RICCO)		F:GO:0016491	F:oxidoreductase activity			G3DSA:3.40.50.720 (GENE3D): IPR0	20,305	21,882	25,365	23,747	25,667									
Solyc01g006650	ETHYLENE INSENSITIVE 3-like 3 protein (AHRD V3.3 *** A0A0B2RCL4_GLYSO)	EIL6	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus			IPR023278 (G3DS EIL	0,946	1,175	0,988	2,148	1,508					1,111	0,026			up
Solyc01g006660	Subtilisin-like protease (AHRD V3.3 *** A0A0B2PIS0_GLYSO)		F:GO:0004252; P:GC	F:serine-type endoț	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	0,124	0,153	0,097	0,047	0,117									
Solyc01g006670	Glycosyltransferase (AHRD V3.3 *** K4D910_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR0	3,791	3,444	9,563	7,833	7,316									
Solyc01g006680	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G20810.5)		F:GO:0003700; P:GC	F:DNA-binding trans	EC:2.1.1.43	Histone-lysine N-met	PF13621 (PFAM): G3DSA:2.60.120.6	5,935	7,941	13,243	9,903	14,986									
Solyc01g006690	DNA double-strand break repair rad50 ATPase (AHRD V3.3 *** A0A061GZ54_THECC)						PTHR31029:SF3 (PANTHER): PTHR3	1,486	2,039	1,307	2,252	1,556									
Solyc01g006700	Protein downstream neighbor of Son (AHRD V3.3 *** A0A0B0NFM1_GOSAR)		C:GO:0005634; P:GC	C:nucleus; P:nuclear DNA replication			IPR024861 (PRINTS): IPR024861 (PA	24,503	22,685	24,662	23,222	25,434									
Solyc01g006710	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RL32_RICCO)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR014720 (SMART): IPR001650 (SM	35,197	28,866	37,848	41,129	36,786									
Solyc01g006720	ABC transporter family protein (AHRD V3.3 *** B9IIG9_POPTR)	ABCG1	F:GO:0005524; C:GC	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF.	9,314	5,044	3,604	3,662	5,266									
Solyc01g006730	Calcium-dependent protein kinase (AHRD V3.3 *** H6UM43_TOBAC)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (SMART): IPR000719 (SM	0,622	0,380	0,050	0,099	0,094									
Solyc01g006740	Sucrose phosphate phosphatase (AHRD V3.3 *** Q5J3N8_ACTCH)		F:GO:0000287; P:GC	F:magnesium ion bi	EC:3.1.3.23; EC:3.1.	Sugar-phosphatase;	G3DSA:3.10.450.50 (GENE3D): IPR0	6,646	6,705	5,231	5,097	5,315									
Solyc01g006770	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT4G11350.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:integral component			G3DSA:3.90.550.50 (GENE3D): IPR0	0,620	0,400	0,000	0,000	0,000									
Solyc01g006780	LOW QUALITY:Nitrate reductase [NADH] 1 (AHRD V3.3 --* NIA1_PHAVU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,760	0,661	0,140	0,167	0,355									
Solyc01g006790	BnaAnng41820D protein (AHRD V3.3 *** A0A078K412_BRANA)						PTHR33264:SF5 (PANTHER): PTHR3	2,195	1,991	0,483	0,592	0,497									
Solyc01g006800	Methionine aminopeptidase 2 (AHRD V3.3 *** K4ASP6_SOLLC)		F:GO:0004177; P:GC	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR001714 (PRINTS): IPR002468 (TI	77,506	78,812	60,212	60,950	62,231									
Solyc01g006810	RING/U-box superfamily protein (AHRD V3.3 --* AT5G15790.5)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	17,029	14,914	19,630	19,117	17,049									
Solyc01g006820	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT5G57150.5)							2,928	1,865	1,027	0,449	1,061									
Solyc01g006825	Fasciclin-like arabinogalactan protein 17 (AHRD V3.3 *** FLA17_ARATH)						IPR000782 (SMART): IPR036378 (G3	80,334	67,666	21,513	16,068	23,558									
Solyc01g006830	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT2G35880.3)						IPR027329 (PFAM): mobidb-lite (MOB	64,600	68,185	35,751	36,954	37,799									
Solyc01g006850	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H9M3_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	2,326	2,882	2,649	1,930	1,974									
Solyc01g006860	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *** AT5G06410.1)		F:GO:0001671; F:GC	F:ATPase activator activity; F:chaperone binding; P:protein con			IPR001623 (SMART): IPR001623 (PF	0,641	0,678	1,377	1,443	1,157									
Solyc01g006870	polyketide cyclase/dehydrase/lipid transport superfamily protein (AHRD V3.3 *-* AT5G06440.3)		F:GO:0001671; F:GC	F:ATPase activator activity; F:lipid binding; F:chaperone bindinc			IPR001623 (SMART): IPR002913 (PF.	44,348	39,407	25,384	27,139	26,617									
Solyc01g006880	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9P7Q5_ZOSMR)		F:GO:0005515; F:GC	F:protein binding; F	EC:2.1.1.43	Histone-lysine N-met	IPR003616 (SMART): IPR001214 (SM	70,435	50,818	66,975	78,427	66,835									
Solyc01g006890	EEIG1/EHBP1 N-terminal domain-containing protein (AHRD V3.3 *** A0A103XH66_CYNCS)						IPR019448 (PFAM): mobidb-lite (MOB	22,226	107,403	4,989	4,697	5,046	2,299	0,000					up		
Solyc01g006900	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein (AHRD V3.3 *** AT3		P:GO:0032366	P:intracellular sterol transport			IPR003172 (SMART): IPR003172 (PF.	242,090	240,564	215,630	176,347	210,759									
Solyc01g006920	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2S1E2_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,836	1,856	1,645	1,408	1,505									
Solyc01g006925	Serine/threonine-protein phosphatase (AHRD V3.3 --* K4DBE7_SOLLC)							0,384	0,661	0,458	0,622	0,517									
Solyc01g006930	Nuclear transcription factor Y subunit A-10, putative (AHRD V3.3 *** A0A061EVQ6_THECC)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRINT NF-YA	9,941	14,460	5,659	6,089	6,431									
Solyc01g006940	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G37220.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR003954 (SM	27,913	35,885	26,648	21,802	35,381			0,406	0,019				up	
Solyc01g006950	Syntaxin, putative (AHRD V3.3 *** B9SDJ9_RICCO)		C:GO:0016020; P:GC	C:membrane; P:vesicle-mediated transport			IPR006011 (SMART): IPR000727 (SM	9,255	36,726	5,169	7,806	10,719			1,045	0,001				up	
Solyc01g006960	Trafficking protein particle complex subunit 8 (AHRD V3.3 *** A0A0B2QRW8_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	64,175	52,661	58,837	63,452	61,341									
Solyc01g006970	RNA helicase family protein (AHRD V3.3 *** AT2G35920.2)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR014001 (SMART): IPR001650 (SM	57,222	49,061	66,826	63,453	69,483									
Solyc01g006980	Malonyl-CoA:Acyl carrier protein transacylase (AHRD V3.3 *** M9PMR7_LINUS)		F:GO:0016740	F:transferase activity			IPR020801 (SMART): G3DSA:3.40.36	51,861	63,545	78,954	69,222	83,649									
Solyc01g006990	F-box family protein (AHRD V3.3 *** E5GBH4_CUCME)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR024682 (PF.	23,196	22,489	30,352	26,152	26,021									
Solyc01g007000	U-box domain-containing family protein (AHRD V3.3 *** B9P691_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR011989 (G3	0,322	0,569	0,527	0,625	0,495									
Solyc01g007010	U-box domain-containing family protein (AHRD V3.3 *** B9P691_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR003613 (PF.	0,198	0,619	0,294	0,735	0,448									
Solyc01g007020	U-box domain-containing family protein (AHRD V3.3 *** B9IIK9_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination:			IPR011989 (G3DSA:1.25.10.GENE3D	0,324	1,423	0,944	0,768	0,870									
Solyc01g007025	U-box domain-containing family protein (AHRD V3.3 *-* B9IIK9_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR013083 (G3	0,021	0,099	0,072	0,051	0,070									
Solyc01g007030	U-box domain-containing family protein (AHRD V3.3 *** B9P691_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination:			IPR011989 (G3DSA:1.25.10.GENE3D	1,612	1,678	0,803	1,494	1,021									
Solyc01g007040	U-box domain-containing family protein (AHRD V3.3 *-* B9P691_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR013083 (G3	0,730	1,111	0,712	1,152	0,656									
Solyc01g007050	U-box domain-containing family protein (AHRD V3.3 *** B9IIL0_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR013083 (G3	0,019	0,021	0,000	0,025	0,047									
Solyc01g007060	BTB/POZ domain-containing protein (AHRD V3.3 *** AT3G05675.3)						G3DSA:3.30.710.10 (GENE3D): IPR0	9,513	9,561	14,437	17,561	16,159									
Solyc01g007070	BEL1-like homeodomain protein 1 (AHRD V3.3 *** A0A151SQ36_CAJCA)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006563 (SMAF TALE	313,747	228,958	408,799	322,579	365,897					-0,339	0,042			down
Solyc01g007100	Digalactosyldiacylglycerol synthase 1 (AHRD V3.3 *** W8SVK3_TOBAC)		C:GO:0009707; P:GC	C:chloroplast outer membrane; P:galactolipid biosynthetic proce			G3DSA:3.40.50.2000 (GENE3D): IPR0	20,184	30,020	9,003	11,687	11,999	0,601	0,036					up		
Solyc01g007110	NC domain-containing protein-like protein (AHRD V3.3 *** AT5G06370.1)		P:GO:0071284	P:cellular response to lead ion			G3DSA:3.90.1720.10 (GENE3D): IPR0	1,194	1,593	0,537	0,740	0,709									
Solyc01g007120	protein serine/threonine kinase (AHRD V3.3 *** AT3G51270.4)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000687 (SMART): G3DSA:3.30.20	5,508	3,795	3,002	6,998	4,085					1,217	0,000			up
Solyc01g007130	Receptor-like protein kinase (AHRD V3.3 *** Q58JF6_SOLPI)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR003591 (SMART): IPR000719 (SM	35,742	21,203	32,982	25,348	23,630	-0,723	0,016	-0,485	0,047			down	down	
Solyc01g007140	ARM repeat superfamily protein (AHRD V3.3 *** AT5G06350.2)		C:GO:0071339; C:GC	C:MLL1 complex; C:Rix1 complex			IPR024679 (PFAM): mobidb-lite (MOB	6,946	7,309	11,815	13,444	10,276									
Solyc01g007150	Coatomer subunit beta (AHRD V3.3 *** K4AST1_SOLLC)		F:GO:0005198; P:GC	F:structural molecule activity; P:intracellular protein transport; P			IPR011989 (G3DSA:1.25.10.GENE3D	139,098	124,050	114,620	114,754	112,025									
Solyc01g007160	N-acetyltransferase ESCO2 (AHRD V3.3 *** A0A1D1YG22_9ARAE)		P:GO:0000070; P:GC	P:mitotic sister chromatid segregation; P:sister chromatid cohe:			IPR028009 (PFAM): IPR028005 (PFA	0,428	0,713	0,118	0,045	0,256									
Solyc01g007170	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT3G03680.1)		C:GO:0016021; C:GC	C:integral component of membrane; C:vesicle			IPR000008 (SMART): IPR035892 (G3	0,547	0,469	0,118	0,100	0,188									
Solyc01g007180	Gamma-tubulin complex component (AHRD V3.3 *** K4AST4_SOLLC)		P:GO:0000278; C:GC	P:mitotic cell cycle; C:equatorial microtubule organizing center; C:centrosome; C:gamma-tubulin ring cor				4,952	4,937	6,234	6,423	5,673									
Solyc01g007190	LOW QUALITY:UvrABC system protein A (AHRD V3.3 *** A0A1D1YSC2_9ARAE)						PTHR36351 (PANTHER)	3,797	3,535	3,247	3,951	3,055									
Solyc01g007200	LOW QUALITY:Integrase-type DNA-binding superfamily protein (AHRD V3.3 -** AT1G72360.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,256	2,477	5,008	5,058	4,755									
Solyc01g007210	LOW QUALITY:glutamate receptor 2 (AHRD V3.3 --* AT2G17260.1)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,022	0,000									
Solyc01g007220	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G52470.1)		C:GO:0009506; C:GC	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM): PTHR31415 (PAN	288,331	320,497	172,125	187,211	211,881									
Solyc01g007230	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family, putative (AHRD V3.3 *** A0A06		C:GO:0009506; C:GC	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM): PTHR31415:SF4	6,711	5,986	8,336	8,443	8,717									
Solyc01g007240	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane			PTHR31415:SF4 (PANTHER): PTHR3	0,019	0,018	0,047	0,100	0,047									
Solyc01g007250	U3 small nucleolar ribonucleoprotein protein imp4, putative (AHRD V3.3 *** B9RGD5_RICCO)		P:GO:0006364; F:GC	P:rRNA processing; F:snoRNA binding; C:small-subunit process			IPR007109 (SMART): G3DSA:3.40.50	13,978	16,906	19,805	19,882	18,728									
Solyc01g007260	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 **		P:GO:0019538	P:protein metabolic process			IPR004176 (PFAM): G3DSA:3.40.50.3	0,278	0,511	0,169	0,194	0,260									
Solyc01g007265	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *-* M1BCW3_SOLTU)		C:GO:0005634; C:GC	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): PTHF	0,507	0,753	1,053	0,913	0,899									
Solyc01g007740	2-Cys peroxiredoxin 2		P:GO:0045454; F:GC	P:cell redox homeo:	EC:1.11.1.15	Peroxiredoxin	IPR024706 (PIRSF): G3DSA:3.40.30.	10,571	12,456	15,740	16,523	15,452									
Solyc01g007750	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT2G36000.1)		F:GO:0003690; P:GC	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR038538 (G3	6,473	7,267	6,070	7,221	6,929									
Solyc01g007760	Transcription factor E2F (AHRD V3.3 *** Q9LEL4_DAUCA)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:transcription facto			IPR003316 (SMAF E2F/DP	18,092	19,814	29,188	29,996	24,675									
Solyc01g007780	HVA22-like protein (AHRD V3.3 *** M1BCP5_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004345 (PFAM): IPR004345 (PAN	2,577	3,415	1,758	1,891	1,740									
Solyc01g007790	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G11620.8)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane; F:hydrolase a			IPR019363 (PFAM): IPR029058 (G3D	9,229	8,333	11,596	11,374	11,656									
Solyc01g007800	ovate family protein 2	OFP2	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (TIGRFAM): IPR006458 (F	0,113	0,181	0,000	0,025	0,023									
Solyc01g007810	LOW QUALITY:ovate family protein 3	OFP3	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (PFAM): IPR006458 (TIGF	0,058	0,019	0,000	0,000	0,000									
Solyc01g007830	Condensin complex subunit 2 (AHRD V3.3 --* CND2_ARATH)		P:GO:0009987; C:GC	P:cellular process; C:intracellular part				1,194	0,841	1,012	1,263	1,034									
Solyc01g007840	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT5G22250.1)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.1.1.13; EC:3.1.1	Acting on ester bond:	IPR036397 (G3DSA:3.30.420.GENE3	23,100	20,333	39,587	33,720	34,841									
Solyc01g007850	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061F6E7_THECC)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (PFA	8,821	8,707	13,822	16,128	15,288									
Solyc01g007855	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G46870.2)							2,479	3,528	5,694	4,936	5,093									
Solyc01g007860	ubiquitin-conjugating enzyme E2 variant 1D		C:GO:0005634; P:GC	C:nucleus; P:postreplication repair; F:ubiquitin conjugating enzy			SM00212 (SMART): IPR016135 (G3D	72,820	78,496	83,830	82,920	78,112									
Solyc01g007870	E3 ubiquitin-protein ligase (AHRD V3.3 *** AT3G11600.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,709	0,622	0,118	0,318	0,349									
Solyc01g007880	1-phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *** B9S7B0_RICCO)		C:GO:0009570; C:GC	C:chloroplast stroma; C:chloroplast outer membrane; P:chlorop			IPR003409 (SMART): IPR036525 (G3	19,399	19,039	18,744	18,972	18,637									
Solyc01g007890	Zinc finger protein, putative (AHRD V3.3 *-* B9S7A8_RICCO)		F:GO:0005488	F:binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	8,254	5,745	1,904	2,729	2,023									
Solyc01g007895	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G31050.6)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): PTHR162	0,301	0,134	0,047	0,050	0,048									
Solyc01g007900	Tobamovirus multiplication 1 homolog (AHRD V3.3 *** Q402F2_SOLLC)		C:GO:0009705; C:GC	C:plant-type vacuole membrane; C:integral component of memb			IPR009457 (PFAM): IPR040226 (PAN	14,966	11,573	20,585	22,894	18,909									
Solyc01g007910	succinyl-CoA ligase alpha 1 subunit	scoa1	F:GO:0003824; F:GC	F:catalytic activity; F:cofactor binding			PR01798 (PRINTS): IPR003781 (SMA	56,095	75,180	67,041	59,968	65,187									
Solyc01g007920	Isochorismatase hydrolase family protein (AHRD V3.3 *** G7IBE1_MEDTR)		F:GO:0003824	F:catalytic activity			IPR000868 (PFAM): IPR036380 (G3D	27,773	20,394	42,570	42,971	43,990									
Solyc01g007930	F-box family protein (AHRD V3.3 *** AT1G70590.1)		F:GO:0005515	F:protein binding			IPR006597 (SMART): IPR006597 (PF.	20,853	18,433	15,758	13,395	14,965									
Solyc01g007940	Alanine aminotransferase 2 (AHRD V3.3 *** A0A151TGW4_CAJCA)		F:GO:0003824; P:GC	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3	10,693	8,484	0,322	1,942	0,023									
Solyc01g007955	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G10740.4)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,994	1,133	0,502	0,747	0,517									
Solyc01g007960	Kinase family protein (AHRD V3.3 *** B9HTV7_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	0,121	0,157	0,211	0,047	0,166									
Solyc01g007970	Kinase family protein (AHRD V3.3 *** U5G1A9_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,000	0,039	0,000	0,000	0,048									
Solyc01g007980	Protein kinase family protein (AHRD V3.3 *** C6ZRU6_SOYBN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,038	0,144	0,050	0,073	0,164									
Solyc01g007990	Kinase family protein (AHRD V3.3 *** U5G1A9_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	13,277	42,083	11,449	11,347	10,663	1,690	0,000					up		
Solyc01g008000	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00177 (SMA	374,035	349,107	375,511	341,920	335,347									
Solyc01g008005	TATA-box-binding protein (AHRD V3.3 *** TBP_SOLTU)		F:GO:0003677; P:GC	F:DNA binding; P:DNA-templated transcription, initiation			IPR000814 (PRINTS): IPR000814 (PF	0,038	0,021	0,049	0,049	0,071									

Solyc01g008010	OBP32pep protein, putative (Domain of unknown function DUF220) (AHRD V3.3 *** AT1G23600.1)						IPR023393 (G3DSA:3.30.530.GENE3I	7,051	8,910	18,006	26,459	16,615					0,559	0,049			up
Solyc01g008020	Equilibrative nucleoside transporter (AHRD V3.3 *** A0A103YAP6_CYNCS)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con			IPR002259 (PFAM): IPR002259 (PIRS	11,764	11,676	0,845	1,096	1,786									
Solyc01g008050	Trichome birefringence-like 27 (AHRD V3.3 *** A0A061E629_THECC)		C:GO:0005794; P:G(	C:Golgi apparatus; P:xyloglucan metabolic process; F:O-acetylt			IPR026057 (PFAM): IPR025846 (PFA	0,019	0,000	0,000	0,025	0,070									
Solyc01g008060	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM): IPR036397 (G3D	33,702	32,303	36,596	39,486	38,058									
Solyc01g008070	Gut esterase (DUF1350) (AHRD V3.3 *** AT5G47860.1)		C:GO:0009507	C:chloroplast			IPR010765 (PFAM): IPR010765 (PAN	23,848	22,334	82,081	83,445	80,119									
Solyc01g008080	40S ribosomal protein S27 (AHRD V3.3 *** M0TJU4_MUSAM)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.20.25.640 (GENE3D): IPR0(	16,887	15,505	7,741	6,963	5,823									
Solyc01g008090	40S ribosomal protein S27 (AHRD V3.3 *-* M0TJU4_MUSAM)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.20.25.640 (GENE3D): IPR0(	90,407	104,905	107,771	99,658	100,784									
Solyc01g008100	Transferase, transferring glycosyl groups, putative (AHRD V3.3 *** B9RG20_RICCO)		C:GO:0005773; C:G(	C:vacuole; C:integral component of membrane; F:transferase a			IPR038941 (PANTHER): PTHR33880:	35,293	33,234	40,195	39,391	40,046									
Solyc01g008110	Cytochrome P450 (AHRD V3.3 *** A0A118JS81_CYNCS)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR001128 (PRINTS): IPR002403 (PF	97,669	100,372	156,827	150,774	138,908									
Solyc01g008120	Histone acetyltransferase (AHRD V3.3 *** A0A0U5B4W5_TOBAC)		F:GO:0003712; F:G(	F:transcription core	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR000197 (SMART): IPR000433 (SM	90,198	85,712	93,183	108,267	104,104									
Solyc01g008130	electron protein, putative (Protein of unknown function, DUF547) (AHRD V3.3 *-* AT1G43020.1)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR000591 (SMART): IPR000591 (PF	19,899	20,931	12,330	11,373	13,954									
Solyc01g008140	Receptor kinase (AHRD V3.3 *** A0A0K9Q671_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	23,210	22,722	41,867	43,070	46,855									
Solyc01g008150	LOW QUALITY:cytochrome B5-like protein (AHRD V3.3 --* AT1G60660.1)							0,219	0,122	0,122	0,097	0,116									
Solyc01g008160	Tetratricopeptide repeat-containing family protein (AHRD V3.3 *** B9HVN0_POPTR)		F:GO:0005515	F:protein binding			PF13432 (PFAM): IPR011990 (G3DS/	13,185	15,502	69,759	70,589	65,140									
Solyc01g008170	Zinc finger transcription factor 5	C3H5	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	39,633	48,358	58,460	51,130	55,602									
Solyc01g008180	Remorin family protein (AHRD V3.3 *** B9HVM6_POPTR)						IPR005516 (PFAM): mobidb-lite (MOB	16,953	25,687	9,813	7,357	10,126									
Solyc01g008190	INO80 complex subunit D-like protein (AHRD V3.3 --* AT2G31600.5)		C:GO:0000123	C:histone acetyltransferase complex				4,262	4,041	8,649	7,981	7,893									
Solyc01g008200	INO80 complex subunit D (AHRD V3.3 *-* A0A0B0MZT7_GOSAR)		C:GO:0000123	C:histone acetyltransferase complex			IPR026316 (PANTHER): PTHR13453:	3,403	3,320	6,596	6,791	5,716									
Solyc01g008220	UPF0664 stress-induced protein C29B12.11c (AHRD V3.3 *** A0A0B2PCL5_GLYSO)		F:GO:0003713; C:G(	F:transcription coactivator activity; C:nucleus; F:chromatin DNA			PTHR31606:SF12 (PANTHER): PTHR:	2,231	3,144	0,789	1,037	1,221									
Solyc01g008230	TCP transcription factor 15	TCP15	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	67,185	45,101	43,698	36,235	39,485	-0,547	0,028					down		
Solyc01g008250	Thioredoxin (AHRD V3.3 *-* A0A103XS29_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored			PR00421 (PRINTS): IPR005746 (TIGF	0,196	0,186	0,248	0,145	0,260									
Solyc01g008260	E2F-associated phosphoprotein (AHRD V3.3 *** AT5G08320.1)		C:GO:0005634; P:G(	C:nucleus; P:positive regulation of cell population proliferation			IPR019370 (PFAM): mobidb-lite (MOB	16,446	12,769	21,388	17,018	18,186									
Solyc01g008270	Prefoldin subunit 5 (AHRD V3.3 *** B6TVU2_MAIZE)		P:GO:0006457; C:G(	P:protein folding; C:prefoldin complex; F:unfolded protein binding			IPR011599 (TIGRFAM): IPR009053 ((	25,521	27,497	22,854	21,595	21,755									
Solyc01g008280	Serine/threonine-protein phosphatase 2A activator (AHRD V3.3 *** K4AT26_SOLLC)		F:GO:0019211	F:phosphatase activator activity			IPR004327 (PFAM): IPR004327 (PIRS	46,645	46,454	61,366	47,750	56,014									
Solyc01g008290	Dihydroorotate dehydrogenase (quinone), mitochondrial (AHRD V3.3 *** K4AT27_SOLLC)		F:GO:0004152; C:G(	F:dihydroorotate de	EC:1.3.5.2	Dihydroorotate dehy	IPR013785 (G3DSA:3.20.20.GENE3D	12,090	13,756	13,804	10,392	11,392									
Solyc01g008300	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM): IPR023213 (G3D	0,384	0,508	0,218	0,223	0,117									
Solyc01g008310	Phenylalanyl-tRNA synthetase beta chain family protein (AHRD V3.3 *** B9N5I6_POPTR)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:6.1.1.2	Phenylalanine--tRNA	IPR005147 (SMART): IPR005146 (SM	104,776	101,269	125,991	134,201	125,812									
Solyc01g008320	shoot gravitropism 2 (SGR2) (AHRD V3.3 *** AT1G31480.1)		F:GO:0046872	F:metal ion binding			IPR004177 (SMART): IPR004177 (PF	55,288	44,436	86,615	85,060	82,975									
Solyc01g008330	Biotin Carboxylase (AHRD V3.3 *** A0A0R5QP93_SALMI)		F:GO:0005524; F:G(	F:ATP binding; F:ligase activity; F:metal ion binding			IPR005482 (SMART): G3DSA:3.30.47	86,571	97,602	130,572	159,929	171,269			0,388	0,023				up	
Solyc01g008340	L19 ribosomal protein		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001857 (PRINTS): IPR001857 (PF	15,700	17,191	25,693	25,181	23,472									
Solyc01g008350	LOW QUALITY:DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *-* AT1G65280.2)						IPR022226 (PFAM): mobidb-lite (MOB	0,021	0,060	0,075	0,000	0,000									
Solyc01g008360	RNA recognition motif (RRM) domain-containg protein		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	51,383	49,983	94,896	83,550	80,949									
Solyc01g008370	putative 26S proteasome subunit		F:GO:0005515; C:G(	F:protein binding; C:proteasome regulatory particle			IPR000555 (SMART): G3DSA:3.40.14	134,798	141,276	163,818	183,148	165,107									
Solyc01g008390	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,952	8,715	1,511	5,395	6,364	3,213	0,000	2,059	0,000	1,827	0,000	up	up	up
Solyc01g008400	mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT1G23230.3)							2,639	3,473	2,956	3,307	3,658									
Solyc01g008405	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JVH5_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,000	0,000	0,025	0,000									
Solyc01g008410	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,000	0,500	0,174	0,576	0,518									
Solyc01g008420	Protein DETOXIFICATION (AHRD V3.3 *** K4AT40_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	10,487	5,281	1,676	1,686	1,805	-0,960	0,005					down		
Solyc01g008430	Ankyrin repeat family protein (AHRD V3.3 --* AT2G24600.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,058	0,000	0,000	0,000									
Solyc01g008440	Calcium-dependent protein kinase (AHRD V3.3 *** F8V179_HEVBR)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): IPR002048 (SM	15,311	13,347	17,422	21,500	16,112									
Solyc01g008460	Ferredoxin (AHRD V3.3 *** Q70SW4_DIGLA)		F:GO:0009055; F:G(	F:electron transfer activity; F:2 iron, 2 sulfur cluster binding			IPR001055 (PRINTS): IPR012675 (G3	14,419	13,572	21,319	20,044	18,645									
Solyc01g008470	Translocation protein sec62 (AHRD V3.3 *** W9RTI5_9ROSA)		P:GO:0015031; C:G(	P:protein transport; C:integral component of endoplasmic reticul			IPR004728 (PFAM): mobidb-lite (MOB	11,252	10,581	12,657	13,253	11,533									
Solyc01g008471	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,025	0,000	0,047									
Solyc01g008472	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein (AHRD V3.3 --* AT2G05160.3)							0,000	0,021	0,000	0,047	0,024									
Solyc01g008474	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,000	0,122	0,000									
Solyc01g008476	Cysteine proteinases superfamily protein (AHRD V3.3 --* AT3G48350.2)							0,000	0,000	0,000	0,050	0,000									
Solyc01g008478	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,021	0,018	0,025	0,000	0,023									
Solyc01g008480	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YH67_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	12,586	9,987	15,671	16,352	15,767									
Solyc01g008485	Translocation sec62 (AHRD V3.3 *-* A0A0B0MVG2_GOSAR)		C:GO:0005783; F:G(	C:endoplasmic reticulum; F:protein transporter activity; P:protein transport; C:membrane; C:integral con				4,013	3,847	5,840	5,269	5,011									
Solyc01g008490	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRIN NF-YA	5,931	4,807	11,746	9,771	8,856									
Solyc01g008493	Nuclear transcription factor Y subunit A-1, putative (AHRD V3.3 *-* B9RID0_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,010	3,810	8,320	7,343	6,405									
Solyc01g008497	Receptor-like kinase (AHRD V3.3 *** G7I982_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,080	0,093	0,075	0,164	0,353									
Solyc01g008510	Photosystem II 5 kDa protein (AHRD V3.3 *** G7IWU5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR040296 (PANTHER): IPR040296 (I	0,848	5,243	4,972	7,522	9,852	2,640	0,000	0,982	0,000			up	up	
Solyc01g008520	DNA repair XRCC2-like protein (AHRD V3.3 *** A0A0B0P902_GOSAR)		P:GO:0000724; C:G(	P:double-strand break repair via homologous recombination; C:i			IPR030547 (PTHR22942:PANTHER): I	3,858	2,766	2,069	1,929	2,638									
Solyc01g008530	phenylacetaldehyde reductase	par1	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	3,124	3,909	0,858	0,803	0,678									
Solyc01g008540	Cinnamoyl CoA reductase-like protein (AHRD V1 ***- B9HNY0_POPTR)	CCR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	0,161	0,383	37,878	52,974	26,154									
Solyc01g008550	phenylacetaldehyde reductase PAR2	par2	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	19,941	35,744	7,796	9,340	12,787	0,870	0,000	0,710	0,035			up	up	
Solyc01g008560	NAD kinase 1 (AHRD V3.3 *** AT3G21070.2)		F:GO:0003951; P:G(	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR017437 (G3DSA:2.60.200.GENE3I	37,692	74,017	25,722	26,681	32,634	0,997	0,015					up		
Solyc01g008570	LOW QUALITY:Receptor-like protein kinase (AHRD V3.3 *-* A0A061EYK6_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,021	0,000	0,000	0,000	0,000									
Solyc01g008600	Zinc finger transcription factor 6	C3H6	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (SMART): IPR000571 (SM	17,154	12,426	16,101	15,153	15,447									
Solyc01g008620	Beta-1,3-glucanase (AHRD V3.3 *** Q9SYX6_TOBAC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00(	0,000	0,204	0,169	0,192	0,404									
Solyc01g008650	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc01g008660	F-box protein (AHRD V3.3 *** W9R8S7_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	6,933	7,264	4,888	4,492	5,275									
Solyc01g008670	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,057	0,324	0,480	0,726	0,661									
Solyc01g008680	S2 self-incompatibility locus-linked pollen 3.2 protein (AHRD V3.3 *** Q7XAE8_PETIN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,345	0,460	2,508	2,932	2,531									
Solyc01g008690	GDP-mannose transporter (AHRD V3.3 *** M5VX95_PRUPE)		C:GO:0016021	C:integral component of membrane			IPR004853 (PFAM): PTHR44371 (PAN	0,078	0,121	0,022	0,000	0,000									
Solyc01g008700	Crossover junction endodeoxyribonuclease, putative (AHRD V3.3 *** A0A072UU82_MEDTR)						PTHR36015:SF2 (PANTHER): PTHR3(	9,219	8,164	76,897	82,561	71,631									
Solyc01g008710	inactive endo-beta-mannanase	man4	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001547 (PFAM): G3DSA:3.20.20.8	16,636	20,850	1886,507	2526,530	1815,309									
Solyc01g008720	Mannan endo-1 4-beta-mannosidase (AHRD V1 ***- A8FDC6_BACP2)%3B contains Interpro domain(s) IPR		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001547 (PFAM): G3DSA:3.20.20.8	0,000	0,077	0,000	0,000	0,000									
Solyc01g008730	BZIP transcription factor (AHRD V3.3 *** Q9SQK1_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	20,738	19,190	31,356	32,871	30,758									
Solyc01g008740	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9SJ93_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (SMART): IPR000719 (SM	0,000	0,000	0,000	0,025	0,000									
Solyc01g008760	Terpene cyclase/mutase family member (AHRD V3.3 --* U5FRE5_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,652	3,885	5,363	4,636	4,613									
Solyc01g008770	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9NLF4_ZOSMR)		P:GO:0007165	P:signal transduction			IPR000198 (SMART): IPR001849 (SM	53,234	40,697	34,154	34,831	34,697									
Solyc01g008780	Phospholipase A2 family protein (AHRD V3.3 *** AT4G29070.2)		F:GO:0004623; P:G(	F:phospholipase A2	EC:3.1.1.1; EC:3.1.1	Carboxylesterase; Pl	IPR036444 (G3DSA:1.20.90.GENE3D	30,807	25,905	69,108	71,243	72,314									
Solyc01g008790	Non specific phospholipase C (AHRD V3.3 *** A0A0K9P3E0_ZOSMR)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR007312 (PFAM): IPR017849 (G3D	69,170	47,550	11,216	5,965	10,510					-0,910	0,004			down
Solyc01g008800	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR001841 (SMA	0,758	3,034	0,478	3,000	2,184	2,015	0,000	2,155	0,000	2,616	0,000	up	up	up
Solyc01g008810	RING/U-box superfamily protein (AHRD V3.3 *** AT5G19430.6)						IPR001841 (SMART): IPR013083 (G3	0,677	0,677	0,587	0,790	0,427									
Solyc01g008820	signal peptide peptidase (AHRD V3.3 *** AT2G03120.1)		F:GO:0004190; C:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR006639 (SMART): IPR007369 (PF	28,364	35,313	50,647	55,158	51,962									
Solyc01g008830	Ascorbate oxidase (AHRD V3.3 *** X5JRX8_NICBE)		F:GO:0005507; C:G(	F:copper ion binding; C:extracellular region; F:oxidoreductase a			IPR011706 (PFAM): IPR001117 (PFA	2,512	3,386	2,061	2,541	2,986									
Solyc01g008840	COP9 signalosome complex subunit 2 (AHRD V3.3 *** W9QZI3_9ROSA)		C:GO:0008180	C:COP9 signalosome			SM00753 (SMART): IPR000717 (SMA	61,125	58,619	73,294	74,196	68,955									
Solyc01g008850	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IV59_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	86,322	99,981	131,663	147,152	156,033									
Solyc01g008860	Protein kinase (AHRD V3.3 *** C6ZRQ9_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,000	0,019	0,000	0,000	0,000									
Solyc01g008870	Protein kinase (AHRD V3.3 *** C6ZRQ9_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,000	0,000	0,025	0,000	0,024									
Solyc01g008880	Solanum lycopersicum Cytokinin Response Factor 8		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,273	0,080	0,050	0,000	0,047									
Solyc01g008890	Solanum lycopersicum Cytokinin Response Factor 3	CRF6	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN AP2	13,349	11,675	14,563	13,998	14,153									
Solyc01g008900	Pyridoxal-5'-phosphate-dependent enzyme family protein (AHRD V3.3 *** AT3G26115.1)		F:GO:0019148	F:D-cysteine desulf	EC:4.4.1.15	D-cysteine desulfhyd	G3DSA:3.40.50.1100 (GENE3D): G3D	5,859	5,819	5,420	6,706	6,169									
Solyc01g008910	Scarecrow-like transcription factor 3 family protein (AHRD V3.3 *** B9HP16_POPTI	GRAS	F:GO:0003712; C:G(	F:transcription coregulator activity; C:nucleus			IPR005202 (PFAM GRAS	3,845	2,746	10,815	15,467	12,098					0,522	0,021			up
Solyc01g008920	NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (AHRD V3.3 *** A0A061GTI3_THECC)		F:GO:0016616; P:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0	2,597	4,355	2,285	2,778	5,393			1,238	0,001				up	
Solyc01g008925	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT4G31530.2)		F:GO:0016616; P:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0	5,276	9,402	5,070	5,825	11,601	0,857	0,019	1,192	0,000			up	up	
Solyc01g008930	AUREA phytochromobilin synthase	aurea/GUN3	P:GO:0010024; F:G(	P:phytochromobilin biosynthetic process; F:oxidoreductase acti			IPR009249 (PFAM): G3DSA:3.40.150	12,294	11,153	11,474	9,104	14,231									
Solyc01g008940	LOW QUALITY:ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 --* AT1G54280.3)							2,904	2,978	0,124	0,251	0,000									
Solyc01g008950	Calmodulin 1	CaM1	F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	176,320	176,409	230,935	218,898	213,600									
Solyc01g008960	Argonaute 4a	AGO4a	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR014811 (SMART): IPR003165 (SM	568,739	473,530	322,862	295,515	319,937									
Solyc01g008970	RNA binding protein (AHRD V3.3 *** B6TJJ4_MAIZE)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	380,085	365,983	336,536	330,025	331,431									
Solyc01g008977	BZIP transcription factor (AHRD V3.3 *-* A0A072UF45_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMART): IPR004827 (PF	0,657	0,740	0,763	0,964	0,964									
Solyc01g008980	BZIP transcription factor (AHRD V3.3 *** A0A072UF45_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	2,059	1,285	1,222	1,369	1,446									
Solyc01g008990	THO complex subunit 7 (AHRD V3.3 *** A0A0B0PUA3_GOSAR)		C:GO:0000445; P:G(	C:THO complex part of transcription export complex; P:mRNA pr			IPR008501 (PFAM): mobidb-lite (MOB	13,156	11,989	18,953	18,889	16,843									
Solyc01g009000	RING/U-box superfamily protein (AHRD V3.3 *** AT3G56580.3)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR001841 (SMART): IPR039525 (PF	31,572	29,176	35,698	32,587	33,113									
Solyc01g009010	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	CMK	F:GO:0005524; P:G(	F:ATP binding; P:te	EC:2.7.1.148	4-(cytidine 5'-diphosp	IPR014721 (G3DSA:3.30.230.GENE3I	8,614	12,058	59,037	66,099	54,984									
Solyc01g009020	Cysteine proteinase inhibitor (AHRD V3.3 *** K4AT98_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			IPR000010 (SMART): IPR000010 (PF	128,332	114,468	143,315	116,016	133,348									
Solyc01g009030	Nuclear control of ATPase 2 (AHRD V3.3 *** A0A0B0N2X0_GOSAR)		C:GO:0005741; C:G(	C:mitochondrial outer membrane; C:integral component of meml			IPR013946 (PFAM): mobidb-lite (MOB	25,079	26,767	48,069	49,976	50,130									
Solyc01g009040	cyclinB1_4	CycB1_4	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	0,509	0,712	0,025	0,000	0,000									
Solyc01g009050	Molybdopterin biosynthesis protein CNX1 (AHRD V3.3 *** CNX1_ARATH)		P:GO:0032324	P:molybdopterin cofactor biosynthetic process			IPR001453 (SMART): IPR001453 (PF	41,710	42,787	54,612	49,054	54,391									
Solyc01g009060	BTB-POZ and MATH domain protein (AHRD V3.3 *** B9VXZ7_CAPAN)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR000210 (SM	28,974	25,156	45,835	44,019	43,099									
Solyc01g009070	gamyb-like 1	R2R3MYB65	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	15,359	12,411	9,088	8,553	10,391									
Solyc01g009080	Zeaxanthin epoxidase, chloroplastic (AHRD V3.3 *** A0A0B0MK82_GOSAR)		F:GO:0005515	F:protein binding			IPR000253 (SMART): IPR000253 (PF	13,204	18,322	8,626	10,133	18,544			1,103	0,000				up	
Solyc01g009090	Serrate RNA effector molecule-like protein (AHRD V3.3 *** A0A0B0MH79_GOSAR)		P:GO:0006397	P:mRNA processing			IPR007042 (PFAM): IPR021933 (PFA	113,746	108,323	146,924	138,048	138,787									
Solyc01g009100	60S ribosomal protein L30 (AHRD V3.3 *** RL30_LUPLU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR004038 (PFAM): IPR029064 (G3D	69,054	83,467	80,399	72,332	72,782									
Solyc01g009120	Histone deacetylase, putative (AHRD V3.3 *** B9RRD2_RICCO)		C:GO:0005634; C:G(	C:nucleus; C:integra	EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS): IPR037138 (G3	9,961	12,242	12,442	11,932	13,368									
Solyc01g009150	Fe(3+) dicitrate transport system permease (AHRD V3.3 *** AT5G21070.1)		C:GO:0016021	C:integral component of membrane			PTHR36394 (PANTHER)	9,045	8,593	8,781	7,673	7,620									
Solyc01g009160	harpin-induced1-like		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	53,482	17,578	14,320	27,407	22,998	-1,582	0,000			0,936	0,002	down		up
Solyc01g009170	EIL-EIN3/EIL	EIL2	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus			IPR023278 (G3DS EIL	101,028	74,746	99,023	90,760	90,934									
Solyc01g009180	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (AHRD V3.3 *** METE_CATRO)		F:GO:0003871; F:G(	F:5-methyltetrahydr	EC:2.1.1.14	5-methyltetrahydropt	IPR038071 (G3DSA:3.20.20.GENE3D	40,866	39,711	78,972	78,252	77,460									
Solyc01g009190	Double-stranded RNA-binding protein 1 (AHRD V3.3 *** W9RGH4_9ROSA)		F:GO:0003723	F:RNA binding			IPR014720 (SMART): G3DSA:3.30.16	0,133	0,041	0,000	0,000	0,000									
Solyc01g009200	Heat shock family protein (AHRD V3.3 *-* B9MYM7_POPTR)	Hsp25.7A	C:GO:0016021	C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc01g009220	Heat shock family protein (AHRD V3.3 *-* U5GG61_POPTR)	Hsp23.8A	C:GO:0016021	C:integral component of membrane			IPR002068 (PFAM): IPR008978 (G3D	0,042	0,094	0,000	0,000	0,000									
Solyc01g009230	sitiens							0,458	0,690	0,330	0,149	0,212									
Solyc01g009235	Aldehyde oxidase (AHRD V3.3 *** Q9FV23_SOLLC)		F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR000674 (SMART): IPR005107 (SM	16,506	17,419	4,801	3,994	6,353									
Solyc01g009240	Beta-glucosidase (AHRD V3.3 *-* A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR036962 (G3DSA:3.20.20.GENE3D	0,080	0,039	0,025	0,025	0,024									
Solyc01g009245	Chlororespiratory reduction 42 (AHRD V3.3 *** A0A0F7J401_9ROSI)						IPR021495 (PFAM): PTHR36799:SF2	2,733	6,233	0,356	0,511	1,617	1,217	0,002					up		
Solyc01g009250	LOW QUALITY:zinc finger (CCCH-type) family protein (AHRD V3.3 --* AT2G28450.2)						mobidb-lite (MOBIDB_LITE): PTHR332	0,660	0,493	0,243	0,313	0,517									
Solyc01g009260	LOW QUALITY:ribosomal protein L5 (AHRD V3.3 *-* ATMG00210.1)						IPR021410 (PFAM): mobidb-lite (MOB	0,000	0,000	0,025	0,022	0,000									
Solyc01g009270	FAF-like protein (DUF3049) (AHRD V3.3 *-* AT5G22090.2)						IPR021410 (PFAM): mobidb-lite (MOB	0,094	0,000	0,115	0,047	0,000									
Solyc01g009280	Serine/threonine-protein phosphatase (AHRD V3.3 *** G8Z292_SOLLC)		F:GO:0004721; F:G(	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threor	IPR006186 (PRINTS): IPR006186 (SM	66,862	49,368	75,455	70,312	68,282									
Solyc01g009290	Protein CLP1 homolog (AHRD V3.3 *** K4ATC5_SOLLC)		C:GO:0005849; P:G(	C:mRNA cleavage factor complex; P:mRNA 3'-end processing			IPR032319 (PFAM): IPR038238 (G3D	23,619	24,341	28,288	29,158	29,114									
Solyc01g009300	Kinase (AHRD V3.3 *** D7LMI5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	35,251	26,439	19,999	21,829	22,266									
Solyc01g009307	myb domain protein 3r-4 (AHRD V3.3 --* AT5G11510.4)							0,000	0,000	0,047	0,050	0,023									
Solyc01g009310	meloidogyne-induced giant cell protein DB217	TOMTRALTBE	C:GO:0016020	C:membrane			IPR001171 (PFAM): G3DSA:1.20.120	108,625	113,262	70,833	77,238	74,393									
Solyc01g009320	U-box domain-containing family protein (AHRD V3.3 *** B9IIL0_POPTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR003613 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc01g009335	LOW QUALITY:Ovate family protein, putative (AHRD V3.3 *-* A0A061EUC3_THECC)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (TIGRFAM): IPR006458 (F	0,159	0,092	0,050	0,000	0,024									
Solyc01g009340	SUN-domain protein2	SUN2	F:GO:0005515	F:protein binding			IPR000048 (SMART): G3DSA:1.20.5.1	0,895	0,670	0,119	0,247	0,072									
Solyc01g009360	Polynucleotidyl transferase%2C ribonuclease H-like superfamily protein (AHRD V3.3 *** AT3G44260.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.13; EC:3.1.1	Acting on ester bonds	IPR006941 (PFAM): IPR006941 (PFA	0,019	0,000	0,000	0,000	0,000									
Solyc01g009370	Cytochrome P450 (AHRD V3.3 *** A9ZT63_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,019	0,060	0,118	0,434	0,236									
Solyc01g009380	Nicalin (AHRD V3.3 *** A0A166DJQ4_DAUCA)		P:GO:0009966; C:G(	P:regulation of signal transduction; C:integral component of mer			G3DSA:3.40.630.10 (GENE3D): IPR0(	17,895	12,161	30,215	26,013	25,427									
Solyc01g009390	mRNA-decapping enzyme-like protein (AHRD V3.3 *** A0A0B2REC5_GLYSO)		P:GO:0000290; F:G(	P:deadenylation-dependent decapping of nuclear-transcribed ml			IPR011993 (G3DSA:2.30.29.GENE3D	10,795	11,614	21,910	22,196	20,439									
Solyc01g009420	UDP-apiose/xylose synthase (AHRD V3.3 *** Q2I2N3_SOLTU)		F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	436,443	348,983	300,026	268,284	262,208									
Solyc01g009430	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	75,680	54,876	226,914	199,033	157,437			-0,530	0,003				down	
Solyc01g009450	Mitochondrial inner membrane protease ATP23 (AHRD V3.3 *** W9R362_9ROSA)		F:GO:0004222	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR019165 (PFAM): IPR019165 (PAN	98,215	97,025	118,876	104,064	106,598									
Solyc01g009470	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4ATE3_SOLLC)		F:GO:0003950; P:G(	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylti	IPR008893 (SMART): IPR001357 (SM	2,736	4,321	0,887	2,022	0,162									
Solyc01g009480	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G44510.2)						IPR000073 (PFAM): IPR029058 (G3D	0,021	0,100	0,000	0,075	0,000									
Solyc01g009500	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G44510.2)						IPR029058 (G3DSA:3.40.50.GENE3D	5,089	5,737	4,697	4,949	5,134									

Solyc01g009510	BZIP transcription factor (AHRD V3.3 *-* A0A142CR61_9FABA)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	2,325	1,737	0,000	0,025	0,000										
Solyc01g009520	Ribosomal protein (AHRD V3.3 *** K4ATE8_SOLLC)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR002143 (PIRSF); IPR016095 (G3D	173,340	176,374	116,939	102,483	102,964										
Solyc01g009530	LOW QUALITY:plant/protein (AHRD V3.3 *-* AT5G43400.1)						IPR011205 (PIRSF); IPR011205 (PFA	0,019	0,000	0,022	0,000	0,000										
Solyc01g009570	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT4G08850.2)		C:GO:0016020	C:membrane			IPR025875 (PFAM); IPR032675 (G3D	0,000	0,043	0,000	0,000	0,000										
Solyc01g009580	Terminal flower 1-like protein (AHRD V3.3 *** A0A0S1LKM5_CHRMO)		C:GO:0005737; P:G(	C:cytoplasm; P:flower development; P:vegetative to reproductiv			IPR036610 (G3DSA:3.90.280.GENE3I	0,058	0,039	0,000	0,000	0,000										
Solyc01g009610	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NN67_ZOSMR)		F:GO:0004864; P:G(	F:protein phosphatase inhibitor activity; P:regulation of signal tr			IPR007062 (PFAM); mobidb-lite (MOB	24,987	24,545	8,572	8,695	8,939										
Solyc01g009620	Cleavage and polyadenylation specificity factor subunit 5 (AHRD V3.3 *** A0A0K9P6H8_ZOSMR)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cleavage factor complex; P:mRNA po			G3DSA:3.90.79.10 (GENE3D); IPR01(	10,098	12,705	16,555	16,576	17,409										
Solyc01g009630	Cleavage and polyadenylation specificity factor subunit 5 (AHRD V3.3 *** A0A0K9P6H8_ZOSMR)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cleavage factor complex; P:mRNA po			IPR016706 (PIRSF); G3DSA:3.90.79.	14,524	16,189	22,956	24,464	23,766										
Solyc01g009660	Low-temperature-induced 65 kDa-like protein (AHRD V3.3 *-* A0A0B0MRR8_GOSAR)		P:GO:0009737	P:response to abscisic acid			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,532	1,021	0,370	1,610	0,139										
Solyc01g009670	Poly(A) polymerase, putative (AHRD V3.3 *** B9RA84_RICCO)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti			G3DSA:1.10.3090.10 (GENE3D); G3D	1,111	1,903	0,578	0,311	0,914										
Solyc01g009680	Lipoxygenase (AHRD V3.3 *** K4ATG3_SOLLC)		F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	PR00019 (PRINTS); IPR013819 (PRII	0,100	0,258	0,576	0,674	1,040										
Solyc01g009690	BnaC05g27570D protein (AHRD V3.3 --* A0A078CAX2_BRANA)							0,040	0,197	0,000	0,050	0,186										
Solyc01g009700	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,019	0,117	0,000	0,022	0,024										
Solyc01g009710	LOW QUALITY:PLAT/LH2 domain-containing lipoxygenase family protein (AHRD V3.3 --* AT1G72520.1)							0,159	0,194	0,044	0,097	0,023										
Solyc01g009715	RING finger protein, putative (AHRD V3.3 *** A0A061E508_THECC)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,037	0,025	0,050	0,000										
Solyc01g009740	Jasmonate zim-domain protein (AHRD V3.3 --* G7LE60_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (SMART); IPR010399 (PF.	0,019	0,000	0,000	0,000	0,000										
Solyc01g009750	cysteine-rich/transmembrane domain protein A (AHRD V3.3 --* AT2G33520.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	127,475	125,418	123,283	108,285	111,242										
Solyc01g009760	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)						IPR004182 (SMART); IPR004182 (PF.	3,200	3,339	2,385	3,390	2,595										
Solyc01g009770	ATP-dependent RNA helicase (AHRD V3.3 *** AT2G33510.1)		F:GO:0005515	F:protein binding			G3DSA:2.20.70.10 (GENE3D); mobidb	1,307	1,642	3,375	5,904	2,744					0,809	0,031			up
Solyc01g009780	LITAF-domain-containing protein (AHRD V3.3 *** A0A0K9NQ82_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR006629 (SMART); IPR006629 (PF.	40,404	42,718	36,656	58,509	43,773					0,676	0,000			up
Solyc01g009810	Leucine-rich repeat receptor-like kinase protein (AHRD V3.3 *-* A0A060H1D1_ELAGV)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,236	0,000	0,100	0,140										
Solyc01g009820	Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *** A0A061E526_THECC)		C:GO:0005886	C:plasma membrane			IPR027267 (G3DSA:1.20.1270.GENE:	45,413	68,191	41,735	42,246	47,261										
Solyc01g009830	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT4G32272.1)		C:GO:0005794; P:G(	C:Golgi apparatus; P:carbohydrate transport; F:antiporter activi			IPR004853 (PFAM); PTHR44680 (PAI	1,308	0,889	0,383	0,048	0,422										
Solyc01g009845	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** A0A1D1YLP0_9ARAE)						IPR016340 (PFAM); PTHR37703 (PAI	0,019	0,018	0,051	0,045	0,048										
Solyc01g009850	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* A0A1D1YLP0_9ARAE)						PTHR37703 (PANTHER)	2,385	2,635	3,816	3,711	3,912										
Solyc01g009860	NAC domain protein (AHRD V3.3 *** B2ZGQ7_SOYBN)	NAC002	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	24,875	69,914	24,501	39,265	27,256	1,518	0,000			0,683	0,000	up		up
Solyc01g009870	Glycerophosphodiester phosphodiesterase, putative (AHRD V3.3 *** B9RM92_RICCO)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR030395 (PFAM); IPR017946 (G3D	35,309	31,370	3,675	6,026	7,778			1,075	0,035				up	
Solyc01g009920	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0MF82_GOSAR)						IPR036890 (G3DSA:3.30.565.GENE3I	0,000	0,000	0,169	0,517	0,591										
Solyc01g009930	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,000	0,000	0,000	0,000	0,024										
Solyc01g009970	catalytic/ hydrolase (AHRD V3.3 *** AT2G35450.1)		F:GO:0016787; F:G(	F:hydrolase activity; F:carboxy-lyase activity			IPR006680 (PFAM); G3DSA:3.20.20.1	15,379	17,047	35,054	33,963	37,899										
Solyc01g009990	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4ATJ4_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS); IPR029000 (G3	71,717	111,644	132,031	118,126	141,668	0,666	0,007					up		
Solyc01g010000	ACT domain containing protein, putative, expressed (AHRD V3.3 *** Q75IY1_ORYSJ)						G3DSA:3.30.70.260 (GENE3D); G3DS	6,594	5,566	15,005	13,036	12,298										
Solyc01g010020	Calmodulin, putative (AHRD V3.3 *** B9RLA1_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	4,272	5,227	0,940	1,648	1,547										
Solyc01g010030	Kinase family protein (AHRD V3.3 *-* B9HIU4_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PR01217 (PRINTS); IPR000719 (SMA	5,690	5,079	5,879	8,774	6,775					0,578	0,045			up
Solyc01g010035	RING/U-box superfamily protein (AHRD V3.3 --* AT1G78420.2)							0,000	0,000	0,050	0,000	0,023										
Solyc01g010050	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 *** K4ATK0_SOLLC)		F:GO:0004014; P:G(	F:adenosylmethioni	EC:4.1.1.5	Adenosylmethionine (	IPR001985 (PIRSF); G3DSA:3.60.90.	28,900	32,953	33,696	35,666	35,577										
Solyc01g010055	S-adenosylmethionine decarboxylase uORF (AHRD V3.3 *-* Q6RUQ6_DAUCA)		F:GO:0004014; P:G(	F:adenosylmethioni	EC:4.1.1.5	Adenosylmethionine (	IPR012511 (PFAM); PTHR35727:SF1	0,126	0,080	0,025	0,195	0,048										
Solyc01g010060	LOW QUALITY:ARM repeat superfamily protein (AHRD V3.3 --* AT5G65920.2)							11,573	11,081	5,929	14,370	7,137					1,279	0,000			up
Solyc01g010080	Potassium channel (AHRD V3.3 *** B6ECZ4_TOBAC)		F:GO:0005249; P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra			IPR003938 (PRINTS); IPR000595 (SM	1,461	0,766	0,366	0,466	0,166										
Solyc01g010087	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM); G3DSA:3.40.395.	0,021	0,000	0,000	0,000	0,000										
Solyc01g010090	Dof-type zinc finger DNA-binding family protein (AHRD V3.3 --* AT3G52440.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,041	0,000	0,000	0,000										
Solyc01g010135	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT1G68920.3)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMART); IPR036638 (G3	5,982	4,577	2,873	3,030	3,814										
Solyc01g010140	LOW QUALITY:18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *** AT2G03810.7)		P:GO:0009786	P:regulation of asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,019	0,000	0,000	0,000										
Solyc01g010150	ACT domain-containing protein (AHRD V3.3 *** A0A118JXJ7_CYNCS)		P:GO:0009735	P:response to cytokinin			G3DSA:3.30.70.260 (GENE3D); G3DS	3,941	5,197	14,530	14,284	13,802										
Solyc01g010160	Beta-glucosidase, putative (AHRD V3.3 *-* B9REF8_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); IPR001360 (PF	0,000	0,000	0,172	0,222	0,047										
Solyc01g010170	Beta-glucosidase, putative (AHRD V3.3 --* B9REF8_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:beta-gluc				0,000	0,000	0,607	0,573	0,144										
Solyc01g010180	DEA(D/H)-box RNA helicase family protein (AHRD V3.3 --* AT3G61240.2)							23,197	81,541	1,843	2,965	4,087	1,841	0,000	1,149	0,001			up	up	
Solyc01g010190	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151RZV3		C:GO:0016020	C:membrane			PF14223 (PFAM); mobidb-lite (MOBID	12,442	17,759	7,121	6,299	6,110										
Solyc01g010200	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151RZV3_CAJCA)		C:GO:0000943; C:G(	C:retrotransposon nucleocapsid; C:membrane; C:integral compc			PF14223 (PFAM); mobidb-lite (MOBID	68,246	72,646	23,058	24,119	18,686										
Solyc01g010220	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151RZV3		C:GO:0000943; C:G(	C:retrotransposon nucleocapsid; C:membrane; C:integral compc			PF14223 (PFAM); mobidb-lite (MOBID	6,924	9,692	2,403	2,864	2,867										
Solyc01g010230	LOW QUALITY:Acanthoscurrin-2 (AHRD V3.3 --* B6TLS9_MAIZE)		C:GO:0016021	C:integral component of membrane			PTHR33333:SF2 (PANTHER); IPR039	12,825	20,588	7,057	6,178	5,782	0,711	0,029					up		
Solyc01g010250	6-phosphogluconolactonase, putative (AHRD V3.3 *** B9REC3_RICCO)		P:GO:0005975; P:G(	P:carbohydrate met	EC:3.1.1.31; EC:3.1.	6-phosphogluconolac	IPR006148 (PFAM); G3DSA:3.40.50.1	7,751	10,724	34,075	45,493	42,098					0,419	0,008			up
Solyc01g010260	Cytochrome P450 (AHRD V3.3 *** A0A103XPY7_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	0,000	0,043	0,000	0,000	0,000										
Solyc01g010270	SPIRAL1-like1 (AHRD V3.3 *** AT1G26355.1)		P:GO:0043622	P:cortical microtubule organization			mobidb-lite (MOBIDB_LITE); mobidb-lit	87,559	71,541	33,416	21,445	26,358					-0,636	0,000			down
Solyc01g010280	suppressor SRP40-like protein (AHRD V3.3 *-* AT2G03630.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,000	0,000	0,000	0,000										
Solyc01g010290	Ureide permease (AHRD V3.3 *** A0A124SG70_CYNCS)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR009834 (PFAM); PTHR31081:SF5	7,989	6,911	7,423	7,869	7,311										
Solyc01g010295	Ureide permease, putative (AHRD V3.3 *-* B9REE2_RICCO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR009834 (PFAM); PTHR31081:SF9	0,811	0,961	0,747	0,978	0,634										
Solyc01g010310	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *-* A0A0B2R8X2_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR012946 (SMART); IPR012946 (PF.	7,697	4,883	1,789	1,459	1,668										
Solyc01g010315	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)						IPR019557 (PFAM); mobidb-lite (MOB	0,000	0,021	0,022	0,000	0,000										
Solyc01g010350	Glucose-6-phosphate translocator		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR004696 (TIGRFAM); IPR004853 (F	0,484	0,113	0,119	0,216	0,142										
Solyc01g010360	14-3-3 protein, putative (AHRD V3.3 *** B9REF4_RICCO)		F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS); IPR023410 (SM	2,773	2,531	1,648	1,479	1,412										
Solyc01g010370	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G78240.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	6,517	5,448	3,138	3,886	3,196										
Solyc01g010390	Beta-glucosidase, putative (AHRD V3.3 *** B9REF8_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); IPR001360 (PF	8,979	9,209	5,662	7,218	8,105										
Solyc01g010410	Zinc finger family protein (AHRD V3.3 *** B9HID5_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMART); PF13912 (PFAI	9,146	6,961	12,179	11,943	11,576										
Solyc01g010420	LOW QUALITY:Actin cross-linking protein (AHRD V3.3 *-* AT1G27100.1)						G3DSA:2.80.10.50 (GENE3D); IPR00	0,040	0,142	0,044	0,047	0,000										
Solyc01g010430	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)						IPR007679 (PFAM); G3DSA:2.80.10.5	48,556	57,826	23,528	28,117	33,446										
Solyc01g010440	glycine-rich protein (AHRD V3.3 *** AT1G27090.1)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE); mobidb-lit	102,171	73,625	79,471	71,407	75,895										
Solyc01g010460	5'-AMP-activated protein kinase-like protein (AHRD V3.3 *** AT1G27070.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	4,935	4,604	4,497	5,136	5,810										
Solyc01g010465	5'-AMP-activated protein kinase subunit beta-1 (AHRD V3.3 *-* A0A1D1Y9A4_9ARAE)						IPR013783 (G3DSA:2.60.40.GENE3D	0,099	0,174	0,050	0,116	0,188										
Solyc01g010470	5'-AMP-activated protein kinase subunit beta-1 (AHRD V3.3 *-* A0A1D1Y9A4_9ARAE)						IPR013783 (G3DSA:2.60.40.GENE3D	0,524	0,473	0,482	0,423	0,471										
Solyc01g010480	LOV/LOV protein (AHRD V3.3 *** E3WH16_SOLLC)		C:GO:0005634	C:nucleus			IPR001610 (SMART); G3DSA:3.30.45	74,782	56,537	84,237	72,593	77,979										
Solyc01g010490	Cytochrome P450 (AHRD V3.3 *** A0A061FSW2_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	6,644	7,693	39,424	46,656	43,201										
Solyc01g010493	Dihydroneopterin aldolase 1 (AHRD V3.3 --* FOLB1_ARATH)							0,019	0,158	0,333	0,000	0,641										
Solyc01g010500	EIN3-binding F-box-like protein (AHRD V3.3 *-* G7I706_MEDTR)		F:GO:0046872	F:metal ion binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,039	0,000	0,000	0,000										
Solyc01g010506	methylcrotonyl-CoA carboxylase alpha chain (AHRD V3.3 --* AT1G03090.2)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,057	0,025	0,025	0,000										
Solyc01g010508	WD-40 repeat family protein / beige-like protein (AHRD V3.3 --* AT2G45540.6)							0,076	0,000	0,000	0,048	0,000										
Solyc01g010510	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G26900.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,258	1,554	1,512	1,622	1,862										
Solyc01g010520	helicase with zinc finger protein (AHRD V3.3 *** AT2G46420.3)						IPR006476 (TIGRFAM); IPR006476 (F	7,260	7,869	1,265	0,957	1,269										
Solyc01g010525	Villin-5 (AHRD V3.3 --* VLN5_ORYSJ)							0,040	0,055	0,000	0,045	0,000										
Solyc01g010530	Sugar transporter protein 5	STP5	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); IPR005828 (PF	0,000	0,000	0,047	0,050	0,024										
Solyc01g010540	40S ribosomal protein S9, putative (AHRD V3.3 *** Q60CZ2_SOLDE)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001912 (SMART); IPR002942 (SM	43,610	53,083	43,792	38,473	40,368										
Solyc01g010570	mucin-like protein (AHRD V3.3 *** AT2G02880.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	39,209	33,662	30,204	31,758	28,050										
Solyc01g010580	40S ribosomal protein S9, putative (AHRD V3.3 *** Q60CZ2_SOLDE)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001912 (SMART); IPR002942 (SM	305,823	279,785	156,460	158,407	145,533										
Solyc01g010590	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4ATQ3_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS); IPR002130 (PF	18,042	16,488	15,889	15,790	16,021										
Solyc01g010640	Cytochrome b6-f complex subunit 5 (AHRD V3.3 --* PETG_FAGEA)		C:GO:0016021	C:integral component of membrane			IPR005182 (PFAM); PTHR35688:SF2	9,427	11,049	24,888	22,689	28,260										
Solyc01g010650	UDP-galactose transporter, putative (AHRD V3.3 *** B9S297_RICCO)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM); PTHR10778:SF1(	64,619	40,929	52,918	45,548	49,077	-0,631	0,022					down		
Solyc01g010660	Protein kinase (AHRD V3.3 *** Q2HTW4_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); IPR001245 (F	34,211	47,919	26,461	29,553	33,643										
Solyc01g010670	LOW QUALITY:Aquaporin NIP3-2 (AHRD V3.3 --* NIP32_ORYSJ)		P:GO:0006486; C:G(	P:protein glycosylation; C:integral component of membrane; F:transferase activity, transferring glycosyl				0,019	0,041	0,047	0,025	0,024										
Solyc01g010690	LOW QUALITY:Quinohemoprotein ethanol dehydrogenase type-1 (AHRD V3.3 *** S1RTP2_THECC)		F:GO:0005515	F:protein binding			IPR018391 (SMART); G3DSA:2.140.1	0,101	0,082	0,094	0,025	0,023										
Solyc01g010700	SNF1-related kinase regulatory subunit gamma 1 (AHRD V3.3 *** G7KB20_MEDTR)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR000644 (SMART); G3DSA:3.10.58	21,319	22,957	36,939	39,871	38,160										
Solyc01g010710	Carboxypeptidase (AHRD V3.3 *-* K4ATR4_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PFAM); G3DSA:3.40.50.1	0,281	0,612	0,022	0,000	0,000										
Solyc01g010720	Carboxypeptidase (AHRD V3.3 *** K4ATR5_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	1,073	1,146	0,000	0,022	0,093										
Solyc01g010740	Pectate lyase (AHRD V3.3 *** K4ATR7_SOLLC)		F:GO:0030570	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS); IPR002022 (SM	0,000	0,000	0,000	0,000	0,023										
Solyc01g010750	Hop-interacting protein THI113 (AHRD V3.3 *** G8Z279_SOLLC)		C:GO:0005634; C:G(	C:nucleus; C:cytoplasm; F:carbohydrate binding; P:defense resı			G3DSA:2.80.10.50 (GENE3D); mobidb	399,255	352,123	738,964	597,509	627,431										
Solyc01g010760	Mitochondrial outer membrane porin (AHRD V3.3 *** VDAC1_WHEAT)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe			IPR027246 (PFAM); IPR023614 (G3D	7,467	7,343	19,981	15,122	18,917										
Solyc01g010770	Hypersensitive-induced response protein (AHRD V3.3 *** Q6UNT3_CUCSA)		C:GO:0005774; C:G(	C:vacuolar membrane; C:plasma membrane; C:plasmodesma; (			IPR001107 (SMART); IPR001107 (PF.	1,869	2,748	2,850	4,599	3,957										
Solyc01g010780	Kinase family protein (AHRD V3.3 *** B9H0D5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); IPR001245 (F	35,964	36,655	47,611	46,723	44,927										
Solyc01g010810	Ran guanine nucleotide release factor-like protein (AHRD V3.3 *** G7KCJ8_MEDTR)						IPR007681 (PFAM); IPR016123 (G3D	11,482	11,132	12,780	11,932	11,749										
Solyc01g010820	Cullin family protein (AHRD V3.3 *** B9HJT6_POPTR)		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR016158 (SMART); IPR019559 (SM	38,961	42,077	48,361	48,207	45,632										
Solyc01g010830	Haloacid dehalogenase-like hydrolase domain protein (AHRD V3.3 *** G7KDV9_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR006439 (PRINTS); IPR006439 (TI(	9,485	10,569	20,529	17,053	18,104										
Solyc01g010835	Haloacid dehalogenase-like hydrolase domain protein (AHRD V3.3 *-* G7KDV9_MEDTR)		F:GO:0016787	F:hydrolase activity			mobidb-lite (MOBIDB_LITE); PTHR127	2,573	2,624	5,604	4,703	4,164										
Solyc01g010860	sphingoid base hydroxylase 2 (AHRD V3.3 *** AT1G14290.1)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM); PTHR11863:SF9	8,152	6,657	14,437	15,373	12,267										
Solyc01g010870	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G26850.2)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	81,924	75,742	181,069	199,882	165,096										
Solyc01g010880	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT2G02960.6)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART); IPR011016 (PF.	12,085	10,679	5,180	8,487	6,704					0,709	0,008			up
Solyc01g010920	O-fucosyltransferase family protein (AHRD V3.3 *-* AT1G14020.1)		C:GO:0005737; P:G(	C:cytoplasm; P:fucose metabolic process; C:integral componen			IPR019378 (PFAM); PTHR31741 (PAI	1,165	1,406	0,800	0,753	0,897										
Solyc01g010930	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G14020.1)		C:GO:0005737; P:G(	C:cytoplasm; P:fucose metabolic process; C:integral componen			IPR024709 (PIRSF); IPR019378 (PFA	1,901	2,105	1,120	1,470	1,742										
Solyc01g010933	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 --* AT2G23060.1)							0,199	0,233	0,049	0,072	0,094										
Solyc01g010940	Transmembrane emp24 domain-containing protein 10 (AHRD V3.3 *** W9SPK8_9ROSA)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR009038 (SMART); IPR009038 (PF.	14,309	15,087	23,868	27,170	23,786										
Solyc01g010950	MAP kinase kinase kinase 2	MAPKKK2	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR001245 (PRINTS); IPR002110 (SM	15,939	14,240	29,447	26,498	25,153										
Solyc01g010960	60S ribosomal L35 (AHRD V3.3 *** A0A0B0PTB9_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.287.310 (GENE3D); mob	0,440	0,592	0,439	0,191	0,470										
Solyc01g010970	Argonaute7	AGO.7	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR003100 (SMART); IPR014811 (SM	0,281	0,576	0,856	0,615	0,851										
Solyc01g010980	LOW QUALITY:30S ribosomal protein S14, chloroplastic (AHRD V3.3 --* RR14_PINKO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,101	0,019	0,000	0,000	0,000										
Solyc01g010990	Transmembrane protein, putative (AHRD V3.3 *** A0A072UY68_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33133:SF1 (PANTHER); PTHR3:	21,116	17,443	12,582	14,407	12,857										
Solyc01g011000	Eukaryotic translation initiation factor 5A (AHRD V3.3 *** K4BNF7_SOLLC)		F:GO:0003746; P:G(	F:translation elongation factor activity; P:translational frameshif			IPR020189 (SMART); IPR020189 (PF.	137,951	154,750	224,970	220,751	205,640										
Solyc01g011010	Phosphatidylinositol 4-phosphate 5-kinase 8 (AHRD V3.3 --* PI5K8_ARATH)							0,405	0,275	0,458	0,718	0,541										
Solyc01g011025	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT2G43700.5)							0,662	0,432	0,732	0,735	0,539										
Solyc01g011030	RING/U-box superfamily protein (AHRD V3.3 *** AT1G69330.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity; F:metal ioı			IPR013083 (G3DSA:3.30.40.GENE3D	18,874	14,738	20,273	19,768	18,794										
Solyc01g011040	leucine-rich repeat (LRR) family protein		F:GO:0005515	F:protein binding			IPR003591 (SMART); IPR032675 (G3	70,995	78,127	70,321	71,776	68,490										
Solyc01g011080	LOW QUALITY:IQ-domain 32 (AHRD V3.3 --* AT1G19870.2)						mobidb-lite (MOBIDB_LITE)	5,209	4,216	4,358	4,227	4,820										
Solyc01g011090	Phospholipid-transporting ATPase (AHRD V3.3 *-* K4BWJ0_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR032631 (PFAM); PTHR24092:SF8	0,000	0,000	0,000	0,000	0,024										
Solyc01g011091	BnaA03g14530D protein (AHRD V3.3 --* A0A078D6I5_BRANA)							0,418	0,403	0,482	0,683	0,378										
Solyc01g011092	Phospholipid-transporting ATPase (AHRD V3.3 *-* A0A0V0IYV6_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PTHR24092:SF85 (PANTHER); IPR00	0,037	0,000	0,025	0,050	0,047										
Solyc01g011095	CLAVATA3/ESR (CLE)-related 25-like protein (AHRD V3.3 *-* A0A0B0NFL0_GOSAR)		P:GO:0045168	P:cell-cell signaling involved in cell fate commitment			PTHR34277:SF3 (PANTHER); IPR039	0,581	0,510	0,126	0,073	0,116										
Solyc01g011180	Sec1 family domain-containing protein 2 (AHRD V3.3 *-* A0A0B2RPU4_GLYSO)		C:GO:0005737; P:G(	C:cytoplasm; P:endoplasmic reticulum to Golgi vesicle-mediated transport; P:vesicle docking involved ir				0,184	0,101	0,115	0,094	0,047										
Solyc01g011190	LOW QUALITY:Sec1 family domain-containing protein 2 (AHRD V3.3 *-* A0A0B2RPU4_GLYSO)		C:GO:0005737; P:G(	C:cytoplasm; P:endoplasmic reticulum to Golgi vesicle-mediated transport; P:vesicle docking involved ir				0,000	0,000	0,000	0,000	0,024										
Solyc01g011195	Jasmonate-zim-domain protein 10, putative (AHRD V3.3 --* A0A061E5T9_THECC)							0,021	0,021	0,022	0,000	0,000										
Solyc01g011200	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT2G36670.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,403	0,422	0,238	0,319	0,234										
Solyc01g011220	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT5G22850.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,352	0,396	0,283	0,214	0,211										
Solyc01g011225	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT2G36670.2)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,260	0,257	0,100	0,146	0,164										
Solyc01g011230	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT2G36670.2)		F:GO:0004190; P:G(	F:aspartic-type endopeptidase activity; P:proteolysis; F:peptidase activity; C:membrane; C:integral com				0,359	0,511	0,118	0,192	0,353										
Solyc01g011333	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT2G36670.2)		F:GO:0004190; P:G(	F:aspartic-type endopeptidase activity; P:proteolysis; F:peptidase activity; C:membrane; C:integral com				0,000	0,039	0,000	0,022	0,047										
Solyc01g011340	protein phosphatase 2A catalytic subunit 2	pp2ac2	F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS); IPR006186 (SM	32,707	31,641	37,201	31,844	33,832										
Solyc01g011350	ZZ-type zinc finger-containing protein 3, putative isoform 1 (AHRD V3.3 *** A0A061EGG8_THECC)		F:GO:0003677	F:DNA binding			IPR022228 (PFAM); mobidb-lite (MOB	88,585	64,027	32,956	32,449	28,809										
Solyc01g011390	NHL domain protein (AHRD V3.3 --* AT3G01430.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,059	0,041	0,000	0,000	0,047										
Solyc01g011393	U-box domain-containing protein 15 (AHRD V3.3 --* A0A151TB12_CAJCA)							0,000	0,019	0,000	0,000	0,000										
Solyc01g011410	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_SOLLC)		F:GO:0016651; F:G(	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindin(			IPR001135 (PFAM); IPR038290 (G3D	0,021	0,149	0,025	0,098	0,094										
Solyc01g011415	Photosystem II CP47 reaction center protein (AHRD V3.3 *-* PSBB_AMBTC)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM); PTHR33180:SF5	0,000	0,142	0,025	0,072	0,165										
Solyc01g011430	O-acyltransferase WSD1-like protein (AHRD V3.3 *** A0A0B0PTU2_GOSAR)		F:GO:0004144; P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR004255 (PFAM); IPR009721 (PFA	0,637	1,099	0,467	1,354	0,070										
Solyc01g011460	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151R160_CAJCA)							0,161	0,132	0,000	0,025	0,000										
Solyc01g011510	Aldehyde dehydrogenase (AHRD V3.3 *** K4ATY6_SOLLC)		P:GO:0006081; F:G(	P:cellular aldehyde metabolic process; F:oxidoreductase activit			IPR016163 (G3DSA:3.40.309.GENE3I	19,964	16,496	9,964	11,519	9,278										
Solyc01g012580	LOW QUALITY:Dicer-like protein 2 (AHRD V3.3 *** F8SXT7_NICAT)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR000999 (PFAM); IPR036389 (G3D	0,040	0,000	0,000	0,025	0,047										

Solyc01g012690	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)	F:GO:0005515	F:protein binding	PR00019 (PRINTS): IPR001611 (PFA	0,021	0,000	0,000	0,000	0,024									
Solyc01g012760	Aldehyde dehydrogenase (AHRD V3.3 *-* K4ATY6_SOLLC)	F:GO:0016620: P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR015590 (PFAM): IPR016163 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc01g013885	LOW QUALITY:Aldehyde dehydrogenase (AHRD V3.3 *-* K4ATY6_SOLLC)	F:GO:0016620: P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR016163 (G3DSA:3.40.309.GENE3	0,492	0,321	0,233	0,533	0,545									
Solyc01g013895	Aldehyde dehydrogenase (AHRD V3.3 *-* K4ATY6_SOLLC)	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR016162 (G3DSA:3.40.605.GENE3	0,019	0,000	0,000	0,000	0,000									
Solyc01g013915	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 --* NDHI_DIOEL)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,025	0,000									
Solyc01g013995	B3 domain-containing protein family (AHRD V3.3 *** A0A151S4J0_CAJCA)	F:GO:0003677	F:DNA binding	IPR003340 (PFAM): IPR015300 (G3D	0,173	0,154	0,000	0,000	0,000									
Solyc01g014075	TATA BOX ASSOCIATED FACTOR II 59 (AHRD V3.3 --* AT1G04950.3)				0,076	0,000	0,025	0,022	0,048									
Solyc01g014090	Synaptotagmin-5 (AHRD V3.3 *-* A0A199VMX5_ANACO)	C:GO:0005783: P:G(	C:endoplasmic reticulum; P:lipid transport; F:lipid binding; C:inte	IPR035892 (G3DSA:2.60.40.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc01g014100	CLE protein 1	C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,342	0,579	0,000	0,000	0,000									
Solyc01g014103	DNA double-strand break repair rad50 ATPase (AHRD V3.3 *** A0A061GZ54_THECC)			PTHR31029:SF3 (PANTHER): PTHR3	6,485	5,172	2,593	2,401	2,925									
Solyc01g014107	DNA double-strand break repair rad50 ATPase (AHRD V3.3 *-* A0A061GZ54_THECC)			PTHR31029 (PANTHER): PTHR31029	0,098	0,076	0,093	0,142	0,117									
Solyc01g014140	Hcr9-OR3A (AHRD V3.3 *-* Q4VSU2_SOLPI)	C:GO:0016020	C:membrane		0,021	0,039	0,000	0,000	0,046									
Solyc01g014143	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)	C:GO:0016020: P:G(	C:membrane; P:defense response to fungus	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,021	0,000	0,000	0,000									
Solyc01g014147	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)	F:GO:0005515	F:protein binding	PR00019 (PRINTS): IPR001611 (PFA	0,042	0,341	0,025	0,288	0,306									
Solyc01g014150	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)	C:GO:0016020: P:G(	C:membrane; P:defense response to fungus	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,018	0,000	0,000	0,024									
Solyc01g014180	A20/AN1 zinc finger protein	F:GO:0003677: F:G(	F:DNA binding; F:zinc ion binding	IPR002653 (SMART): IPR000058 (SM	346,024	333,695	453,374	433,802	416,035									
Solyc01g014220	strawberry notch protein (DUF616) (AHRD V3.3 *-* AT1G28240.1)	P:GO:0006672: C:G(	P:ceramide metabolic process; C:integral component of membra	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,025	0,000	0,000									
Solyc01g014225	DUF616 family protein (AHRD V3.3 *-* G7IPT3_MEDTR)	P:GO:0006672: C:G(	P:ceramide metabolic process; C:integral component of membra	IPR006852 (PFAM): IPR008901 (PAN	0,021	0,021	0,000	0,000	0,024									
Solyc01g014230	U-box domain-containing protein 4 (AHRD V3.3 *** W9QMI4_9ROSA)	F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR000225 (SMART): IPR003613 (SM	18,101	27,305	17,515	14,781	18,065	0,619	0,037					up		
Solyc01g014245	Protein kinase superfamily protein (AHRD V3.3 --* AT5G01850.2)				4,578	3,335	13,755	13,477	13,351									
Solyc01g014250	LOW QUALITY:Sec23/Sec24 protein transport family protein (AHRD V3.3 --* AT3G23660.2)				2,438	2,252	8,254	7,362	6,158									
Solyc01g014260	LOW QUALITY:Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT1G74390.4)				0,000	0,000	0,025	0,000	0,000									
Solyc01g014270	LETM1-like protein (AHRD V3.3 --* AT3G11560.4)				10,075	9,909	7,263	7,843	9,229									
Solyc01g014310	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)	F:GO:0005515	F:protein binding	PR00019 (PRINTS): IPR001611 (PFA	0,000	0,043	0,000	0,000	0,000									
Solyc01g014320	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, putative (AHRD V3.3 *** A0A06	F:GO:0008168	F:methyltransferase activity	IPR005299 (PFAM): G3DSA:3.40.50.1	0,084	0,347	0,000	0,000	0,000									
Solyc01g014370	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *-* AT1G05500.2)	C:GO:0005783: C:G(	C:endoplasmic reticulum; C:membrane	IPR035892 (G3DSA:2.60.40.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc01g014375	DNA double-strand break repair rad50 ATPase (AHRD V3.3 *** A0A061GZ54_THECC)			PTHR31029:SF3 (PANTHER): PTHR3	2,044	1,653	1,508	1,235	1,482									
Solyc01g014390	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_CRYJA)				0,280	0,395	0,235	0,214	0,400									
Solyc01g014470	LOW QUALITY:RHO guanyl-nucleotide exchange factor 2 (AHRD V3.3 --* AT1G01700.4)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,315	0,139	0,284	0,281	0,401									
Solyc01g014480	ETHYLENE INSENSITIVE 3-like 3 protein (AHRD V3.3 *** W9RBN4_9ROSA) EIL5	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus	IPR006957 (PFAM EIL	24,276	27,388	29,011	28,055	27,618									
Solyc01g014490	DNA topoisomerase 6 subunit B (AHRD V3.3 *** K4AU86_SOLLC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:3.6.1.3; EC:5.99. Adenosinetriphospha	G3DSA:1.10.8.50 (GENE3D): IPR015:	13,291	12,705	13,729	15,082	14,661									
Solyc01g014495	DNA topoisomerase 6 subunit B (AHRD V3.3 *-* K4AU86_SOLLC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:3.6.1.3; EC:5.99. Adenosinetriphospha	IPR003594 (PFAM): mobidb-lite (MOB	11,006	9,468	10,483	10,601	10,505									
Solyc01g014520	Serine/threonine-protein kinase (AHRD V3.3 *** M1DYE5_SOLTU)	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	0,040	0,000	0,000	0,025	0,046									
Solyc01g014530	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 *-* K7N5H4_SOYBN)	F:GO:0000166: F:G(	F:nucleotide binding; F:protein kinase activity; C:membrane; P:r	IPR036426 (G3DSA:2.90.10.GENE3D	9,765	7,051	17,898	16,053	14,667									
Solyc01g014534	Physalis organ size 1 (AHRD V3.3 *** A0A097F7F7_9SOLA)	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; C:nu	mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,024									
Solyc01g014537	Ethylene-responsive transcription factor, putative (AHRD V3.3 *-* B9RGV0_RICCO)	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (SMART): IPR036955 (G3	0,000	0,019	0,000	0,000	0,000									
Solyc01g014550	Serine/threonine-protein kinase (AHRD V3.3 *** M1DYE5_SOLTU)	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	0,061	0,000	1,654	1,160	1,320									
Solyc01g014560	Serine/threonine-protein kinase (AHRD V3.3 *** K4ASL8_SOLLC)	F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation; F:carbohydrate binding; P:	IPR001480 (SMART): IPR001480 (PF.	1,219	1,331	21,097	22,406	17,885									
Solyc01g014620	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G41670.1)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,062	0,050	0,022	0,023									
Solyc01g014680	Serine/threonine-protein kinase (AHRD V3.3 *-* M1DYE5_SOLTU)	F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phosphorus-containing groups		0,021	0,021	0,165	0,271	0,257									
Solyc01g014690	Serine/threonine-protein kinase (AHRD V3.3 *-* M1CXJ4_SOLTU)	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:1.10.510	0,059	0,019	0,337	0,285	0,260									
Solyc01g014700	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 *-* K4ASL8_SOLLC)	F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation; F:carbohydrate binding; P:	IPR036426 (G3DSA:2.90.10.GENE3D	0,082	0,160	0,933	1,207	0,891									
Solyc01g014705	Physalis organ size 1 (AHRD V3.3 *-* A0A097F7A0_9SOLA)	F:GO:0003700	F:DNA-binding transcription factor activity	IPR017392 (PIRSF): mobidb-lite (MOE	0,000	0,039	0,000	0,000	0,000									
Solyc01g014710	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)			IPR012876 (PFAM): IPR012876 (PAN	0,139	0,272	0,097	0,147	0,094									
Solyc01g014720	Solanum lycopersicum Cytokinin Response Factor 7 CRF9	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,038	0,039	0,000	0,000	0,000									
Solyc01g014740	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT5G38100.1)				0,038	0,021	0,000	0,000	0,024									
Solyc01g014830	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)			PTHR35022 (PANTHER)	0,000	0,021	0,000	0,000	0,000									
Solyc01g014840	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.2)	F:GO:0005515: P:G(	F:protein binding; P:signal transduction; F:ADP binding	PR00364 (PRINTS): IPR000157 (SMA	33,199	61,338	9,405	19,065	19,827			1,072	0,006	1,017	0,000		up	up
Solyc01g014850	Zinc finger transcription factor 7 C3H7	F:GO:0003723: F:G(	F:RNA binding; F:metal ion binding	IPR004087 (SMAF C3H	24,084	31,851	28,945	28,404	28,669									
Solyc01g014860	Unknown protein (AHRD V3.3)				3,651	4,597	3,647	4,023	3,963									
Solyc01g014910	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT1G49770.1)	F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	0,019	0,058	0,022	0,000	0,000									
Solyc01g014930	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1	F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,077	1,022	0,320	0,710	1,035									
Solyc01g014940	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2	C:GO:0016020: P:G(	C:membrane; P:defense response to fungus	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,343	0,099	0,142	0,351									
Solyc01g014960	LOW QUALITY:Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0H3YC60_SALMI)	F:GO:0046983	F:protein dimerization activity	PTHR11514:SF96 bHLH	0,019	0,021	0,000	0,000	0,000									
Solyc01g014980	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT4G26600.8)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,000	0,000									
Solyc01g014990	ferrochelatase 2 (AHRD V3.3 --* AT2G30390.2) FC2			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,039	0,000	0,000	0,000									
Solyc01g015000	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *-* A0A0D2UFH3_GOSRA)	F:GO:0003824: P:G(	F:catalytic activity; P:regulation of nitrogen utilization; F:enzyme	IPR002187 (PRINTS): IPR002187 (SM	0,195	0,269	0,099	0,051	0,144									
Solyc01g015010	LOW QUALITY:Pseudouridine synthase family protein (AHRD V3.3 --* AT1G09800.2)				0,000	0,018	0,000	0,000	0,000									
Solyc01g015020	PRLI-interacting factor (AHRD V3.3 *** AT5G19900.5)			mobidb-lite (MOBIDB_LITE): mobidb-lit	93,577	92,999	112,044	101,076	96,902									
Solyc01g015040	LOW QUALITY:BTB/POZ domain-containing protein (AHRD V3.3 --* AT2G30600.5)				0,125	0,000	0,000	0,000	0,000									
Solyc01g015050	LOW QUALITY:XH/XS domain-containing protein (AHRD V3.3 --* AT5G59390.5)	P:GO:0031047	P:gene silencing by RNA	mobidb-lite (MOBIDB_LITE)	0,332	0,000	0,000	0,000	0,000									
Solyc01g015060	LOW QUALITY:XH/XS domain-containing protein (AHRD V3.3 *-* AT5G59390.5)	P:GO:0031047	P:gene silencing by RNA	IPR038588 (G3DSA:3.30.70.GENE3D	0,146	0,000	0,000	0,000	0,000									
Solyc01g015070	Lipoxygenase 3, chloroplastic (AHRD V3.3 --* LOX3_ARATH)				0,564	0,082	0,000	0,000	0,000									
Solyc01g015210	LOW QUALITY:B3 domain-containing protein family (AHRD V3.3 *-* A0A151RF19_CAJCA)	F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	0,000	0,019	0,000	0,000	0,000									
Solyc01g015250	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G41750.2)			mobidb-lite (MOBIDB_LITE): mobidb-lit	5,102	5,433	7,076	7,949	6,909									
Solyc01g015285	Phytoene synthase 1, chloroplastic (AHRD V3.3 --* PSY1_SOLLC)				3,922	4,862	4,159	1,602	4,477					-1,361	0,004			down
Solyc01g016360	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT3G24240.1)	P:GO:0050832	P:defense response to fungus	IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc01g016370	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)	F:GO:0005515	F:protein binding	PR00019 (PRINTS): IPR013210 (PFA	0,042	0,000	0,000	0,000	0,024									
Solyc01g016400	LOW QUALITY:aluminum activated malate transporter family protein (AHRD V3.3 --* AT1G18420.2)				0,138	0,059	0,593	0,740	0,704									
Solyc01g016410	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G08139.1)	F:GO:0008270	F:zinc ion binding	IPR011016 (SMART): IPR001841 (SM	12,079	8,466	20,040	19,955	16,020									
Solyc01g016413	LOW QUALITY:TCP family transcription factor (AHRD V3.3 *-* F1T102_9ERIC)			IPR017887 (PFAM): mobidb-lite (MOB	0,101	0,059	0,025	0,000	0,047									
Solyc01g016470	60S acidic ribosomal protein P1 (AHRD V3.3 *** B9IDH5_POPTR)	F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translationa	PF00428 (PFAM): IPR038716 (G3DS/	20,038	21,752	18,256	16,387	15,173									
Solyc01g016550	photosystem II reaction center protein H (AHRD V3.3 --* ATCG00710.1)				0,019	0,021	0,000	0,022	0,070									
Solyc01g016620	LOW QUALITY:oxidoreductase/transition metal ion-binding protein (AHRD V3.3 --* AT5G52410.2)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc01g016630	LOW QUALITY:WAS/WASL-interacting family protein (AHRD V3.3 --* AT1G55160.1)			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,000	0,000	0,000									
Solyc01g016700	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT2G27120.2)				0,000	0,000	0,025	0,000	0,000									
Solyc01g016720	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G36150.1)				0,517	0,378	0,377	0,221	0,235									
Solyc01g016730	LOW QUALITY:Cytochrome P450 82A3 (AHRD V3.3 --* C82A3_SOYBN)				0,000	0,021	0,000	0,000	0,000									
Solyc01g016770	Transcription factor Myb (AHRD V3.3 *-* Q71KV1_CAPAN)	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	0,021	0,000	0,022	0,000	0,000									
Solyc01g016780	LOW QUALITY:Transcription factor Myb (AHRD V3.3 --* Q71KV1_CAPAN)	C:GO:0005634: P:G(	C:nucleus; P:cell differentiation; F:sequence-specific DNA binding	F:transcription regulatory region DN/	0,038	0,019	0,000	0,000	0,000									
Solyc01g016800	LOW QUALITY:Chaperone DnaJ-domain superfamily protein, putative isoform 1 (AHRD V3.3 *-* A0A061EB22_THECC)			PTHR36335 (PANTHER)	0,000	0,000	0,000	0,073	0,000									
Solyc01g016805	plant/protein (AHRD V3.3 --* AT2G41150.2)				2,093	0,359	1,674	0,389	0,164									
Solyc01g016850	LOW QUALITY:embryo defective 1303 (AHRD V3.3 --* AT1G56200.2)			mobidb-lite (MOBIDB_LITE)	0,063	0,000	0,000	0,000	0,000									
Solyc01g016970	LOW QUALITY:Autophagy protein 5 (AHRD V3.3 --* ATG5_ORYSJ)			mobidb-lite (MOBIDB_LITE)	0,617	0,623	2,153	2,742	1,876									
Solyc01g017050	LOW QUALITY:ATP synthase subunit alpha, chloroplastic (AHRD V3.3 --* ATPA_IPOPU)	F:GO:0003676	F:nucleic acid binding	PTHR38146 (PANTHER)	1,020	1,698	0,795	1,655	1,276									
Solyc01g017080	Ycf15 protein (AHRD V3.3 *-* A0A0C5C0V6_9SOLA)	F:GO:0005524: C:G(	F:ATP binding; C:chloroplast	IPR019645 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,000	0,023									
Solyc01g017083	50S ribosomal protein L20, chloroplastic (AHRD V3.3 *** RK20_PANGI)	F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR005813 (PRINTS): IPR005813 (PF	0,000	0,000	0,000	0,050	0,023									
Solyc01g017087	30S ribosomal protein S18, chloroplastic (AHRD V3.3 *** RR18_TOBAC)	F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001648 (PRINTS): IPR001648 (PF	0,019	0,165	0,025	0,025	0,023									
Solyc01g017090	NADH dehydrogenase subunit (AHRD V3.3 *-* Q8HSD4_9SOLN)	F:GO:0008137: P:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	PR01434 (PRINTS): IPR018393 (PRIN	0,000	0,062	0,025	0,025	0,000									
Solyc01g017100	NADH dehydrogenase subunit (AHRD V3.3 *-* B7SRI7_9SOLA)	C:GO:0009536: C:G(	C:plastid; C:membrane	PR01434 (PRINTS): IPR001750 (PFA	0,000	0,000	0,000	0,025	0,000									
Solyc01g017140	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)	F:GO:0005524: C:G(	F:ATP binding; C:chloroplast	IPR003959 (PFAM): G3DSA:3.40.50.3	0,000	0,000	0,075	0,025	0,046									
Solyc01g017170	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* A0A161V440_9MAGN)	C:GO:0005886: F:G(	C:plasma membrane EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001750 (PFAM): PTHR22773 (PAI	0,097	0,078	0,049	0,050	0,023									
Solyc01g017183	30S ribosomal protein S7, chloroplastic (AHRD V3.3 *** RR7_TOBAC)	P:GO:0006412	P:translation	IPR000235 (PIRSF): IPR036823 (G3D	0,082	0,248	0,100	0,147	0,094									
Solyc01g017187	Ribosomal protein S12 (AHRD V3.3 *** A0A0C5G6K8_IPOBA)	C:GO:0043229: C:G(	C:intracellular organelle; C:cytoplasmic part	G3DSA:2.40.50.140 (GENE3D): IPR0	0,000	0,000	0,000	0,000	0,023									
Solyc01g017200	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 *-* ACCD_SOL	F:GO:0003824: P:G(	F:catalytic activity; P:lipid metabolic process; C:plastid; F:ion bi	G3DSA:3.90.226.10 (GENE3D): PTHF	0,000	0,235	0,151	0,201	0,212									
Solyc01g017210	NAD(P)H-quinone oxidoreductase subunit 3, chloroplastic (AHRD V3.3 *** NU3C_LEMMI)	F:GO:0008137: P:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR000440 (PFAM): IPR038430 (G3D	0,000	0,041	0,000	0,000	0,000									
Solyc01g017220	ATP synthase epsilon chain, chloroplastic (AHRD V3.3 *** ATPE_SOLLC)	P:GO:0015986: C:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR020546 (PFAM): IPR001469 (TIGF	0,864	3,011	0,412	0,825	0,893	1,810	0,000					up		
Solyc01g017260	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_COECR)	C:GO:0005739: C:G(	C:mitochondrion; C: EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001750 (PFAM): PTHR22773 (PAI	0,000	0,000	0,000	0,000	0,024									
Solyc01g017300	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_POPAL)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR014724 (G3DSA:2.40.50.GENE3D	0,000	0,000	0,000	0,025	0,070									
Solyc01g017320	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_JASNU)	C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis; C:integral component of me	IPR001280 (PFAM): IPR036408 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc01g017330	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_NICTO)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR036408 (G3DSA:1.20.1130.GENE	0,038	0,061	0,174	0,101	0,119									
Solyc01g017333	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLTU)	F:GO:0008137: P:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR022997 (PTHR43507:PANTHER):	0,021	0,043	0,000	0,000	0,023									
Solyc01g017337	Cytochrome c biogenesis protein CcsA (AHRD V3.3 *-* CCSA_SOLBU)	P:GO:0017004: F:G(	P:cytochrome complex assembly; F:heme binding	IPR002541 (PFAM): PTHR30071:SF8	0,000	0,021	0,000	0,000	0,000									
Solyc01g017360	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_TOBAC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR007641 (PFAM): IPR037033 (G3D	0,000	0,021	0,000	0,022	0,000									
Solyc01g017370	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0C5CUM7_SOLLC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR007080 (PFAM): SSF64484 (SUPI	0,038	0,043	0,050	0,075	0,070									
Solyc01g017380	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0K1ZCY1_9LAMI)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	G3DSA:2.40.40.20 (GENE3D): IPR00	0,019	0,039	0,050	0,025	0,047									
Solyc01g017400	30S ribosomal protein S7, chloroplastic (AHRD V3.3 *** RR7_PHAAO)	P:GO:0006412	P:translation	IPR023798 (PFAM): IPR036823 (G3D	0,117	0,327	0,289	0,245	0,470									
Solyc01g017420	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLLC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001268 (PFAM): IPR007081 (PFA	0,040	0,000	0,000	0,000	0,023									
Solyc01g017440	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 *** RPOA_SOLLC)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR036603 (G3DSA:3.30.1360.GENE	0,057	0,288	0,025	0,175	0,140									
Solyc01g017450	30S ribosomal protein S11, chloroplastic (AHRD V3.3 *** RR11_NICTO)	F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001971 (PFAM): IPR036967 (G3D	0,019	0,000	0,100	0,050	0,000									
Solyc01g017460	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0S0ZL28_9ASTE)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR007080 (PFAM): G3DSA:2.40.40.2	0,019	0,000	0,025	0,050	0,000									
Solyc01g017470	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0V0INT8_SOLCH)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR006592 (SMART): G3DSA:2.40.40	0,000	0,000	0,025	0,000	0,000									
Solyc01g017485	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* M7YBH1_TRIUA)	F:GO:0005524	F:ATP binding		0,059	0,083	0,000	0,072	0,119									
Solyc01g017490	calcium-dependent lipid-binding family protein (AHRD V3.3 --* AT1G48090.6)			mobidb-lite (MOBIDB_LITE)	0,040	0,060	0,072	0,000	0,119									
Solyc01g017500	Flowering time control FCA-like protein (AHRD V3.3 --* A0A072UF76_MEDTR)				0,019	0,062	0,150	0,216	0,118									
Solyc01g017510	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SPIOL)	F:GO:0016740: C:G(	F:transferase activity; C:intracellular membrane-bounded organ	PTHR34995 (PANTHER)	0,000	0,000	0,022	0,000	0,000									
Solyc01g017530	30S ribosomal protein S2, chloroplastic (AHRD V3.3 *** RR2_SOLLC)	F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:small ribos	IPR001865 (PRINTS): G3DSA:3.40.5(	0,099	0,364	0,074	0,271	0,189									
Solyc01g017560	response regulator 11 (AHRD V3.3 --* AT1G67710.1)				0,000	0,021	0,000	0,000	0,024									
Solyc01g017567	Exosome complex exonuclease RRP44 (AHRD V3.3 *-* A0A068EX93_COCNU)	F:GO:0000175: C:G(	F:3'-5'-exoribonucle EC:3.1.13; EC:3.1.1! Acting on ester bond:	IPR033771 (PFAM): G3DSA:2.40.50.6	0,098	0,021	0,122	0,000	0,071									
Solyc01g017600	Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)	C:GO:0016021	C:integral component of membrane	IPR006904 (PFAM): PTHR16007:SF2	0,426	0,228	0,235	0,829	0,399									
Solyc01g017710	LOW QUALITY:ferredoxin-fold anticodon-binding domain protein (AHRD V3.3 --* AT1G55790.1)				0,076	0,320	0,075	0,075	0,094									
Solyc01g017720	Maturase K (AHRD V3.3 --* H9NKB3_9ASTR)				0,021	0,041	0,050	0,000	0,047									
Solyc01g017730	LOW QUALITY:ARM repeat superfamily protein (AHRD V3.3 --* AT5G37290.3)				0,021	0,075	0,000	0,022	0,023									
Solyc01g017740	LOW QUALITY:Cytochrome b6 (AHRD V3.3 *-* CYB6_HORVU)	F:GO:0005506: C:G(	F:iron ion binding; C:integral component of membrane; F:heme b	IPR027387 (G3DSA:1.20.810.GENE3I	0,000	0,235	0,096	0,223	0,234									
Solyc01g017760	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072TVC2_MEDTR)			IPR025558 (PFAM): PTHR31286:SF1	0,021	0,000	0,000	0,000	0,000									
Solyc01g017775	AT-rich interactive domain protein (AHRD V3.3 --* G7K2M1_MEDTR)				0,019	0,000	0,000	0,000	0,000									
Solyc01g017860	Delta-1-pyrroline-5-carboxylate synthase (AHRD V3.3 --* P5CS_VIGAC)			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,854	7,984	10,528	12,226	10,166									
Solyc01g017870	low-molecular-weight cysteine-rich 13 (AHRD V3.3 -** AT4G09795.1)				0,061	0,043	0,000	0,047	0,047									
Solyc01g018010	Mitogen-activated protein kinase 5 (AHRD V3.3 --* MPK5_ARATH)				2,460	2,323	2,443	2,955	2,812									
Solyc01g018020	Transketolase, putative (AHRD V3.3 *** B9T0B2_RICCO)	F:GO:0004802	F:transketolase act EC:2.2.1.1 Transketolase	IPR005475 (SMART): IPR005474 (PF.	0,460	1,413	0,633	2,043	0,662					1,680	0,010			up
Solyc01g018060	30S ribosomal protein S7, chloroplastic (AHRD V3.3 *-* RR7_TOBAC)	P:GO:0000028: F:G(	P:ribosomal small subunit assembly; F:mRNA binding; F:structur	IPR036823 (G3DSA:1.10.455.GENE3I	0,019	0,043	0,050	0,100	0,094									
Solyc01g018090	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_ENCLE)	C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis; C:integral component of me	IPR001280 (PRINTS): IPR036408 (G3	0,000	0,000	0,047	0,075	0,023									
Solyc01g020115	NADP-dependent alkenal double bond reductase P1 (AHRD V3.3 *-* A0A0B2RWA9_GLYSO)	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	G3DSA:3.40.50.720 (GENE3D): PTHF	0,000	0,000	0,000	0,025	0,000									
Solyc01g020120	DNA helicase (AHRD V3.3 *-* M1B2A8_SOLTU)	F:GO:0003677: F:G(	F:DNA binding; F:DI EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.30.1640.10 (GENE3D): IPR(	0,019	0,000	0,025	0,000	0,000									
Solyc01g020125	Glycosyltransferase (AHRD V3.3 *-* Q50HV0_SOLLC)	F:GO:0015018: C:G(	F:galactosylgalacto EC:2.4.1.17; EC:2.4. Glucuronosyltransfer	IPR005027 (PFAM): IPR005027 (PAN	0,257	0,114	0,065	0,123	0,141									
Solyc01g020130	Glycosyltransferase (AHRD V3.3 *-* Q50HV0_SOLLC)	F:GO:0015018: C:G(	F:galactosylgalacto EC:2.4.1.17; EC:2.4. Glucuronosyltransfer	IPR029044 (G3DSA:3.90.550.GENE3I	0,333	0,252	0,265	0,224	0,260									
Solyc01g020150	Glycosyltransferase (AHRD V3.3 *-* Q50HV0_SOLLC)	F:GO:0015018: C:G(	F:galactosylgalacto EC:2.4.1.17; EC:2.4. Glucuronosyltransfer	PTHR10896:SF17 (PANTHER): IPR00	0,082	0,082	0,072	0,025	0,071									
Solyc01g020190	LOW QUALITY:RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *-* AT4G32670.2)	F:GO:0008270	F:zinc ion binding	IPR011016 (SMART): IPR013083 (G3	0,419	0,311	0,515	0,242	0,259									
Solyc01g020200	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0C5C9W8_SOLLC)	C:GO:0016021	C:integral component of membrane	IPR008896 (PANTHER)	0,000	0,021	0,000	0,050	0,000									
Solyc01g020220	Replication factor C subunit 3 (AHRD V3.3 *** RFC3_ARATH),Pfam:PF13177	F:GO:0003689: C:G(	F:DNA clamp loade EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): PF13	0,282	0,318	0,237	0,245	0,166									
Solyc01g020230	Replication factor C subunit 3 (AHRD V3.3 *** RFC3_ARATH)	F:GO:0003677: P:G(	F:DNA binding; P:DNA replication	IPR003593 (SMART): PF13177 (PFAM	0,296	0,201	0,342	0,188	0,259									

Solyc01g020240	THUMP domain-containing protein 1 (AHRD V3.3 *** A0A1D1ZBW7_9ARAE)		F:GO:0003723; P:GC	F:RNA binding; P:tRNA modification			IPR004114 (PFAM); IPR040183 (PAN	14,348	14,118	21,198	22,221	23,564									
Solyc01g020285	SU(VAR)3-9 homolog 5 (AHRD V3.3 --* AT2G35160.5)		C:GO:0005739; C:GC	C:mitochondrion; C:chloroplast			PD169947 (PRODOM)	0,080	0,273	0,424	0,988	0,569									
Solyc01g020290	LOW QUALITY:60S ribosomal protein L7A-like (AHRD V3.3 *-* Q2VCI3_SOLTU)		P:GO:0000470; F:GC	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large ribo			IPR038524 (G3DSA:3.30.1330 GENE	0,222	0,099	0,097	0,076	0,069									
Solyc01g020320	calmodulin-binding receptor-like cytoplasmic kinase 1 (AHRD V3.3 --* AT5G58940.4)						mobidb-lite (MOBIDB_LITE); PTHR372	6,113	5,489	6,407	6,655	6,027									
Solyc01g020340	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XHN5_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (TIGF	1,601	1,369	1,265	1,428	1,442									
Solyc01g020371	LOW QUALITY:GRF zinc finger family protein (AHRD V3.3 --* Q2QWQ9_ORYSJ)		F:GO:0008270	F:zinc ion binding			IPR010666 (PFAM); PTHR33248 (PAN	0,021	0,000	0,000	0,000	0,000									
Solyc01g020378	LOW QUALITY:Calcium-binding EF-hand family protein, putative (AHRD V3.3 *** A0A061FAV4_THECC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); IPR002048 (PF	0,181	0,359	0,075	0,000	0,024									
Solyc01g020440	Replication factor C subunit 3 (AHRD V3.3 *** RFC3_ARATH)		F:GO:0003677; P:GC	F:DNA binding; P:DNA replication			IPR003593 (SMART); G3DSA:1.10.8.6	16,984	18,681	8,069	4,999	6,901									
Solyc01g020500	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G53600.2)							1,087	0,823	1,116	0,745	0,732									
Solyc01g020520	Protease m50 membrane-bound transcription factor site 2 protease, putative (AHRD V3.3 *-* A0A061F386		F:GO:0008233; C:GC	F:peptidase activity; C:membrane				0,000	0,000	0,000	0,022	0,000									
Solyc01g020525	Protease m50 membrane-bound transcription factor site 2 protease, putative (AHRD V3.3 *** A0A061F386		F:GO:0004222; F:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR008915 (PFAM); G3DSA:2.30.42.1	2,258	2,130	1,601	1,574	1,416									
Solyc01g020570	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0000166	F:nucleotide binding			G3DSA:1.20.1110.10 (GENE3D); PTH	0,061	0,118	0,074	0,025	0,095									
Solyc01g021600	Dirigent protein (AHRD V3.3 *** K4AV41_SOLLC)		C:GO:0016021; C:GC	C:integral component of membrane; C:apoplast			IPR004265 (PFAM); PTHR21495 (PAN	0,079	0,257	0,044	0,000	0,023									
Solyc01g021640	Katanin p80 subunit B1 (AHRD V3.3 *** A0A103XBA3_CYNCS)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10 GENE3	12,099	12,030	16,198	17,546	16,415									
Solyc01g021670	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *-* AT5G19860.1)		C:GO:0005773	C:vacuole			IPR007493 (PFAM); IPR036758 (G3D	58,054	43,272	54,315	52,782	45,921									
Solyc01g021675	Integrase-type DNA-binding superfamily protein (AHRD V3.3 --* AT4G13040.7)							32,110	25,165	32,336	24,534	26,995					-0,394	0,029			down
Solyc01g021690	LOW QUALITY:Alpha/beta hydrolase domain containing protein 1,3, putative (AHRD V3.3 --* B9T6L2_RICCI		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc01g021720	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT5G54050.1)						mobidb-lite (MOBIDB_LITE)	0,217	0,057	0,122	0,171	0,117									
Solyc01g021730	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 *-* B9T476_R_NAC003		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS_NAC	2,520	0,180	3,861	12,834	2,941					1,734	0,000			up
Solyc01g021740	LOW QUALITY:Mitochondrial carrier family (AHRD V3.3 *-* A0A0K9NTE2_ZOSMR)		F:GO:0022857	F:transmembrane transporter activity			IPR018108 (PFAM); IPR023395 (G3D	0,218	0,218	0,349	0,167	0,237									
Solyc01g022740	F-box/kelch-repeat protein (AHRD V3.3 *** W9S3L7_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR006652 (SM	6,615	6,604	7,700	7,156	7,363									
Solyc01g022750	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 (AHRD V3.3 *** A0A1D1XVP9_9ARAE)		C:GO:0005747; P:GC	C:mitochondrial respiratory chain complex I; P:response to oxid			IPR016488 (PANTHER)	31,707	33,954	76,820	69,329	73,719									
Solyc01g022780	LOW QUALITY:Nascent polypeptide-associated complex subunit beta (AHRD V3.3 *-* B8BHJ4_ORYSI)		F:GO:0003677; F:GC	F:DNA binding; F:zinc ion binding; C:membrane; C:integral comp			PTHR33715 (PANTHER)	0,063	0,106	0,075	0,176	0,094									
Solyc01g028800	RNA binding protein, putative (AHRD V3.3 *** B9SBN7_RICCO)		F:GO:0003723	F:RNA binding			IPR001313 (SMART); IPR001313 (PF	2,190	2,067	1,884	2,308	2,168									
Solyc01g028805	Cytochrome P450 (AHRD V3.3 *** A0A061GI36_THECC)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,867	2,345	5,310	8,072	6,395	1,445	0,003			0,610	0,047	up		up
Solyc01g028810	Chaperonin-60 beta subunit (AHRD V3.3 *** P93570_SOLTU)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS); IPR001844 (TIG	798,357	926,562	1434,871	1282,066	1434,521									
Solyc01g028830	Protein kinase (AHRD V3.3 *** C6ZRP4_SOYBN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF); G3DSA:1.10.5	34,756	33,210	17,403	17,533	18,052									
Solyc01g028860	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *** AT3G13460.1)		F:GO:0003723	F:RNA binding			G3DSA:3.10.590.10 (GENE3D); IPR0	620,864	646,341	475,552	489,255	509,643									
Solyc01g028870	N utilization substance B (AHRD V3.3 *** A0A0B0MRW6_GOSAR)		F:GO:0003723; P:GC	F:RNA binding; P:DNA-templated transcription, termination; P:re			IPR006027 (PFAM); IPR035926 (G3D	13,735	15,647	22,536	23,561	21,538									
Solyc01g028900	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** A0A0K9PF29_DXS3		F:GO:0003824	F:catalytic activity			IPR005475 (SMART); IPR009014 (G3	95,232	108,732	147,397	131,767	132,577									
Solyc01g028930	TATA-box-binding protein (AHRD V3.3 *** TBP_SOLTU)		F:GO:0003677; P:GC	F:DNA binding; P:DNA-templated transcription, initiation			IPR000814 (PRINTS); IPR000814 (PF	19,061	19,577	23,610	23,130	21,278									
Solyc01g028935	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072TVC2_MEDTR)						IPR025558 (PFAM); PTHR34427 (PAN	0,021	0,018	0,025	0,025	0,048									
Solyc01g028987	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RDP2_RICCO)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D); IPR0	0,037	0,000	0,000	0,000	0,000									
Solyc01g034010	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)						IPR019557 (PFAM); mobidb-lite (MOB	0,094	0,201	0,000	0,075	0,000									
Solyc01g034020	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0IAM6_SOLCH)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS); IPR006186 (SM	58,192	63,088	77,385	80,852	76,399									
Solyc01g034023	Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 --* AT3G23080.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc01g034063	replication factor-A carboxy-terminal domain protein (AHRD V3.3 *-* AT2G28105.2)						mobidb-lite (MOBIDB_LITE); PTHR232	0,000	0,000	0,000	0,022	0,000									
Solyc01g034080	Amino acid permease family protein (AHRD V3.3 *** AT3G13620.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmem			IPR002293 (PFAM); G3DSA:1.20.174	0,139	0,200	0,100	0,195	0,118									
Solyc01g034150	DNA polymerase eta (AHRD V3.3 *** A0A0B2R9V1_GLYSO)		F:GO:0003684; P:GC	F:damaged DNA binding; P:DNA repair			IPR036775 (G3DSA:3.30.1490.GENE	9,281	7,580	8,653	7,825	8,774									
Solyc01g034155	DNA polymerase eta (AHRD V3.3 *** POLH_ARATH)		P:GO:0006281	P:DNA repair			G3DSA:3.30.70.270 (GENE3D); G3DS	3,954	3,664	3,531	3,713	4,313									
Solyc01g035220	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_SILLA)		C:GO:0005739; C:GC	C:mitochondrion; C:	EC:1.6.99.5; EC:1.6.	Acting on NADH or NADPH: NADH dehydrogenase: NADH:ub		0,000	0,019	0,000	0,000	0,000									
Solyc01g044240	Soluble inorganic pyrophosphatase 1 (AHRD V3.3 --* IPYR1_ARATH)							30,366	33,327	17,677	20,587	23,523									
Solyc01g044270	DnaJ domain-containing protein (AHRD V3.3 *** A0A103YAX8_CYNCS)						IPR001623 (SMART); IPR001623 (PF	34,009	37,078	34,254	32,866	35,188									
Solyc01g044307	RING/U-box superfamily protein (AHRD V3.3 *** AT1G05890.1)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR001876 (SMART); IPR002867 (SM	6,266	6,112	7,942	7,529	7,905									
Solyc01g044350	Zinc finger family protein (AHRD V3.3 *-* B9HHY6_POPTR)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR001876 (SMART); IPR001876 (PF	0,482	0,429	0,537	0,806	0,707									
Solyc01g044360	Importin 5 (AHRD V3.3 *** A0A0U3C0Z7_HEVBR)		F:GO:0005515; P:GC	F:protein binding; P:protein import into nucleus			IPR034085 (SMART); PF18808 (PFAM	251,205	243,089	236,687	224,399	233,676									
Solyc01g044370	Molybdenum cofactor sulfurase family protein (AHRD V3.3 *-* AT1G30910.1)		F:GO:0003824; F:GC	F:catalytic activity; F:molybdenum ion binding; F:pyridoxal phosi			IPR005302 (PFAM); PTHR44907 (PAN	0,820	0,825	0,599	0,964	0,751									
Solyc01g044371	Molybdenum cofactor sulfurase family protein (AHRD V3.3 *-* AT1G30910.1)		F:GO:0003824; F:GC	F:catalytic activity; F:molybdenum ion binding; F:pyridoxal phosi			IPR005303 (PFAM); IPR005302 (PFA	1,250	1,683	1,097	1,261	1,418									
Solyc01g044372	Molybdenum cofactor sulfurase family protein (AHRD V3.3 --* AT5G44720.2)		F:GO:0003824; F:GC	F:catalytic activity; F:molybdenum ion binding; F:pyridoxal phosi			mobidb-lite (MOBIDB_LITE)	0,452	0,600	0,169	0,503	0,588									
Solyc01g044373	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2QRD1_ORYSJ)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); PTHR23272:SF9	0,040	0,000	0,096	0,096	0,234									
Solyc01g044420	calmodulin-binding family protein (AHRD V3.3 *** AT3G13600.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,158	0,079	0,091	0,098	0,024									
Solyc01g044480	Elongation factor P (AHRD V3.3 *-* B6TAH3_MAIZE)		F:GO:0003746; P:GC	F:translation elongation factor activity; P:translational elongatio			IPR001059 (SMART); IPR020599 (PIF	0,495	0,532	0,608	0,941	0,730									
Solyc01g044520	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)						IPR004883 (PFAM_LBD	0,059	0,019	0,050	0,045	0,024									
Solyc01g044540	LOW QUALITY:cleavage and polyadenylation specificity factor 100 (AHRD V3.3 --* AT5G23880.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,448	0,176	0,334	0,236	0,259									
Solyc01g044565	Cytochrome P450, putative (AHRD V3.3 *-* B9S4U5_RICCO)		F:GO:0005506; C:GC	F:iron ion binding; C:integral component of membrane; F:oxidore			PTHR24296:SF11 (PANTHER); PTHR2	0,309	0,287	0,022	0,025	0,047									
Solyc01g047590	Signal recognition particle subunit SRP72 (AHRD V3.3 *** K4D938_SOLLC)		P:GO:0006614; F:GC	P:SRP-dependent cotranslational protein targeting to membrane			IPR013699 (PFAM); mobidb-lite (MOB	0,084	0,128	0,075	0,025	0,095									
Solyc01g047593	Signal recognition particle subunit SRP72 (AHRD V3.3 *-* K4D938_SOLLC)		C:GO:0005786; P:GC	C:signal recognition particle, endoplasmic reticulum targeting; P:SRP-dependent cotranslational protein				0,040	0,043	0,000	0,074	0,000									
Solyc01g047597	Signal recognition particle subunit SRP72 (AHRD V3.3 *-* K4D938_SOLLC)		F:GO:0005515; P:GC	F:protein binding; P:SRP-dependent cotranslational protein targ			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc01g048590	LOW QUALITY:Photosystem II protein D1 (AHRD V3.3 *-* PSBA_CHLVU)		P:GO:0009772; F:GC	P:photosynthetic electron transport in photosystem II; F:electroi			IPR000484 (PFAM); IPR036854 (G3D	0,565	0,934	0,891	1,773	2,667			1,576	0,048				up	
Solyc01g049650	Pyruvate kinase (AHRD V3.3 *** K4AVE6_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS); IPR015806 (G3	164,806	139,581	56,142	41,987	51,170					-0,417	0,013			down
Solyc01g049680	Transcription factor Pur-alpha 1 (AHRD V3.3 *** A0A061GR22_THECC)						IPR006628 (SMART); IPR006628 (PF	37,947	42,859	66,350	63,470	61,684									
Solyc01g049685	Transcription factor Pur-alpha 1 (AHRD V3.3 *-* PUR_ARATH)		P:GO:0000122; F:GC	P:negative regulation of transcription by RNA polymerase II; F:F			IPR006628 (PFAM); G3DSA:3.10.450	0,019	0,021	0,000	0,000	0,000									
Solyc01g049690	Transcription factor Pur-alpha 1 (AHRD V3.3 *-* A0A151UB56_CAJCA)		P:GO:0000122; F:GC	P:negative regulation of transcription by RNA polymerase II; F:F			IPR006628 (SMART); G3DSA:3.10.45	3,195	3,833	5,166	5,787	5,547									
Solyc01g049770	LOW QUALITY:SPT2 chromatin protein (AHRD V3.3 --* AT4G37860.2)							3,507	3,932	2,521	3,275	3,813									
Solyc01g049810	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SBK7_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	0,507	0,470	0,876	0,862	1,060									
Solyc01g049820	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative isoform 1		F:GO:0003777; P:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	PTHR24115:SF391 (PANTHER); IPR0	0,021	0,018	0,000	0,000	0,000									
Solyc01g049825	DCD (Development and Cell Death) domain protein (AHRD V3.3 --* AT5G61910.5)							0,021	0,019	0,000	0,025	0,000									
Solyc01g049880	DegP protease 7 (AHRD V3.3 --* AT3G03380.2)							1,712	5,297	1,687	3,338	3,598	1,651	0,000			0,992	0,035	up		up
Solyc01g049890	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (AHRD V3.3 *** AT3G13410.1)		C:GO:0005783; C:GC	C:endoplasmic reticulum; C:integral component of membrane			PTHR35285 (PANTHER)	329,170	274,624	343,066	311,108	314,074									
Solyc01g049910	Protease m50 membrane-bound transcription factor site 2 protease, putative (AHRD V3.3 *** A0A061F386		F:GO:0004222; F:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	G3DSA:2.30.42.10 (GENE3D); IPR00	3,523	3,188	3,371	3,673	2,750									
Solyc01g049912	Protease m50 membrane-bound transcription factor site 2 protease, putative (AHRD V3.3 --* A0A061F386		F:GO:0004222; P:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bonds (peptidases)		0,215	0,241	0,241	0,294	0,212									
Solyc01g049914	Protease m50 membrane-bound transcription factor site 2 protease, putative (AHRD V3.3 *-* A0A061F386		F:GO:0004222; P:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR001193 (PANTHER)	0,019	0,000	0,000	0,022	0,000									
Solyc01g049920	Cytochrome c oxidase biogenesis protein Cmc1-like protein (AHRD V3.3 --* AT4G21192.2)						mobidb-lite (MOBIDB_LITE)	1,195	1,134	1,705	1,081	1,454									
Solyc01g049925	Cytochrome b (AHRD V3.3 --* CYB_VICFA)							0,141	0,271	0,244	0,562	0,517									
Solyc01g049960	Chromosome-associated kinesin KIF4 (AHRD V3.3 *** A0A0B0MX86_GOSAR)						PTHR34554:SF2 (PANTHER); PTHR3	32,945	38,696	39,942	37,870	43,201									
Solyc01g049975	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061FID3_THECC)		F:GO:0003677	F:DNA binding			IPR025525 (PFAM); PTHR23272 (PAN	2,508	2,136	1,750	2,219	1,932									
Solyc01g050010	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061FVD3_THECC)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR025525 (PFAM); IPR008906 (PFA	2,855	3,564	2,909	2,348	3,042									
Solyc01g050020	LOW QUALITY:Photosystem II CP47 reaction center protein (AHRD V3.3 *-* PSBB_LEMMI)		C:GO:0009522; P:GC	C:photosystem I; P:photosynthetic electron transport chain; C:ir			IPR000932 (PFAM); IPR000932 (PAN	0,019	0,060	0,000	0,170	0,000									
Solyc01g050040	RING/U-box superfamily protein (AHRD V3.3 *** AT1G55530.2)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR001841 (SMART); IPR039525 (PF	18,438	15,543	15,230	16,690	14,665									
Solyc01g050047	Unknown protein (AHRD V3.3)							0,323	0,244	0,147	0,248	0,143									
Solyc01g050050	LOW QUALITY:CTP synthase (AHRD V3.3 --* A0A0E0L5X3_ORYPU)							0,021	0,000	0,000	0,000	0,000									
Solyc01g050070	transmembrane protein (AHRD V3.3 *** AT1G55535.3)		C:GO:0016021	C:integral component of membrane			PTHR35471 (PANTHER)	5,992	5,855	5,626	5,758	5,958									
Solyc01g050075	protein-l-isoaspartate methyltransferase 2 (AHRD V3.3 --* AT5G50240.1)							0,737	0,413	0,409	0,491	0,728									
Solyc01g056200	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 --* AT1G80160.3)		C:GO:0016021	C:integral component of membrane			PTHR34562:SF1 (PANTHER); PTHR3	0,000	0,000	0,000	0,050	0,024									
Solyc01g056260	LOW QUALITY:protein kinase family protein (AHRD V3.3 --* AT5G21222.4)							0,040	0,081	0,000	0,000	0,000									
Solyc01g056270	LOW QUALITY:Unknown protein (AHRD V3.3)							0,042	0,169	0,000	0,000	0,000									
Solyc01g056310	anther-specific LAT51	lat51	F:GO:0005507; F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	0,019	0,021	0,000	0,000	0,000									
Solyc01g056320	transcription elongation factor B polypeptide (AHRD V3.3 --* AT2G42780.2)							0,779	0,591	0,626	1,307	0,682									
Solyc01g056340	Light-mediated development protein DET1 (AHRD V3.3 *** DET1_SOLLC)	DET1	F:GO:0003824	F:catalytic activity			IPR019138 (PFAM); IPR019138 (PAN	8,358	9,338	13,483	16,073	12,411									
Solyc01g056360	LOW QUALITY:Dehydrin family protein, expressed (AHRD V3.3 -** Q40711_ORYSJ)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,098	0,750	0,022	0,025	0,000									
Solyc01g056370	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --* AT1G61080.6)							0,427	0,055	0,000	0,000	0,000									
Solyc01g056455	50S ribosomal protein L20, chloroplastic (AHRD V3.3 *** A0A0A8LFP3_9FABA)		P:GO:0000027; F:GC	P:ribosomal large subunit assembly; F:RNA binding; F:structural constituent of ribosome; C:ribosome; P				0,000	0,043	0,000	0,075	0,047									
Solyc01g056470	Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_SOLBU)		C:GO:0009521; P:GC	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM); PTHR33180:SF4	0,019	0,064	0,000	0,025	0,047									
Solyc01g056480	LOW QUALITY:cytochrome P450, family 81, subfamily F, polypeptide 2 (AHRD V3.3 --* AT5G57220.1)							1,271	0,900	1,108	1,012	0,827									
Solyc01g056520	ARM repeat superfamily protein (AHRD V3.3 *** AT5G06120.6)		P:GO:0006886; F:GC	P:intracellular protein transport; F:Ran GTPase binding			IPR001494 (SMART); IPR011989 (G3	28,714	26,748	39,619	43,202	40,133									
Solyc01g056530	Oligopeptide transporter, putative (AHRD V3.3 *-* B9SUI4_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM); PTHR22601 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc01g056570	ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 ***		F:GO:0005515	F:protein binding			IPR000408 (PRINTS); IPR002110 (SM	56,001	50,609	74,936	69,696	71,368									
Solyc01g056580	L-aspartate oxidase (AHRD V3.3 *** K4DCY8_SOLLC)		F:GO:0008734; P:GC	F:L-aspartate oxida	EC:1.4.3.16; EC:1.4.	L-aspartate oxidase;	IPR027477 (G3DSA:3.90.700.GENE3	0,180	0,241	0,025	0,022	0,048									
Solyc01g056590	Transcription initiation factor TFIID subunit 8 (AHRD V3.3 *-* A0A0B0P5F6_GOSAR)		F:GO:0046982	F:protein heterodimerization activity			PTHR37604 (PANTHER)	0,058	0,000	0,000	0,045	0,000									
Solyc01g056620	Double-stranded RNA binding protein (AHRD V3.3 *-* A9TDF6_PHYPA)		F:GO:0003723	F:RNA binding			IPR014720 (SMART); IPR014720 (PF	5,168	4,332	5,011	4,471	4,615									
Solyc01g056625	Double-stranded RNA-binding (AHRD V3.3 *-* A0A103Y040_CYNCS)		F:GO:0003723	F:RNA binding			IPR014720 (SMART); G3DSA:3.30.16	10,794	9,977	10,398	11,336	10,852									
Solyc01g056640	LOW QUALITY:Peroxidase (AHRD V3.3 --* M7ZGL7_TRIUA)							0,019	0,000	0,000	0,000	0,000									
Solyc01g056655	Somatic embryogenesis receptor-like kinase-like protein (AHRD V3.3 --* C6FF61_SOYBN)							2,401	0,000	0,000	0,407	0,000									
Solyc01g056670	NADH dehydrogenase subunit 4L (AHRD V3.3 *** ATMG00650.1)		F:GO:0016651; P:GC	F:oxidoreductase activity, acting on NAD(P)H; P:ATP synthesis			PTHR11434:SF5 (PANTHER); IPR001	0,040	0,043	0,000	0,125	0,024									
Solyc01g056690	Protein kinase, putative (AHRD V3.3 *** B9SJN7_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001932 (SMART); IPR000719 (SM	25,055	23,407	22,897	20,897	23,260									
Solyc01g056720	small basic intrinsic protein 2.1	SIP2.1	F:GO:0015267; C:GC	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR023271 (G3	14,613	19,761	16,189	19,317	18,214									
Solyc01g056725	NADH dehydrogenase subunit 5 (AHRD V3.3 *-* A0A1C9IAH4_9LAMI)		C:GO:0005743; F:GC	C:mitochondrial inne	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	mobidb-lite (MOBIDB_LITE); mobidb-lit	1,540	1,702	1,899	1,436	1,628									
Solyc01g056730	zinc knuckle (CCHC-type) family protein (AHRD V3.3 *-* AT3G43590.1)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART); G3DSA:4.10.60	3,071	3,193	1,861	1,887	1,879									
Solyc01g056750	zinc knuckle (CCHC-type) family protein (AHRD V3.3 *-* AT3G43590.1)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	PTHR23002:SF97 (PANTHER); PTHR	0,299	0,292	0,218	0,245	0,401									
Solyc01g056760	Zinc knuckle family protein (AHRD V3.3 *-* U5GMH6_POPTR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART); G3DSA:4.10.60	0,082	0,039	0,000	0,022	0,000									
Solyc01g056770	Nucleotide/sugar transporter family protein (AHRD V3.3 --* AT5G55950.2)		F:GO:0005488	F:binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,822	0,790	0,240	0,385	0,491									
Solyc01g056780	50S ribosomal protein L34 (AHRD V3.3 *** W9QWL4_9ROSA)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000271 (PFAM); mobidb-lite (MOB	6,896	14,844	7,720	8,280	11,770	1,134	0,000	0,606	0,011			up	up	
Solyc01g056790	Exostosin-like protein (AHRD V3.3 *** A0A124SBF9_CYNCS)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc			IPR004263 (PFAM); IPR004263 (PAN	1,113	1,209	0,463	0,629	0,681									
Solyc01g056810	Syntaxin (AHRD V3.3 *** A0F0A7_NICBE)		C:GO:0016020; P:GC	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART); IPR006011 (SM	10,622	10,473	5,672	5,681	4,609									
Solyc01g056830	Syntaxin (AHRD V3.3 *-* A0F0A7_NICBE)		F:GO:0000149; F:GC	F:SNARE binding; F:SNAP receptor activity; C:plasma membrar			mobidb-lite (MOBIDB_LITE)	0,118	0,021	0,072	0,094	0,070									
Solyc01g056850	CTP synthase (AHRD V3.3 *** W8SVJ8_TOBAC)		F:GO:0003883; P:GC	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR004468 (TIGRFAM); IPR017456 (F	27,212	52,829	4,719	5,787	8,596	0,982	0,001	0,859	0,035			up	up	
Solyc01g056875	two-component response regulator (AHRD V3.3 --* AT3G62670.1)							0,000	0,021	0,000	0,000	0,000									
Solyc01g056880	Soul heme-binding family protein (AHRD V3.3 *-* D7L8V8_ARALL)		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:plastoglobule; F:heme binc			IPR011256 (G3DSA:3.20.80.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc01g056890	LOW QUALITY:F-box/RNI-like/FBD-like domains-containing protein (AHRD V3.3 --* AT3G58960.1)		C:GO:0009579	C:thylakoid			IPR033344 (PANTHER); PTHR33222:	0,000	0,039	0,121	0,022	0,048									
Solyc01g056910	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT3G44480.5)		F:GO:0004252; P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	PTHR22939 (PANTHER); PTHR22939	0,000	0,021	0,000	0,000	0,000									
Solyc01g056940	Ubiquitin		F:GO:0003735; F:GC	F:structural constituent of ribosome; F:protein binding; C:ribosoi			PTHR19956 (PRINTS); IPR002906 (SM	295,735	328,714	248,835	212,323	217,518									
Solyc01g056990	Methyl-CpG-binding domain protein 4 (AHRD V3.3 *** A0A1D1YE90_9ARAE)		C:GO:0016021	C:integral component of membrane			PTHR36065 (PANTHER)	1,497	2,661	0,495	0,268	0,304									
Solyc01g057000	Universal stress protein						IPR006015 (PRINTS); IPR006016 (PF	232,076	171,377	1813,458	1554,818	1355,692									
Solyc01g057020	Pigment defective 320 protein (AHRD V3.3 *-* G7INF5_MEDTR)		C:GO:0005739; C:GC	C:mitochondrion; C:vacuolar membrane; C:chloroplast envelope			PTHR34954:SF1 (PANTHER); PTHR3	6,119	5,611	7,710	7,537	8,880									
Solyc01g057030	LOW QUALITY:nitric oxide synthase-interacting protein (AHRD V3.3 --* AT5G10210.1)							0,101	0,061	0,025	0,075	0,118									
Solyc01g057040	pigment defective 320 (AHRD V3.3 *** AT3G06960.1)		C:GO:0043231; C:GC	C:intracellular membrane-bounded organelle; C:cytoplasmic part			PTHR34954:SF1 (PANTHER); PTHR3	5,508	5,948	8,482	8,980	9,272									
Solyc01g057070	methyltransferase (AHRD V3.3 *-* AT3G28460.1)		F:GO:0008168; P:GC	F:methyltransferase activity; P:methylation			PS51257 (PROSITE_PROFILES)	0,019	0,000	0,025	0,025	0,024									
Solyc01g057080	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A0K9P1G2_ZOSMR)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN_ERF	0,040	0,681	0,000	0,000	0,000									
Solyc01g057090	Transmembrane protein 194A (AHRD V3.3 *** A0A0B2RS82_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR019358 (PFAM); mobidb-lite (MOB	24,236	16,769	25,570	25,514	24,999									
Solyc01g057130	LOW QUALITY:ATP synthase epsilon chain, chloroplastic (AHRD V3.3 --* ATPE_IPOBA)						mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,000	0,000	0,000									
Solyc01g057150	LOW QUALITY:General transcription factor 2-related zinc finger protein (AHRD V3.3 --* AT3G31402.2)							0,000	0,000	0,000	0,022	0,023									
Solyc01g057160	LOW QUALITY:basic helix loop helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT4G38065.1)							0,442	0,309	0,361	0,550	0,352									
Solyc01g057170	DEAD-box ATP-dependent RNA helicase 48 (AHRD V3.3 --* RH48_ORYSJ)							0,366	0,238	0,455	0,268	0,424									
Solyc01g057175	Potassium channel (AHRD V3.3 --* A0A059Q2G9_9POAL)							0,019	0,000	0,000	0,000	0,000									
Solyc01g057200	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103TWN9_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	8,326	10,480	9,006	9,041	9,921									
Solyc01g057210	pyruvate dehydrogenase kinase (AHRD V3.3 *** AT3G06483.1)		F:GO:0004672; P:GC	F:protein kinase activity; P:phosphorylation			IPR004358 (PRINTS); IPR003594 (SM	43,265	39,378	41,463	41,390	49,776									
Solyc01g057260	transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT3G50140.2)		C:GO:0016020	C:membrane			IPR004158 (PFAM); IPR004158 (PAN	0,218	0,096	0,022	0,125	0,000									
Solyc01g057270	Calmodulin-binding transcription activator (AHRD V3.3 *-* A0A072TUJ0_MEDTR)		F:GO:0003677	F:DNA binding			IPR013783 (G3DS_CAMTA	0,601	0,658	0,719	0,783	0,820									
Solyc01g057275	Calmodulin-binding transcription activator (AHRD V3.3 *-* A0A072TUJ0_MEDTR)		F:GO:0005515	F:protein binding			IPR000048 (SMART); IPR000048 (PF	0,404	0,596	0,540	0,585	0,398									
Solyc01g057280	LOW QUALITY:26S proteasome non-ATPase regulatory subunit-like protein (AHRD V3.3 *** A0A072V9K9_M		F:GO:0005515; P:GC	F:protein binding; P:proteasome regulatory particle assembly			G3DSA:2.30.42.10 (GENE3D); mobidt	0,733	0,648	0,548	0,686	0,728									
Solyc01g057300	bHLH transcription factor 002		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF_bHLH	0,114	0,215	0,075	0,145	0,071									

Solyc01g057310	Kinesin-like protein KIF15 (AHRD V3.3 *** A0A0B2P1R3_GLYSO)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	5,708	5,709	1,394	2,215	2,135									
Solyc01g057320	Kinesin-like protein (AHRD V3.3 *** K4AVU3_SOLLC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	1,254	1,299	0,549	0,215	0,497									
Solyc01g057330	LOW QUALITY:Yellow stripe-like transporter 1 (AHRD V3.3 *-* T1Q4G6_ARAHY)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM): PTHR31645 (PAN	0,157	0,158	0,025	0,000	0,070									
Solyc01g057340	WD-40 repeat family protein-2 (AHRD V3.3 --* A0A172CCS3_POPTO)							5,980	8,772	4,534	4,485	4,434									
Solyc01g057380	Unknown protein (AHRD V3.3)							0,000	0,000	0,000	0,022	0,000									
Solyc01g057390	LOW QUALITY:protein kinase family protein (AHRD V3.3 --* AT5G26150.1)		F:GO:0003677	F:DNA binding				0,000	0,000	0,000	0,000	0,023									
Solyc01g057430	Carboxyltransferase alpha Subunit (AHRD V3.3 *-* A0A0G2SJ78_SALMI)		F:GO:0003989: P:G(	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR001095 (PFAM): IPR001095 (PAN	0,492	0,738	0,502	0,460	0,543									
Solyc01g057440	NAC domain containing protein 71 (AHRD V3.3 --* AT4G17980.2)							0,977	0,611	1,055	1,000	1,179									
Solyc01g057460	mediator of RNA polymerase II transcription subunit 15a-like protein (AHRD V3.3 *-* AT1G15780.2)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,			G3DSA:1.10.246.20 (GENE3D): IPR0:	10,787	14,493	14,249	13,932	14,006									
Solyc01g057465	Metal tolerance protein (AHRD V3.3 --* E5GC92_CUCME)		F:GO:0000166: P:G(	F:nucleotide binding; P:telomere maintenance; F:DNA helicase a			PTHR11562:SF54 (PANTHER): PTHR	0,000	0,021	0,025	0,000	0,000									
Solyc01g057473	DNA helicase homolog, putative (AHRD V3.3 *-* Q1EPC6_MUSAC)		P:GO:0000723: F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosphate phosphatase		1,714	1,882	1,296	1,503	1,159									
Solyc01g057475	Pentatricopeptide repeat-containing protein (AHRD V3.3 --* V5QPJ8_GOSHI)							0,000	0,021	0,000	0,000	0,000									
Solyc01g057477	mediator of RNA polymerase II transcription subunit 15a-like protein (AHRD V3.3 --* AT1G15780.3)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,			IPR036546 (PFAM)	0,867	0,948	0,922	0,910	1,293									
Solyc01g057480	PIF1 helicase (AHRD V3.3 *-* G7J5Q6_MEDTR)		P:GO:0000723: F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR010285 (PFAM): IPR003840 (PFA	0,000	0,000	0,000	0,072	0,023									
Solyc01g057490	mediator of RNA polymerase II transcription subunit 15a-like protein (AHRD V3.3 --* AT1G15780.3)							1,197	0,451	1,081	1,085	0,755	-1,349	0,046					down		
Solyc01g057520	ARM repeat superfamily protein (AHRD V3.3 *** A0A061EX70_THECC)		C:GO:0005623: P:G(	C:cell; P:intracellular protein transport; F:Ran GTPase binding			IPR011989 (G3DSA:1.25.10.GENE3D	39,222	50,511	24,123	20,979	20,586									
Solyc01g057530	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT5G65560.3)							0,000	0,000	0,025	0,000	0,023									
Solyc01g057535	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* A0A0B0PXE6_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,080	0,019	0,000	0,025	0,024									
Solyc01g057570	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** A0A0G4AMM0_9ROSI)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027450 (PFAM): IPR037151 (G3D	9,951	10,246	11,038	11,664	11,915									
Solyc01g057580	LOW QUALITY:Kinase, putative (AHRD V3.3 *-* B9RND0_RICCO)		F:GO:0004675: F:G(	F:transmembrane re	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): mobic	0,040	0,039	0,175	0,000	0,095									
Solyc01g057590	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT5G62710.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane				0,000	0,000	0,025	0,000	0,000									
Solyc01g057600	4-hydroxy-3-methylbut-2-enyl diphosphate synthase (AHRD V3.3 --* AT5G60600.5)							0,320	0,220	0,100	0,075	0,023									
Solyc01g057640	LOW QUALITY:CASP-like protein 5A1 (AHRD V3.3 --* CSPL2_GINBI)							0,000	0,000	0,000	0,025	0,000									
Solyc01g057680	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT2G26330.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:kinase activity; P:phosph			IPR013210 (PFAM)	0,000	0,036	0,049	0,543	0,238									
Solyc01g057685	SKP1-like 8 (AHRD V3.3 --* AT3G21830.1)		F:GO:0003677	F:DNA binding			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,025	0,000	0,023									
Solyc01g057705	Histidyl-tRNA synthetase (AHRD V3.3 *-* A0A072U3T0_MEDTR)		P:GO:0006486: C:G(	P:protein glycosylation; C:integral component of membrane; F:tr			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,037	0,000	0,000	0,000	0,000									
Solyc01g057743	BED zinc finger,hAT family dimerization domain (AHRD V3.3 --* A0A061FVD3_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM)	0,021	0,019	0,000	0,000	0,000									
Solyc01g057747	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THECC)		F:GO:0005488	F:binding			PTHR23272:SF54 (PANTHER): PTHR:	0,000	0,018	0,000	0,000	0,000									
Solyc01g057760	RNA helicase DEAD2	DEAD2	F:GO:0003676: F:G(	F:nucleic acid binding; F:protein binding; F:ATP binding			IPR014001 (SMART): IPR001202 (SM	78,649	90,466	100,828	97,314	99,762									
Solyc01g057770	Boron transporter (AHRD V3.3 *** B6V758_VITVI)		F:GO:0005452: P:G(	F:inorganic anion exchanger activity; P:anion transport; C:integ			IPR011531 (PFAM): mobidb-lite (MOB	445,342	463,902	133,608	170,683	265,681			0,988	0,026				up	
Solyc01g057780	Zinc finger protein (AHRD V3.3 *** W9QKV5_9ROSA)		F:GO:0046872	F:metal ion binding			IPR001876 (SMART): G3DSA:4.10.10	38,661	37,629	59,240	54,132	57,953									
Solyc01g057805	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 --* PFPB_RICCO)							4,054	4,698	4,409	5,052	4,888									
Solyc01g057830	30S ribosomal protein S1 (AHRD V3.3 *** W9RV42_9ROSA)		F:GO:0003676	F:nucleic acid binding			PR00681 (PRINTS): IPR022967 (SMA	45,570	80,534	87,922	88,745	141,165	0,848	0,001	0,680	0,000			up	up	
Solyc01g057840	Nuclear export mediator factor Nemf (AHRD V3.3 *-* A0A0B0NE50_GOSAR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR021846 (PF	0,393	0,488	0,400	0,663	0,212									
Solyc01g057850	Nuclear export mediator factor Nemf (AHRD V3.3 *** A0A0B0NE50_GOSAR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): G3DSA:4.10.60	19,256	16,824	17,627	19,076	19,405									
Solyc01g057852	Protein-S-isoprenylcysteine O-methyltransferase (AHRD V3.3 *** K4BP57_SOLLC)		F:GO:0004671: P:G(	F:protein C-termina	EC:2.1.1.1	Protein-S-isoprenylcy	IPR007269 (PFAM)	0,000	0,019	0,000	0,000	0,000									
Solyc01g057854	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						IPR015410 (PFAM): mobidb-lite (MOB	0,075	0,000	0,000	0,000	0,000									
Solyc01g057856	Non-legume hemoglobin (AHRD V3.3 --* HBPL_PARRI)						mobidb-lite (MOBIDB_LITE)	0,000	0,082	0,000	0,000	0,000									
Solyc01g057900	Ubiquitin-protein ligase, putative (AHRD V3.3 *** B9RZW1_RICCO)		F:GO:0004842	F:ubiquitin-protein transferase activity			IPR000569 (SMART): G3DSA:3.30.24	55,126	47,190	80,910	87,311	83,057									
Solyc01g057910	R2R3MYB transcription factor 2	R2R3MYB2	F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB	2,809	1,349	1,593	1,669	1,607									
Solyc01g058010	Neutral/alkaline invertase (AHRD V3.3 *** G5DC09_MANES)		F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetylc	IPR024746 (PFAM): IPR024746 (PAN	14,970	19,679	8,966	11,272	11,097									
Solyc01g058020	Alkaline/neutral invertase (AHRD V3.3 *-* A0A0D5CUF6_9ROSI)		F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetylc	IPR024746 (PFAM): IPR012341 (G3D	7,429	10,489	4,642	6,242	5,568									
Solyc01g058030	Gibberellin 2-oxidase (AHRD V3.3 *** A4GVL5_SOLLC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,000	0,000	0,050	0,000									
Solyc01g058040	Gibberellin 2-oxidase (AHRD V3.3 *-* A4GVL5_SOLLC)		F:GO:0046872: F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR027443 (G3DSA:2.60.120.GENE3I	0,019	0,000	0,000	0,000	0,000									
Solyc01g058060	40S ribosomal protein S15-like (AHRD V3.3 --* Q2V999_SOLTU)		P:GO:0000028: F:G(	P:ribosomal small subunit assembly; F:RNA binding; F:structural constituent of ribosome; C:ribosome; P				0,021	0,000	0,000	0,000	0,000									
Solyc01g058070	LOW QUALITY:Nucleosome assembly protein 1-1 (AHRD V3.3 --* NAP1A_ARATH)		C:GO:0005634: P:G(	C:nucleus; P:nucleosome assembly				0,019	0,041	0,022	0,000	0,000									
Solyc01g058100	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_ANTFO)							0,063	0,043	0,000	0,000	0,023									
Solyc01g058140	beta-glycosidase 2	sfr2	F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS): IPR001360 (PF	52,439	47,172	42,394	39,523	42,775									
Solyc01g058160	agenet domain-containing protein (AHRD V3.3 *** AT3G06520.2)						IPR014002 (SMART): IPR008395 (PF.	5,853	4,032	3,194	3,167	4,370									
Solyc01g058170	agenet domain-containing protein (AHRD V3.3 *** AT3G06520.2)						IPR014002 (SMART): IPR008395 (PF.	3,689	3,698	2,532	2,285	3,031									
Solyc01g058190	30S ribosomal protein S6 (AHRD V3.3 *** W9RJT9_9ROSA)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR000529 (PFAM): IPR000529 (TIGF	10,143	11,052	31,249	29,479	29,809									
Solyc01g058200	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 --* AT3G24570.2)							1,463	1,886	4,656	4,513	4,262									
Solyc01g058210	HCO3- transporter family (AHRD V3.3 --* AT1G15460.4)							9,051	8,365	7,210	7,120	8,603									
Solyc01g058220	F-box family protein (AHRD V3.3 --* AT2G32560.1)							0,019	0,021	0,050	0,000	0,000									
Solyc01g058230	LOW QUALITY:Reverse transcriptase like protein (AHRD V3.3 --* O23303_ARATH)							0,059	0,039	1,122	1,426	0,755									
Solyc01g058240	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 --* AT4G28550.3)							0,019	0,000	0,050	0,097	0,071									
Solyc01g058260	Poly(A) polymerase, putative (AHRD V3.3 *** B9RZU0_RICCO)		F:GO:0003723: F:G(	F:RNA binding; F:pc	EC:2.7.7.19	Polynucleotide aden	G3DSA:3.30.460.10 (GENE3D): G3DS	71,847	65,873	109,849	143,073	127,941					0,384	0,018			up
Solyc01g058270	O-acetyltransferase family protein (AHRD V3.3 *** AT3G06550.1)		C:GO:0005794: P:G(	C:Golgi apparatus; P:plant-type secondary cell wall biogenesis;			IPR012419 (PFAM): PTHR13533:SF1	18,192	13,775	2,214	1,542	1,533									
Solyc01g058280	Transmembrane 93 (AHRD V3.3 *** A0A0B0PFK3_GOSAR)		C:GO:0072546	C:ER membrane protein complex			IPR029008 (PFAM): PTHR20994:SF3	18,340	15,927	19,770	21,244	18,956									
Solyc01g058320	transmembrane protein (AHRD V3.3 *** AT3G17120.5)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	111,747	88,217	7,395	9,680	8,942									
Solyc01g058350	LOW QUALITY:tRNA modification GTPase (AHRD V3.3 --* AT1G78010.1)							0,323	0,216	0,412	0,318	0,283									
Solyc01g058360	zinc induced facilitator-like 1 (AHRD V3.3 *-* AT5G13750.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR011701 (PFAM): IPR005828 (PFA	0,000	0,043	0,000	0,000	0,000									
Solyc01g058380	Coatomer subunit gamma (AHRD V3.3 *-* K4B3G7_SOLLC)		P:GO:0006886: P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR002553 (PFAM): IPR011989 (G3D	0,194	0,233	0,000	0,150	0,117									
Solyc01g058390	Galactokinase, putative (AHRD V3.3 *** B9RZT4_RICCO)		F:GO:0004335: F:G(	F:galactokinase act	EC:2.7.1.6	Galactokinase	IPR000705 (PRINTS): PR00959 (PRII	33,030	31,726	14,332	15,020	16,878									
Solyc01g058400	DHBP synthase RibB-like alpha/beta domain-containing protein (AHRD V3.3 --* AT3G01920.2)		F:GO:0046983	F:protein dimerization activity				0,000	0,021	0,000	0,075	0,000									
Solyc01g058410	LOW QUALITY:Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* J7MFY4_MALDO)		F:GO:0004129: F:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	PTHR22888:SF16 (PANTHER): PTHR:	0,038	0,021	0,050	0,075	0,046									
Solyc01g058450	Flowering time control protein FCA, putative (AHRD V3.3 *** B9RZT3_RICCO)		F:GO:0003723: F:G(	F:RNA binding; F:protein binding			IPR002343 (PRINTS): IPR001202 (SM	37,171	35,793	46,730	49,111	48,660									
Solyc01g058470	LOW QUALITY:Neutral/alkaline non-lysosomal ceramidase (AHRD V3.3 --* AT2G38010.3)							1,366	1,660	0,859	0,718	0,895									
Solyc01g058500	LOW QUALITY:TBP-associated factor 2 (AHRD V3.3 --* AT1G73960.2)							27,797	37,885	29,601	72,790	42,211					1,305	0,000			up
Solyc01g058510	LOW QUALITY:GATA transcription factor 17 (AHRD V3.3 --* GAT17_ORYSJ)							0,573	0,345	0,781	0,690	0,515									
Solyc01g058520	Peroxidase (AHRD V3.3 *** K4AW60_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,831	0,599	0,460	0,446	0,402									
Solyc01g058530	30S ribosomal S18 (AHRD V3.3 *** A0A0B0MLA2_GOSAR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001648 (PRINTS): IPR001648 (PF	5,184	5,006	3,881	4,323	3,841									
Solyc01g058540	WRKY transcription factor 47	WRKY47	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF_WRKY	1,516	1,604	0,025	0,120	0,071									
Solyc01g058550	LOW QUALITY:DNA binding,zinc ion binding,DNA binding, putative isoform 6 (AHRD V3.3 --* A0A061GSH6		F:GO:0046872	F:metal ion binding			PTHR22880:SF196 (PANTHER): PTHI	0,019	0,000	0,000	0,000	0,000									
Solyc01g058595	LOW QUALITY:Polyprotein, putative (AHRD V3.3 *-* Q0KIN7_SOLDE)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): IPR012337 (SUP	0,061	0,082	0,098	0,125	0,094									
Solyc01g058650	LOW QUALITY:Prefoldin subunit 3 (AHRD V3.3 *-* B9RZT0_RICCO)		P:GO:0006457: C:G(	P:protein folding; C:prefoldin complex			IPR016655 (PANTHER)	0,157	0,174	0,168	0,025	0,095									
Solyc01g058660	LOW QUALITY:Unknown protein (AHRD V3.3)							0,409	0,436	0,332	0,195	0,212									
Solyc01g058670	Transcription factor protein (AHRD V3.3 *** A0A0B0PZR8_GOSAR)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	80,459	62,735	56,282	61,101	50,384									
Solyc01g058690	LOW QUALITY:Zinc finger CCCH domain-containing protein 41 (AHRD V3.3 *-* W9S0N7_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,000	0,000	0,025	0,000	0,023									
Solyc01g058720	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XT58_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	2,318	3,888	1,441	1,252	1,084									
Solyc01g058730	transmembrane protein (AHRD V3.3 *** AT4G16180.2)		C:GO:0016021	C:integral component of membrane			PTHR31515 (PANTHER): PTHR31515	94,818	78,371	88,376	82,865	83,931									
Solyc01g058733	embryo sac development arrest 7 (AHRD V3.3 --* AT3G56990.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,050	0,000	0,000									
Solyc01g058735	Phosphonates import ATP-binding protein PhnC 2 (AHRD V3.3 *-* A0A1D1Z394_9ARAE)		C:GO:0016021	C:integral component of membrane				13,198	10,591	13,094	11,101	12,950									
Solyc01g058740	Ninja-family protein AFP3 (AHRD V3.3 --* A0A199V6N7_ANACO)		C:GO:0005634: P:G(	C:nucleus; P:signal transduction; P:negative regulation of transcription, DNA-templated				0,000	0,021	0,000	0,000	0,000									
Solyc01g059760	Sentrin-specific protease 1 (AHRD V3.3 *-* W9RLZ4_9ROSA)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM): IPR015410 (PFA	0,173	0,235	0,000	0,025	0,000									
Solyc01g059800	LOW QUALITY:Transcriptional factor B3 family protein (AHRD V3.3 --* AT2G24645.4)							0,000	0,019	0,000	0,000	0,000									
Solyc01g059830	Enoyl-CoA hydratase (AHRD V3.3 *** C1K4P1_ELAOL)		F:GO:0003824	F:catalytic activity			IPR001753 (PFAM): G3DSA:3.90.226	37,137	35,730	85,591	84,234	81,209									
Solyc01g059840	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2P5N2_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,057	0,039	0,000	0,000	0,000									
Solyc01g059860	MAP kinase kinase kinase 3	MAPKKK3	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:regulation of transcri			IPR001245 (PRINTS): IPR000014 (SM	57,007	49,621	21,706	21,707	20,602									
Solyc01g059870	phytochrome B1	PHYB1	F:GO:0000155: P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR001294 (PRINTS): IPR003594 (SM	46,419	33,646	22,110	22,625	24,447									
Solyc01g059880	ATP-citrate synthase, putative (AHRD V3.3 *** B9RZR0_RICCO)		F:GO:0046912	F:transferase activity, transferring acyl groups, acyl groups con			IPR002020 (PFAM): IPR016143 (G3D	101,430	99,523	73,255	63,958	64,997									
Solyc01g059920	Nucleic acid-binding proteins superfamily (AHRD V3.3 *** AT3G17030.1)						IPR035200 (PFAM): G3DSA:2.40.50.1	6,219	4,946	3,403	2,797	3,691									
Solyc01g059930	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G17020.1)		C:GO:0005886: P:G(	C:plasma membrane; P:response to cold			IPR006015 (PRINTS): IPR006016 (PF	80,830	84,978	51,825	49,727	57,500									
Solyc01g059950	LOW QUALITY:GAI-like protein 1	GRAS					IPR005202 (PFAN_GRAS	0,560	0,354	0,312	0,381	0,352									
Solyc01g059960	LOW QUALITY:GAI-like protein 1 (AHRD V3.3 *** A1YWM9_9ROSI)	GRAS	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAN_GRAS	0,000	0,000	0,000	0,000	0,023									
Solyc01g059990	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SHP6_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,000	0,051	0,000	0,000									
Solyc01g060030	Zinc finger CCHC domain-containing 10 (AHRD V3.3 *** A0A0B0MPC6_GOSAR)						PF13917 (PFAM): mobidb-lite (MOBID	81,085	71,834	75,704	68,516	68,620									
Solyc01g060040	Bromodomain and WD repeat-containing protein 1 (AHRD V3.3 *** W9QVV9_9ROSA)		F:GO:0005515	F:protein binding			IPR036427 (G3DSA:1.20.920.GENE3I	24,799	21,397	28,613	30,951	29,384									
Solyc01g060050	WD-repeat protein, putative (AHRD V3.3 *-* B9RZN7_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	7,347	5,954	8,234	9,777	8,851									
Solyc01g060070	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		P:GO:0003333: F:G(	P:amino acid transmembrane transport; F:amino acid transmem			PF02466 (PFAM): mobidb-lite (MOBID	3,664	5,648	3,856	4,320	3,872									
Solyc01g060080	Serine/threonine-protein phosphatase 4 regulatory subunit 3 (AHRD V3.3 *** A0A0B2PYQ7_GLYSO)						IPR011993 (G3DSA:2.30.29.GENE3D	29,980	30,517	44,649	48,591	42,648									
Solyc01g060085	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_LAVLA)		F:GO:0000287: P:G(	F:magnesium ion bi	EC:4.1.1.39	Ribulose-bisphospha	IPR036376 (G3DSA:3.20.20.GENE3D	0,737	2,468	3,288	5,432	4,006	1,738	0,046					up		
Solyc01g060130	TOMGTPASE_Mill. GTPase	sar2	F:GO:0005525: C:G(	F:GTP binding; C:intracellular; P:intracellular protein transport			IPR006689 (PRINTS): SM00178 (SMA	20,606	18,629	32,661	34,943	29,354									
Solyc01g060140	calmodulin-binding transcription activator (AHRD V3.3 *** AT3G16940.3)		F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR002110 (SM	87,931	102,336	93,716	91,662	94,624									
Solyc01g060160	LOW QUALITY:Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 *-* A0A151SL68_CAJCA)						IPR025558 (PFAM): mobidb-lite (MOB	0,163	0,417	0,100	0,117	0,023									
Solyc01g060170	calmodulin-binding transcription activator (AHRD V3.3 *-* AT3G16940.2)		F:GO:0003677	F:DNA binding			IPR005559 (SMAF_CAMTA	18,388	17,452	16,398	17,892	16,753									
Solyc01g060180	CoA ligase (AHRD V3.3 *** A0A0K9PM15_ZOSMR)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D): IPF	25,774	38,082	10,189	11,278	15,762	0,590	0,015	0,623	0,007			up	up	
Solyc01g060200	3'-5' exonuclease domain-containing protein (AHRD V3.3 *** A0A103XRN2_CYNCS)		F:GO:0003676: P:G(	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR002562 (PFAM): G3DSA:3.30.420	0,157	0,207	0,122	0,098	0,165									
Solyc01g060205	XH/XS domain-containing family protein (AHRD V3.3 *-* B9HTH7_POPTR)		P:GO:0031047	P:gene silencing by RNA			PTHR21596:SF23 (PANTHER): PTHR:	0,740	0,625	0,624	0,510	0,702									
Solyc01g060210	XH/XS domain-containing protein (AHRD V3.3 *-* AT3G48670.3)		P:GO:0031047	P:gene silencing by RNA			IPR005380 (PFAM): IPR038588 (G3D	0,815	0,912	0,489	0,437	0,755									
Solyc01g060215	embryo defective 2410 (AHRD V3.3 --* AT2G25660.4)		P:GO:0031047	P:gene silencing by RNA				0,317	0,391	0,313	0,142	0,190									
Solyc01g060220	Cleavage and polyadenylation specificity factor subunit 1 (AHRD V3.3 --* CPSF1_ARATH)							0,000	0,190	0,000	0,000	0,000									
Solyc01g060240	cAMP-regulated phosphoprotein 19-related protein (AHRD V3.3 --* AT4G16146.1)						mobidb-lite (MOBIDB_LITE)	11,192	14,176	7,924	8,714	8,382									
Solyc01g060245	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RZM2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	4,422	3,551	3,525	3,365	3,934									
Solyc01g060250	RING/U-box superfamily protein (AHRD V3.3 --* AT2G37150.9)						mobidb-lite (MOBIDB_LITE)	1,155	0,647	0,509	0,631	0,730									
Solyc01g060260	Glycine-rich protein family (AHRD V3.3 *-* AT5G49350.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			PTHR34366 (PANTHER): PTHR34366	0,613	0,364	0,427	0,414	0,539									
Solyc01g060280	AMSH-like ubiquitin thioesterase 1 (AHRD V3.3 *** A0A0B0NE95_GOSAR)		F:GO:0005515	F:protein binding			IPR000555 (SMART): IPR000555 (PF.	20,929	22,341	29,968	30,217	26,232									
Solyc01g060300	damaged DNA binding 2 (AHRD V3.3 --* AT5G58760.2)						M-type_MADS	0,037	0,055	0,000	0,000	0,000									
Solyc01g060350	LOW QUALITY:Mediator of RNA polymerase II transcription subunit 33A (AHRD V3.3 --* MD33A_ARATH)							0,471	0,285	0,390	0,907	0,422									
Solyc01g060380	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT5G50130.9)						PTHR44422:SF1 (PANTHER): PTHR4	0,000	0,079	0,025	0,000	0,000									
Solyc01g060390	Ubiquitin-conjugating enzyme 23 isoform 1 (AHRD V3.3 *-* A0A061DYZ5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,077	0,000	0,022	0,023									
Solyc01g060410	cation calcium exchanger 4 (AHRD V3.3 --* AT1G54115.1)							0,040	0,000	0,000	0,000	0,000									
Solyc01g060415	DUF4378 domain protein (AHRD V3.3 *** G7IMV9_MEDTR)						IPR032795 (PFAM): IPR025486 (PFA	0,787	0,701	0,191	0,214	0,070									
Solyc01g060450	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT5G49320.1)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769 (PAI	0,000	0,000	0,000	0,000	0,024									
Solyc01g060455	chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR001650 (SMART): IPR014001 (SM	0,019	0,000	0,292	0,317	0,237									
Solyc01g060460	chromatin remodeling 31 (AHRD V3.3 *** AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR001650 (SM	0,000	0,000	0,245	0,287	0,119									
Solyc01g060470	Importin subunit alpha (AHRD V3.3 *** K4AWF0_SOLLC)		F:GO:0005515: C:G(	F:protein binding; C:nucleus; C:cytoplasm; P:protein import into			IPR000225 (SMART): IPR032413 (PF	265,346	257,238	368,863	329,312	323,479									
Solyc01g060490	GATA transcription factor, putative (AHRD V3.3 *** B9RZK8_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMAF_GATA	0,450	0,632	0,000	0,025	0,000									
Solyc01g065490	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *-* AT1G60690.1)						IPR036812 (G3DSA:3.20.20.GENE3D	5,032	3,728	5,767	5,112	5,792									
Solyc01g065495	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *-* AT1G60730.3)						IPR023210 (PFAM): IPR036812 (G3D	10,163	9,747	13,262	11,126	11,258									
Solyc01g065500	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT5G17980.1)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:plasma membrane; C:plasmodesma			IPR000008 (SMART): IPR000008 (PF.	14,754	21,404	2,475	2,725	3,069									
Solyc01g065510	CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			PR01217 (PRINTS): mobidb-lite (MOB	5,739	4,352	1,048	0,952	0,849									
Solyc01g065540	Two-component response regulator (AHRD V3.3 *** W9RS74_9ROSA)		P:GO:0000160: F:G(	P:phosphorelay signal transduction system; F:DNA binding; F:D			IPR001789 (SMAF_ARR-B	23,646	18,592	17,233	15,698	16,877									
Solyc01g065550	Dehydration-induced 19-like protein (AHRD V3.3 *** E3T7S4_GOSHI)						IPR008598 (PFAM): IPR027935 (PFA	5,054	6,949	3,784	4,564	4,318									
Solyc01g065560	DUF789 family protein (AHRD V3.3 *** A0A072UTC8_MEDTR)						IPR008507 (PFAM): mobidb-lite (MOB	10,978	8,998	12,316	12,780	11,362									
Solyc01g065577	Glucose-6-phosphate isomerase, cytosolic 1 (AHRD V3.3 --* G6PI1_CLAAR)		F:GO:0003723: F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome; P:translation; C:chloroplast				0,000	0,000	0,000	0,025	0,000									
Solyc01g065580	Pumilio-like protein (AHRD V3.3 *** A0A0B0MGW0_GOSAR)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR012959 (PF.	41,806	39,529	38,675	37,431	35,661									
Solyc01g065590	Cell wall-associated hydrolase (AHRD V3.3 *-* A0A061S5B2_9CHLO)		C:GO:0009507	C:chloroplast				0,394	0,360	0,541	0,272	0,848									
Solyc01g065597	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLLC)		F:GO:0008137: P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N.	IPR003918 (PRINTS): IPR001750 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc01g065610	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_TOBAC)		F:GO:0008137: P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N.	IPR001750 (PFAM): IPR022997 (PTH	0,000	0,064	0,000	0,000	0,023									
Solyc01g065620	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLLC)		F:GO:0008137: P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N.	IPR003918 (PANTHER): IPR022997 (I	0,000	0,064	0,000	0,000	0,000									

Solyc01g065630	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLLC)		F:GO:0008137; P:GO	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR003918 (PANTHER); IPR022997 (I	0,021	0,000	0,000	0,025	0,000									
Solyc01g065640	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 --* NU4C_DAUCA)					0,000	0,019	0,000	0,050	0,023									
Solyc01g065645	Transducin/WD40 repeat protein (AHRD V3.3 --* G7KUQ2_MEDTR)					0,000	0,000	0,000	0,000	0,024									
Solyc01g065680	LOW QUALITY:Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein (AHRD V3.3 --* A0A199V352_ANACO)				mobidb-lite (MOBIDB_LITE)	1,441	1,394	0,290	0,441	0,307									
Solyc01g065690	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *-* A0A061EP42_THECC)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D); IPR0	7,163	7,892	5,401	5,762	6,759									
Solyc01g065700	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G27930.2)		F:GO:0004722; P:GO	F:protein serine/thr EC:3.1.3.16 Protein-serine/threon	IPR001932 (SMART); IPR001932 (PF	0,042	0,060	0,071	0,047	0,024									
Solyc01g065710	CST complex subunit TEN1 (AHRD V3.3 *** A0A0B0NF61_GOSAR)		F:GO:0003697; C:GO	F:single-stranded DNA binding; C:CST complex	G3DSA:2.40.50.140 (GENE3D); IPR0	3,393	3,455	1,855	1,819	2,043									
Solyc01g065720	Phospholipase D (AHRD V3.3 *** I1NJ37_SOYBN)		F:GO:0004630; P:GO	F:phospholipase D EC:3.1.4.4 Phospholipase D	IPR001849 (SMART); IPR001736 (SM	78,875	59,290	132,306	138,285	135,368									
Solyc01g065740	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR001810 (PF	3,737	3,437	3,331	2,930	2,379									
Solyc01g065770	NADH dehydrogenase subunit 7 (AHRD V3.3 *** ATMG00510.1)		F:GO:0016651; F:GO	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindin	IPR038290 (G3DSA:1.10.645.GENE3	0,021	0,120	0,022	0,000	0,024									
Solyc01g065780	NADH dehydrogenase subunit 7 (AHRD V3.3 --* ATMG00510.1)		C:GO:0005739; C:GO	C:mitochondrion; C:plasma membrane; F:NADH dehydrogenase	IPR038290 (G3DSA:1.10.645.GENE3	0,063	0,000	0,000	0,000	0,000									
Solyc01g065790	LOW QUALITY:Retrotransposon protein, putative, unclassified (AHRD V3.3 --* Q2QRU0_ORYSJ)		C:GO:0005739	C:mitochondrion	PS51257 (PROSITE_PROFILES)	0,040	0,021	0,000	0,000	0,024									
Solyc01g065795	BnaCnng48510D protein (AHRD V3.3 *-* A0A078JK64_BRANA)				mobidb-lite (MOBIDB_LITE)	0,021	0,018	0,000	0,000	0,000									
Solyc01g065800	LOW QUALITY:AUXIN RESPONSE FACTOR 13 (AHRD V3.3 --* AT1G34170.3)					0,037	0,000	0,000	0,000	0,024									
Solyc01g065810	NADH dehydrogenase subunit 7 (AHRD V3.3 *-* ATMG00510.1)		F:GO:0016651; F:GO	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindin	IPR001135 (PFAM); IPR038290 (G3D	0,000	0,039	0,000	0,000	0,000									
Solyc01g065820	LOW QUALITY:Dehydrin protein (AHRD V3.3 *-* V9M5C3_MANES)		P:GO:0009415	P:response to water	IPR000167 (PFAM); mobidb-lite (MOB	0,000	0,060	0,000	0,000	0,000									
Solyc01g065840	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR013101 (PF	20,407	18,168	20,311	18,876	19,099									
Solyc01g065847	Trihelix transcription factor ASR3 (AHRD V3.3 *-* ASR3_ARATH),Pfam:PF13837				PF13837 (PFAM); PTHR33492:SF3 (F	0,000	0,000	0,025	0,000	0,000									
Solyc01g065915	Protein CHLOROPLAST ENHANCING STRESS TOLERANCE, chloroplastic (AHRD V3.3 --* CEST_ORYSI)					0,000	0,019	0,072	0,050	0,234									
Solyc01g065960	Gamma-interferon-inducible lysosomal thiol reductase (AHRD V3.3 --* A0A151RU75_CAJCA)		C:GO:0016020; F:GO	C:membrane; F:kinase activity; P:phosphorylation		0,040	0,039	0,000	0,025	0,000									
Solyc01g065980	Ethylene Response Factor E.4	ERF.E4	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	277,515	261,301	801,303	709,527	659,713									
Solyc01g065985	Elongation factor G, III-V domain-containing protein (AHRD V3.3 --* A0A103Y9Q4_CYNCS)				mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,000	0,000									
Solyc01g066000	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)				IPR012876 (PFAM); IPR012876 (PAN	0,021	0,043	0,072	0,073	0,023									
Solyc01g066010	RNA-binding domain CCCH-type zinc finger protein (AHRD V3.3 *-* A0A072UWB6_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	0,040	0,138	0,047	0,076	0,116									
Solyc01g066020	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.2)		F:GO:0005515; P:GO	F:protein binding; P:signal transduction; F:ADP binding	PR00364 (PRINTS); IPR000157 (SMA	1,169	1,166	0,000	0,000	0,048									
Solyc01g066040	LOW QUALITY:WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)				PTHR33484 (PANTHER)	0,037	0,099	0,202	0,125	0,094									
Solyc01g066050	Tetratricopeptide repeat-containing protein (AHRD V3.3 *** D7L668_ARALL)		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR011990 (G3	93,179	109,765	120,636	124,837	113,372									
Solyc01g066060	DAG protein (AHRD V3.3 *** K7TSG0_MAIZE)		P:GO:0016554	P:cytidine to uridine editing	mobidb-lite (MOBIDB_LITE); mobidb-lit	12,308	12,338	16,835	17,162	15,157									
Solyc01g066070	Pectin lyase-like superfamily protein, putative (AHRD V3.3 *** A0A061EWE0_THEC PG44		F:GO:0004650; P:GO	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR006626 (SMART); IPR000743 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc01g066080	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		F:GO:0008194; F:GO	F:UDP-glycosyltransferase activity; F:transferase activity, trans	G3DSA:3.40.50.2000 (GENE3D); G3D	0,021	0,021	0,000	0,000	0,000									
Solyc01g066100	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR0	0,096	0,157	0,000	0,000	0,000									
Solyc01g066110	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		C:GO:0043231; F:GO	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl	G3DSA:3.40.50.2000 (GENE3D); G3D	0,078	0,160	0,000	0,000	0,000									
Solyc01g066120	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR0	0,040	0,021	0,000	0,000	0,000									
Solyc01g066150	Glycosyltransferase (AHRD V3.3 *-* K4AWL3_SOLLC)		F:GO:0008194; F:GO	F:UDP-glycosyltransferase activity; F:transferase activity, trans	G3DSA:3.40.50.2000 (GENE3D); PTH	0,000	0,057	0,022	0,000	0,000									
Solyc01g066160	LOW QUALITY:WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)				PTHR33484 (PANTHER)	0,000	0,000	0,022	0,000	0,000									
Solyc01g066190	LOW QUALITY:Splicing factor 3B subunit 3 (AHRD V3.3 --* A0A0B2RZM2_GLYSO)				PTHR33484 (PANTHER)	0,000	0,043	0,000	0,051	0,072									
Solyc01g066200	LOW QUALITY:Glucan endo-1,3-beta-glucosidase 8 (AHRD V3.3 --* W9S9M9_9ROSA)				mobidb-lite (MOBIDB_LITE)	0,080	0,121	0,022	0,191	0,047									
Solyc01g066260	LOW QUALITY:dyggve-melchior-clausen syndrome protein (AHRD V3.3 --* AT1G04200.2)				PTHR33484 (PANTHER)	0,000	0,061	0,047	0,025	0,071									
Solyc01g066270	LOW QUALITY:AT-hook motif nuclear-localized protein 1 (AHRD V3.3 --* AT4G12080.1)				mobidb-lite (MOBIDB_LITE); PTHR334	0,000	0,018	0,000	0,000	0,000									
Solyc01g066290	LOW QUALITY:Xaa-Pro aminopeptidase 1 (AHRD V3.3 --* A0A199W6F4_ANACO)				PTHR33484 (PANTHER)	0,252	0,686	0,369	0,709	0,494									
Solyc01g066310	acyl-CoA dehydrogenase-like protein (AHRD V3.3 *** AT3G06810.1)		F:GO:0016627; F:GO	F:oxidoreductase activity, acting on the CH-CH group of donors	G3DSA:1.20.140.10 (GENE3D); G3DS	84,331	80,473	116,108	118,999	120,462									
Solyc01g066340	LOW QUALITY:Peptidyl-prolyl cis-trans isomerase CYP21-3, mitochondrial (AHRD V3.3 --* CP21C_ARATH)					6,909	6,140	2,779	3,468	3,929									
Solyc01g066430	RING/U-box superfamily protein (AHRD V3.3 *** AT2G47560.1)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART); IPR001841 (PF	204,027	51,696	51,094	195,580	67,387	-1,956	0,000			1,940	0,000	down		up
Solyc01g066440	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 --* AT1G18335.3)				mobidb-lite (MOBIDB_LITE); mobidb-lit	6,394	6,321	3,778	3,116	2,515									
Solyc01g066450	Epoxide hydrolase (AHRD V3.3 *** A0A072UTA2_MEDTR)		F:GO:0003824	F:catalytic activity	IPR000639 (PRINTS); IPR000073 (PF	0,040	0,160	0,000	0,000	0,023									
Solyc01g066453	Epoxide hydrolase (AHRD V3.3 *-* S8E221_9LAMI)		F:GO:0003824	F:catalytic activity	IPR000073 (PRINTS); IPR000639 (PF	2,557	4,378	1,041	0,368	0,446									
Solyc01g066457	Epoxide hydrolase-like protein (AHRD V3.3 *** A0A103YM44_CYNCS)		F:GO:0003824	F:catalytic activity	IPR000639 (PRINTS); IPR000073 (PF	1,799	3,537	0,759	0,732	1,224									
Solyc01g066480	Fumarylacetoacetate hydrolase, putative (AHRD V3.3 *** B9RT83_RICCO)		F:GO:0003824	F:catalytic activity	IPR011234 (PFAM); IPR036663 (G3D	27,097	27,962	47,096	40,190	42,420									
Solyc01g066490	Unknown protein (AHRD V3.3)					0,082	0,064	0,000	0,022	0,000									
Solyc01g066500	MADS-box transcription factor family protein (AHRD V3.3 *-* AT4G36590.1)		F:GO:0003677; F:GO	F:DNA binding; F:protein dimerization activity	IPR002100 (PRIN M-type_MADS	0,138	0,120	0,000	0,025	0,000									
Solyc01g066510	Gamete expressed 2 (AHRD V3.3 *-* A0A061ENE4_THECC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,034	0,976	0,329	0,097	0,350									
Solyc01g066513	Gamete expressed 2 (AHRD V3.3 *-* A0A061ENE4_THECC)		C:GO:0016021	C:integral component of membrane	IPR013783 (G3DSA:2.60.40.GENE3D	0,236	0,136	0,022	0,000	0,070									
Solyc01g066515	Gamete expressed 2 (AHRD V3.3 *-* A0A061ENE4_THECC)		C:GO:0016021	C:integral component of membrane	IPR017868 (PFAM); IPR013783 (G3D	0,382	0,431	0,069	0,022	0,119									
Solyc01g066517	gamete expressed 2 (AHRD V3.3 *-* AT5G49150.4)		C:GO:0016021	C:integral component of membrane	PTHR38537 (PANTHER)	0,349	0,122	0,022	0,022	0,000									
Solyc01g066520	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4AW		F:GO:0016746	F:transferase activity, transferring acyl groups	G3DSA:2.40.50.100 (GENE3D); IPR0	23,427	26,678	44,716	49,319	39,911									
Solyc01g066525	Agenet and bromo-adjacent homology (BAH) domain-containing protein (AHRD V3.3 --* AT1G68580.5)					0,690	0,339	0,470	0,466	0,353									
Solyc01g066560	Protein DETOXIFICATION (AHRD V3.3 *** K4AWQ7_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transp	IPR002528 (TIGRFAM); IPR002528 (F	1,517	1,007	0,677	0,658	0,755									
Solyc01g066570	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)		C:GO:0000932	C:P-body	IPR007650 (PFAM); mobidb-lite (MOB	42,805	31,633	40,630	29,712	36,704									
Solyc01g066590	Dynein light chain (AHRD V3.3 *** K9P0T9_9ROSI)		P:GO:0007017; C:GO	P:microtubule-based process; C:dynein complex	IPR001372 (SMART); IPR037177 (G3	29,352	29,775	24,737	22,336	25,451									
Solyc01g066610	fanconi anemia group I-like protein (AHRD V3.3 *** AT5G49110.4)		P:GO:0006281	P:DNA repair	IPR029308 (PFAM); IPR029315 (PFA	2,707	2,693	0,913	0,670	1,295									
Solyc01g066613	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR015894 (PFAM); IPR013955 (PFA	12,898	14,181	8,080	8,216	9,569									
Solyc01g066620	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857; P:GO	F:3-hydroxyacyl-Co EC:1.1.1.35 3-hydroxyacyl-CoA d	IPR006108 (PFAM); G3DSA:3.40.50.7	1,835	2,055	1,712	1,920	2,280									
Solyc01g066640	LOW QUALITY:vitellogenin-like protein (AHRD V3.3 *** AT3G06868.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	9,664	7,316	1,345	1,217	1,502									
Solyc01g066690	eukaryotic translation initiation factor 2 gamma subunit (AHRD V3.3 *** AT1G04170.2)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR000795 (PRINTS); G3DSA:2.40.30	49,025	52,281	56,695	54,351	53,463									
Solyc01g066700	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 *** AT3G53520.1)		C:GO:0016021	C:integral component of membrane	PR01713 (PRINTS); G3DSA:3.40.50.7	2,041	2,379	3,065	2,946	3,170									
Solyc01g066710	UDP-glucuronate decarboxylase protein 1 (AHRD V3.3 *-* N0A0E7_POPTO)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane	IPR016040 (PFAM); G3DSA:3.40.50.7	1,113	1,110	1,460	1,451	1,570									
Solyc01g066720	Hypoxia-responsive family protein (AHRD V3.3 *** G7I8Q8_MEDTR)		C:GO:0031305; P:GO	C:integral component of mitochondrial inner membrane; P:mitoc	IPR007667 (PFAM); IPR040153 (PAN	76,627	97,892	313,295	289,913	290,453									
Solyc01g066730	MADS-box transcription factor family protein (AHRD V3.3 *-* AT1G72350.1)		F:GO:0003677; F:GO	F:DNA binding; F:protein dimerization activity	IPR002100 (PRIN M-type_MADS	0,000	0,000	0,000	0,022	0,000									
Solyc01g066740	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G06880.2)		F:GO:0005515; P:GO	F:protein binding; P:signal transduction	IPR001680 (SMART); IPR001680 (PF	42,228	31,187	4,459	3,529	4,520									
Solyc01g066760	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_LOLPR)					0,500	0,832	0,115	0,048	0,048									
Solyc01g066770	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9RT65_RICCO)		C:GO:0016021	C:integral component of membrane	IPR001623 (PRINTS); IPR001623 (SM	22,070	23,614	12,271	11,300	12,902									
Solyc01g066790	LOW QUALITY:Diacylglycerol O-acyltransferase 2 (AHRD V3.3 --* DGAT2_ARATH)					0,000	0,064	0,000	0,025	0,094									
Solyc01g066810	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT2G47710.1)		C:GO:0005773; C:GO	C:vacuole; C:Golgi apparatus; C:plasma membrane	IPR006015 (PRINTS); IPR006016 (PF	0,339	0,289	0,000	0,000	0,046									
Solyc01g066820	Kinesin-like protein (AHRD V3.3 *** K4AWT2_SOLLC)		F:GO:0003777; F:GO	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	5,812	5,716	4,410	3,123	4,227									
Solyc01g066830	Ubiquitin-like-specific protease ESD4 (AHRD V3.3 *** A0A0B0MXS6_GOSAR)		P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity	IPR003653 (PFAM); G3DSA:3.40.395	15,221	15,873	17,570	18,325	18,092									
Solyc01g066840	40S ribosomal protein S21 (AHRD V3.3 *** A0A0V0GU27_SOLCH)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001931 (PFAM); IPR038579 (G3D	128,257	155,787	171,952	161,145	160,215									
Solyc01g066850	WAT1-related protein (AHRD V3.3 *** K4AWT5_SOLLC)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); mobidb-lite (MOB	1,443	1,281	0,470	0,222	0,187									
Solyc01g066860	LOW QUALITY:BnaCnng45880D protein (AHRD V3.3 *** A0A078JHJ1_BRANA)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,733	0,867	0,096	0,025	0,118									
Solyc01g066870	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G16560.4)		F:GO:0004722; P:GO	F:protein serine/thr EC:3.1.3.16 Protein-serine/threon	IPR001932 (SMART); IPR036457 (G3	7,793	6,997	6,426	6,336	6,649									
Solyc01g066880	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G27690.1)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D); IPR0	4,234	3,109	2,587	3,660	3,395									
Solyc01g066890	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT4G32660.3)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane		0,000	0,000	0,022	0,025	0,000									
Solyc01g066900	cationic amino acid transporter 9 (AHRD V3.3 --* AT1G05940.2)					6,282	7,552	2,461	2,407	2,378									
Solyc01g066910	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)		F:GO:0005504; P:GO	F:fatty acid binding; P:systemic acquired resistance	IPR016140 (SMART); IPR016140 (PF	1,941	2,722	0,025	0,000	0,000									
Solyc01g066940	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9RT39_RICCO)		C:GO:0016021; P:GO	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS); IPR010908 (SM	13,499	14,401	9,540	8,986	8,708									
Solyc01g066970	Flowering promoting factor 1 (AHRD V3.3 *** A0A061EW40_THECC)		P:GO:0009909	P:regulation of flower development	IPR039274 (PANTHER); PTHR33433:	0,084	0,054	0,025	0,000	0,000									
Solyc01g067000	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G16510.1)				IPR000008 (SMART); IPR035892 (G3	35,336	48,833	19,332	18,535	21,158									
Solyc01g067010	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYN		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR001810 (PF	10,912	5,275	15,147	21,952	13,649	-1,022	0,009			0,537	0,026	down		up
Solyc01g067020	Atypical receptor-like kinase 1 (AHRD V3.3 *** C5H8K0_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (PFAM); IPR001611 (PFA	4,245	12,504	5,998	9,611	9,675					0,685	0,018			up
Solyc01g067025	LOW QUALITY:F-box/RNI superfamily protein, putative (AHRD V3.3 *** G7KI75_MEDTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR001810 (PF	0,470	0,324	0,291	0,224	0,376									
Solyc01g067030	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYN		F:GO:0005515	F:protein binding	IPR001810 (SMART); IPR001810 (PF	1,724	1,709	1,776	1,043	1,344									
Solyc01g067040	PWWP domain-containing family protein (AHRD V3.3 *-* U5GDF3_POPTR)		F:GO:0003676	F:nucleic acid binding	IPR000313 (SMART); G3DSA:2.30.30	0,317	0,295	0,118	0,025	0,000									
Solyc01g067070	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G48970.1)		F:GO:0022857; P:GO	F:transmembrane transporter activity; P:transmembrane transp	IPR002067 (PRINTS); IPR023395 (G3	30,990	26,750	17,779	14,505	16,406									
Solyc01g067080	dynein beta chain, ciliary protein (AHRD V3.3 *** AT3G21400.1)		C:GO:0005739; P:GO	C:mitochondrion; P:mitochondrial respiratory chain complex I as	mobidb-lite (MOBIDB_LITE); mobidb-lit	8,408	9,615	33,894	32,012	23,622									
Solyc01g067090	Arginine-glutamic acid dipeptide repeats protein (AHRD V3.3 *** A0A1D1ZEZ0_9ARAE)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 (GENE3D); mobidb	17,674	16,350	32,855	62,224	29,742					0,926	0,000			up
Solyc01g067100	cullin 1 (AHRD V3.3 *** AT4G02570.4)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR016158 (SMART); IPR019559 (SM	106,032	97,230	143,643	135,603	128,903									
Solyc01g067103	Cullin-1, putative (AHRD V3.3 *-* B9RT30_RICCO)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	G3DSA:1.20.1310.10 (GENE3D); IPR0	39,335	33,972	50,355	48,760	48,849									
Solyc01g067107	ARABIDILLO-1 (AHRD V3.3 --* AT2G44900.2)					3,938	2,939	4,846	3,991	5,289									
Solyc01g067120	Cullin 1, putative (AHRD V3.3 *** A0A061EP85_THECC)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR001373 (PFAM); G3DSA:1.20.131	0,584	2,630	0,025	0,220	0,259	2,184	0,000					up		
Solyc01g067125	Cullin 1, putative (AHRD V3.3 *-* A0A061EP85_THECC)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	G3DSA:1.20.1310.10 (GENE3D); IPR0	0,080	0,774	0,000	0,025	0,046									
Solyc01g067130	Nuclear transcription factor Y protein (AHRD V3.3 *** G7JKC3_MEDTR)		F:GO:0046982	F:protein heterodimerization activity	PR00615 (PRINTS NF-YB	0,278	0,619	0,170	0,260	0,259									
Solyc01g067140	Cullin-1 (AHRD V3.3 *** A0A151STJ7_CAJCA)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR016158 (SMART); IPR019559 (SM	0,103	0,041	0,047	0,075	0,211									
Solyc01g067147	asterix-like protein (AHRD V3.3 *-* AT5G07960.1)		C:GO:0016021	C:integral component of membrane	IPR005351 (PFAM); IPR005351 (PRC	0,000	0,021	0,000	0,000	0,000									
Solyc01g067160	DNA topoisomerase 4 subunit B (DUF810) (AHRD V3.3 --* AT4G11670.4)					0,080	0,000	0,096	0,125	0,024									
Solyc01g067165	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072VNI6_MEDTR)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); G3DSA:3.40.50.3	0,801	0,986	0,921	0,465	0,540									
Solyc01g067170	LOW QUALITY:cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0006511; C:GO	P:ubiquitin-dependent protein catabolic process; C:cullin-RING	IPR019559 (SMART); IPR036388 (G3	0,040	0,082	0,000	0,000	0,000									
Solyc01g067180	Cullin-1 (AHRD V3.3 *-* A0A0B2STE7_GLYSO)		P:GO:0044267	P:cellular protein metabolic process	PTHR11932:SF97 (PANTHER); PTHR	1,763	1,402	1,099	0,972	0,921									
Solyc01g067190	LOW QUALITY:Succinate dehydrogenase subunit 7, mitochondrial (AHRD V3.3 --* SDH7_ORYSJ)				mobidb-lite (MOBIDB_LITE)	0,173	0,077	0,162	0,119	0,094									
Solyc01g067210	cullin 1 (AHRD V3.3 *** AT4G02570.4)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR019559 (SMART); IPR016158 (SM	2,643	2,027	1,827	2,553	2,069									
Solyc01g067215	cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0006511; C:GO	P:ubiquitin-dependent protein catabolic process; C:cullin-RING	G3DSA:1.20.1310.10 (GENE3D); PTH	0,021	0,059	0,096	0,050	0,093									
Solyc01g067220	RING/U-box superfamily protein (AHRD V3.3 --* AT1G32361.1)					0,495	0,444	0,209	0,489	0,425									
Solyc01g067230	cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process	G3DSA:1.20.1310.10 (GENE3D); PTH	0,467	0,239	0,169	0,166	0,212									
Solyc01g067250	cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0016567; C:GO	P:protein ubiquitination; C:SCF ubiquitin ligase complex; P:SCF-	PTHR11932:SF97 (PANTHER); PTHR	1,132	1,330	0,623	1,092	0,755									
Solyc01g067273	Cullin 1 (AHRD V3.3 *-* A0A172MAB9_VITPS)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR001373 (PFAM); G3DSA:1.20.131	3,389	3,214	3,258	3,927	2,633									
Solyc01g067280	F-box-like protein (AHRD V3.3 *** G7JJ28_MEDTR)		F:GO:0005515; P:GO	F:protein binding; P:SCF-dependent proteasomal ubiquitin-depe	IPR001810 (SMART); G3DSA:1.20.12	11,356	10,748	16,331	13,852	13,560									
Solyc01g067295	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** O24373_SOLTU)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane	IPR004231 (PFAM); IPR009632 (PRC	0,082	0,000	0,076	0,025	0,000									
Solyc01g067300	CASP-like protein (AHRD V3.3 *** K4AWX9_SOLLC)		C:GO:0005794; C:GO	C:Golgi apparatus; C:plasma membrane; C:integral component	IPR006702 (PFAM); IPR006459 (TIGF	4,616	8,403	15,512	33,272	24,335			0,644	0,016	1,100	0,000		up	up
Solyc01g067330	CASP-like protein (AHRD V3.3 *** K4AWY2_SOLLC)		C:GO:0005886; C:GO	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM); IPR006459 (TIGF	0,099	0,037	0,115	0,050	0,094									
Solyc01g067340	bHLH transcription factor 075		F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	0,019	0,000	0,000	0,000	0,000									
Solyc01g067350	Glycosyltransferase (AHRD V3.3 *** K4AWY4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM); G3DSA:3.40.50.2	0,000	0,037	0,000	0,000	0,000									
Solyc01g067360	CHY-type/CTCHY-type/RING-type Zinc finger protein (AHRD V3.3 *** AT5G18650.1)		F:GO:0008270; P:GO	F:zinc ion binding; P:protein ubiquitination	IPR001841 (SMART); G3DSA:2.20.28	0,534	1,090	0,243	0,709	0,445									
Solyc01g067370	TSB				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,099	0,078	0,000	0,000	0,000									
Solyc01g067380	Lipase (AHRD V3.3 *** B6V3M3_JATCU)		P:GO:0006629	P:lipid metabolic process	IPR002921 (PFAM); IPR029058 (G3D	18,394	11,655	31,392	32,276	26,406	-0,630	0,049					down		
Solyc01g067390	RNA helicase DEAH-box1	DEAH1	F:GO:0003677; F:GO	F:DNA binding; F:A EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR014001 (SMART); IPR001650 (SM	214,765	170,756	210,101	202,497	205,346									
Solyc01g067400	Kinase family protein (AHRD V3.3 *** D7LYF0_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	37,900	35,829	40,930	39,908	38,886									
Solyc01g067410	Pectinesterase (AHRD V3.3 *** K4AWZ0_SOLLC)		F:GO:0030599; P:GO	F:pectinesterase ac EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR000070 (PFAM); IPR012334 (G3D	0,040	0,178	0,000	0,022	0,023									
Solyc01g067417	LOW QUALITY:Invertase inhibitor (AHRD V3.3 *** A7IZL3_COFCA)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART); IPR006501 (TIG	0,000	0,057	0,000	0,000	0,000									
Solyc01g067420	Pectinesterase (AHRD V3.3 *** K4AWZ1_SOLLC)		F:GO:0030599; P:GO	F:pectinesterase ac EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3	0,021	0,000	0,000	0,000	0,000									
Solyc01g067440	Glutaredoxin family protein (AHRD V3.3 *** AT3G21460.1)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR011905 (TIGRFAM); G3DSA:3.40.3	0,436	0,848	0,923	1,965	1,323					1,093	0,023			up
Solyc01g067460	Glutaredoxin family protein (AHRD V3.3 *** D7MAE7_ARALL)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS); IPR002109 (PF	2,796	6,294	0,313	0,345	0,401	1,194	0,004					up		
Solyc01g067480	Acyl-CoA-binding domain-containing protein 4 (AHRD V3.3 *** A0A0B0MQV8_GOSAR)		F:GO:0005515	F:protein binding	IPR015915 (G3DSA:2.120.10.GENE3	22,688	21,438	7,070	5,320	8,019									
Solyc01g067490	Anaphase-promoting complex subunit 7-like protein (AHRD V3.3 *** A0A0B0MSH3_GOSAR)		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR011990 (G3	15,992	14,047	18,346	17,703	17,475									
Solyc01g067500	Serine/threonine-protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** G7JK96_MEDTR)		F:GO:0005509; P:GO	F:calcium ion binding; P:regulation of dephosphorylation	G3DSA:1.10.238.10 (GENE3D); IPR0	55,035	50,138	65,268	62,804	64,921									
Solyc01g067510	Kinase family protein (AHRD V3.3 *** B9GNF8_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	PIRSF000654 (PIRSF); IPR001245 (F	9,858	5,905	0,025	0,047	0,000									
Solyc01g067520	Cellulose synthase, putative (AHRD V3.3 *** B9RKY2_RICCO)		C:GO:0016020; F:GO	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (U	IPR029044 (G3DSA:3.90.550.GENE3	0,000	0,000	0,148	0,148	0,072									
Solyc01g067530	GTPase obg (AHRD V3.3 *** W9RHI6_9ROSA)		F:GO:0000287; F:GO	F:magnesium ion bi EC:3.6.1.15 Nucleoside-triphosph	IPR006073 (PRINTS); IPR036346 (G3	25,696	32,163	73,557	78,593	71,546									
Solyc01g067550	Zinc finger transcription factor 8	C3H8	F:GO:0046872	F:metal ion binding	IPR000571 (SMAF C3H	68,053	61,015	73,518	75,276	72,984									
Solyc01g067560	Always early, putative (AHRD V3.3 *** B9RT24_RICCO)		F:GO:0003677; P:GO	F:DNA binding; P:transcription, DNA-templated; C:transcriptiona	IPR001005 (SMAF MYB_related	41,111	36,658	33,128	30,357	29,980									
Solyc01g067570	Adaptin family protein (AHRD V3.3 --* AT4G23460.1)		F:GO:0046872	F:metal ion binding		19,614	14,158	21,593	15,218	22,253					-0,501	0,011			down
Solyc01g067580	E3 ubiquitin-protein ligase (AHRD V3.3 *** AT5G18540.2)				mobidb-lite (MOBIDB_LITE); mobidb-lit	5,760	6,027	7,224	8,177	6,880									
Solyc01g067590	Sucrose nonfermenting 4-like protein (AHRD V3.3 *** A0A0B2SMB8_GLYSO)				IPR000644 (SMART); G3DSA:3.10.58	31,546	29,011	39,925	40,078	36,801									
Solyc01g067600	Zinc finger, CW-type (AHRD V3.3 *** A0A103XJ19_CYNCS)		F:GO:0008270	F:zinc ion binding	G3DSA:3.30.40.100 (GENE3D); IPR0	79,124	59,736	70,048	83,659	79,709									

Solyc01g067610	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_OENEH)							9,656	8,180	11,270	11,674	10,912									
Solyc01g067620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G21420.1)		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	6,731	5,424	2,473	2,048	2,242									
Solyc01g067630	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G39080.1)						G3DSA:3.40.50.720 (GENE3D): PTHR	20,112	24,772	12,219	9,690	13,653									
Solyc01g067640	Protein kinase superfamily protein (AHRD V3.3 *** AT1G54610.3)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	19,295	20,073	11,681	10,277	11,607									
Solyc01g067650	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT1G15750.4)		C:GO:0016020: C:G	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,149	0,074	0,375	0,023									
Solyc01g067660	1,4-alpha-glucan-maltohydrolase	bmy3	P:GO:0000272: F:G	P:polysaccharide c	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS): G3DSA:3.20.2	281,200	269,696	706,324	796,728	677,984									
Solyc01g067680	Tubby-like F-box protein (AHRD V3.3 *** M1APZ0_SOLTU)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS): IPR001810 (PF	57,011	56,261	141,272	170,041	141,578									
Solyc01g067690	Sgf11 (Transcriptional regulation protein) protein (AHRD V3.3 --* A0A072TU18_MEDTR)						mobidb-lite (MOBIDB_LITE)	2,383	1,894	2,331	2,572	2,163									
Solyc01g067700	SAGA-associated factor 11 (AHRD V3.3 *-* J3NDX3_ORYBR)						PTHR15117 (PANTHER): PTHR15117	3,302	2,624	1,667	2,006	2,399									
Solyc01g067710	(Sodium/potassium)/proton exchanger 3	nhx3	C:GO:0005774: C:G	C:vacuolar membrane; C:plasma membrane; P:sodium ion trans			IPR004709 (PRINTS): IPR004709 (TI	14,484	10,018	29,029	35,396	28,362									
Solyc01g067720	Vesicle-associated 2-2-like protein (AHRD V3.3 *** A0A0B0PX66_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR013783 (G3DSA:2.60.40.GENE3D	5,901	6,091	5,963	5,640	5,745									
Solyc01g067730	Acyl carrier protein (AHRD V3.3 *** K4AX21_SOLLC)		P:GO:0006633: F:G	P:fatty acid biosynthetic process; F:phosphopantetheine bindinc			IPR020806 (SMART): IPR009081 (PF	356,700	394,431	396,176	447,664	479,791									
Solyc01g067740	Superoxide dismutase [Cu-Zn] 1	SODCC1	P:GO:0006801: F:G	P:superoxide metabolic process; F:metal ion binding			IPR001424 (PRINTS): IPR036423 (G3	417,520	406,076	1204,339	1013,270	936,801									
Solyc01g067750	dehydroquinate dehydratase/shikimate:NADP oxidoreductase	SDH/DHQ1	F:GO:0003855: F:G	F:3-dehydroquinate	EC:1.1.1.25; EC:4.2.	Shikimate dehydroge	IPR011342 (TIGRFAM): IPR001381 (F	34,461	34,116	61,791	69,632	62,281									
Solyc01g067780	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XIV0_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	2,993	1,832	0,149	0,148	0,094									
Solyc01g067790	BRCT domain-containing DNA repair protein, putative isoform 1 (AHRD V3.3 *** A0A061ENE5_THECC)						IPR001357 (SMART): IPR036420 (G3	6,037	4,497	1,852	1,381	1,647									
Solyc01g067800	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EMU5_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR011016 (PF	38,931	47,470	18,431	17,930	22,913									
Solyc01g067810	LOW QUALITY:Condensin complex subunit 1 (AHRD V3.3 --* K4D2L4_SOLLC)						mobidb-lite (MOBIDB_LITE)	0,000	0,075	0,022	0,000	0,000									
Solyc01g067820	DNA mismatch repair protein (AHRD V3.3 *** AT3G62450.1)		C:GO:0016021	C:integral component of membrane			PTHR36377 (PANTHER): PTHR36377	5,738	6,015	9,127	10,447	8,728									
Solyc01g067830	U1 small nuclear ribonucleoprotein C (AHRD V3.3 *** K4AX31_SOLLC)		P:GO:0000387: F:G	P:spliceosomal snRNP assembly; F:nucleic acid binding; C:U1 s			IPR003604 (SMART): IPR017340 (PIF	16,135	13,043	24,465	25,454	23,799									
Solyc01g067840	LOW QUALITY:breaking of asymmetry in the stomatal lineage (AHRD V3.3 --* AT5G60880.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,019	0,000	0,000	0,000									
Solyc01g067850	Peroxidase (AHRD V3.3 *** K4AX33_SOLLC)		F:GO:0004601: P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,018	0,047	0,000	0,023									
Solyc01g067860	Peroxidase (AHRD V3.3 *** K4AX34_SOLLC)		F:GO:0004601: P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,019	0,000	0,000	0,000	0,000									
Solyc01g067880	Peroxidase (AHRD V3.3 *-* K4AX36_SOLLC)		F:GO:0004601: P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): G3DSA:1.10.42	0,059	0,018	0,000	0,000	0,000									
Solyc01g067890	1-D-deoxyxylulose 5-phosphate synthase	DXS1	F:GO:0008661: P:G	F:1-deoxy-D-xylulos	EC:2.2.1.7	1-deoxy-D-xylulose-5	IPR005475 (SMART): IPR005475 (PF	147,387	185,836	442,118	420,749	511,145									
Solyc01g067900	Rapid ALkalinization Factor (AHRD V3.3 *** A0A118JUQ8_CYNCS)		C:GO:0009506: P:G	C:plasmodesma; P:calcium-mediated signaling			IPR008801 (PFAM): PTHR33136 (PAN	46,820	37,275	71,440	67,484	56,583									
Solyc01g067905	Heat shock factor-binding protein 1 (AHRD V3.3 *** A0A0B2P7Y6_GLYSO)		F:GO:0003714	F:transcription corepressor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,203	9,916	24,355	22,904	18,282									
Solyc01g067910	Unknown protein (AHRD V3.3)							0,059	0,037	0,736	0,610	0,520									
Solyc01g067930	Xyloglucan alpha-1,6-xylosyltransferase (AHRD V3.3 *** X2CZ83_PINRA)		C:GO:0016021: F:G	C:integral component of membrane; F:transferase activity, trans			IPR008630 (PFAM): IPR029044 (G3D	67,368	50,283	27,494	37,331	30,907					0,442	0,025			up
Solyc01g067940	LOW QUALITY:Citrate synthase family protein (AHRD V3.3 --* AT2G44350.4)							0,891	0,832	0,352	0,414	0,519									
Solyc01g067980	LOW QUALITY:Protein phosphatase 2C-like protein (AHRD V3.3 *-* G7IBT6_MEDTR)		F:GO:0004722: P:G	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc01g068000	Protein phosphatase 2C-like protein (AHRD V3.3 *** G7IBT5_MEDTR)		F:GO:0004722: P:G	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	86,587	69,832	94,183	102,368	97,945									
Solyc01g068020	Polyketide cyclase / dehydrase and lipid transport protein (AHRD V3.3 *** AT4G01883.1)						IPR005031 (PFAM): IPR023393 (G3D	4,922	5,816	7,037	7,012	7,856									
Solyc01g068030	Polyketide cyclase / dehydrase and lipid transport protein (AHRD V3.3 *** AT4G01883.1)						IPR023393 (G3DSA:3.30.530.GENE3	8,858	11,904	19,479	23,574	25,207									
Solyc01g068040	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* H6T2Q9_9POAL)		F:GO:0003676	F:nucleic acid binding			IPR036397 (G3DSA:3.30.420.GENE3	0,000	0,039	0,000	0,000	0,000									
Solyc01g068050	tRNA guanosine-2'-O-methyltransferase TRM13 (AHRD V3.3 *** A0A0B0MRQ4_GOSAR)		P:GO:0030488: F:G	P:tRNA methylation; F:tRNA 2'-O-methyltransferase activity			IPR021721 (PFAM): IPR022776 (PFA	11,715	10,613	7,435	6,938	7,511									
Solyc01g068060	Autophagy-related protein (AHRD V3.3 *-* K7VT17_SOLTU)		F:GO:0005515: C:G	F:protein binding; C:cytoplasm; P:autophagy; P:cellular respons			G3DSA:3.10.20.90 (GENE3D): IPR00	7,927	7,887	13,634	11,564	14,600									
Solyc01g068065	Autophagy-related protein (AHRD V3.3 *** F2YHL2_SOLLC)		F:GO:0005515: C:G	F:protein binding; C:cytoplasm; P:autophagy; P:cellular respons			PTHR10969:SF25 (PANTHER): IPR00	11,678	11,280	20,718	17,897	20,415									
Solyc01g068070	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7KTS0_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	18,892	16,799	13,583	14,269	14,827									
Solyc01g068080	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *** B9T062_RICCO)	CCR	F:GO:0003824: F:G	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	9,326	9,246	14,261	23,494	18,048					0,726	0,001			up
Solyc01g068100	Squamosa promoter binding protein12a		F:GO:0003677: C:G	F:DNA binding; C:nucleus			IPR036893 (G3DS SBP	379,669	413,806	313,100	361,381	351,955									
Solyc01g068130	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)						PTHR33916:SF4 (PANTHER): PTHR3	52,471	51,703	4,658	5,292	7,225			0,624	0,044				up	
Solyc01g068140	Transferase family protein (AHRD V3.3 *** B9I9B9_POPTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	0,911	0,864	1,309	1,058	1,365									
Solyc01g068150	NEFA-interacting nuclear protein NIP30, putative (AHRD V3.3 *** B9RN44_RICCO)		C:GO:0005634	C:nucleus			IPR019331 (PFAM): mobidb-lite (MOB	7,261	8,245	7,212	6,482	6,444									
Solyc01g068155	Transducin/WD40 repeat-like superfamily protein isoform 1 (AHRD V3.3 --* A0A061DF50_THECC)							0,364	0,503	0,483	0,189	0,519									
Solyc01g068160	Isopenicillin N epimerase (AHRD V3.3 *** A0A0B0PU12_GOSAR)		F:GO:0003824	F:catalytic activity			IPR000192 (PFAM): IPR015421 (G3D	30,608	28,217	42,272	40,586	42,526									
Solyc01g068170	oxidoreductase/transition metal ion-binding protein (AHRD V3.3 *-* AT3G51940.2)		F:GO:0016798: P:G	F:hydrolase activity, acting on glycosyl bonds; P:xylan catabolic			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,222	7,438	7,950	6,543	5,993									
Solyc01g068180	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y1F7_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	8,733	8,243	8,822	9,104	8,438									
Solyc01g068190	HIGH CHLOROPHYLL FLUORESCENCE 153-like protein		P:GO:0010190: C:G	P:cytochrome b6f complex assembly; C:integral component of n			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,187	4,924	8,537	8,654	9,220									
Solyc01g068200	Elongation defective 1 family protein (AHRD V3.3 *** A0A172CF10_POPTO)		C:GO:0005768: C:G	C:endosome; C:trans-Golgi network; C:plasma membrane; C:pla			mobidb-lite (MOBIDB_LITE): PTHR107	42,617	31,220	41,628	38,289	35,737									
Solyc01g068210	Glutamate dehydrogenase, putative (AHRD V3.3 *** B9RQ63_RICCO)		P:GO:0006520: F:G	P:cellular amino acid metabolic process; F:oxidoreductase activ			IPR006095 (PRINTS): IPR006096 (SM	61,603	52,163	64,774	64,639	62,893									
Solyc01g068240	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** G7IGQ8_MEDTR)		P:GO:0016579: F:G	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	33,065	33,055	47,127	47,259	46,537									
Solyc01g068250	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061FJT3_THECC)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	0,447	0,512	1,074	0,806	1,087									
Solyc01g068260	BRCT domain-containing family protein (AHRD V3.3 *-* U5GIX9_POPTR)		F:GO:0016853	F:isomerase activity			IPR001357 (SMART): IPR001357 (PF	9,802	12,317	14,473	12,112	15,166									
Solyc01g068263	DNA topoisomerase 2-binding protein 1 (AHRD V3.3 *-* A0A1D1Y397_9ARAE)		F:GO:0016853	F:isomerase activity			IPR036420 (G3DSA:3.40.50.GENE3D	4,467	4,866	7,231	5,798	7,402									
Solyc01g068267	DNA topoisomerase 2-binding 1 (AHRD V3.3 *-* A0A0B0N3F4_GOSAR)		F:GO:0016853	F:isomerase activity			IPR001357 (SMART): IPR001357 (PF	4,235	3,396	7,128	5,897	6,757									
Solyc01g068270	Kinase family protein (AHRD V3.3 *** B9H7J5_POPTR)		F:GO:0004674: F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR006016 (PF	33,908	27,308	44,500	39,062	40,113									
Solyc01g068280	chromatin remodeling 24 (AHRD V3.3 *** AT5G63950.1)		F:GO:0005524	F:ATP binding			IPR001650 (SMART): IPR014001 (SM	17,159	16,523	10,785	10,109	12,183									
Solyc01g068290	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (AHRD V3.3 *** A0A1D1ZGW0_9AR		P:GO:0002098: F:G	P:tRNA wobble uridine modification; F:flavin adenine dinucleotid			PR00411 (PRINTS): SM01228 (SMAR	14,366	14,266	27,384	31,225	33,943									
Solyc01g068320	chromatin remodeling 31 (AHRD V3.3 *** AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR001650 (SM	0,487	0,567	0,100	0,025	0,118									
Solyc01g068330	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:1.10.8.6	41,139	38,518	45,534	46,816	42,377									
Solyc01g068340	Crossover junction endonuclease MUS81-like protein (AHRD V3.3 *** G7J1L2_MEDTR)		F:GO:0003677: F:G	F:DNA binding; F:nuclease activity			IPR006166 (SMART): IPR036388 (G3	1,982	1,095	0,595	0,674	0,893									
Solyc01g068350	Crossover junction endonuclease MUS81-like protein (AHRD V3.3 *-* G7J1L2_MEDTR)		F:GO:0003677: F:G	F:DNA binding; F:endonuclease activity; P:nucleic acid phospho			G3DSA:3.40.50.10130 (GENE3D): PT	0,819	0,535	0,485	0,500	0,496									
Solyc01g068360	Protein kinase (AHRD V3.3 *** Q2HVC0_MEDTR)		F:GO:0004672: F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR032675 (G3DSA:3.80.10.GENE3D	0,225	0,159	0,118	0,189	0,118									
Solyc01g068370	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9QN21_9ROSA)		F:GO:0005515: C:G	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR007728 (SMART): IPR001214 (SM	4,107	3,433	5,622	4,957	4,943									
Solyc01g068380	Purple acid phosphatase (AHRD V3.3 *** K4AX84_SOLLC)		F:GO:0003993: F:G	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR015914 (PFAM): IPR025733 (PFA	0,199	0,450	0,626	2,309	1,104					1,872	0,000			up
Solyc01g068390	LIM domain and RING finger protein (AHRD V3.3 *** A0A0B2SF36_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMART): mobidb-lite (MO	46,018	48,754	65,180	63,502	57,507									
Solyc01g068400	Tubulin-specific chaperone A (AHRD V3.3 *** M4M6P8_GOSAR)		P:GO:0007021: P:G	P:tubulin complex assembly; P:post-chaperonin tubulin folding pa			IPR004226 (PFAM): G3DSA:1.20.58.9	48,446	45,300	55,731	50,327	49,157									
Solyc01g068410	SIPIN5	PIN5	C:GO:0016021: P:G	C:integral component of membrane; P:transmembrane transport			IPR014024 (TIGRFAM): IPR004776 (F	3,311	3,016	0,313	0,366	0,143									
Solyc01g068430	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794: F:G	C:Golgi apparatus; F:O-acetyltransferase activity			IPR026057 (PFAM): IPR025846 (PFA	9,084	11,525	1,425	2,462	2,244									
Solyc01g068440	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794: C:G	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFA	0,000	0,000	0,075	0,069	0,070									
Solyc01g068450	Essential protein Yae1, N-terminal (AHRD V3.3 *** A0A118K080_CYNCS)						IPR019191 (PFAM): IPR038881 (PAN	16,054	13,181	18,799	13,862	15,426					-0,439	0,042			down
Solyc01g068470	cytochrome C oxidase subunit (AHRD V3.3 *-* AT2G38780.4)		C:GO:0016021	C:integral component of membrane			PTHR35482 (PANTHER)	1,338	1,309	0,954	1,073	1,462									
Solyc01g068475	cytochrome C oxidase subunit (AHRD V3.3 *-* AT2G38780.6)		C:GO:0016021	C:integral component of membrane			PTHR35482 (PANTHER)	3,777	4,245	2,739	3,203	3,812									
Solyc01g068480	Embryo defective 2765 (AHRD V3.3 *** Q8L5Y4_ARATH)		P:GO:0000398: C:G	P:mRNA splicing, via spliceosome; C:spliceosomal complex			G3DSA:3.40.50.300 (GENE3D): IPR0	130,497	98,367	93,521	84,993	89,319									
Solyc01g068490	U-box domain-containing protein (AHRD V3.3 *** A0A0K9NJR6_ZOSMR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	0,959	5,476	2,174	3,541	3,382	2,519	0,000					up		
Solyc01g068500	ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *** G7IW32_MEDTR)		C:GO:0016020	C:membrane			IPR032880 (PFAM): IPR003864 (PFA	2,990	3,289	21,082	30,584	23,457					0,542	0,046			up
Solyc01g068510	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** G7JV71_MEDTR)		F:GO:0016301: P:G	F:kinase activity; P:phosphorylation			PTHR33088 (PANTHER): PTHR33088	0,056	0,157	1,025	0,895	0,543									
Solyc01g068520	LOW QUALITY:UDP-glucosyl transferase 72B3 (AHRD V3.3 --* AT1G01420.2)							0,000	0,021	0,046	0,000	0,000									
Solyc01g068530	Ribosomal protein S16 (AHRD V3.3 *** A9P8S1_POPTR)		F:GO:0003735: C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014721 (G3DSA:3.30.230.GENE3	181,554	187,702	122,107	108,232	116,825									
Solyc01g068540	Homeodomain-like superfamily protein, putative (AHRD V3.3 *** A0A061DHF1_THECC)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): mobidb	1,983	1,940	1,781	1,612	1,156									
Solyc01g068560	Agglutinin-like protein ALA1, putative isoform 3 (AHRD V3.3 --* A0A061FRH3_THECC)		P:GO:0006355: P:G	P:regulation of transcription, DNA-templated; P:circadian rhythm			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,470	14,919	6,345	7,502	8,671									
Solyc01g068580	COP1 SUPPRESSOR 2-like protein		C:GO:0005681: P:G	C:spliceosomal complex; P:regulation of photomorphogenesis; (			IPR010756 (PFAM): mobidb-lite (MOB	18,405	18,790	27,325	29,780	28,743									
Solyc01g068590	metal ion-binding protein (AHRD V3.3 *** AT3G62010.1)		F:GO:0016787	F:hydrolase activity			SM01301 (SMART): IPR010237 (TIGF	57,836	102,260	60,401	58,998	68,995	0,848	0,001					up		
Solyc01g068620	Polyketide cyclase / dehydrase and lipid transport protein (AHRD V3.3 *** AT4G01650.2)		C:GO:0009507	C:chloroplast			IPR023393 (G3DSA:3.30.530.GENE3	0,040	0,000	0,025	0,025	0,070									
Solyc01g068630	Haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** B9I993_POPTR)		F:GO:0016787	F:hydrolase activity			IPR010237 (TIGRFAM): IPR023214 ((	0,061	0,076	0,000	0,072	0,000									
Solyc01g068640	aarF domain-containing protein kinase		P:GO:0006744: F:G	P:ubiquinone biosynthetic process; F:kinase activity; P:phosphc			IPR004147 (PFAM): PTHR43851:SF3	9,580	11,001	8,458	9,240	9,221									
Solyc01g073640	alcohol dehydrogenase-3,Pfam:PF13561	gad3	F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	12,254	22,480	1,611	1,957	2,040	0,901	0,004					up		
Solyc01g073650	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A068ERL0_CARTI)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	111,616	105,664	110,856	114,860	107,703									
Solyc01g073660	Major facilitator superfamily protein (AHRD V3.3 *** AT2G44280.4),Pfam:PF13347		P:GO:0008643: F:G	P:carbohydrate transport; F:symporter activity; C:integral comp			PF13347 (PFAM): G3DSA:1.20.1250.	9,002	9,038	25,574	38,146	33,111					0,582	0,001			up
Solyc01g073670	Major facilitator superfamily protein (AHRD V3.3 *** AT3G60070.5),Pfam:PF13347		P:GO:0008643: F:G	P:carbohydrate transport; F:symporter activity; C:integral comp			PF13347 (PFAM): G3DSA:1.20.1250.	0,318	0,353	0,341	0,599	0,258									
Solyc01g073680	Lipid transfer protein (AHRD V3.3 *** A0A072TPI6_MEDTR)		P:GO:0006869: F:G	P:lipid transport; F:lipid binding; C:integral component of membra			IPR016140 (SMART): G3DSA:1.10.11	14,192	17,046	3,568	2,979	4,998									
Solyc01g073690	V-type proton ATPase subunit D (AHRD V3.3 *** W9SN12_9ROSA)		F:GO:0042626	F:ATPase activity, (	EC:3.6.1.3; EC:3.6.1.	Adenosinetriphospha	IPR002699 (TIGRFAM): IPR002699 (F	184,834	214,104	310,306	305,754	301,768									
Solyc01g073710	LOW QUALITY:Calcium-binding EF hand family protein (AHRD V3.3 *** A9PCU6_POPTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	9,582	15,018	5,446	6,173	6,810	0,672	0,026					up		
Solyc01g073720	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT3G26730.8)		C:GO:0016021	C:integral component of membrane			PTHR34268 (PANTHER): PTHR34268	0,143	0,360	0,025	0,051	0,046									
Solyc01g073725	ATPase, V1 complex, subunit B protein (AHRD V3.3 --* AT4G38510.5)							0,501	0,622	0,445	0,357	0,475									
Solyc01g073730	cofactor of nitrate reductase and xanthine dehydrogenase 2 (AHRD V3.3 *** AT2G31955.5)		F:GO:0003824: P:G	F:catalytic activity; P:Mo-molybdopterin cofactor biosynthetic pr			IPR006638 (SMART): IPR013483 (TIG	12,343	10,865	10,408	12,547	10,827									
Solyc01g073740	Citrate synthase (AHRD V3.3 *** M1CTV7_SOLTU)		F:GO:0004108: P:G	F:citrate (Si)-syntha	EC:2.3.3.1	Citrate (Si)-synthase	IPR002020 (PRINTS): IPR002020 (PF	72,805	72,320	64,504	62,068	60,569									
Solyc01g073750	Glucan synthase-like protein (AHRD V3.3 *** G7KWP5_MEDTR)		C:GO:0000148: F:G	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan synth	IPR026899 (SMART): IPR003440 (PF	205,857	181,002	119,929	134,319	144,878									
Solyc01g073755	Callose synthase (AHRD V3.3 *-* K7PRK8_MAIZE)		C:GO:0000148: F:G	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan synth	IPR003440 (PFAM): PTHR12741 (PAN	0,021	0,000	0,000	0,000	0,023									
Solyc01g073770	LOW QUALITY:PRLI-interacting factor A (AHRD V3.3 *-* Q9FUB4_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	18,942	16,220	30,334	25,779	27,069									
Solyc01g073780	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *-* AT2G44380.1)		F:GO:0046872	F:metal ion binding			IPR004146 (PFAM): mobidb-lite (MOB	0,037	0,036	0,000	0,000	0,000									
Solyc01g073800	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)		F:GO:0046872	F:metal ion binding			IPR004146 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc01g073810	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)		F:GO:0046872	F:metal ion binding			IPR001965 (SMART): IPR004146 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc01g073820	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)		F:GO:0046872	F:metal ion binding			IPR004146 (PFAM): mobidb-lite (MOB	0,019	0,358	0,271	0,194	0,144									
Solyc01g073830	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *-* AT2G27660.1)		P:GO:0035556	P:intracellular signal transduction			IPR004146 (PFAM): mobidb-lite (MOB	0,021	0,156	0,050	0,025	0,000									
Solyc01g073840	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)		P:GO:0035556: F:G	P:intracellular signal transduction; F:metal ion binding			IPR001965 (SMART): IPR004146 (PF	0,000	0,060	0,000	0,000	0,000									
Solyc01g073860	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)		P:GO:0035556: F:G	P:intracellular signal transduction; F:metal ion binding			IPR004146 (PFAM): PTHR13871 (PAN	0,021	0,000	0,000	0,000	0,000									
Solyc01g073870	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q10C76_ORYSJ)						IPR004252 (PFAM): mobidb-lite (MOB	39,410	40,657	41,444	43,419	41,255									
Solyc01g073880	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)						IPR004146 (PFAM): PTHR13871 (PAN	0,058	0,085	0,025	0,268	0,047									
Solyc01g073890	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *-* AT2G27660.1)						IPR004146 (PFAM): PTHR13871:SF5	2,874	4,428	0,850	2,533	1,459					1,567	0,003			up
Solyc01g073900	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G44410.1)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): PF13920 (PFAM	25,847	37,888	38,369	37,811	36,381	0,577	0,043					up		
Solyc01g073910	homeobox leucine zipper protein (AHRD V3.3 *** AT5G06710.1)		F:GO:0003700: P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001356 (SMAF HD-ZIP	0,818	5,579	0,928	0,575	0,568	2,780	0,000					up		
Solyc01g073920	Hydroxyproline-rich glycoprotein (AHRD V3.3 *** B9N6I3_POPTR)		C:GO:0017053	C:transcriptional repressor complex			IPR028226 (PFAM): mobidb-lite (MOB	12,348	12,655	12,810	11,776	12,772									
Solyc01g073930	N-terminal asparagine amidohydrolase family protein (AHRD V3.3 *** B9HPS4_POPTR)		F:GO:0008418	F:protein-N-terminal asparagine amidohydrolase activity			IPR026750 (PFAM): IPR026750 (PAN	6,998	6,399	11,735	10,149	10,697									
Solyc01g073940	Zinc finger transcription factor 9	C3H9	F:GO:0003723: F:G	F:RNA binding; F:metal ion binding			IPR004087 (SMAF C3H	17,808	17,624	22,702	20,994	21,635									
Solyc01g073950	DNA-binding bromodomain-containing protein, putative (AHRD V3.3 *** A0A061EYH0_THECC)		F:GO:0003677: F:G	F:DNA binding; F:protein binding			IPR001487 (SMAF MYB_related	43,755	64,004	49,365	43,960	50,991									
Solyc01g073960	Emsy N terminus domain-containing family protein (AHRD V3.3 *** B9HPS6_POPTR)		P:GO:0050832	P:defense response to fungus			IPR005491 (SMART): IPR005491 (PF	49,603	46,538	53,779	52,040	49,511									
Solyc01g073970	Histone H3 (AHRD V3.3 *** A0A068VC55_COFCA)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS): IPR000164 (SM	0,098	0,078	0,000	0,000	0,000									
Solyc01g074000	Histone H3 (AHRD V3.3 *** A0A0E0P928_ORYRU)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS): IPR000164 (SM	0,040	0,019	0,000	0,000	0,000									
Solyc01g074010	Protein kinase superfamily protein (AHRD V3.3 *** AT2G32850.2)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; F:protein kinase activity; F:ATP			IPR000164 (PRINTS): IPR000164 (SM	71,174	88,053	62,978	55,429	57,652									
Solyc01g074020	LOW QUALITY:HIT-type Zinc finger family protein (AHRD V3.3 *** AT1G04945.4)		P:GO:0000463: P:G	P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU			G3DSA:3.30.60.190 (GENE3D): IPR0	6,842	6,327	10,223	9,940	9,461									
Solyc01g074030	Beta-glucosidase 01 (AHRD V3.3 *** B5M9E4_SOLLC)		F:GO:0004553: P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS): IPR001360 (PF	42,046	51,914	4,933	6,720	12,562			1,338	0,001				up	
Solyc01g079060	Charged multivesicular body 7 (AHRD V3.3 *-* A0A0B0PQU1_GOSAR)		P:GO:0007034	P:vacuolar transport			PTHR22761 (PANTHER): PTHR22761	12,721	13,427	14,360	13,762	12,571									
Solyc01g079080	asynaptic protein (AHRD V3.3 *** AT2G46980.2)		P:GO:0051321	P:meiotic cell cycle			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,566	12,846	0,983	0,316	0,842									
Solyc01g079090	Protoporphyrinogen oxidase (AHRD V3.3 *** O64384_SOLTU)	HEMG/PPOX	F:GO:0004729: P:G	F:oxygen-depender	EC:1.3.3.4	Protoporphyrinogen (	G3DSA:1.10.3110.10 (GENE3D): IPR	54,574	78,865	83,529	74,653	94,510	0,558	0,030					up		
Solyc01g079100	S-acyltransferase (AHRD V3.3 *** K4AXF6_SOLLC)		C:GO:0005783: C:G	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	0,312	0,177	0,074	0,072	0,023									
Solyc01g079110	Histone H3 (AHRD V3.3 *** A0A0V0H170_SOLCH)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS): IPR000164 (SM	12,916	13,156	2,113	0,913	1,198					-1,197	0,014			down
Solyc01g079130	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G02460.1)	PG4	F:GO:0004650: P:G	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,021	0,081	0,025	0,000	0,000									
Solyc01g079140	LOW QUALITY:evolutionarily conserved C-terminal region 2 (AHRD V3.3 --* AT3G13460.4)							0,000	0,213	0,000	0,025	0,046									
Solyc01g079150	Boron transporter (AHRD V3.3 *** B6V758_VITVI)		F:GO:0005452: P:G	F:inorganic anion exchanger activity; P:anion transport; C:integ			IPR011531 (PFAM): mobidb-lite (MOB	11,782	11,900	3,857	3,004	4,163									
Solyc01g079160	GDSL esterase/lipase (AHRD V3.3 *** W9R6R2_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,123	0,060	0,000	0,000	0,000									
Solyc01g079170	Hexosyltransferase (AHRD V3.3 *** K4AXG3_SOLLC)		P:GO:0006012: F:G	P:galactose metabo	EC:2.4.1.123	Inositol 3-alpha-galac	IPR029044 (G3DSA:3.90.550.GENE3	8,396	8,822	3,431	3,370	4,615									
Solyc01g079180	Pectinesterase (AHRD V3.3 *** K4AXG4_SOLLC)		F:GO:0030599: P:G	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3	0,019	0,101	0,000	0,025	0,000									
Solyc01g079190	LOW QUALITY:Sucrose-6F-phosphate phosphohydrolase family protein (AHRD V3.3 --* AT2G35840.4)							0,000	0,000	0,000	0,025	0,000									
Solyc01g079200	gibberellin 2-oxidase 3	ga2ox-3	F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR005123 (PFA	0,326	2,818	0,540	0,274	0,541	3,116	0,000					up		
Solyc01g079210	DNA methyltransferase 1-associated protein, putative (AHRD V3.3 *** B9RN98_RICCO)		F:GO:0003677: P:G	F:DNA binding; P:DNA repair; P:chromatin remodeling; C:NuA4			IPR001005 (SMAF MYB_related	17,884	16,257	22,629	23,095	22,634									
Solyc01g079220	NifU-like protein 1 (AHRD V3.3 *** W9R6P7_9ROSA)		F:GO:0005506: P:G	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl			IPR034904 (G3DSA:3.30.300.GENE3	11,107	14,446	31,170	30,490	34,924									
Solyc01g079230	Agenet-like domain-containing protein (AHRD V3.3 *-* A0A103YNT6_CYNCS)		P:GO:0006306	P:DNA methylation			IPR014002 (SMART): IPR008395 (PF	9,703	7,514	10,063	11,843	11,916									
Solyc01g079235	Agenet-like domain-containing protein (AHRD V3.3 *** A0A103YNT6_CYNCS)		P:GO:0006306	P:DNA methylation			IPR014002 (SMART): IPR008395 (PF	72,052	66,759	92,264	93,039	91,254									
Solyc01g079240	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0G2SJE2_SALMI)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D): IPF	47,500	43,917	63,565	66,168	62,714									

Solyc01g079250	RNA helicase DEAH-box2	DEAH2	F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR014001 (SMART); IPR001650 (SM	314,171	288,366	243,261	235,585	251,042									
Solyc01g079260	WRKY transcription factor 23	WRKY23	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	7,379	12,734	27,414	41,754	38,008			0,469	0,004	0,610	0,001		up	up
Solyc01g079280	LOW QUALITY:Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein (DUF828) (AHRD V3.3 --* AT5G58600.1)							0,021	0,000	0,022	0,025	0,023									
Solyc01g079290	LOW QUALITY:Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* AT1G53025.2)		P:GO:0016567; F:GO	P:protein ubiquitination; F:ubiquitin conjugating enzyme activity			SM00212 (SMART); IPR016135 (G3D	0,533	0,709	0,554	0,683	0,823									
Solyc01g079300	Stachyose synthase, putative (AHRD V3.3 *** B9RNB5_RICCO)		P:GO:0010325; F:GO	P:raffinose family oligosaccharide biosynthetic process; F:trans			IPR008811 (PFAM); PTHR31268:SF8	0,187	0,138	0,097	0,309	0,141									
Solyc01g079310	heme binding protein (AHRD V3.3 *** AT3G62370.1)		F:GO:0020037	F:heme binding			IPR019020 (SMART); IPR019020 (PF	15,343	13,264	12,174	10,319	12,257									
Solyc01g079320	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RNC6_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,125	8,046	6,049	5,203	5,254									
Solyc01g079330	RNA helicase DEAD3	DEAD3	F:GO:0003676; F:GO	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART); IPR014001 (SM	45,405	41,129	53,511	52,828	52,018									
Solyc01g079340	protein kinase superfamily protein		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); G3DS	45,388	38,776	36,796	32,664	35,145									
Solyc01g079350	HIT zinc finger,PAPA-1-like conserved region, putative (AHRD V3.3 *** A0A061F305_THECC)		P:GO:0006338; C:GO	P:chromatin remodeling; C:Ino80 complex			IPR006880 (SMART); IPR007529 (PF	123,965	95,199	64,226	54,364	58,552									
Solyc01g079360	WRKY transcription factor 37	WRKY37	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	3,602	4,608	3,863	3,124	3,246									
Solyc01g079370	GRAS family transcription factor, putative (AHRD V3.3 *** A0A061EWU1_THECC)	GRAS	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	0,141	0,037	0,000	0,050	0,093									
Solyc01g079375	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G47820.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,042	0,019	0,000	0,000	0,000									
Solyc01g079380	LOW QUALITY:GRAS family transcription factor, putative (AHRD V3.3 *** A0A061E	GRAS	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	0,186	0,079	0,025	0,025	0,000									
Solyc01g079385	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A072VP41_MEDTR)		C:GO:0031519	C:PcG protein complex			PTHR22884 (PANTHER); IPR025778 (	16,018	12,854	12,816	13,427	13,163									
Solyc01g079390	Histone-lysine N-methyltransferase MEDEA (AHRD V3.3 *-* MEDEA_ARATH)	EZ1	F:GO:0005515; C:GO	F:protein binding; C:PcG protein complex			IPR033467 (SMART); IPR001214 (SM	44,493	44,083	37,699	36,924	37,443									
Solyc01g079400	TRICHOME BIREFRINGENCE-LIKE 6 (AHRD V3.3 *** AT3G62390.1)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	5,570	3,806	1,104	1,739	1,931									
Solyc01g079410	Calcium-dependent phosphotriesterase superfamily protein (AHRD V3.3 *** A0A061DRE0_THECC)		C:GO:0005783; C:GO	C:endoplasmic reticulum; C:integral component of membrane			IPR011042 (G3DSA:2.120.10.GENE3	16,530	13,516	0,843	0,649	0,821									
Solyc01g079420	Cytochrome c oxidase subunit 5C (AHRD V3.3 *** M1AI67_SOLTU)		C:GO:0005746	C:mitochondrial respirasome			IPR008432 (PIRSF); IPR008432 (PAN	68,574	72,432	98,422	97,639	90,882									
Solyc01g079425	H -ATPase 7 (AHRD V3.3 --* AT3G60330.4)						mobidb-lite (MOBIDB_LITE)	1,334	1,485	1,375	1,190	1,293									
Solyc01g079430	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT5G21970.2)		P:GO:0006979	P:response to oxidative stress			IPR021099 (PFAM); mobidb-lite (MOB	2,130	2,593	2,080	1,783	2,639									
Solyc01g079450	Dipeptidyl-peptidase, putative (AHRD V3.3 *** B9RNE4_RICCO)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity			IPR001375 (PFAM); IPR029058 (G3D	131,726	141,587	209,010	195,178	223,622									
Solyc01g079460	LOW QUALITY:BnaC09g16130D protein (AHRD V3.3 *** A0A078E278_BRANA)						PTHR35702:SF1 (PANTHER); PTHR3	0,021	0,099	0,000	0,022	0,048									
Solyc01g079470	CP12 (AHRD V3.3 *** O24136_TOBAC)		C:GO:0009507; P:GO	C:chloroplast; P:negative regulation of reductive pentose-phosp			IPR003823 (SMART); IPR003823 (PF	6,131	34,102	14,468	15,937	49,632	2,499	0,000	1,773	0,000			up	up	
Solyc01g079480	BZIP transcription factor (AHRD V3.3 *** Q1HW69_CAPAN)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	114,378	81,539	52,275	81,694	73,655			0,491	0,006	0,646	0,000		up	up
Solyc01g079500	Vps51/Vps67 family (components of vesicular transport) protein (AHRD V3.3 *** AT4G02030.1)		C:GO:0000938; C:GO	C:GARP complex; C:trans-Golgi network; C:cytosol; P:Golgi org			mobidb-lite (MOBIDB_LITE); mobidb-lit	34,393	34,110	18,306	22,111	19,075									
Solyc01g079507	DNA helicase (AHRD V3.3 *** K4AXJ5_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:3.6.1.15	Nucleoside-triphosph	IPR001208 (PRINTS); IPR008050 (PF	12,343	10,491	11,469	8,426	10,955									
Solyc01g079510	WD40/YVTN repeat-like-containing domain,Bromodomain isoform 1 (AHRD V3.3 *** A0A061DT52_THECC)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	117,718	104,459	112,418	118,086	116,365									
Solyc01g079520	DNA mismatch repair protein (AHRD V3.3 *** Q6DQL6_PETHY)		F:GO:0005524; P:GO	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			IPR000432 (SMART); IPR007696 (SM	9,883	10,342	7,815	6,304	6,523									
Solyc01g079530	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT1G02610.1)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART); IPR013083 (G3	0,162	0,257	0,075	0,224	0,354									
Solyc01g079540	GTP-binding protein (AHRD V3.3 *** Q9SDK4_ORYSJ)		F:GO:0005525; C:GO	F:GTP binding; C:intracellular; P:intracellular protein transport			IPR006689 (PRINTS); SM00177 (SMA	102,661	109,592	135,357	132,537	127,274									
Solyc01g079550	LOW QUALITY:Multidrug resistance protein ABC transporter family protein, putative (AHRD V3.3 *** A0A061DZ20_THECC)						IPR025322 (PFAM); PTHR33052 (PAN	0,037	0,141	0,072	0,194	0,119									
Solyc01g079570	Beta-D-xylosidase family protein (AHRD V3.3 *** B9HWX2_POPTR)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS); IPR026891 (SM	0,611	1,233	0,025	0,000	0,000									
Solyc01g079580	DNAJ heat shock N-terminal domain-containing family protein (AHRD V3.3 *** B9GSH4_POPTR)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	19,120	17,859	1,378	2,281	2,301									
Solyc01g079590	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 *** AT3G62580.1)		C:GO:0005783; C:GO	C:endoplasmic reticulum; C:integral component of membrane			IPR025423 (PFAM); PTHR23241 (PAN	84,686	63,497	187,177	210,257	186,976									
Solyc01g079600	Lipase (AHRD V3.3 *** A0A151RYE9_CAJCA)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	97,579	47,544	71,854	162,568	103,001	-1,011	0,000	0,517	0,005	1,180	0,000	down	up	up
Solyc01g079610	DNAJ heat shock family protein (AHRD V3.3 *** AT3G62600.1)		P:GO:0006457; F:GO	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS); IPR001623 (SM	28,997	30,569	43,113	49,207	46,256									
Solyc01g079620	colorless fruit epidermis	MYB12	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	12,527	7,610	47,542	57,400	46,583									
Solyc01g079630	Sucrose-phosphatase-related family protein (AHRD V3.3 *** B9GSG4_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR035979 (SUPERFAMILY)	0,566	0,678	0,476	0,779	0,802									
Solyc01g079640	tRNA (Guanine(26)-N(2))-dimethyltransferase (AHRD V3.3 *** A0A1D1XTE5_9ARAE)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,274	0,806	1,154	0,866	1,159									
Solyc01g079650	CTP synthase (AHRD V3.3 *** A0A0V0IPL0_SOLCH)		F:GO:0003883; P:GO	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR004468 (TIGRFAM); IPR029062 ((	38,056	29,966	39,393	36,902	36,514									
Solyc01g079670	LOW QUALITY:cotton fiber protein (AHRD V3.3 *** AT5G38700.1)						IPR008480 (PFAM); PTHR33265 (PAN	0,487	0,076	0,265	0,988	0,469									
Solyc01g079680	Ran GTPase activating protein 2 (AHRD V3.3 *** I7JP53_9SOLN)		F:GO:0005515	F:protein binding			SM00368 (SMART); IPR038214 (G3D	3,302	3,201	2,198	1,846	2,491									
Solyc01g079700	Transcription regulatory protein SNF2 (AHRD V3.3 *-* W9S7A6_9ROSA)		F:GO:0004386; F:GO	F:helicase activity;	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,570	2,199	2,836	2,507	2,879									
Solyc01g079710	OB-fold-like isoform 1 (AHRD V3.3 *** A0A061ELQ4_THECC)		F:GO:0008168; P:GO	F:methyltransferase activity; P:methylation			IPR003750 (PFAM); G3DSA:2.40.50.1	56,354	43,294	44,019	35,944	40,453									
Solyc01g079720	Kinase-associated protein phosphatase 1 (AHRD V3.3 *** A6N8J3_SOLPE)		F:GO:0004722; F:GO	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR000253 (SMART); IPR001932 (SM	43,375	37,363	77,251	77,626	71,849									
Solyc01g079740	LOW QUALITY:Fantastic four-like protein (AHRD V3.3 *** G7IE53_MEDTR)						IPR021410 (PFAM); mobidb-lite (MOB	0,201	0,216	0,000	0,000	0,024									
Solyc01g079750	MAP kinase kinase kinase 4	MAPKKK4	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	8,183	8,308	6,436	7,268	6,933									
Solyc01g079760	Peroxisomal carrier protein (AHRD V3.3 *** B4FBM4_MAIZE)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	18,772	19,102	38,009	39,861	36,994									
Solyc01g079780	Glycoprotein membrane GPI-anchored (AHRD V3.3 *** A0A061ELP1_THECC)		C:GO:0016021	C:integral component of membrane			PTHR33976:SF1 (PANTHER); PTHR3	0,096	0,082	0,125	0,162	0,071									
Solyc01g079790	ADP-glucose pyrophosphorylase large subunit 3	AGPase L3	P:GO:0005978; F:GO	P:glycogen biosynt	EC:2.7.7.27	Glucose-1-phosphate	IPR029044 (G3DSA:3.90.550.GENE3	7,774	25,772	3,758	4,295	9,370	1,755	0,000	1,309	0,000			up	up	
Solyc01g079800	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RTX6_RICCO)		F:GO:0003676; F:GO	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART); IPR014001 (SM	5,921	6,550	14,596	12,522	15,546									
Solyc01g079810	RING/U-box superfamily protein (AHRD V3.3 --* AT5G38895.3)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	35,277	70,777	20,339	20,340	28,986	1,029	0,002	0,507	0,021			up	up	
Solyc01g079820	Peroxiredoxin (AHRD V3.3 *** Q5JBR7_IPOBA)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:cell redox homeostasis			IPR013740 (PFAM); G3DSA:3.40.30.1	37,768	40,926	51,066	47,117	54,065									
Solyc01g079830	Fatty acid hydroxylase superfamily (AHRD V3.3 --* AT1G02205.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,040	0,019	0,000	0,000	0,000									
Solyc01g079840	NEDD8-activating enzyme E1 catalytic subunit-like protein (AHRD V3.3 *** A0A0B0N4J5_GOSAR)		F:GO:0005524; F:GO	F:ATP binding; F:acid-amino acid ligase activity; F:NEDD8 activ			IPR014929 (SMART); IPR014929 (PF	63,802	63,279	106,493	94,871	98,584									
Solyc01g079850	TRICHOME BIREFRINGENCE-LIKE 11 (AHRD V3.3 *** AT5G19160.1)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM); IPR026057 (PFA	1,294	1,502	7,922	8,115	8,859									
Solyc01g079860	ATP-dependent (S)-NAD(P)H-hydrate dehydratase (AHRD V3.3 *** K4AXN1_SOLLC)		F:GO:0052855	F:ADP-dependent N	EC:4.2.1.136	ADP-dependent NAD	IPR000631 (TIGRFAM); IPR029056 ((	33,600	30,720	98,800	84,343	93,788									
Solyc01g079865	Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase (AHRD V3.3 --* CCAMK_PEA)							5,294	6,088	8,151	5,121	6,030					-0,666	0,031			down
Solyc01g079870	CONSTANS interacting protein 2b	cip2b	F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YC	118,496	112,354	155,745	146,775	150,222									
Solyc01g079880	Stem-specific TSJT1 (AHRD V3.3 *** A0A0B0MRD0_GOSAR)						IPR024286 (SMART); IPR029055 (G3	747,449	476,940	466,907	363,569	510,317	-0,620	0,033					down		
Solyc01g079920	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,000	0,097	0,000	0,000	0,000									
Solyc01g079930	Xyloglucan-specific endoglucanase inhibitor 9 (AHRD V3.3 *** G8GYH9_SOLTU)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM); IPR021109 (G3D	0,096	0,146	0,000	0,089	0,023									
Solyc01g079940	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	1,029	1,727	0,329	0,242	0,258									
Solyc01g079950	Xyloglucan-specific endoglucanase inhibitor protein 2 (AHRD V3.3 *** F1DHN5_SOLTU)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM); IPR032861 (PFA	2,950	3,993	0,405	0,819	0,662									
Solyc01g079960	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,000	0,000	0,000	0,000	0,023									
Solyc01g079980	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM); IPR021109 (G3D	0,042	0,118	0,000	0,076	0,000									
Solyc01g080000	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM); IPR032861 (PFA	8,422	6,849	0,099	0,127	0,023									
Solyc01g080010	xyloglucan endoglucanase inhibitor	xegip	F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM); IPR021109 (G3D	76,064	76,965	116,115	120,834	131,399									
Solyc01g080020	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061ELJ0_THECC)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	45,636	47,378	7,601	8,889	12,091									
Solyc01g080030	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D); G3DS	0,134	0,483	0,212	1,581	1,011									
Solyc01g080040	Dual specificity protein phosphatase, putative (AHRD V3.3 *** B9RTU2_RICCO)		P:GO:0006470; F:GO	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART); IPR000340 (PF	4,608	4,481	6,709	8,048	7,944									
Solyc01g080070	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT3G06130.1)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM); G3DSA:3.30.70.1	84,838	68,691	7,439	5,812	6,779									
Solyc01g080080	RING/U-box superfamily protein (AHRD V3.3 *** AT3G06140.1)		F:GO:0016874	F:ligase activity			IPR001841 (SMART); IPR013083 (G3	22,847	18,527	25,034	25,688	25,172									
Solyc01g080100	LOW QUALITY:RING zinc finger protein, putative (AHRD V3.3 *** A0A072USX7_MEDTR)							0,717	0,546	0,000	0,025	0,024									
Solyc01g080110	TVP38/TMEM64 family membrane protein (AHRD V3.3 *** A0A0B2RII2_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR032816 (PFAM); PTHR12677:SF3	22,142	19,375	23,795	28,354	25,334									
Solyc01g080120	cytochrome P450 family protein (AHRD V3.3 *** AT3G06150.1)		C:GO:0016021	C:integral component of membrane			PTHR35124 (PANTHER)	0,416	0,134	0,022	0,000	0,000									
Solyc01g080130	cytochrome P450 family protein (AHRD V3.3 *** AT3G06150.1)		C:GO:0016021	C:integral component of membrane			PTHR35124 (PANTHER)	38,122	20,332	8,072	6,317	9,163	-0,877	0,016					down		
Solyc01g080140	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G19050.1)						IPR029058 (G3DSA:3.40.50.GENE3D	10,329	12,245	19,433	23,225	18,951									
Solyc01g080150	tRNA dimethylallyltransferase		P:GO:0008033	P:tRNA processing			IPR018022 (PFAM); G3DSA:1.10.287	3,743	3,238	3,023	2,405	2,328									
Solyc01g080160	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2P6Y2_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM); mobidb-lite (MOB	14,542	13,944	10,071	10,925	11,159									
Solyc01g080170	Hydroxymethylglutaryl-CoA lyase (AHRD V3.3 *** W9QRW1_9ROSA)		F:GO:0004419; C:GO	F:hydroxymethylglut	EC:4.1.3.4	Hydroxymethylglutary	IPR013785 (G3DSA:3.20.20.GENE3D	16,262	16,806	19,975	21,703	24,327									
Solyc01g080180	Ribosomal protein L34e superfamily protein (AHRD V3.3 *** AT3G06180.1)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			mobidb-lite (MOBIDB_LITE); IPR0081	4,153	5,054	6,393	6,514	5,792									
Solyc01g080200	Mediator of RNA polymerase II transcription subunit 33A (AHRD V3.3 *** MD33A_ARATH)		C:GO:0016592; P:GO	C:mediator complex; P:regulation of phenylpropanoid metabolic			PTHR33739:SF5 (PANTHER); IPR039	50,673	30,108	11,676	12,947	17,101	-0,723	0,013	0,545	0,022			down	up	
Solyc01g080210	Ribonucleoside-diphosphate reductase small chain family protein (AHRD V3.3 *** B9HMC3_POPTR)		P:GO:0009263; F:GO	P:deoxyribonucleotide biosynthetic process; F:oxidoreductase a			IPR000358 (PFAM); IPR012348 (G3D	3,704	3,678	28,931	36,902	28,191									
Solyc01g080220	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9RSS3_RICCO)		F:GO:0016787	F:hydrolase activity			IPR002925 (PFAM); IPR029058 (G3D	16,741	24,246	132,234	147,774	164,407									
Solyc01g080240	mitogen-activated protein kinase 13	mapk13	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	115,337	103,581	84,289	84,777	88,595									
Solyc01g080250	BTB-POZ and MATH domain 2 (AHRD V3.3 *** AT3G06190.1)		F:GO:0005515	F:protein binding			IPR002083 (SMART); IPR000210 (SM	60,948	65,126	96,618	112,290	95,132									
Solyc01g080260	ARM repeat superfamily protein (AHRD V3.3 *** AT5G18980.1)		C:GO:0016021	C:integral component of membrane			IPR011989 (G3DSA:1.25.10.GENE3D	1,687	1,997	2,437	6,792	5,544			1,171	0,039	1,469	0,002		up	up
Solyc01g080270	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G14290.1)						IPR022742 (PFAM); IPR029058 (G3D	33,060	27,684	44,832	44,549	40,086									
Solyc01g080280	chloroplast glutamine synthetase	cgs	F:GO:0004356; P:GO	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetase	IPR008146 (SMART); IPR008147 (PF	27,503	75,128	5,812	9,969	22,293	1,477	0,000	1,935	0,000			up	up	
Solyc01g080290	AWPM-19-like membrane family protein (AHRD V3.3 *** B9HMA9_POPTR)		C:GO:0016021	C:integral component of membrane			IPR008390 (PFAM); IPR008390 (PAN	0,302	0,491	0,000	0,243	0,140									
Solyc01g080300	cobalt ion transmembrane transporter (AHRD V3.3 *** AT3G21580.1)		C:GO:0009507; C:GO	C:chloroplast; C:integral component of membrane			IPR003339 (PFAM); PTHR33514:SF3	9,201	7,127	13,964	17,539	15,454									
Solyc01g080310	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151TET9_CAJCA)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	10,416	6,069	5,500	6,418	6,369	-0,748	0,045					down		
Solyc01g080320	phospholipase D gamma 3 (AHRD V3.3 --* AT4G11840.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,651	1,940	1,437	1,531	1,583									
Solyc01g080330	Bax inhibitor-1 family protein (AHRD V3.3 *** AT4G15470.1)		C:GO:0016021	C:integral component of membrane			IPR006214 (PFAM); PTHR23291:SF3	217,615	194,239	267,514	279,497	250,852									
Solyc01g080340	LOW QUALITY:BSD domain-containing protein 1 (AHRD V3.3 *** A0A151U0M7_CAJCA)		C:GO:0009507	C:chloroplast			IPR005607 (SMART); IPR005607 (PF	22,088	24,075	22,717	15,851	16,690					-0,515	0,007			down
Solyc01g080350	Calcium-binding protein 39 (AHRD V3.3 *** A0A151U0E3_CAJCA)		F:GO:0004674; P:GO	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR013878 (PFAM); IPR011989 (G3D	10,744	9,549	12,276	12,747	10,609									
Solyc01g080360	clathrin adaptor complexes medium subunit family protein (AHRD V3.3 *** AT2G20790.1)		P:GO:0015031; C:GO	P:protein transport; C:membrane			G3DSA:2.60.40.1170 (GENE3D); IPR(	24,862	18,243	29,851	32,219	31,027									
Solyc01g080363	Charged multivesicular body protein 1 (AHRD V3.3 *** A0A1D1YV61_9ARAE)		P:GO:0006810	P:transport			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,019	0,000	0,000	0,047									
Solyc01g080367	Hexosyltransferase (AHRD V3.3 *** K4AXT1_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR029044 (G3DSA:3.90.550.GENE3	0,576	0,305	0,050	0,069	0,211									
Solyc01g080370	wall associated kinase-like 5 (AHRD V3.3 --* AT1G16160.1)							0,000	0,018	0,000	0,000	0,000									
Solyc01g080380	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 *** A0A068TRL8_COFCA)		F:GO:0004014; P:GO	F:adenosylmethioni	EC:4.1.1.5	Adenosylmethionine	IPR001985 (TIGRFAM); G3DSA:3.60.	0,261	0,211	0,000	0,000	0,000									
Solyc01g080400	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G06270.1)		F:GO:0003824	F:catalytic activity			IPR001932 (SMART); IPR001932 (PF	20,916	15,206	21,073	21,663	19,923									
Solyc01g080410	Methionine sulfoxide reductase, putative (AHRD V3.3 *** B9RX37_RICCO)		P:GO:0006979; P:GO	P:response to oxida	EC:1.8.4.12	Peptide-methionine (!	G3DSA:2.170.150.20 (GENE3D); IPR(	9,089	7,239	604,491	732,035	498,073									
Solyc01g080415	Cox19-like CHCH family protein (AHRD V3.3 --* AT5G18920.2)		C:GO:0005758; P:GO	C:mitochondrial intermembrane space; P:mitochondrial respirato			mobidb-lite (MOBIDB_LITE)	6,500	5,838	24,194	31,616	17,643									
Solyc01g080430	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03000.2)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	108,744	103,144	131,626	134,339	128,804									
Solyc01g080450	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G16830.1)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	12,547	10,475	16,592	17,180	14,783									
Solyc01g080460	pyruvate orthophosphate dikinase (AHRD V3.3 *** AT4G15530.6)		F:GO:0005524; P:GO	F:ATP binding; P:py	EC:2.7.9.1	Pyruvate, phosphate	IPR002192 (PFAM); IPR008279 (PFA	1257,971	722,372	2636,196	2124,459	2093,382	-0,773	0,001					down		
Solyc01g080470	tRNA/rRNA methyltransferase family protein (AHRD V3.3 *** A9PAZ0_POPTR)		F:GO:0003723; P:GO	F:RNA binding; P:RNA processing; F:RNA methyltransferase ac			IPR001537 (PFAM); IPR029026 (G3D	1,974	1,930	3,005	2,436	2,402									
Solyc01g080480	Endonuclease/exonuclease/phosphatase family protein (AHRD V3.3 *** B9HM94_POPTR)		F:GO:0003723; P:GO	F:RNA binding; P:RNA processing; F:RNA methyltransferase ac			IPR036691 (G3DSA:3.60.10.GENE3D	0,021	0,078	0,119	0,200	0,284									
Solyc01g080490	LOW QUALITY:transmembrane protein, putative (DUF679 domain membrane protein 2) (AHRD V3.3 *** AT3		C:GO:0005783; C:GO	C:endoplasmic reticulum; C:plant-type vacuole membrane; P:ab			IPR007770 (PFAM); IPR007770 (PAN	1,615	2,563	1,296	1,391	1,456									
Solyc01g080500	LOW QUALITY:Plant/F10N7-170 protein, putative (AHRD V3.3 *** G7IFN2_MEDTR)						PF15365 (PFAM); mobidb-lite (MOBID	346,840	327,321	130,768	233,369	157,208					0,838	0,000			up
Solyc01g080510	PH-response transcription factor pacC/RIM101 isoform 1 (AHRD V3.3 *** A0A061EVN3_THECC)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			G3DSA:3.40.50.300 (GENE3D); mobic	9,897	12,187	15,052	18,562	19,447									
Solyc01g080530	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9RSW4_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR006620 (SMART); IPR003582 (PF	26,113	24,493	19,474	17,156	18,144									
Solyc01g080540	Histidine-containing phosphotransfer protein (AHRD V3.3 *** Q94KS0_CATRO)		P:GO:0000160	P:phosphorelay signal transduction system			IPR008207 (PFAM); IPR036641 (G3D	16,958	18,319	9,443	9,048	10,982									
Solyc01g080550	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)		C:GO:0016021	C:integral component of membrane			IPR036452 (G3DSA:3.90.245.GENE3	0,000	0,036	0,000	0,025	0,046									
Solyc01g080570	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)		C:GO:0016021	C:integral component of membrane			IPR001910 (PFAM); IPR036452 (G3D	0,021	0,036	0,462	0,778	0,943									
Solyc01g080580	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)		C:GO:0016021	C:integral component of membrane			IPR001910 (PFAM); IPR036452 (G3D	0,357	1,017	0,219	0,339	0,353									
Solyc01g080590	Low-density lipoprotein receptor-related (AHRD V3.3 *** A0A0B0MXM6_GOSAR)		C:GO:0016021	C:integral component of membrane				25,037	23,862	46,706	43,576	44,270									
Solyc01g080600	Histone H3 (AHRD V3.3 *** A0A068VC55_COFCA)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS); IPR000164 (SM	6,043	7,490	1,227	0,584	0,638									
Solyc01g080610	Farnesyl pyrophosphate synthase (AHRD V3.3 --* E7EJI5_ALIPL)						IPR005508 (PFAM); PTHR31541 (PAN	0,038	0,000	0,000	0,000	0,000									
Solyc01g080620	BTB/POZ domain-containing protein isoform 1 (AHRD V3.3 *** A0A061EQ91_THECC)		F:GO:0005515	F:protein binding			IPR000210 (SMART); IPR000210 (PF	37,478	32,021	42,065	40,536	40,822									
Solyc01g080640	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *** G7IF78_	ABCC1	F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR003439 (PF	206,974	297,344	311,612	338,635	300,032									
Solyc01g080660	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT2G21440.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR003954 (SM	11,264	11,898	12,022	10,193	10,221									
Solyc01g080670	Squamosa promoter binding protein 7		F:GO:0003677; C:GO	F:DNA binding; C:nucleus			IPR036893 (G3DS SBP	103,598	88,215	72,869	65,636	70,960									
Solyc01g080680	Sugar facilitator protein 3	SFP3	C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); G3DSA:1.20.12	10,935	20,154	1,485	1,779	1,691									
Solyc01g080690	WD40 repeat-containing protein (AHRD V3.3 *** A0A118JWM1_CYNCS)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	33,111	32,358	78,330	77,634	72,180									
Solyc01g080700	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)		C:GO:0016021	C:integral component of membrane			IPR036452 (G3DSA:3.90.245.GENE3	12,337	11,357	7,552	8,181	9,606									
Solyc01g080705	Inosine-uridine preferring nucleoside hydrolase-related family protein (AHRD V3.3 *-* B9P577_POPTR)		C:GO:0016021	C:integral component of membrane			IPR036452 (G3DSA:3.90.245.GENE3	5,565	5,311	3,617	4,236	4,074									
Solyc01g080720	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061ENU5_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,913	5,184	4,593	5,411	4,640									
Solyc01g080725	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,041	0,000	0,000	0,000									
Solyc01g080760	Embryo defective 1703 protein, putative (AHRD V3.3 *-* G8A2Y6_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	12,696	16,527	18,216	17,614	19,711									
Solyc01g080770	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4AXX0_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART); IPR000719 (SM	3,545	3,706	1,996	2,265	2,263									
Solyc01g080780	Translocase of chloroplast (AHRD V3.3 *** A0A0K9PDK5_ZOSMR)		F:GO:0005525; F:GO	F:GTP binding; F:hydrolase activity, acting on acid anhydrides			IPR006703 (PFAM); G3DSA:3.40.50.3	11,687	12,958	18,943	21,051	22,278									
Solyc01g080810	Isoleucyl-tRNA synthetase (AHRD V3.3 *** F4K4Q2_ARATH)		F:GO:0000049; F:GO	F:tRNA binding; F:a	EC:6.1.1.5; EC:3.1.1	Isoleucine--tRNA liga	IPR002301 (PRINTS); IPR013155 (PF	34,590	41,821	36,771	34,574	45,076									
Solyc01g080820	LOW QUALITY:Poly [ADP-ribose] polymerase (AHRD V3.3 *-* K4BW60_SOLLC)		F:GO:0003950; C:GO	F:NAD+ ADP-ribosyltransferase activity; C:membrane; C:integra			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,080	0,000	0,000	0,000									
Solyc01g080830	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein (AHRD V3.3 *** AT4G01790.1)						IPR029064 (G3DSA:3.30.1330.GENE	0,000	0,000	0,025	0,025	0,000									
Solyc01g080840	Protein translocase subunit SecA (AHRD V3.3 *** K4AXX7_SOLLC)		F:GO:0005524; P:GO	F:ATP binding; P:protein targeting; C:membrane; P:protein impo			IPR000185 (PRINTS); IPR011115 (SM	58,803	74,194	71,829	78,297	95,759			0,412	0,014				up	
Solyc01g080850	Protein transport protein SEC23 (AHRD V3.3 *** W9QYF9_9ROSA)		P:GO:0006886; P:GO	P:intracellular protein transport; P:endoplasmic reticulum to Gol			IPR006896 (PFAM); IPR036465 (G3D	98,246	86,533	109,370	114,901	106,712									
Solyc01g080860	Protoheme IX farnesyltransferase, mitochondrial-like protein (AHRD V3.3 *** A0A0B0P8P0_GOSAR)		F:GO:0008495; C:GO	F:protoheme IX farr	EC:2.5.1.29	Geranylgeranyl diphc	IPR006369 (TIGRFAM); IPR016315 (F	64,204	62,938	108,032	99,511	103,688									

Solyc01g080870	Peptide transporter, putative (AHRD V3.3 *** B9SKJ1_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D); IPR(	43,834	28,258	115,122	157,087	99,357	-0,605	0,023			0,451	0,010	down		up
Solyc01g080880	Kinase family protein (AHRD V3.3 *** D7MRC6_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR011990 (G3DSA:1.25.40.GENE3D	66,407	71,475	77,968	73,864	70,237									
Solyc01g080890	KH domain-containing protein / zinc finger (CCCH type) family protein (AHRD V3.3 --* AT5G06770.6)						PTHR35282:SF5 (PANTHER); PTHR3!	43,695	51,248	68,294	54,028	40,005			-0,774	0,000				down	
Solyc01g080900	Cytochrome P450 (AHRD V3.3 *** A0A124SDJ5_CYNCS)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR001128 (PRINTS); IPR002403 (PF	16,006	13,791	15,675	9,351	19,365					-0,742	0,004			down
Solyc01g080910	LOW QUALITY:polyadenylate-binding protein 1-B-binding protein (AHRD V3.3 *** AT4G19950.1)		C:GO:0016021	C:integral component of membrane			PTHR33133 (PANTHER); PTHR33133	164,849	97,575	93,989	59,245	90,234	-0,728	0,009			-0,663	0,005	down		down
Solyc01g080930	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072TX02_MEDTR)		F:GO:0003860	F:3-hydroxyisobuty	EC:3.1.2.4	3-hydroxyisobutyryl-(	G3DSA:3.90.226.40 (GENE3D); IPR0	53,361	51,893	122,782	115,824	109,129									
Solyc01g080940	Transthyretin-like S-allantoin synthase protein (AHRD V3.3 *** A0A0G2T5A0_9ROSI)		P:GO:0006144; F:G(	P:purine nucleobas	EC:3.5.2.17	Hydroxyisourate hydı	IPR000895 (PRINTS); IPR036778 (G3	35,218	32,446	43,488	38,748	46,306									
Solyc01g080950	Late embryogenesis abundant protein (AHRD V3.3 *** A0A072TZA1_MEDTR)		P:GO:0009793	P:embryo development ending in seed dormancy			IPR005513 (PFAM); mobidb-lite (MOB	0,000	0,019	0,000	0,025	0,000									
Solyc01g080960	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7KSI4_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM); G3DSA:3.30.13	0,000	0,000	0,000	0,022	0,000									
Solyc01g080970	Methyltransferase (AHRD V3.3 *** Q9LRL5_ARATH)		F:GO:0008168	F:methyltransferase activity			G3DSA:1.10.1200.270 (GENE3D); G3	0,000	0,000	0,000	0,000	0,024									
Solyc01g080990	Carboxyl methyltransferase (AHRD V3.3 *** Q70T29_BIXOR)		F:GO:0008168	F:methyltransferase activity			G3DSA:1.10.1200.270 (GENE3D); G3	0,078	0,055	0,000	0,000	0,024									
Solyc01g081000	Phosphatase 2C family protein, putative (AHRD V3.3 *** A0A061GDE7_THECC)		F:GO:0003824	F:catalytic activity			IPR001932 (SMART); IPR001932 (SM	1,407	1,524	3,190	2,300	2,271									
Solyc01g081010	Nucleolar GTP-binding protein 1 (AHRD V3.3 *** K4AXZ3_SOLLC)		F:GO:0005525; C:G(	F:GTP binding; C:nucleolus			IPR006073 (PRINTS); IPR010674 (PF	840,617	720,446	499,492	464,338	455,605									
Solyc01g081020	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MAN3_ARALL)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM); IPR032867 (PFA	0,412	0,625	0,573	0,900	0,724									
Solyc01g081030	SCAI-like protein (AHRD V3.3 *** A0A0M4KE35_SOLTU)		F:GO:0003714; P:G(	F:transcription corepressor activity; P:transcription, DNA-templa			IPR022709 (PFAM); mobidb-lite (MOB	48,306	42,209	69,741	75,480	70,051									
Solyc01g081040	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061F730_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination			IPR001841 (SMART); IPR001841 (PF	0,119	0,480	0,050	0,022	0,023									
Solyc01g081050	D-alanine--poly(phosphoribitol) ligase subunit 1 (AHRD V1 *--- DLTA_BACSU)%3B contains Interpro domain(		F:GO:0003824; F:G(	F:catalytic activity; F:protein binding			IPR018391 (SMART); IPR025110 (PF	43,753	43,278	41,725	53,398	44,091					0,358	0,042			up
Solyc01g081060	xyloglucan endotransglucosylase-hydrolase XTH5		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR016455 (PIRSF); IPR000757 (PFA	35,183	58,152	212,070	283,745	196,775					0,424	0,049			up
Solyc01g081070	Protein transport protein sec23, putative (AHRD V3.3 *** B9SKJ9_RICCO)		P:GO:0006886; F:G(	P:intracellular protein transport; F:zinc ion binding; C:COPII vesi			IPR036465 (G3DSA:3.40.50.GENE3D	57,696	51,868	133,287	151,704	128,008									
Solyc01g081080	Replication factor C subunit, putative (AHRD V3.3 *-* B9T608_RICCO)		F:GO:0003677; P:G(	F:DNA binding; P:DNA replication			G3DSA:3.40.50.300 (GENE3D); G3DS	0,019	0,076	0,000	0,000	0,000									
Solyc01g081090	bHLH transcription factor 003		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,040	0,019	0,022	0,000	0,000									
Solyc01g081100	bHLH transcription factor 004		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,000	0,021	0,000	0,000	0,000									
Solyc01g081110	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A118K4S4_CYNCS)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMART); IPR002885 (PF	1,294	1,449	1,173	1,190	1,271									
Solyc01g081115	COMPLEX 1 LYR-like protein (AHRD V3.3 *** AT1G65032.1)						IPR008011 (PFAM); PTHR36724 (PAN	0,158	0,120	0,150	0,270	0,259									
Solyc01g081120	COMPLEX 1 LYR-like protein (AHRD V3.3 *** AT1G65032.1)						PTHR36724 (PANTHER)	0,059	0,041	0,025	0,170	0,071									
Solyc01g081140	Phototropic-responsive NPH3 family protein, putative (AHRD V3.3 *** A0A061EZT3_THECC)		F:GO:0005515	F:protein binding			IPR000210 (SMART); G3DSA:3.30.71	0,019	0,000	0,051	0,000	0,023									
Solyc01g081150	DNA-directed RNA polymerases I, II, and III subunit rpabc3 (AHRD V3.3 *** W9RLU0_9ROSA)		P:GO:0006351	P:transcription, DNA-templated			IPR005570 (SMART); IPR005570 (PF	36,827	37,260	44,598	42,086	38,469									
Solyc01g081160	Beta-glucosidase, putative (AHRD V3.3 *-* B9SAQ1_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D); IPR00	7,408	10,466	1,986	1,674	2,544									
Solyc01g081170	Beta-glucosidase, putative (AHRD V3.3 --* B9SAQ6_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process				1,991	2,383	0,368	0,428	0,800									
Solyc01g081173	Beta-glucosidase, putative (AHRD V3.3 *-* B9SAQ6_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); G3DSA:3.20.2(	1,609	2,002	0,476	0,314	0,588									
Solyc01g081175	Serine/threonine protein kinase (AHRD V3.3 --* F5C0G2_SOLCH)							0,076	0,036	0,000	0,120	0,046									
Solyc01g081177	Calcium-binding EF hand family protein (AHRD V3.3 *** AT1G64850.1)		F:GO:0005509; C:G(	F:calcium ion binding; C:integral component of membrane			PTHR11639 (PANTHER); PTHR11639	0,953	0,688	0,803	0,481	0,541									
Solyc01g081190	LOW QUALITY:Calcium-binding EF hand family protein (AHRD V3.3 *** AT1G64850.1)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,346	0,240	0,739	0,773	0,681									
Solyc01g081200	Protein OS-9 (AHRD V3.3 *** A0A1D1ZFI5_9ARAE)		C:GO:0005783	C:endoplasmic reticulum			IPR031985 (PFAM); IPR031985 (PAN	11,594	9,271	14,354	12,043	13,539									
Solyc01g081210	F-box/kelch-repeat protein SKIP25, putative (AHRD V3.3 *** G7K6R4_MEDTR)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	0,180	0,099	0,953	1,130	0,453									
Solyc01g081240	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y130_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	6,994	8,169	4,286	4,995	5,472									
Solyc01g081250	Glutathione s-transferase, putative (AHRD V3.3 *** B9SPC9_RICCO)	GSTU1	F:GO:0005515	F:protein binding			IPR004045 (PFAM); IPR004046 (PFA	42,092	13,679	25,226	11,399	9,929					-1,142	0,001			down
Solyc01g081270	Glutathione s-transferase, putative (AHRD V3.3 *** B9SPC9_RICCO)	GSTU3	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D); IPR00	7,696	5,991	30,328	32,541	35,130									
Solyc01g081280	Redox-regulatory protein FAM213A (AHRD V3.3 *-* A0A199V9J3_ANACO)		P:GO:0055114	P:oxidation-reduction process			PTHR28630:SF13 (PANTHER); IPR03	0,000	0,000	0,022	0,025	0,000									
Solyc01g081290	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y132_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,072	4,142	2,657	2,458	2,616									
Solyc01g081293	Redox-regulatory protein FAM213A-like protein (AHRD V3.3 *** A0A0B2R8Q7_GLYSO)		P:GO:0055114	P:oxidation-reduction process			IPR032801 (PFAM); PTHR28630:SF1	0,862	1,159	0,630	0,866	0,849									
Solyc01g081297	phosphoenolpyruvate carboxylase-related kinase 2 (AHRD V3.3 *** AT1G12680.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	9,434	8,758	17,703	14,446	14,050									
Solyc01g081300	Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic (AHRD V3.3 *** PUR7_ARATH)		F:GO:0004639; P:G(	F:phosphoribosylan	EC:6.3.2.6	Phosphoribosylaminc	G3DSA:3.30.470.20 (GENE3D); G3DS	11,599	12,801	55,757	57,733	48,749									
Solyc01g081310	glutathione S-transferase T3	GSTU4	F:GO:0005515	F:protein binding			IPR004046 (PFAM); G3DSA:1.20.105	1,974	2,017	0,878	1,696	1,481									
Solyc01g081320	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RJS7_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	0,000	0,019	0,025	0,000	0,000									
Solyc01g081330	Chaperone protein DNAj, putative (AHRD V3.3 *** B9RJS6_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS); IPR001623 (SM	3,914	3,222	2,142	2,838	2,146									
Solyc01g081340	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1 (AHRD V3.3 *** B5TVE1_TOBAC)		F:GO:0008168	F:methyltransferase activity			G3DSA:1.10.1200.270 (GENE3D); IPF	0,097	0,080	0,000	0,025	0,024									
Solyc01g081350	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G64830.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,234	1,241	0,000	0,000	0,000									
Solyc01g081370	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G64830.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	1,052	2,110	0,025	0,000	0,000									
Solyc01g081380	nuclear matrix protein 1	nmp1	F:GO:0051011	F:microtubule minus-end binding			IPR010604 (PIRSF); IPR010604 (PFA	10,505	9,404	9,401	10,216	8,692									
Solyc01g081390	Glucose-6-phosphate/phosphate translocator (AHRD V3.3 *** Q6YZC3_ORYSJ)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR004853 (PFAM); IPR004696 (TIGF	17,009	25,435	28,083	26,930	28,656	0,610	0,033					up		
Solyc01g081410	Major facilitator superfamily protein (AHRD V3.3 *** AT5G45275.1)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM); G3DSA:1.20.125	6,416	4,217	4,398	4,792	4,320									
Solyc01g081420	Serrate RNA effector molecule (AHRD V3.3 *-* A0A1D1Y9V9_9ARAE)						IPR008979 (G3DSA:2.60.120.GENE3	16,617	11,280	17,527	20,723	19,448									
Solyc01g081430	DNA replication and repair recF (AHRD V3.3 *-* A0A0B0P660_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	6,699	6,184	7,759	6,822	7,935									
Solyc01g081440	nuclear factor 1 A-type protein (DUF1005) (AHRD V3.3 *** AT5G17640.1)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity			IPR010410 (PFAM); IPR010410 (PAN	14,340	9,475	11,227	7,983	10,210					-0,489	0,045			down
Solyc01g081450	Glycine-rich protein A3 (AHRD V3.3 *** A0A1D1Y762_9ARAE)						PTHR31248 (PANTHER); PTHR31248	52,610	65,195	48,924	51,511	52,545									
Solyc01g081460	tRNA (guanine-N-7) methyltransferase (AHRD V3.3 *** AT5G17660.1)		P:GO:0006400; F:G(	P:tRNA modificatior	EC:2.1.1.33	tRNA (guanine(46)-N	PF02390 (PFAM); G3DSA:3.40.50.15(	5,104	4,682	7,593	8,109	8,295									
Solyc01g081470	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial (AHRD V3.3 *** K4AY39_SOLLC)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	9,324	12,366	14,542	13,153	15,016									
Solyc01g081480	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G17670.1)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR012908 (PFAM); IPR039529 (PAN	3,358	5,142	2,761	3,458	3,784									
Solyc01g081490	Sigma factor (AHRD V3.3 *** A0A0G2STP3_9ROSI)	SIG2	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra			IPR000943 (PRINTS); G3DSA:1.10.6(	17,188	25,724	38,773	40,075	48,584	0,610	0,033					up		
Solyc01g081500	heterochromatin protein 1-like protein	hp1L	C:GO:0005634	C:nucleus			IPR008251 (SMART); IPR000953 (SM	85,357	82,947	73,959	65,467	74,741									
Solyc01g081510	3-hydroxyisobutyrate dehydrogenase, putative (AHRD V3.3 *** B9STG2_RICCO)		F:GO:0016491; F:G(	F:oxidoreductase activity; F:NADP binding; F:NAD binding; P:ox			IPR015815 (PIRSF); IPR006115 (PFA	10,535	9,840	15,057	10,455	12,742					-0,522	0,037			down
Solyc01g081520	30S ribosomal S2 (AHRD V3.3 *** A0A0B0MLM4_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR001865 (PRINTS); IPR001865 (PF	57,357	58,164	63,310	57,448	57,810									
Solyc01g081530	Annexin (AHRD V3.3 *** M1DLM8_SOLTU)		F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS); IPR018502 (SM	0,019	0,000	0,000	0,000	0,000									
Solyc01g081535	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT3G58120.2)							0,021	0,000	0,025	0,000	0,024									
Solyc01g081540	Myosin family protein, putative, expressed (AHRD V3.3 *** Q10CX1_ORYSJ)		F:GO:0003774; F:G(	F:motor activity; F:ı	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (SMART); IPR002710 (SM	82,778	64,430	32,690	39,342	32,497									
Solyc01g081545	Myosin (AHRD V3.3 *-* W6A1M7_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS); IPR001609 (SM	16,441	9,121	5,283	7,593	4,668	-0,820	0,040					down		
Solyc01g081560	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UML1_ANACO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,502	1,731	2,379	2,107	2,067									
Solyc01g081570	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)						IPR025521 (PFAM); G3DSA:3.90.132	43,107	38,924	11,439	10,309	13,709									
Solyc01g081590	Non-specific lipid-transfer protein (AHRD V3.3 *** A0A059B8S7_EUCGR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS); G3DSA:1.10.11	0,019	0,082	0,074	0,475	0,046									
Solyc01g081600	Non-specific lipid-transfer protein (AHRD V3.3 *** K4AY52_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS); IPR016140 (SM	0,473	0,269	0,631	1,031	1,127									
Solyc01g081610	Beta-hexosaminidase (AHRD V3.3 *** D3TI69_SOLLC)		F:GO:0004563; P:G(	F:beta-N-acetylhex	EC:3.2.1.52	Beta-N-acetylhexosa	IPR025705 (PRINTS); IPR015883 (PF	15,942	24,395	54,462	76,330	58,296	0,640	0,021			0,492	0,018	up		up
Solyc01g081620	Vacuolar protein sorting-associated protein 62 (AHRD V3.3 *** A0A103Y146_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR009291 (PFAM); mobidb-lite (MOB	0,335	0,487	0,287	0,790	0,941									
Solyc01g081640	DUF936 family protein (AHRD V3.3 *** A2Q3C0_MEDTR)		F:GO:0008017	F:microtubule binding			IPR010341 (PFAM); mobidb-lite (MOB	0,415	1,254	0,000	0,025	0,000									
Solyc01g086640	LOW QUALITY:O-fucosyltransferase family protein (AHRD V3.3 *** AT2G44500.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:chloroplast; C:integral componei			IPR019378 (PFAM); IPR024709 (PIRS	21,911	8,434	4,189	7,709	10,921	-1,349	0,000	1,370	0,000			down	up	
Solyc01g086650	Siroheme synthase (AHRD V3.3 *** W8SGE9_TOBAC)		F:GO:0008168; P:G(	F:methyltransferase activity; P:siroheme biosynthetic process			IPR014777 (G3DSA:3.40.1010.GENE	10,599	15,960	11,689	12,387	11,524									
Solyc01g086660	LOW QUALITY:agenet domain protein (DOMAIN OF UNKNOWN FUNCTION 724 2) (AHRD V3.3 --* AT1G11420.1)							0,605	3,473	0,125	0,197	0,048	2,533	0,000					up		
Solyc01g086670	LOW QUALITY:Expressed protein-RZ53 (AHRD V3.3 --* E0CW61_9ORYZ)						PTHR37748 (PANTHER)	0,220	1,672	0,100	0,148	0,513									
Solyc01g086680	glutathione S-transferase T1	GSTU5	F:GO:0005515	F:protein binding			IPR004045 (PFAM); IPR004046 (PFA	0,846	2,836	1,743	3,320	6,631			1,914	0,001				up	
Solyc01g086690	LOW QUALITY:Sister chromatid cohesion 1 protein 3 (AHRD V3.3 *** W9R9I5_9ROSA)		F:GO:0005515; P:G(	F:protein binding; P:sister chromatid cohesion; C:cohesin comp			IPR006909 (PFAM); IPR006910 (PFA	1,779	1,830	0,243	0,069	0,166									
Solyc01g086700	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072TGP1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000008 (SMART); IPR013583 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc01g086710	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** K4AY64_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:3.90.1800.10 (GENE3D); IPR(	40,802	36,858	33,118	33,523	33,333									
Solyc01g086720	C2 domain-containing family protein (AHRD V3.3 *** B9GFS0_POPTR)		C:GO:0016021	C:integral component of membrane			IPR000008 (SMART); IPR013583 (PF	0,599	0,826	0,197	0,075	0,117									
Solyc01g086730	magnesium transporter, putative (DUF803) (AHRD V3.3 *** AT3G26670.4)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM); PTHR12570:SF4	1,345	1,172	0,615	1,152	0,400									
Solyc01g086740	DnaJ-like protein (AHRD V3.3 *** C4T7Z2_TOBAC)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS); IPR001623 (SM	55,034	58,268	79,277	72,195	73,761									
Solyc01g086750	Clustered mitochondria protein homolog (AHRD V3.3 *** K4AY68_SOLLC)		F:GO:0005515; P:G(	F:protein binding; P:intracellular distribution of mitochondria			IPR019734 (SMART); IPR007967 (PF	173,664	152,376	172,353	175,791	179,786									
Solyc01g086755	LOW QUALITY:Polyprotein, putative (AHRD V3.3 *-* Q0KIN7_SOLDE)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); PTHR23272:SF5	0,021	0,021	0,025	0,000	0,000									
Solyc01g086760	Histone H3 (AHRD V3.3 *** H3_VOLCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS); IPR000164 (SM	0,132	0,118	0,000	0,000	0,000									
Solyc01g086800	Histone H3 (AHRD V3.3 *** H3_VOLCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS); IPR000164 (SM	0,078	0,043	0,000	0,000	0,000									
Solyc01g086810	NBS-LRR disease resistance protein (AHRD V3.3 *** G7IVT3_MEDTR)		F:GO:0005515; F:G(	F:protein binding; F:ADP binding			PR00364 (PRINTS); IPR001611 (PFA	46,876	38,848	33,354	37,695	40,543									
Solyc01g086820	Histone H3 (AHRD V3.3 *** A0A068VC55_COFCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS); IPR000164 (SM	13,565	15,850	3,225	1,272	2,145					-1,326	0,015			down
Solyc01g086840	Thaumatin-like protein (AHRD V1 ***- Q5DWG1_CRYJA)%3B contains Interpro domain(s) IPR001938						IPR001938 (PRINTS); IPR001938 (SM	0,019	0,018	0,000	0,000	0,000									
Solyc01g086845	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 --* RPOA_HUPLU)							0,000	0,039	0,025	0,022	0,046									
Solyc01g086850	Ras-related protein RGP1 (AHRD V3.3 *** RLGP1_ORYSJ)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00177 (SMAR	8,184	9,369	7,446	7,711	7,397									
Solyc01g086860	DUF3128 family protein (AHRD V3.3 *** G7J0G9_MEDTR)						IPR021475 (PFAM); IPR021475 (PAN	29,802	24,609	23,625	20,322	20,581									
Solyc01g086870	bHLH transcription factor 076		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	37,103	68,662	15,505	11,335	14,010	0,913	0,003					up		
Solyc01g086890	G-patch domain-containing protein (AHRD V3.3 *** A0A103XTL2_CYNCS)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing			IPR000061 (SMART); IPR000467 (SM	200,997	195,949	186,690	175,256	183,356									
Solyc01g086893	CBL-interacting protein kinase 9 (AHRD V3.3 --* AT1G01140.2)							10,347	9,069	6,836	7,986	7,636									
Solyc01g086895	Potassium transporter (AHRD V3.3 --* A0A0D3GJS3_9ORYZ)							6,760	5,444	3,900	5,246	4,357									
Solyc01g086900	tRNA (cytidine(34)-2'-O)-methyltransferase (AHRD V3.3 *** AT5G26880.1)		P:GO:0001510; F:G(	P:RNA methylation; F:RNA binding; P:RNA processing; F:RNA n			IPR029026 (G3DSA:3.40.1280.GENE	8,816	9,537	7,666	6,751	8,045									
Solyc01g086920	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PVU5_ZOSMR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,482	0,200	0,000	0,000	0,000									
Solyc01g086930	GAMMA RESPONSE 1 family protein (AHRD V3.3 *** B9GFQ6_POPTR)		F:GO:0004519; P:G(	F:endonuclease activity; P:DNA repair			IPR013882 (PFAM); mobidb-lite (MOB	2,445	2,550	0,556	0,673	0,917									
Solyc01g086950	SWIB/MDM2 and Plus-3 and GYF domain-containing protein (AHRD V3.3 *** AT5G08430.2)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR004343 (SMART); IPR036885 (G3	14,191	11,882	16,744	18,804	18,789									
Solyc01g086953	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 *-*		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR026960 (PFAM)	0,037	0,039	0,000	0,000	0,047									
Solyc01g086957	GYF domain protein (AHRD V3.3 *-* A0A072UAG4_MEDTR)		F:GO:0005515	F:protein binding			IPR003169 (SMART); IPR003169 (PF	17,059	14,737	20,680	22,434	21,354									
Solyc01g086960	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** A0A0K9Q649_ZOSM		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR002653 (SMART); IPR000058 (SM	366,615	364,461	234,399	386,345	297,546					0,724	0,000			up
Solyc01g086970	A20/AN1 zinc finger protein SAP4		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR002653 (SMART); IPR000058 (SM	348,454	303,090	457,331	437,815	384,041									
Solyc01g086980	RNA binding family protein, putative (AHRD V3.3 *** A0A061DVK1_THECC)		F:GO:0003676; P:G(	F:nucleic acid binding; P:mRNA processing			IPR000504 (SMART); IPR000504 (PF	36,941	32,181	47,615	47,105	43,890									
Solyc01g086990	Pre-mRNA-splicing factor SYF1 (AHRD V3.3 *** A0A0B0P9F3_GOSAR)		F:GO:0005515; P:G(	F:protein binding; P:RNA processing			IPR003107 (SMART); IPR011990 (G3	71,685	64,418	67,689	62,890	66,347									
Solyc01g086995	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)						IPR005181 (PFAM); IPR036514 (G3D	1,075	1,091	2,451	1,744	1,347									
Solyc01g087000	Leucine-rich repeat receptor protein kinase EXS (AHRD V3.3 --* M8BQ53_AEGTA)							0,101	0,140	0,124	0,173	0,120									
Solyc01g087003	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	0,572	0,581	0,622	0,555	0,612									
Solyc01g087007	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *-* AT1G63080.3)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	0,558	0,519	0,762	0,874	0,820									
Solyc01g087010	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7I2A7_MEDTR)		C:GO:0016020	C:membrane			IPR036514 (G3DSA:3.40.50.GENE3D	0,040	0,000	0,000	0,050	0,000									
Solyc01g087020	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7IZE0_MEDTR)						PTHR33659 (PANTHER); PTHR33659	81,026	86,089	41,414	40,435	56,536									
Solyc01g087030	Zinc finger transcription factor 10	C3H10	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	75,115	49,367	58,387	49,593	51,580	-0,579	0,023					down		
Solyc01g087035	asparagine synthetase 2 (AHRD V3.3 --* AT5G65010.2)							4,627	2,791	3,354	2,897	3,177									
Solyc01g087040	PsbP-like (AHRD V3.3 *** A0A0U9HL69_KLEFL)	PsbP-like	F:GO:0005509; C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR002683 (PFAM); IPR016123 (G3D	5,454	11,443	5,363	7,239	11,031	1,095	0,004	1,035	0,000			up	up	
Solyc01g087050	Protein TRANSPARENT TESTA 1 (AHRD V3.3 *** A0A0B2QDT4_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR013087 (PFAN C2H2	0,158	0,105	0,022	0,000	0,000									
Solyc01g087060	E3 ubiquitin ligase BIG brother, putative (AHRD V3.3 *-* G7LDM4_MEDTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			PTHR14155 (PANTHER); IPR033276 (	0,544	0,798	0,101	0,385	0,187									
Solyc01g087070	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 *** ADT1_SOLTU)		C:GO:0005743; F:G(	C:mitochondrial inner membrane; F:transmembrane transporter			IPR002113 (PRINTS); IPR002067 (PF	10,931	19,232	2,660	3,319	4,220									
Solyc01g087080	interferon-activable protein (AHRD V3.3 *** AT3G52110.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,749	0,849	0,431	0,686	0,377									
Solyc01g087095	Telomerase reverse transcriptase (AHRD V3.3 *** F4YIN0_TOBAC)		F:GO:0003677; F:G(	F:DNA binding; F:te	EC:2.7.7.49	RNA-directed DNA pc	IPR003545 (PRINTS); IPR021891 (SM	0,156	0,101	0,000	0,025	0,000									
Solyc01g087120	F1-ATP synthase delta subunit (AHRD V3.3 *** Q9SXX1_IPOBA)		P:GO:0015986; F:G(	P:ATP synthesis co	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR000711 (PRINTS); IPR000711 (TI(	224,567	241,539	280,514	268,551	279,696									
Solyc01g087130	R2R3MYB transcription factor 47	R2R3MYB47	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,040	0,041	0,000	0,000	0,000									
Solyc01g087140	Late embryogenesis abundant protein (AHRD V3.3 *** G7II20_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR318	0,352	0,380	0,000	0,051	0,000									
Solyc01g087150	Protein DETOXIFICATION (AHRD V3.3 *** K4AYA6_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM); IPR002528 (TIGF	0,613	0,932	0,072	0,146	0,235									
Solyc01g087170	Zinc finger transcription factor 11	C3H11	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding			IPR000571 (SMAF C3H	47,577	62,380	80,486	83,431	73,324									
Solyc01g087180	Microspore-specific promoter 2, putative (AHRD V3.3 --* A0A061G480_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,163	0,247	1,162	2,858	1,732									
Solyc01g087190	Chaperonin-like RbcX protein (AHRD V3.3 *** G7J266_MEDTR)		C:GO:0009570; F:G(	C:chloroplast stroma; F:protein folding chaperone; P:chaperone			IPR038052 (G3DSA:1.10.1200.GENE	6,812	6,865	5,851	7,291	6,575									
Solyc01g087200	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR002182 (PFA	2,555	3,077	3,298	3,852	3,271									
Solyc01g087210	Cellulose synthase family protein (AHRD V3.3 *** AT5G05170.1)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (l	IPR013083 (G3DSA:3.30.40.GENE3D	1049,497	711,603	227,540	182,810	229,596									
Solyc01g087230	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT3G09180.3)		C:GO:0016592	C:mediator complex			IPR021627 (PFAM); mobidb-lite (MOB	11,260	12,638	15,145	16,281	15,773									
Solyc01g087235	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT2G34300.3)							0,162	0,175	0,144	0,189	0,119									
Solyc01g087240	nuclear transcription factor Y subunit A-9		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRINT NF-YA	42,095	47,069	22,315	22,115	25,015									
Solyc01g087250	carotenoid cleavage dioxygenase 1A	ccd1a	F:GO:0016702; P:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR004294 (PFAM); PTHR10543:SF3	26,533	30,767	22,565	22,136	24,523									
Solyc01g087260	carotenoid cleavage dioxygenase 1B	ccd1b	F:GO:0016702; P:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR004294 (PFAM); PTHR10543:SF3	344,702	295,750	533,899	418,229	522,869					-0,349	0,050			down
Solyc01g087270	Carotenoid cleavage dioxygenase (AHRD V3.3 *-* A0A166HYX6_DAUCA)		C:GO:0009570; P:G(	C:chloroplast strom	EC:1.13.11; EC:1.13	Acting on single donors with incorporation of molecular oxyge		0,019	0,000	0,000	0,000	0,023									
Solyc01g087290	tRNA-dihydrouridine synthase (AHRD V3.3 *** A0A0V0I8M3_SOLCH)		P:GO:0002943; F:G(	P:tRNA dihydrouridine synthesis; F:tRNA dihydrouridine synthas			IPR013785 (G3DSA:3.20.20.GENE3D	20,751	21,154	20,724	21,287	23,759									
Solyc01g087300	tRNA-dihydrouridine synthase		P:GO:0002943; F:G(	P:tRNA dihydrouridine synthesis; F:tRNA dihydrouridine synthas			IPR001269 (PIRSF); IPR001269 (PFA	12,831	12,753	23,494	25,844	23,919									
Solyc01g087320	PHD finger family protein (AHRD V3.3 *-* AT3G08020.1)		F:GO:0046872	F:metal ion binding			IPR001965 (SMART); IPR013083 (G3	28,214	23,970	24,868	26,351	24,386									

Solyc01g087330	Histone-lysine N-methyltransferase MLL4 (AHRD V3.3 --* W9QFC2_9ROSA)		F:GO:0046872	F:metal ion binding				0,097	0,078	0,147	0,072	0,116									
Solyc01g087332	Histone-lysine N-methyltransferase MLL4 (AHRD V3.3 *-* W9QFC2_9ROSA)						IPR013083 (G3DSA:3.30.40.GENE3D	1,013	0,890	0,996	1,256	1,296									
Solyc01g087336	tRNA-dihydrouridine synthase (AHRD V3.3 *-* K4AYC0_SOLLC)		P:GO:0002943; F:G(	P:tRNA dihydrouridine synthesis; F:tRNA dihydrouridine synthas			IPR004653 (PANTHER)	0,198	0,177	0,289	0,151	0,164									
Solyc01g087340	tRNA-dihydrouridine synthase (AHRD V3.3 *-* K4AYC0_SOLLC)		F:GO:0046872	F:metal ion binding			PTHR10615 (PANTHER): PTHR10615	2,753	2,033	2,821	2,479	2,352									
Solyc01g087360	Histone-lysine N-methyltransferase MLL4 (AHRD V3.3 *-* W9QFC2_9ROSA)		F:GO:0046872	F:metal ion binding			PTHR10615:SF130 (PANTHER): PTHI	0,994	0,690	1,577	0,944	1,222									
Solyc01g087380	PHD finger family protein (AHRD V3.3 *-* B9GFC9_POPTR)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,737	6,553	8,051	6,232	6,704									
Solyc01g087385	tRNA-dihydrouridine synthase (AHRD V3.3 *-* K4AYC0_SOLLC)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	7,025	5,557	7,017	7,205	7,181									
Solyc01g087400	Histone-lysine N-methyltransferase MLL4 (AHRD V3.3 *** A0A0B0PKG0_GOSAR)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	30,507	24,788	33,075	31,664	32,312									
Solyc01g087410	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* A0A072UJ97_MEDTR)		F:GO:0046872	F:metal ion binding			IPR001965 (SMART): IPR013083 (G3	11,285	8,261	12,499	13,810	13,373									
Solyc01g087420	PHD finger family protein (AHRD V3.3 *** AT3G08020.1)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR001965 (SM	16,814	16,144	13,948	17,458	17,160									
Solyc01g087430	PHD finger family protein (AHRD V3.3 *** AT3G08020.1)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR001965 (SM	38,122	30,986	44,810	38,749	40,409									
Solyc01g087440	Protein EFR3 like B (AHRD V3.3 *-* A0A0B2PVI4_GLYSO)		P:GO:0072659	P:protein localization to plasma membrane			IPR039786 (PANTHER): PTHR12444:	0,783	0,670	0,755	0,791	0,824									
Solyc01g087450	Protein EFR3 B (AHRD V3.3 *** A0A1D1ZEH0_9ARAE)		P:GO:0072659	P:protein localization to plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,685	5,668	4,307	4,702	4,968									
Solyc01g087460	protein phosphatase 2C family protein (AHRD V3.3 *** AT2G34740.1)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	0,058	0,340	0,247	0,728	0,046									
Solyc01g087470	Peptidyl-prolyl cis-trans isomerase FKBP42 (AHRD V3.3 *** A0A0B2RKD3_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR001179 (PF.	1,070	0,876	1,471	2,308	2,002									
Solyc01g087480	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* A0A151UEH4_CAJCA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:mitochondrion; C:ribosome; P:translation; F:electron transfer act				0,000	0,000	0,025	0,000	0,000									
Solyc01g087490	Peptidyl-prolyl cis-trans isomerase FKBP42 (AHRD V3.3 *-* A0A0B2RKD3_GLYSO)		F:GO:0005515	F:protein binding			IPR004082 (PRINTS): IPR019734 (SM	3,598	3,479	3,128	3,885	3,629									
Solyc01g087500	DNA topoisomerase 2 (AHRD V3.3 *** K4AYE0_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:3.6.1.3; EC:5.99.	Adenosinetriphospha	PR00418 (PRINTS): IPR001154 (PRII	2,724	3,279	0,722	1,141	1,033									
Solyc01g087520	Ferredoxin-thioredoxin reductase, variable chain (AHRD V3.3 *** I3SXR8_MEDTR)		P:GO:0009107; P:G(	P:lipoate biosynthet	EC:2.8.1.8	Lipoyl synthase	G3DSA:2.30.30.50 (GENE3D): IPR00	34,561	43,037	38,713	43,396	45,865									
Solyc01g087530	Zinc transporter (AHRD V3.3 *** A0A0K9NP89_ZOSMR)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR003689 (PFAM): PTHR11040 (PAI	21,420	22,576	35,957	41,185	35,741									
Solyc01g087540	imidazolonepropionase (Protein of unknown function, DUF642) (AHRD V3.3 *** AT2G41810.1)		C:GO:0005618; C:G(	C:cell wall; C:plasma membrane			IPR008979 (G3DSA:2.60.120.GENE3I	35,103	34,580	5,431	2,755	4,044									
Solyc01g087550	Cytochrome b5 reductase 4 (AHRD V3.3 *** A0A0B2RKL5_GLYSO)		C:GO:0005829; F:G(	C:cytosol; F:oxidoreductase activity; F:heme binding; F:metal ic			IPR001199 (PRINTS): IPR001199 (SM	22,721	21,352	26,452	26,691	25,848									
Solyc01g087560	Methyltransferase (AHRD V3.3 *** K4AYE6_SOLLC)		P:GO:0006694; F:G(	P:steroid biosynthetic process; F:methyltransferase activity			IPR013705 (PFAM): IPR013216 (PFA	71,227	62,847	129,643	132,927	121,402									
Solyc01g087565	calmodulin-binding receptor-like cytoplasmic kinase 1 (AHRD V3.3 --* AT5G58940.4)							0,000	0,018	0,000	0,000	0,000									
Solyc01g087570	BnaA09g36760D protein (AHRD V3.3 *** A0A078EZT5_BRANA)						mobidb-lite (MOBIDB_LITE): PTHR339	0,000	0,021	0,072	0,000	0,023									
Solyc01g087580	LOW QUALITY:SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like		P:GO:0008150	P:biological_process			mobidb-lite (MOBIDB_LITE): mobidb-lit	21,128	5,628	3,864	7,875	3,371	-1,885	0,000			1,030	0,000	down		up
Solyc01g087590	Polyamine oxidase (AHRD V3.3 *** Q4H439_TOBAC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001613 (PRINTS): IPR036188 (G3	27,764	35,757	6,170	3,451	6,913									
Solyc01g087600	transmembrane protein, putative (DUF288) (AHRD V3.3 *** AT2G41770.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity			IPR005049 (PFAM): PTHR31362 (PAI	36,669	28,231	22,230	22,677	20,845									
Solyc01g087610	Alpha-N-acetylglucosaminidase (AHRD V3.3 *** Q9ZR45_TOBAC)		C:GO:0005773; P:G(	C:vacuole; P:embryo development ending in seed dormancy; P:			IPR024733 (PFAM): IPR024732 (PFA	15,176	19,256	16,344	20,091	20,193									
Solyc01g087620	ubiquitin-like protein 5 (AHRD V3.3 *** AT5G42300.1)		F:GO:0005515; P:G(	F:protein binding; P:cellular protein modification process			G3DSA:3.10.20.90 (GENE3D): IPR00(	0,886	1,404	1,166	1,140	1,388									
Solyc01g087640	alcohol dehydrogenase	adh	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	14,242	15,233	37,531	40,082	37,370									
Solyc01g087650	Conserved oligomeric Golgi complex component (AHRD V3.3 *** F8WL71_CITUN)		C:GO:0017119	C:Golgi transport complex			IPR016632 (PIRSF): IPR007255 (PFA	24,456	21,796	25,383	24,950	25,745									
Solyc01g087670	Transducin/WD40 repeat protein (AHRD V3.3 *** A0A072UCU5_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:rRNA processing; C:small-subunit processo			IPR001680 (SMART): IPR024977 (PF.	46,129	39,224	38,283	36,649	33,973									
Solyc01g087680	Structural constituent of ribosome, putative (AHRD V3.3 *** A0A061EZC6_THECC)		C:GO:0016021	C:integral component of membrane			IPR016804 (PIRSF): IPR005134 (PFA	16,416	18,896	40,822	48,237	46,777									
Solyc01g087690	Sigma factor (AHRD V3.3 *** A0A0G2STQ4_9ROSI)	SIG4	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra			IPR000943 (PRINTS): IPR036388 (G3	0,019	0,076	0,000	0,000	0,000									
Solyc01g087700	LOW QUALITY:adenosine kinase 2 (AHRD V3.3 --* AT5G03300.3)							0,040	0,041	0,000	0,025	0,000									
Solyc01g087720	structural maintenance of chromosomes 5 (AHRD V3.3 *** AT5G15920.1)		P:GO:0000724; P:G(	P:double-strand break repair via homologous recombination; P:s			IPR005134 (PFAM): G3DSA:3.40.50.3	77,533	56,710	99,245	105,739	95,180									
Solyc01g087730	Ribosomal protein (AHRD V3.3 *** K4AYG3_SOLLC)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR028364 (PFAM): IPR016095 (G3D	77,864	117,363	85,616	106,679	148,645	0,620	0,033	0,793	0,000			up	up	
Solyc01g087740	Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	0,644	0,529	0,022	0,047	0,023									
Solyc01g087750	Protein RETICULATA-RELATED 4, chloroplastic (AHRD V3.3 *** A0A199V226_ANACO)		C:GO:0016021	C:integral component of membrane			IPR021825 (PFAM): mobidb-lite (MOBI	0,438	1,075	0,000	0,145	0,143									
Solyc01g087770	Subtilisin-like protease (AHRD V3.3 *** A0A0B2SDI9_GLYSO)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR000209 (PFAM): G3DSA:3.50.30.3	0,473	0,662	0,068	0,150	0,283									
Solyc01g087775	Subtilisin-like protease (AHRD V3.3 *-* Q38708_ALNGL)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	0,544	0,584	0,050	0,072	0,210									
Solyc01g087780	LOW QUALITY:serine protease SBT4A	sbt4a	F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	0,019	0,653	0,044	0,000	0,093									
Solyc01g087785	Subtilisin-like protease SDD1 (AHRD V3.3 *-* A0A1D1XBY5_9ARAE)		F:GO:0004252; P:G(	F:serine-type endopeptidase activity; P:proteolysis; F:peptidase			PTHR10795:SF514 (PANTHER): PTHI	0,040	0,099	0,022	0,022	0,024									
Solyc01g087790	LOW QUALITY:subtilisin-like serine protease family protein		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	7,238	9,815	1,683	0,675	2,612									
Solyc01g087800	LOW QUALITY:Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	2,129	4,215	1,667	0,561	2,046									
Solyc01g087810	subtilisin-like serine protease family protein		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.30	3,505	11,379	1,485	1,090	1,686									
Solyc01g087820	subtilisin-like protease 4B		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): PF17766 (PFAI	31,695	46,328	22,721	19,313	28,749	0,575	0,038					up		
Solyc01g087830	LOW QUALITY:Subtilisin-like protease (AHRD V3.3 *-* O82777_SOLLC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	0,412	0,347	0,137	0,117	0,187									
Solyc01g087840	Subtilisin-like protease (AHRD V3.3 *** O82006_SOLLC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR000209 (PFAM): PF17766 (PFAM)	6,952	5,130	1,399	1,148	1,291									
Solyc01g087850	serine protease SBT3	sbt3	F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:2.60.40	58,778	54,402	13,297	11,400	13,369									
Solyc01g087860	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT1G35430.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR363	2,107	1,517	1,410	2,071	2,025									
Solyc01g087870	Glucosamine-fructose-6-phosphate aminotransferase, putative (AHRD V3.3 *** B9RM60_RICCO)		F:GO:0097367; P:G(	F:carbohydrate derivative binding; P:carbohydrate derivative m			IPR001347 (PFAM): IPR029055 (G3D	7,708	7,210	3,328	4,067	4,364									
Solyc01g087880	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (AHRD V3.3 *** A0A0B0Q2A1_GOSAR)						IPR019034 (PFAM): mobidb-lite (MOBI	5,609	8,133	6,380	6,331	6,530									
Solyc01g087890	Plasma-membrane choline transporter family protein (AHRD V3.3 *** AT5G13760.1)		C:GO:0016021	C:integral component of membrane			IPR007603 (PFAM): mobidb-lite (MOBI	23,072	14,738	44,227	43,366	40,770	-0,617	0,037					down		
Solyc01g087900	N-terminal acetyltransferase A complex subunit NAA10		C:GO:0005829; F:G(	C:cytosol; F:N-acet	EC:2.3.1.5	Arylamine N-acetyltra	G3DSA:3.40.630.30 (GENE3D): IPR0(	75,933	77,747	103,722	95,654	93,080									
Solyc01g087910	F-box family protein with WD40/YVTN repeat doamin (AHRD V3.3 *** AT3G52030.2)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001680 (SM	14,124	11,474	12,848	11,125	12,277									
Solyc01g087920	Carboxypeptidase (AHRD V3.3 *** K4AYI2_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	0,494	0,980	0,022	0,000	0,000									
Solyc01g087940	Carboxypeptidase (AHRD V3.3 *** K4AYI4_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	0,057	0,039	0,523	1,091	0,259									
Solyc01g087950	Carboxypeptidase (AHRD V3.3 *** K4AYI5_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	1,218	2,411	78,289	142,538	72,979					0,869	0,000			up
Solyc01g087960	Carboxypeptidase (AHRD V3.3 *** K4AYI6_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	0,000	0,000	0,000	0,025	0,024									
Solyc01g087970	Carboxypeptidase (AHRD V3.3 *** K4AYI7_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	0,818	0,936	0,989	3,369	1,617					1,743	0,000			up
Solyc01g087980	LOW QUALITY:BPS1, putative (AHRD V3.3 *** A0A072TVX0_MEDTR)						IPR008511 (PFAM): PTHR31509 (PAI	0,000	0,000	0,075	0,000	0,023									
Solyc01g087990	MADS-box transcription factor AGAMOUS-like protein (AHRD V3.3 *** A0A142CJ66_CAMSI)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN' MIKC_MADS	23,077	21,051	34,032	30,332	34,071									
Solyc01g087995	Catalase (AHRD V3.3 --* CATA_VIGRR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,637	9,424	5,945	4,945	5,096									
Solyc01g088000	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT3G60910.2)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			G3DSA:3.40.50.150 (GENE3D): PTHR	19,628	20,874	12,325	12,982	13,425									
Solyc01g088005	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9SPN8_RICCO)		F:GO:0008757	F:S-adenosylmethionine-dependent methyltransferase activity			IPR008854 (PFAM): G3DSA:3.40.50.1	13,520	13,155	7,923	9,009	10,132									
Solyc01g088010	LOW QUALITY:Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT2G28420.1)		F:GO:0016740; F:G(	F:transferase activity; F:lyase activity			IPR029068 (G3DSA:3.10.180.GENE3I	0,580	0,989	0,322	0,725	0,141									
Solyc01g088020	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G18830.3)		F:GO:0005515; P:G(	F:protein binding; P:endoplasmic reticulum to Golgi vesicle-medi			IPR001680 (SMART): IPR015943 (G3	293,402	286,318	339,540	344,440	338,967									
Solyc01g088030	Structure-specific endonuclease subunit SLX1-like protein (AHRD V3.3 *-* A0A072TLC3_MEDTR)		F:GO:0004519; P:G(	F:endonuclease activity; P:nucleic acid phosphodiester bond hy			IPR035901 (G3DSA:3.40.1440.GENE:	2,492	2,186	4,114	6,769	5,346					0,721	0,019			up
Solyc01g088040	V-type proton ATPase catalytic subunit A (AHRD V3.3 --* VATA_VIGRR)							54,258	58,238	79,288	67,618	70,185									
Solyc01g088050	Kinase family protein (AHRD V3.3 *** D7LU09_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	2,351	2,240	4,667	4,269	5,665									
Solyc01g088060	Nbs-lrr resistance protein, putative (AHRD V3.3 *** A0A061FEU3_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	7,448	6,849	8,537	8,555	8,476									
Solyc01g088080	T-complex protein 1 subunit theta (AHRD V3.3 *** W9RAQ1_9ROSA)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR012721 (TI(	98,363	96,813	94,990	84,631	89,452									
Solyc01g088090	Alpha/beta hydrolase, putative (AHRD V3.3 *** B9RIY7_RICCO)	PPH					IPR029058 (G3DSA:3.40.50.GENE3D	28,585	26,198	239,685	202,445	240,533									
Solyc01g088100	Zinc finger transcription factor 12	C3H12	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (SMART): IPR000571 (SM	131,905	99,578	66,631	74,321	76,637									
Solyc01g088120	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G03140.9)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,099	0,019	0,025	0,072	0,023									
Solyc01g088130	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A118JWL2_CYNCS)		F:GO:0003676	F:nucleic acid binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	1,198	1,156	1,309	1,926	1,504									
Solyc01g088140	30S ribosomal protein S12, chloroplastic (AHRD V3.3 *-* A0A1D1YJ71_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	12,108	10,767	15,319	15,463	14,310									
Solyc01g088150	Glycerol-3-phosphate dehydrogenase [NAD(+)] (AHRD V3.3 *** K4AYK5_SOLLC)		F:GO:0004367; P:G(	F:glycerol-3-phosph	EC:1.1.1.8; EC:1.1.1	Glycerol-3-phosphate	IPR006168 (PRINTS): IPR011128 (PF	14,115	20,915	8,995	10,314	9,261									
Solyc01g088160	cytokinin oxidase2	CKX2	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR006094 (PFAM): IPR016167 (G3D	1,612	2,401	0,093	0,069	0,140									
Solyc01g088170	aldehyde oxidase 2	ao2	F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR000674 (SMART): IPR005107 (SM	45,854	48,925	51,435	55,431	58,366									
Solyc01g088180	Aldehyde oxidase (AHRD V1 ***- Q9FV24_SOLLC)%3B contains Interpro domain(s) IPR001041 Ferredoxin		F:GO:0009055; F:G(	F:electron transfer activity; F:iron-sulfur cluster binding			IPR012675 (G3DSA:3.10.20.GENE3D	0,000	0,000	0,022	0,000	0,000									
Solyc01g088200	Aldehyde oxidase	ao4	F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR005107 (SMART): IPR000674 (SM	2,393	2,817	1,723	1,701	2,239									
Solyc01g088230	Aldehyde oxidase (AHRD V3.3 *-* Q9FV24_SOLLC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR005107 (SMART): IPR002346 (PF.	0,000	0,018	0,000	0,000	0,047									
Solyc01g088240	F-box FBW2-like protein (AHRD V3.3 *-* A0A0B0NRC7_GOSAR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	6,146	4,993	14,283	12,607	10,662									
Solyc01g088245	F-box FBW2-like protein (AHRD V3.3 *** A0A0B0NRC7_GOSAR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	17,525	14,604	39,468	36,587	33,145									
Solyc01g088250	SUN domain protein3	SUN3	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR025064 (PF.	53,917	51,617	12,168	12,856	16,145									
Solyc01g088290	Germin-like protein 1 (AHRD V3.3 *** B9NCV4_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SM	0,000	0,000	0,025	0,097	0,000									
Solyc01g088300	Germin-like protein 1 (AHRD V3.3 *** B9NCV4_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SM	0,019	0,000	0,000	0,025	0,023									
Solyc01g088310	Geranylgeranyl reductase (AHRD V3.3 *** A0A097P6G1_SOLHA)		P:GO:0015979; P:G(	P:photosynthesis; P:chlorophyll biosynthetic process; F:oxidore			PR00420 (PRINTS): IPR011774 (TIGF	20,254	26,638	17,021	19,638	18,914									
Solyc01g088320	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *-* A0A118JRY8_CYNCS)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal			PF05664 (PFAM): IPR008528 (PANTH	0,545	0,485	0,402	0,444	0,422									
Solyc01g088323	Maturase K (AHRD V3.3 --* MATK_ARABL)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal movement				0,096	0,018	0,022	0,025	0,046									
Solyc01g088327	TRICHOME BIREFRINGENCE-LIKE 41 (AHRD V3.3 --* AT3G14850.2)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal			IPR008528 (PANTHER): PTHR31280:	0,099	0,098	0,049	0,025	0,024									
Solyc01g088330	glucan synthase-like 9 (AHRD V3.3 --* AT5G36870.5)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal movement				0,099	0,043	0,025	0,000	0,000									
Solyc01g088340	FBD%2C F-box and Leucine Rich Repeat domains containing protein (AHRD V3.3 --* AT3G56780.2)							0,042	0,074	0,025	0,025	0,094									
Solyc01g088350	NADH dehydrogenase 1 alpha subcomplex assembly factor 3-like protein (AHRD V3.3 *** A0A0M4KXJ9_SO		P:GO:0032981	P:mitochondrial respiratory chain complex I assembly			IPR036748 (G3DSA:3.40.1230.GENE:	10,634	9,624	17,264	16,140	16,347									
Solyc01g088370	Eukaryotic translation initiation factor 3 subunit B (AHRD V3.3 *** K4AYM7_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			IPR012677 (G3DSA:3.30.70.GENE3D	232,648	255,261	261,834	251,542	237,347									
Solyc01g088380	DNA replication helicase (AHRD V3.3 *** AT1G08840.4)		F:GO:0017108; P:G(	F:5'-flap endonuclea	EC:3.1.3; EC:3.6.1.3	Acting on ester bonds	PF13086 (PFAM): G3DSA:3.40.50.30(	3,145	2,471	0,690	0,600	0,775									
Solyc01g088390	Sister chromatid cohesion protein DCC1 (AHRD V3.3 *** A0A072TGP8_MEDTR)		P:GO:0007064; C:G(	P:mitotic sister chromatid cohesion; C:Ctf18 RFC-like complex			IPR019128 (PFAM): IPR019128 (PAN	2,589	2,595	8,349	33,218	5,692					1,999	0,000			up
Solyc01g088400	ECERIFERUM 1	CER1	F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): IPR021940 (PFA	2,694	5,090	1550,634	3206,174	993,416					1,052	0,004			up
Solyc01g088410	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT1G02205.5)		F:GO:0000170; F:G(	F:sphingosine hydroxylase activity; F:iron ion binding; C:endopl			IPR021940 (PFAM): PTHR11863 (PAI	0,000	0,019	0,000	0,022	0,000									
Solyc01g088420	Fatty acid hydroxylase superfamily (AHRD V3.3 *-* AT1G02205.3)		F:GO:0000170; F:G(	F:sphingosine hydroxylase activity; F:iron ion binding; C:endopl			PTHR11863:SF41 (PANTHER): PTHR	0,553	0,565	0,347	0,433	0,282									
Solyc01g088430	Fatty acid hydroxylase superfamily protein (AHRD V3.3 *** A0A072TKE8_MEDTR)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR021940 (PFAM): IPR006694 (PFA	0,159	0,043	0,167	0,264	0,071									
Solyc01g088440	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FKE5_THECC)		C:GO:0016020; P:G(	C:membrane; P:protein ubiquitination; F:ubiquitin protein ligase I			IPR001841 (SMART): IPR001841 (PF.	3,199	1,398	2,479	3,387	2,311	-1,166	0,024					down		
Solyc01g088450	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G53820.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	5,564	3,477	2,060	3,104	2,467									
Solyc01g088480	UMP-CMP kinase (AHRD V3.3 *** K4AYN8_SOLLC)		F:GO:0004127; F:G(	F:cytidylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS): PF00406 (PFAI	63,054	77,071	23,674	21,306	23,102									
Solyc01g088490	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XV88_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	1,090	1,271	1,389	1,619	1,292									
Solyc01g088500	Wall-associated receptor kinase-like 20 (AHRD V3.3 *** A0A0B0PGP7_GOSAR)		F:GO:0030247	F:polysaccharide binding			IPR025287 (PFAM): PTHR33355:SF6	0,156	0,223	0,140	0,288	0,094									
Solyc01g088505	Dynamin, putative (AHRD V3.3 *** B9SKH8_RICCO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001401 (SMART): IPR003130 (SM	95,598	119,526	91,047	93,879	97,033									
Solyc01g088520	Dynamin (AHRD V3.3 *-* A0A118JT45_CYNCS)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PANTHER): PTHR11566:	0,156	0,338	0,197	0,173	0,167									
Solyc01g088530	Transposon protein (AHRD V3.3 *** B6TXP6_MAIZE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,360	3,493	1,773	1,719	1,347									
Solyc01g088550	Purine permease family protein (AHRD V3.3 *** B9I8W9_POPTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	16,001	25,902	15,443	15,109	15,913									
Solyc01g088560	Rab family GTPase (AHRD V3.3 *** D8RBQ4_SELML)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	75,373	96,972	78,866	80,534	83,569									
Solyc01g088570	Acyl carrier protein (AHRD V3.3 *** K4AYP7_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR036736 (G3DSA:1.10.1200.GENE:	30,783	34,386	56,779	47,752	47,749									
Solyc01g088590	invertase/pectin methylesterase inhibitor		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (SMART): IPR035513 (G3	0,995	1,105	22,901	29,293	17,333									
Solyc01g088600	Protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic (AHRD V3.3 *** A0A199W3Y6_ANACO)		C:GO:0005739; C:G(	C:mitochondrion; C:vacuolar membrane; C:chloroplast envelope			PTHR34954:SF2 (PANTHER): PTHR3	11,295	12,828	5,045	4,283	8,028									
Solyc01g088610	10 kDa chaperonin (AHRD V3.3 *** A0A0B2PT56_GLYSO)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding			IPR020818 (PRINTS): IPR020818 (SM	60,611	86,589	83,050	78,307	90,663									
Solyc01g088620	Ferredoxin-related (AHRD V3.3 *** A0A061E2R5_THECC)		C:GO:0016021	C:integral component of membrane			PTHR34537:SF2 (PANTHER): PTHR3	3,974	2,325	0,732	0,707	0,823									
Solyc01g088630	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G20030.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination; F:li			IPR001841 (SMART): IPR001841 (PF.	0,687	0,637	0,612	1,164	0,826									
Solyc01g088640	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G45290.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR001841 (PF.	11,605	10,423	21,361	21,855	18,018									
Solyc01g088650	ALG6, ALG8 glycosyltransferase family (AHRD V3.3 *** AT2G44660.1)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:oligosaccharide-lipid inte			IPR004856 (PFAM): mobidb-lite (MOBI	10,932	7,585	8,574	11,288	9,350									
Solyc01g088660	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT2G44670.1)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR013088 (G3DSA:3.30.50.GENE3D	57,538	69,852	38,154	26,698	26,682			-0,520	0,009	-0,513	0,001		down	down
Solyc01g088690	Kinase family protein (AHRD V3.3 *** B9MTV7_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRSI	0,394	0,316	0,218	0,287	0,237									
Solyc01g088700	Eukaryotic translation initiation factor 4g, putative (AHRD V3.3 *** B9SKF9_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:protein binding			IPR003890 (SMART): IPR003891 (SM	342,917	339,427	379,019	359,952	371,930									
Solyc01g088710	Metacaspase-1 (AHRD V3.3 *** M9WJ17_VITVI),Pfam:PF00656		F:GO:0004197; P:G(	F:cysteine-type enc	EC:3.4.22	Acting on peptide bor	PF00656 (PFAM): IPR005735 (TIGRF	15,085	18,680	18,128	17,646	16,385									
Solyc01g088720	Transcription factor IIIB subunit (AHRD V3.3 *** A0A1D1ZC65_9ARAE)		C:GO:0000126; F:G(	C:transcription factor TFIIIB complex; F:RNA polymerase III ger			IPR000812 (PRINTS): IPR013150 (PF	25,325	22,241	29,045	33,904	30,043									
Solyc01g088730	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XTD5_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR001623 (PRINTS): IPR001623 (SM	31,754	28,022	39,377	35,363	33,922									
Solyc01g088740	Casein kinase II subunit beta (AHRD V3.3 *** M0ZNA5_SOLTU)		C:GO:0005956; F:G(	C:protein kinase CK2 complex; F:protein kinase regulator activit			IPR000704 (PRINTS): IPR000704 (SM	18,509	18,796	20,325	19,673	18,543									
Solyc01g088750	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HIE4_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	5,634	4,889	5,619	4,954	5,920									
Solyc01g088760	Cytochrome P450, putative (AHRD V3.3 *** A0A061DWV1_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	16,044	14,994	45,954	45,782	41,918									
Solyc01g088780	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	0,000	0,055	0,000	0,000	0,000									
Solyc01g088800	RNA binding protein, putative (AHRD V3.3 *** B9SKE9_RICCO)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	SM00173 (SMART): SM00174 (SMAR	74,212	81,334	118,124	101,007	102,498									
Solyc01g088810	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A118K0H6_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (SMART): PIRSF000654 (	0,540	0,776	0,368	0,980	0,731									
Solyc01g088820	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *** B9SKE7_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:glucosinolate metabolic process; F:sequence-spec			IPR006578 (SMAF Trihelix	13,608	15,140	8,596	7,346	8,184									
Solyc01g088830	LOW QUALITY:Ankyrin repeat-containing protein (AHRD V3.3 *** A0A118K0H6_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	0,040	0,018	0,068	0,168	0,071									
Solyc01g089840	LOW QUALITY:Glutamyl-tRNA reductase (AHRD V3.3 *-* M1D2W4_SOLTU)		F:GO:0008883; P:G(	F:glutamyl-tRNA rec	EC:1.2.1.7	Glutamyl-tRNA reduc	IPR015895 (PFAM): IPR036343 (G3D	0,000	0,000	0,025	0,069	0,023									
Solyc01g089850	cyclinU4_1	CycU4_1	P:GO:0000079; F:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR012389 (PIRSF): IPR013922 (PFA	0,474	0,542	0,151	0,122	0,142									
Solyc01g089855	BnaC01g16300D protein (AHRD V3.3 *** A0A078EQV8_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,023									
Solyc01g089860	BnaA01g13870D protein (AHRD V3.3 *** A0A078H9V8_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,774	4,644	4,058	4,106	3,252									
Solyc01g089870	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GP78_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	16,231	21,743	40,715	39,590	41,039									

Solyc01g089880	LOW QUALITY:PRA1 family protein (AHRD V3.3 *** K4AYS9_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR38519 (PAN	1,974	3,022	0,621	0,346	0,872									
Solyc01g089890	PRA1 family protein (AHRD V3.3 *** K4AYT0_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR38519 (PAN	0,344	1,082	0,403	0,412	0,967									
Solyc01g089900	Mannosyltransferase (AHRD V3.3 *-* K4AYT1_SOLLC)		C:GO:0005788: C:G(	C:endoplasmic retic	EC:2.4.1.232	Initiation-specific alpha-1,6-mannosyltransferase		2,196	2,264	3,521	3,790	3,563									
Solyc01g089903	Mannosyltransferase (AHRD V3.3 *-* K4AYT1_SOLLC)		C:GO:0005788: P:G(	C:endoplasmic retic	EC:2.4.1.232	Initiation-specific alpl	IPR039485 (PTHR22760:PANTHER):	1,747	1,659	2,756	3,706	3,013									
Solyc01g089907	Mannosyltransferase (AHRD V3.3 *-* K4AYT1_SOLLC)		C:GO:0005788: P:G(	C:endoplasmic retic	EC:2.4.1.232	Initiation-specific alpl	IPR039485 (PTHR22760:PANTHER):	1,589	1,626	2,375	2,889	3,196									
Solyc01g089910	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT5G25260.1)						IPR001107 (PFAM): G3DSA:3.30.479	0,180	0,514	0,122	0,094	0,046									
Solyc01g089920	Bax inhibitor 1-like protein (AHRD V3.3 *** A0A0B0PIU1_GOSAR)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR006214 (PANTHER): PTHR23291::	0,000	0,043	0,050	0,025	0,024									
Solyc01g089930	Riboflavin biosynthesis protein RibD (AHRD V3.3 *-* A0A0B2R4V5_GLYSO)		F:GO:0008703: F:G(	F:5-amino-6-(5-pho	EC:3.5.4.26; EC:1.1.	Diaminohydroxyphos	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,000	0,050	0,000	0,048									
Solyc01g089940	LOW QUALITY:BAX inhibitor 1 (AHRD V3.3 *-* AT5G47120.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR232	0,000	0,000	0,025	0,000	0,000									
Solyc01g089950	F-box family protein (AHRD V3.3 *-* D7MLR5_ARALL)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF.	2,679	1,413	2,969	3,280	2,569									
Solyc01g089960	WRKY transcription factor 12	WRKY12	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF WRKY	0,360	0,434	0,317	0,092	0,071									
Solyc01g089970	Nucleoside diphosphate kinase (AHRD V3.3 *** NDK_CAPAN)		F:GO:0004550: P:G(	F:nucleoside diphos	EC:2.7.4.6	Nucleoside-diphosph	IPR001564 (PRINTS): IPR034907 (SM	444,951	449,038	283,904	242,127	281,033									
Solyc01g089980	ELMO/CED-12 domain-containing protein (AHRD V3.3 *** F4JAP3_ARATH)						IPR006816 (PFAM): PTHR12771:SF2(	66,969	47,530	35,441	33,022	36,226									
Solyc01g089990	Major facilitator superfamily protein (AHRD V3.3 *-* AT2G44280.4)		P:GO:0008643: F:G(	P:carbohydrate transport; F:symporter activity; C:integral compo			IPR039672 (PANTHER): PTHR11328::	0,019	0,165	0,047	0,195	0,071									
Solyc01g090010	BAX inhibitor 1 (AHRD V3.3 *** AT5G47120.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR006214 (PANTHER): PTHR23291::	0,000	0,000	0,025	0,000	0,000									
Solyc01g090020	RING/U-box superfamily protein (AHRD V3.3 --* AT4G26580.2)		C:GO:0016020	C:membrane				0,037	0,000	0,000	0,000	0,000									
Solyc01g090030	BAX inhibitor 1 (AHRD V3.3 *** AT5G47120.1)		C:GO:0016021	C:integral component of membrane			IPR006214 (PANTHER): PTHR23291::	0,000	0,021	0,000	0,000	0,047									
Solyc01g090040	Kinase family protein (AHRD V3.3 --* B9HC64_POPTR)							3,221	2,338	1,489	1,517	1,625									
Solyc01g090050	Bax inhibitor 1-related protein (AHRD V3.3 *-* A0A124SB73_CYNCS)		C:GO:0016021	C:integral component of membrane			PTHR23291:SF34 (PANTHER): PTHR:	0,080	0,060	0,025	0,025	0,000									
Solyc01g090100	Bax inhibitor 1-related protein (AHRD V3.3 *** A0A103XDF0_CYNCS)		C:GO:0016021	C:integral component of membrane			PTHR23291:SF34 (PANTHER): PTHR:	0,079	0,037	0,119	0,116	0,402									
Solyc01g090110	Bax inhibitor 1 (AHRD V3.3 *** A0A151TJ92_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR006214 (PANTHER): PTHR23291::	0,019	0,021	0,000	0,000	0,047									
Solyc01g090120	Blue copper (AHRD V3.3 *-* A0A0B0MZW4_GOSAR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,278	0,459	0,094	0,290	0,116									
Solyc01g090130	Pectinesterase (AHRD V3.3 *** K4AYV4_SOLLC)		F:GO:0030599: P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM): IPR012334 (G3D	0,101	0,154	0,025	0,047	0,072									
Solyc01g090135	pfkB-like carbohydrate kinase family protein (AHRD V3.3 --* AT2G31390.1)							0,000	0,000	0,025	0,025	0,000									
Solyc01g090140	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G44800.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,868	0,983	0,287	0,218	0,378									
Solyc01g090160	Glycogen synthase kinase-3 homolog MsK-3 (AHRD V3.3 --* MSK3_MEDSA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,103	0,098	0,022	0,047	0,072									
Solyc01g090170	ras-related protein Rab-1A		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	39,080	43,645	59,192	63,843	57,960									
Solyc01g090180	4,5-dioxygenase-like protein (AHRD V3.3 *** A0A0G2UQU6_9CARY)		P:GO:0006725: F:G(	P:cellular aromatic compound metabolic process; F:ferrous iron			IPR014436 (PIRSF): IPR004183 (PFA	2,531	1,988	1,190	1,013	0,916									
Solyc01g090190	Nuclear RNA binding protein (AHRD V3.3 *** C7TPG6_SOLTU)		F:GO:0003723	F:RNA binding			IPR006861 (SMART): IPR006861 (PF.	195,809	194,506	276,977	245,498	254,500									
Solyc01g090200	glycine-tRNA ligase (AHRD V3.3 *** AT3G48110.1)		F:GO:0004820: F:G(	F:glycine-tRNA ligas	EC:6.1.1.14	Glycine--tRNA ligase	IPR002310 (PRINTS): G3DSA:3.30.93	71,982	99,856	106,383	109,077	102,767									
Solyc01g090210	U-box domain-containing protein 33 (AHRD V3.3 *** W9RCI3_9ROSA)						IPR014729 (G3DSA:3.40.50.GENE3D	4,671	4,883	2,746	2,924	3,150									
Solyc01g090225	RING finger protein, putative (AHRD V3.3 *** B9RCZ1_RICCO)		F:GO:0005515: F:G(	F:protein binding; F:ubiquitin protein ligase activity			IPR001841 (SMART): IPR006575 (SM	18,146	13,337	15,594	12,103	13,922									
Solyc01g090230	GRAM domain family protein (AHRD V3.3 *** AT1G02120.1)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:response to ethylene; P:response to			IPR004182 (SMART): IPR011993 (G3	37,048	35,787	40,682	43,052	38,076									
Solyc01g090240	AvrPto-dependent Pto-interacting protein 3	adi3	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	12,916	19,881	1,806	1,096	1,945									
Solyc01g090250	Integrator complex subunit 4 (AHRD V1 *-*- C0HAD1_SALSA)%3B contains Interpro domain(s) IPR016024 Armadillo-type fold						IPR011989 (G3DSA:1.25.10.GENE3D	5,764	4,372	2,924	3,363	3,678									
Solyc01g090260	HEAT repeat family protein expressed (AHRD V1 ***- Q10N57_ORYSJ)						PTHR20938 (PANTHER)	8,846	7,226	5,927	6,110	6,217									
Solyc01g090270	bZIP domain class transcription factor (DUF630 and DUF632) (AHRD V3.3 *** AT3G60320.1)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM): IPR006868 (PFA	112,173	91,648	24,602	21,412	25,337									
Solyc01g090280	Leucine carboxyl methyltransferase, putative (AHRD V3.3 *** B9RCZ7_RICCO)		F:GO:0018423: P:G(	F:protein C-terminal leucine carboxyl O-methyltransferase activi			G3DSA:3.40.50.150 (GENE3D): IPR0(	25,518	24,955	37,539	41,921	38,060									
Solyc01g090290	COP9 signalosome complex subunit 7 (AHRD V3.3 *** W9QI01_9ROSA)		P:GO:0000338: C:G(	P:protein deneddylation; C:cytosol; C:COP9 signalosome; P:CC			SM00753 (SMART): IPR000717 (SMA	36,353	37,492	63,237	55,957	54,113									
Solyc01g090300	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RD03_RICCO)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,021	0,103	0,000	0,000	0,000									
Solyc01g090310	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RCZ9_RICCO)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,156	0,650	0,099	0,200	0,048									
Solyc01g090340	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RD03_RICCO)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,218	0,719	0,000	0,000	0,000									
Solyc01g090350	non-specific lipid-transfer protein		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	31,263	88,617	10,148	47,995	0,768									
Solyc01g090360	non-specific lipid-transfer protein		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	66,861	186,089	17,351	78,357	1,508									
Solyc01g090370	Ethylene-responsive transcription factor, putative (AHRD V3.3 *-* B9RD03_RICCO)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,000	0,000	0,069	0,022	0,000									
Solyc01g090380	UPF0565 protein C2orf69 (AHRD V3.3 *** A0A1D1Y7Z6_9ARAE)						IPR018881 (PFAM): IPR018881 (PAN	7,992	7,814	6,995	7,068	6,312									
Solyc01g090390	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 *** AT2G44880.2)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,580	2,456	1,535	1,406	1,172									
Solyc01g090400	Calcium-binding EF hand family protein (AHRD V3.3 *** A0A0K9NS82_ZOSMR)						PTHR37754 (PANTHER)	0,990	1,336	0,532	0,666	0,540									
Solyc01g090410	Palmitoyl protein thioesterase (AHRD V3.3 *** A0A118JUB1_CYNCS)		F:GO:0098599	F:palmitoyl hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,278	0,180	0,144	0,218	0,119									
Solyc01g090420	ARABIDILLO-1 (AHRD V3.3 *-* AT2G44900.2)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	2,988	2,983	4,114	3,186	4,187									
Solyc01g090425	ABA-inducible BHLH-type transcription factor (AHRD V3.3 --* AT2G46510.1)							4,134	2,775	4,466	3,142	3,890									
Solyc01g090430	NRC1	NRC1	F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	12,840	28,895	10,678	15,738	15,382	1,195	0,000	0,523	0,016	0,562	0,010	up	up	up
Solyc01g090440	LOW QUALITY:Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *-* A0A061G512_THEC		C:GO:0016021	C:integral component of membrane			IPR008480 (PFAM): mobidb-lite (MOB	6,472	6,498	2,202	1,786	1,863									
Solyc01g090450	Actin-related protein 2/3 complex subunit 5 (AHRD V3.3 *** A0A0V0HA93_SOLCH)		C:GO:0005885: P:G(	C:Arp2/3 protein complex; P:Arp2/3 complex-mediated actin nuc			IPR006789 (PFAM): IPR036743 (G3D	7,432	6,636	10,974	11,048	10,532									
Solyc01g090460	HD-ZIP	thom1	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR001356 (SMAF HD-ZIP	8,296	5,550	4,012	3,706	4,933									
Solyc01g090470	Protein AATF (AHRD V3.3 *** W9SMH5_9ROSA)		C:GO:0005634	C:nucleus			IPR025160 (PFAM): IPR012617 (PFA	30,254	30,081	50,558	54,080	44,872									
Solyc01g090480	RNA-binding KH domain-containing protein isoform 1 (AHRD V3.3 *** A0A061DUL9_THECC)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR004088 (PF.	28,693	32,190	30,812	29,333	29,264									
Solyc01g090500	Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 *** A0A061DUF5_THECC)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR003690 (PF.	26,779	25,915	50,593	45,123	45,535									
Solyc01g090510	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061GHG1_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,607	2,276	1,644	1,658	1,456									
Solyc01g090515	myb-related protein 1 (AHRD V3.3 --* AT5G18240.6)							0,480	0,768	0,358	0,172	0,283									
Solyc01g090520	plant/protein (AHRD V3.3 --* AT5G43400.1)							0,356	0,189	0,000	0,000	0,000									
Solyc01g090530	R2R3MYB transcription factor 104	R2R3MYB104	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,219	0,356	0,144	0,125	0,211									
Solyc01g090550	DnaJ-like protein (AHRD V3.3 *** W9QHL5_9ROSA)		F:GO:0005524: P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS): IPR001623 (SM	111,440	86,842	259,340	244,899	229,825									
Solyc01g090560	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9R3T6_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	2,704	2,681	0,151	0,149	0,213									
Solyc01g090590	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G44970.3)						IPR029058 (G3DSA:3.40.50.GENE3D	21,216	18,408	49,473	46,824	42,177									
Solyc01g090610	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** A0A061G9S7_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,021	0,019	0,000	0,050	0,000									
Solyc01g090630	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** A0A061G9S7_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc01g090640	Chromodomain helicase-DNA-binding-like protein (AHRD V3.3 *-* A0A072TXT9_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:A'	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.220.10 (GENE3D): SSF5	1,627	2,468	0,978	1,172	0,919									
Solyc01g090645	SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 *** AT2G44980.3)		F:GO:0004003: F:G(	F:ATP-dependent D	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR014001 (SMART): G3DSA:3.40.50	0,000	0,021	0,022	0,000	0,000									
Solyc01g090670	nucleoporin-like protein		C:GO:0005643: F:G(	C:nuclear pore; F:structural constituent of nuclear pore			G3DSA:1.20.5.170 (GENE3D): IPR00'	27,912	26,878	20,197	17,504	18,406									
Solyc01g090680	Cation/H(+) antiporter 11 (AHRD V3.3 *-* A0A1D1XXR2_9ARAE)		C:GO:0016020	C:membrane			PTHR33625 (PANTHER): PTHR33625	0,000	0,000	0,000	0,000	0,024									
Solyc01g090690	Elongation factor G, mitochondrial (AHRD V3.3 *** K4AZ10_SOLLC)		F:GO:0003746: F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR000640 (SM	150,121	141,527	179,456	154,786	166,131									
Solyc01g090700	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A0K9Q5H5_ZOSMR)		F:GO:0003860	F:3-hydroxyisobutyı	EC:3.1.2.4	3-hydroxyisobutyryl-(	G3DSA:3.90.226.40 (GENE3D): IPR0:	65,978	65,173	196,429	192,200	195,035									
Solyc01g090710	cytosolic malate dehydrogenase	cmdh	P:GO:0005975: P:G(	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR015955 (G3DSA:3.90.110.GENE3I	0,554	0,550	0,435	0,651	0,844									
Solyc01g090720	P53/DNA damage-regulated protein (AHRD V3.3 *** AT3G15351.5)						IPR030482 (PANTHER)	9,730	8,637	11,699	12,394	10,948									
Solyc01g090730	Squamosa promoter binding protein 8b		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			IPR036893 (G3DS SBP	10,147	16,597	0,000	0,048	0,023									
Solyc01g090740	Zinc finger protein (AHRD V3.3 *** A0A0B0MVF4_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	12,419	16,196	12,337	9,573	12,570									
Solyc01g090750	T-complex protein 1 alpha subunit (AHRD V3.3 *** AT3G20050.1)		F:GO:0005524: P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR027409 (G3	127,300	126,510	196,664	180,208	189,417									
Solyc01g090760	GATA transcription factor (AHRD V3.3 *** K4AZ17_SOLLC)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ior			IPR000679 (SMAF GATA	2,781	1,015	0,025	0,126	0,000									
Solyc01g090770	alanine-tRNA ligase (AHRD V3.3 *** AT2G45060.1)		C:GO:0005739: C:G(	C:mitochondrion; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR345	31,072	27,291	37,988	33,514	34,947									
Solyc01g090780	CCR4-NOT transcription complex subunit 1 (AHRD V3.3 *** A0A0B2PP65_GLYSO)		P:GO:0006417: C:G(	P:regulation of translation; C:CCR4-NOT core complex			IPR032191 (PFAM): G3DSA:1.25.40.7	193,543	159,011	196,721	219,622	210,405									
Solyc01g090790	bHLH transcription factor		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	34,842	29,298	1,837	0,979	3,576									
Solyc01g090800	cyclinU2_1	CycU2_1	P:GO:0000079: F:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR013922 (PFAM): G3DSA:1.10.472.	0,216	0,399	0,047	0,025	0,024									
Solyc01g090810	beta-expansin precursor	EXPB8	C:GO:0005576: P:G(	C:extracellular region; P:sexual reproduction			IPR007118 (PRINTS): IPR005795 (PF	0,496	1,350	1,640	1,214	1,863									
Solyc01g090840	Zinc finger family protein (AHRD V3.3 *** B9GPC0_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	1,434	1,499	0,294	0,146	0,357									
Solyc01g090850	Phosphatidate cytidylyltransferase (AHRD V3.3 *-* A0A0B0MV12_GOSAR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR003604 (SMART): G3DSA:3.30.16	13,614	12,466	23,252	21,688	20,851									
Solyc01g090860	Nucleotidyltransferase family protein (AHRD V3.3 *** AT4G00060.4)		F:GO:0016779	F:nucleotidyltransferase activity			IPR002934 (PFAM): G3DSA:1.10.141(	86,224	63,173	71,258	78,306	79,173									
Solyc01g090880	Holliday junction resolvase-like protein (AHRD V3.3 *** A0A072UJ99_MEDTR)		P:GO:0006364	P:rRNA processing			IPR006641 (SMART): IPR005227 (TIG	32,851	32,597	21,875	20,461	22,165									
Solyc01g090890	SPX domain-containing protein (AHRD V3.3 *** D7LBV7_ARALL)		P:GO:0016036	P:cellular response to phosphate starvation			IPR004331 (PFAM): IPR031142 (PTH	0,000	0,060	0,000	0,045	0,023									
Solyc01g090900	Cytochrome P450 (AHRD V3.3 *** A0A0B0N0U7_GOSAR)		C:GO:0009706: C:G(	C:chloroplast inner membrane; C:integral component of membra			PTHR33918 (PANTHER): PTHR33918	0,019	0,021	0,071	0,047	0,047									
Solyc01g090910	Vesicle-associated protein 1-1 (AHRD V3.3 *** VAP11_ARATH)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR013783 (G3DSA:2.60.40.GENE3D	14,179	19,513	5,091	7,169	6,743									
Solyc01g090920	Calmodulin, putative (AHRD V3.3 *** B9RD69_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF.	8,119	8,494	4,909	5,338	5,417									
Solyc01g090940	Phosphatidate cytidylyltransferase (AHRD V3.3 *** K4AZ34_SOLLC),Pfam:PF01148		C:GO:0016020: F:G(	C:membrane; F:transferase activity, transferring phosphorus-co			PF01148 (PFAM): mobidb-lite (MOBID	25,952	27,990	33,432	35,291	33,106									
Solyc01g090950	Transcription factor GRAS (AHRD V3.3 *** A0A103XI66_CYNCS)	GRAS	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	17,922	11,882	9,569	10,233	11,079									
Solyc01g090960	hydroxysteroid dehydrogenase 1 (AHRD V3.3 --* AT5G50700.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc01g090970	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *** A0A151QNX1_CAJCA)						IPR016140 (SMART): IPR027923 (PF	0,038	0,212	0,000	0,000	0,000									
Solyc01g090990	vesicle-associated membrane protein		C:GO:0005789	C:endoplasmic reticulum membrane			IPR016763 (PIRSF): IPR000535 (PFA	12,295	13,850	12,774	11,652	12,976									
Solyc01g091000	PLATZ transcription factor family protein (AHRD V3.3 *** A0A061DW44_THECC)		F:GO:0008270	F:zinc ion binding			IPR006734 (PFAM): PTHR31065:SF1	0,994	0,882	0,291	0,287	0,375									
Solyc01g091010	CRABS CLAW-like protein1a	YABBY1a	P:GO:0007275	P:multicellular organism development			IPR036910 (G3DS YABBY	0,638	0,306	0,000	0,025	0,000									
Solyc01g091020	Golgi SNAP receptor complex member 1 (AHRD V3.3 *** A0A0V0HMI7_SOLCH)		C:GO:0000139: C:G(	C:Golgi membrane; C:cis-Golgi network; P:endoplasmic reticulu			PF12352 (PFAM): IPR023601 (PIRSF	19,352	19,262	22,515	19,870	20,142									
Solyc01g091030	Small auxin up-regulated RNA1	SAUR1	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	2,334	3,118	0,961	0,552	1,079									
Solyc01g091040	Cysteine-rich repeat secretory protein 15 (AHRD V3.3 *** A0A151RVB1_CAJCA)		C:GO:0009506: C:G(	C:plasmodesma; C:integral component of membrane			IPR038408 (G3DSA:3.30.430.GENE3I	3,498	2,827	2,175	2,312	2,353									
Solyc01g091050	Pectinesterase (AHRD V3.3 *** K4AZ45_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR000070 (PF.	1,198	0,987	0,416	2,688	1,407					2,626	0,000			up
Solyc01g091060	Pectinesterase (AHRD V3.3 *** K4AZ46_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (PF.	1,069	1,971	0,611	0,894	0,214									
Solyc01g091070	Methionine aminopeptidase 1 (AHRD V3.3 *** K4AZ47_SOLLC)		F:GO:0004177: P:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR001714 (PRINTS): IPR002467 (TIG	55,171	51,244	57,707	51,493	55,840									
Solyc01g091080	Tubulin-folding cofactor D (AHRD V3.3 *** TBCD_ARATH)		F:GO:0005096: P:G(	F:GTPase activator activity; P:tubulin complex assembly; P:pos			IPR022577 (PFAM): IPR033162 (PAN	16,176	13,916	12,930	11,483	12,461									
Solyc01g091090	Tubulin-folding cofactor D (AHRD V3.3 *-* TBCD_ARATH)		F:GO:0005096: P:G(	F:GTPase activator activity; P:tubulin complex assembly; P:pos			IPR033162 (PANTHER): PTHR12658::	16,888	13,191	11,523	11,017	11,894									
Solyc01g091100	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** G7KG88_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (SMART): IPR006501 (PF.	0,194	0,260	0,000	0,047	0,186									
Solyc01g091120	myosin-4 protein (DUF641) (AHRD V3.3 *** AT2G45260.1)		P:GO:0009639: P:G(	P:response to red or far red light; P:negative gravitropism			IPR006943 (PFAM): mobidb-lite (MOB	59,536	60,941	79,244	80,382	75,019									
Solyc01g091130	Nitroreductase (AHRD V3.3 *** A0A0B0N3I7_GOSAR)		F:GO:0016491	F:oxidoreductase activity			IPR000415 (G3DSA:3.40.109.GENE3I	5,309	3,788	19,159	18,536	16,900									
Solyc01g091140	Nitroreductase-like protein (AHRD V3.3 *-* A0A103XIC5_CYNCS)		F:GO:0016491	F:oxidoreductase activity			IPR000415 (G3DSA:3.40.109.GENE3I	1,960	1,815	1,052	0,981	0,846									
Solyc01g091145	Golgi SNAP receptor complex member 1 (AHRD V3.3 *-* K4AZ42_SOLLC)		C:GO:0000139: C:G(	C:Golgi membrane; C:cis-Golgi network; P:endoplasmic reticulu			PTHR21094:SF2 (PANTHER): IPR023	0,634	0,294	0,292	0,288	0,330									
Solyc01g091160	arginase 1 ARG1	arg1	F:GO:0046872	F:metal ion binding			IPR006035 (PFAM): G3DSA:3.40.800	46,019	49,114	50,232	51,360	56,284									
Solyc01g091170	arginase 2 ARG2	ARG2	F:GO:0046872	F:metal ion binding			IPR006035 (PIRSF): G3DSA:3.40.800	56,063	62,981	1,783	0,765	1,567									
Solyc01g091180	peptide transporter 1 (AHRD V3.3 *** AT3G54140.2)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,174	0,497	0,000	0,000	0,000									
Solyc01g091190	5-enolpyruvylshikimate-3-phosphate synthase	EPSPS2	F:GO:0003866: P:G(	F:3-phosphoshikima	EC:2.5.1.19	3-phosphoshikimate	IPR001986 (PFAM): IPR036968 (G3D	61,139	62,781	140,998	140,539	132,469									
Solyc01g091200	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE3	F:GO:0003824: F:G(	F:catalytic activity; F:coenzyme binding			PR01713 (PRINTS): IPR001509 (PFA	6,813	5,576	2,186	2,406	2,304									
Solyc01g091210	RNA 2'-phosphotransferase isoform 2 (AHRD V3.3 *** A0A061DV31_THECC)		P:GO:0006388: F:G(	P:tRNA splicing, via endonucleolytic cleavage and ligation; F:tra			G3DSA:1.10.10.970 (GENE3D): G3DS	12,819	13,125	17,358	17,357	17,486									
Solyc01g091220	40S ribosomal protein S13 (AHRD V3.3 *** RS13_SOYBN)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012606 (SMART): IPR000589 (SM	52,588	63,370	45,049	37,491	42,662									
Solyc01g091230	Receptor-like kinase (AHRD V3.3 *** A0A191UPW4_CASSA)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			G3DSA:1.10.510.10 (GENE3D): IPR0(	1,207	1,638	0,075	0,000	0,046									
Solyc01g091240	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A0D5ZZN7_NICSY)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	1,773	1,860	2,555	2,012	2,077									
Solyc01g091250	DUF1442 family protein (AHRD V3.3 *** G7J167_MEDTR)						IPR009902 (PFAM): G3DSA:3.40.50.1	0,019	0,000	0,025	0,095	0,024									
Solyc01g091260	Myeloid leukemia factor 1 (AHRD V3.3 *** A0A0B0Q1A9_GOSAR)						IPR019376 (PFAM): mobidb-lite (MOB	62,500	47,488	25,784	19,735	24,727									
Solyc01g091270	Myeloid leukemia factor 1 (AHRD V3.3 *** A0A0B0Q047_GOSAR)						IPR019376 (PFAM): mobidb-lite (MOB	58,582	40,393	302,865	266,678	259,732									
Solyc01g091280	S-acyltransferase (AHRD V3.3 *** K4AZ68_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	33,565	27,769	40,940	37,701	34,849									
Solyc01g091290	SNARE-interacting protein KEULE (AHRD V3.3 *-* KEULE_ARATH)		P:GO:0006904	P:vesicle docking involved in exocytosis			G3DSA:3.40.50.2060 (GENE3D): IPR(	0,019	0,000	0,141	0,171	0,024									
Solyc01g091300	SNARE-interacting protein KEULE (AHRD V3.3 *** A0A1D1XCK2_9ARAE)		P:GO:0006904	P:vesicle docking involved in exocytosis			IPR001619 (PFAM): IPR001619 (PIRS	0,523	0,422	1,021	1,530	1,087									
Solyc01g091310	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G00090.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	50,921	50,920	61,317	53,538	54,985									
Solyc01g091320	sterol C4-methyl oxidase 1-2 (AHRD V3.3 *** AT4G22756.1)		F:GO:0005506: P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR11863:SF6'	0,653	1,060	0,000	0,000	0,000									
Solyc01g091330	Glutathione S-transferase (AHRD V3.3 *** A5YRT3_CAPAN)	GSTZ1	F:GO:0003824: F:G(	F:catalytic activity; F:protein binding; C:cytoplasm; P:aromatic a			IPR005955 (TIGRFAM): G3DSA:1.20.'	1,277	1,890	2,140	2,162	2,254									
Solyc01g091340	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *-* A0A0K9P1Y7_ZOSMR)		P:GO:0000413: F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer	IPR001179 (PFAM): G3DSA:2.60.120	11,416	12,781	7,673	6,903	7,031									
Solyc01g091350	ATP-dependent DNA helicase 2 subunit KU80 (AHRD V3.3 *** K4AZ75_SOLLC)		P:GO:0000723: F:G(	P:telomere mainten	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR006164 (SMART): IPR036494 (G3	18,108	17,082	29,289	26,748	27,661									
Solyc01g091360	DUF1499 family protein (AHRD V3.3 *** AT3G60810.1)						IPR010865 (PFAM): PTHR34801:SF1	0,639	1,715	0,094	0,025	0,257	1,440	0,021					up		
Solyc01g091370	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072U297_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): mobidb-lite (MOB	11,045	19,595	1,729	1,143	2,225	0,853	0,005					up		
Solyc01g091380	Microtubule-associated protein-like (AHRD V3.3 *** A0A0K9PJG1_ZOSMR)		P:GO:0000226: F:G(	P:microtubule cytoskeleton organization; F:microtubule binding			G3DSA:1.20.58.1520 (GENE3D): PF0	3,903	4,205	2,467	2,438	2,493									
Solyc01g091385	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT1G06070.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,196	4,383	4,410	4,473	4,284									
Solyc01g091420	LOB domain-containing protein, putative (AHRD V3.3 *** B9RDE1_RICCO)		C:GO:0005634: P:G(	C:nucleus; P:xylem development; P:lateral root formation; P:pos			IPR004883 (PFAM LBD	3,245	4,173	0,761	0,956	0,801									
Solyc01g091430	ATP-dependent DNA helicase 2 subunit KU80 (AHRD V3.3 *-* K4AZ75_SOLLC)		F:GO:0016817	F:hydrolase activity, acting on acid anhydrides			IPR014893 (PFAM): IPR036494 (G3D	0,520	0,294	0,241	0,740	0,517									
Solyc01g091435	ATP-dependent DNA helicase 2 subunit KU80 (AHRD V3.3 *-* A0A0V0IS37_SOLCH)		P:GO:0000723: C:G(	P:telomere mainten	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,215	0,036	0,097	0,095	0,047									
Solyc01g091440	ATP-dependent DNA helicase 2 subunit KU80 (AHRD V3.3 *-* M1AYS8_SOLTU)		F:GO:0003677: P:G(	F:DNA binding; P:DNA metabolic process; P:cellular response tc			PTHR12604:SF4 (PANTHER): PTHR1:	0,038	0,039	0,025	0,095	0,000									
Solyc01g091450	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2QJT4_GLYSO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	6,494	7,967	19,040	20,540	17,527									

Solyc01g091460	Brefeldin A-inhibited guanine nucleotide-exchange protein (AHRD V3.3 *** G7L099_MEDTR)		F:GO:0005086; P:G(	F:ARF guanyl-nucleotide exchange factor activity; P:regulation (			IPR000904 (SMART); IPR023394 (G3	112,148	107,583	89,552	98,980	91,165									
Solyc01g091465	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XUP9_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,000	0,043	0,000	0,000	0,000									
Solyc01g091470	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TPA5_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D); IPR(	0,585	0,735	0,598	1,248	0,586									
Solyc01g091480	Kinesin-like protein (AHRD V3.3 *** K4AZ88_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	31,666	37,192	16,546	15,746	18,783									
Solyc01g091490	Class III homeobox-leucine zipper protein (AHRD V3.3 --* I0IUI3_9ASPA)						PTHR33601:SF1 (PANTHER); IPR039	0,061	0,059	0,000	0,000	0,000									
Solyc01g091500	Smad/FHA domain protein (AHRD V3.3 *** G7L0A8_MEDTR)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:r			IPR000253 (SMART); G3DSA:2.60.20	20,888	17,680	21,064	18,135	19,034									
Solyc01g091510	Ankyrin repeat and zinc finger domain-containing 1 (AHRD V3.3 *** A0A0B0PTB1_GOSAR)		F:GO:0005515	F:protein binding			PF18716 (PFAM); PF18826 (PFAM); I	37,326	33,176	36,657	38,207	35,118									
Solyc01g091520	Enoyl-CoA hydratase/isomerase family protein (AHRD V3.3 *** B9HTL0_POPTR)		F:GO:0003824	F:catalytic activity			IPR001753 (PFAM); G3DSA:3.90.226	69,061	49,408	31,031	33,402	36,312									
Solyc01g091530	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** E3WHD6_9ROSI)		C:GO:0016021; C:G(	C:integral component of membrane; C:anchored component of r			IPR000782 (SMART); IPR036378 (G3	268,503	168,856	16,453	18,308	23,034									
Solyc01g091540	Growth-regulating factor (AHRD V3.3 *** M4T4B6_ARAHY)		C:GO:0005634; P:G(	C:nucleus; P:transcription, DNA-templated; P:developmental pro			IPR014977 (PFAN GRF	2,329	1,180	0,000	0,050	0,000									
Solyc01g091550	Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9RDM1_RICCO)		F:GO:0047617	F:acyl-CoA hydrola:	EC:3.1.2.2	Acyl-CoA hydrolase	IPR006683 (PFAM); G3DSA:3.10.129	13,681	11,308	15,875	14,864	16,208									
Solyc01g091560	LOW QUALITY:Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9RDM1_RICCO)		F:GO:0047617	F:acyl-CoA hydrola:	EC:3.1.2.2	Acyl-CoA hydrolase	IPR006683 (PFAM); G3DSA:3.10.129	0,058	0,082	0,025	0,025	0,046									
Solyc01g091570	Thioesterase family protein (AHRD V3.3 *** B9IC93_POPTR)		F:GO:0047617	F:acyl-CoA hydrola:	EC:3.1.2.2	Acyl-CoA hydrolase	IPR006683 (PFAM); G3DSA:3.10.129	0,021	0,041	0,000	0,050	0,000									
Solyc01g091580	Signal recognition particle receptor family protein (AHRD V3.3 *** B9IC92_POPTR)		F:GO:0005525; P:G(	F:GTP binding; P:SRP-dependent cotranslational protein targeti			IPR013822 (SMART); IPR003593 (SM	19,650	28,045	37,153	37,266	38,947	0,541	0,042					up		
Solyc01g091585	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT1G56540.2)							0,021	0,000	0,025	0,047	0,000									
Solyc01g091600	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61180.1)		C:GO:0005774; C:G(	C:vacuolar membrane; C:integral component of membrane; F:lig			IPR001841 (SMART); IPR001841 (PF.	23,220	23,437	21,588	18,768	19,494									
Solyc01g091610	LOW QUALITY:Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151TBJ2_CAJCA)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40 GENE3D	2,889	2,759	2,339	1,959	2,354									
Solyc01g091620	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	58,992	66,574	50,705	54,016	54,581									
Solyc01g091630	cutin deficient 2	CD2	F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			IPR002913 (SMAF HD-ZIP	61,715	99,731	78,813	92,438	89,841	0,719	0,006					up		
Solyc01g091640	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G00740.2)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR(	79,083	76,698	54,618	47,591	50,100									
Solyc01g091650	COP9 signalosome complex subunit 1 (AHRD V3.3 *** AT3G61140.1)		P:GO:0000338; C:G(	P:protein deneddylation; C:COP9 signalosome			IPR000717 (SMART); SM00753 (SMA	42,473	43,841	60,440	60,917	54,705									
Solyc01g091660	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G47140.1),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	0,061	0,268	0,200	0,073	0,070									
Solyc01g091670	Progesterone 5-beta-reductase (AHRD V3.3 *** D6N9X0_NEROL)		F:GO:0016229; F:G(	F:steroid dehydrogenase activity; F:oxidoreductase activity, ac			G3DSA:3.40.50.720 (GENE3D); PTHF	0,099	0,000	0,165	0,097	0,095									
Solyc01g091690	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G00750.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	194,042	156,467	674,910	701,135	670,873									
Solyc01g091700	F-box family protein (AHRD V3.3 *** B9IC61_POPTR)		F:GO:0005515	F:protein binding			PTHR31960:SF3 (PANTHER); PTHR3	2,347	1,749	0,487	0,932	0,683									
Solyc01g091705	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein (AHRD V3.3 *-* AT4G12600.2)		F:GO:0003723; C:G(	F:RNA binding; C:nucleolus			IPR002415 (PRINTS); IPR029064 (G3	3,261	2,336	4,064	5,016	5,183									
Solyc01g091710	F-box protein (AHRD V3.3 *** A0A0B2RBZ5_GLYSO)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); PTH	22,937	22,576	25,161	23,958	26,052									
Solyc01g091715	Cysteine proteinases superfamily protein (AHRD V3.3 *** AT3G57810.4)		C:GO:0009507	C:chloroplast			G3DSA:3.90.70.80 (GENE3D); IPR00:	6,786	6,602	13,231	15,243	14,686									
Solyc01g091720	F-box family protein (AHRD V3.3 *** AT4G00755.2)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); PTH	5,935	5,634	6,555	6,755	6,583									
Solyc01g091730	Peroxisomal membrane protein 11-1 (AHRD V3.3 *** PX111_ORYSJ)		C:GO:0005779; P:G(	C:integral component of peroxisomal membrane; P:peroxisome			IPR008733 (PFAM); PTHR12652 (PAN	2,723	2,624	3,801	3,888	4,352									
Solyc01g091740	U-box domain-containing protein 3 (AHRD V3.3 *** A0A0B2R036_GLYSO)		F:GO:0005515	F:protein binding			IPR000225 (SMART); IPR000225 (PF	47,923	22,227	14,018	12,104	15,597	-1,081	0,000					down		
Solyc01g091750	Arginine/serine-rich splicing factor (AHRD V3.3 *** D8L816_9POAL)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spli			IPR000504 (SMART); IPR000504 (PF.	28,034	31,770	37,825	33,363	34,338									
Solyc01g091770	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DVK5_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART); IPR001841 (PF.	1,717	2,161	0,125	0,239	0,448									
Solyc01g091780	Kinase, putative (AHRD V3.3 *** B9RDK2_RICCO)		C:GO:0009507; F:G(	C:chloroplast; F:kin:	EC:2.7.1.172	Protein-ribulosamine	G3DSA:3.90.1200.10 (GENE3D); IPR(	15,354	15,677	11,790	8,430	13,019									
Solyc01g091800	rRNA adenine N(6)-methyltransferase (AHRD V3.3 *** K4AZC0_SOLLC)		P:GO:0000154; F:G(	P:rRNA modification; F:rRNA (adenine-N6,N6-)-dimethyltransfer			IPR020598 (SMART); IPR011530 (TIG	4,359	10,324	6,980	7,166	8,861	1,271	0,000					up		
Solyc01g091810	LOW QUALITY:Two-component response regulator (AHRD V3.3 *-* W9QMB4_9ROSA)		F:GO:0003677	F:DNA binding			G3DSA:3.40.50.23 G2-like	0,000	0,019	0,047	0,000	0,000									
Solyc01g091820	Flap endonuclease GEN-like 1 (AHRD V3.3 *** W9SAV0_9ROSA)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR006084 (PRINTS); IPR006085 (SM	7,921	8,889	8,001	8,208	8,526									
Solyc01g091830	DUF4378 domain protein (AHRD V3.3 *** AT4G00770.1)						PTHR33623 (PANTHER); PTHR33623	0,040	0,085	0,000	0,000	0,000									
Solyc01g091840	UDP-galactose transporter (AHRD V3.3 *** M4QC22_PRUPE)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM); mobidb-lite (MOB	3,830	5,045	2,254	2,964	3,112									
Solyc01g091850	Vacuolar iron family transporter (AHRD V3.3 *** C1E094_MICCC)		F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ior			IPR008217 (PFAM); IPR008217 (PAN	0,533	0,458	0,611	0,658	0,447									
Solyc01g091860	SET domain-containing protein (AHRD V3.3 *** AT1G01920.2)		F:GO:0005515	F:protein binding			IPR001214 (PFAM); PTHR13271 (PAN	7,893	6,662	8,076	7,136	7,637									
Solyc01g091870	SPX domain-containing family protein (AHRD V3.3 *** B9GW54_POPTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004331 (PFAM); IPR011701 (PFA	0,715	0,539	0,046	0,097	0,071									
Solyc01g091880	ATPase ASNA1 homolog (AHRD V3.3 *** K4AZC8_SOLLC)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR016300 (TIGRFAM); G3DSA:3.40.5	24,112	25,412	32,124	35,783	29,862									
Solyc01g091890	Ubiquitin-related modifier 1 homolog (AHRD V3.3 *** K4AZC9_SOLLC)		C:GO:0005737; P:G(	C:cytoplasm; P:tRNA thio-modification			IPR015221 (PFAM); IPR015221 (PIRS	32,807	31,280	38,146	32,164	33,926									
Solyc01g091900	Peroxisome biogenesis 16-like protein (AHRD V3.3 *** A0A0B0MSZ8_GOSAR)		C:GO:0005778; P:G(	C:peroxisomal membrane; P:peroxisome organization; C:integra			IPR013919 (PFAM); IPR013919 (PAN	28,477	30,794	21,910	20,863	22,229									
Solyc01g091910	phospholipase PLDb2	pldb2	F:GO:0003824	F:catalytic activity			IPR000008 (SMART); IPR001736 (SM	112,118	334,055	61,959	37,919	57,322	1,595	0,013					up		
Solyc01g091920	Subtilisin-like protease (AHRD V3.3 *** A0A151S7J5_CAJCA)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); G3DSA:3.50.30	0,455	0,999	0,075	0,123	0,046									
Solyc01g091930	Subtilisin-like serine protease (AHRD V3.3 *** A0A072TZN1_MEDTR)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); G3DSA:2.60.40	0,571	0,584	0,171	0,097	0,281									
Solyc01g091940	CRS2-associated factor 1		F:GO:0003723	F:RNA binding			IPR001890 (SMART); IPR001890 (PF.	8,185	7,160	10,573	11,376	11,242									
Solyc01g091950	1-acylglycerophosphocholine O-acyltransferase 1 (AHRD V3.3 *** A0A0B0N8P7_GOSAR)		F:GO:0005509; F:G(	F:calcium ion binding; F:transferase activity, transferring acyl gr			IPR002048 (SMART); IPR002123 (SM	94,293	68,634	45,517	36,537	42,948									
Solyc01g092950	MADS-box transcription factor (AHRD V3.3 *** A0A072TQ92_MEDTR)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM); PTHR11945:SF3	0,021	0,064	0,000	0,000	0,024									
Solyc01g093960	MADS-box transcription factor (AHRD V3.3 *** A0A072TNM9_MEDTR)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN' MIKC_MADS	0,962	2,153	2,252	1,752	2,461									
Solyc01g093970	Glycosyltransferase (AHRD V1 **-- B9IC41_POPTR)%3B contains Interpro domain	GAUT1	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM); IPR029044 (G3D	39,953	39,953	33,411	38,862	32,510									
Solyc01g093980	Gibberellin 20-oxidase 4 (AHRD V1 ***- B2MWW5_SOLLC)%3B contains Interpro domain(s) IPR005123 O>		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS); IPR027443 (G3D	0,438	0,463	0,184	0,048	0,210									
Solyc01g093990	Glyoxylate reductase (AHRD V3.3 *** A0A0B0NFA9_GOSAR)		F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			IPR006140 (PFAM); G3DSA:3.40.50.7	3,088	4,158	1,755	1,907	2,781									
Solyc01g094000	Poly(A) RNA polymerase cid11 (AHRD V3.3 *** W9RV71_9ROSA)		F:GO:0016779	F:nucleotidyltransferase activity			IPR002934 (PFAM); G3DSA:1.10.141	71,433	50,933	61,141	57,099	58,490									
Solyc01g094010	alpha/beta-hydrolases superfamily protein		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM); IPR029058 (G3D	46,595	56,802	2,954	2,284	2,135									
Solyc01g094020	Kinase family protein (AHRD V3.3 *** B9IC34_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF.	13,496	12,256	6,222	8,266	7,726									
Solyc01g094030	CLB1	CLB1	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:lipid binding			IPR000008 (SMART); IPR039010 (PF.	66,223	66,411	78,034	78,717	77,091									
Solyc01g094040	Blue copper protein (AHRD V3.3 *** A0A199UNZ4_ANACO)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM); IPR008972 (G3D	41,821	65,767	36,560	43,632	39,452	0,678	0,025					up		
Solyc01g094050	beige/BEACH domain protein (AHRD V3.3 *-* AT3G60920.2)						IPR031570 (PFAM); mobidb-lite (MOB	35,696	24,388	29,387	32,558	33,003									
Solyc01g094060	BEACH domain-containing protein (AHRD V3.3 *** A0A124SBD7_CYNCS)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR000409 (SM	94,294	74,186	85,429	88,990	87,860									
Solyc01g094070	Dihydroflavonol-4-reductase-like (AHRD V3.3 *** A0A0N6XTN7_LYCRU)	DFR	F:GO:0003854; P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	IPR002225 (PFAM); G3DSA:3.40.50.7	0,019	0,000	0,025	0,000	0,000									
Solyc01g094080	Cytochrome P450 family protein (AHRD V3.3 *** A0A061DTU0_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	8,237	8,631	21,134	19,790	23,545									
Solyc01g094090	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072TX02_MEDTR)		F:GO:0003860	F:3-hydroxyisobutyı	EC:3.1.2.4	3-hydroxyisobutyryl-(	IPR032259 (PFAM); G3DSA:3.90.226	0,000	0,388	0,000	0,025	0,000									
Solyc01g094110	11S globulin seed storage protein 2 (AHRD V3.3 *** A0A0B2RJF9_GLYSO)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS); IPR006045 (SM	0,000	0,000	1,209	1,600	1,560									
Solyc01g094120	Cytochrome P450 family protein (AHRD V3.3 *** A0A061DTZ5_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	0,113	0,255	0,025	0,201	0,000									
Solyc01g094130	Cytochrome P450, putative (AHRD V3.3 *** B9RDF6_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	0,377	0,215	0,187	0,049	0,235									
Solyc01g094140	Cytochrome P450 family protein (AHRD V3.3 *** B9IC22_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	13,782	9,557	2,450	0,920	1,475					-1,409	0,025			down
Solyc01g094150	Katanin p60 ATPase-containing subunit (AHRD V3.3 *-* A0A1D1Y047_9ARAE)		F:GO:0005524	F:ATP binding			IPR003593 (SMART); IPR007330 (SM	30,050	24,951	47,664	46,454	46,807									
Solyc01g094160	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHF		F:GO:0003677	F:DNA binding				0,000	0,058	0,000	0,000	0,000									
Solyc01g094170	Digalactosyldiacylglycerol synthase (AHRD V3.3 *** A2Q3N6_MEDTR)		F:GO:0008194; C:G(	F:UDP-glycosyltransferase activity; C:chloroplast outer membra			PF13692 (PFAM); G3DSA:3.40.50.20(	25,486	21,057	23,433	22,829	24,156									
Solyc01g094180	Transmembrane protein, putative (AHRD V3.3 *** G7L2K1_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,213	1,115	1,010	1,028	0,890									
Solyc01g094190	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G00560.1)		F:GO:0016740	F:transferase activity			IPR029903 (PFAM); G3DSA:3.40.50.7	10,466	9,386	6,896	6,991	7,773									
Solyc01g094200	Malic enzyme (AHRD V3.3 *** K4AZG1_SOLLC)		F:GO:0004471; F:G(	F:malate dehydroge	EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS); IPR012302 (SM	166,239	167,185	102,590	84,186	98,951									
Solyc01g094210	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)		P:GO:0055114	P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	7,244	6,985	0,365	0,509	0,824									
Solyc01g094220	carbonyl reductase-like		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	14,755	13,877	49,702	44,759	45,154									
Solyc01g094230	ATP synthase subunit c, chloroplastic (AHRD V3.3 --* ATPH_CHAGL)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,276	0,162	0,025	0,100	0,094									
Solyc01g094240	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)		P:GO:0006952; F:G(	P:defense response	EC:1.1.1.28	(+)-neomenthol dehy	IPR002347 (PRINTS); IPR002347 (PF	0,572	0,459	0,065	0,000	0,071									
Solyc01g094250	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)		P:GO:0006952; F:G(	P:defense response	EC:1.1.1.28	(+)-neomenthol dehy	IPR002347 (PRINTS); PF13561 (PFAI	1,903	2,251	0,197	0,122	0,211									
Solyc01g094260	(+)-neomenthol dehydrogenase (AHRD V3.3 *** MNR1_CAPAN)		P:GO:0006952; F:G(	P:defense response	EC:1.1.1.28	(+)-neomenthol dehy	IPR002347 (PRINTS); G3DSA:3.40.5(	1,603	2,018	0,143	0,025	0,093									
Solyc01g094270	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G24190.2)		P:GO:0006952; F:G(	P:defense response	EC:1.1.1.28	(+)-neomenthol dehy	IPR002347 (PRINTS); IPR002347 (PF	0,616	0,452	0,022	0,000	0,000									
Solyc01g094280	Bifunctional protein FolD (AHRD V3.3 *** W9RX84_9ROSA)		F:GO:0004488; P:G(	F:methylenetetrahy	EC:1.5.1.5	Methylenetetrahydrol	IPR000672 (PRINTS); G3DSA:3.40.5(	23,311	23,871	34,651	29,736	28,500									
Solyc01g094290	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NJL3_ZOSMR)		P:GO:0006813; F:G(	P:potassium ion transport; F:solute:proton antiporter activity; C:			IPR003148 (PFAM); G3DSA:3.40.50.7	77,983	74,316	93,036	89,347	97,328									
Solyc01g094310	LOW QUALITY:U4/U6 small nuclear ribonucleoprotein Prp31 (AHRD V3.3 *-* A0A0B0PVX3_GOSAR)		P:GO:0000244; C:G(	P:spliceosomal tri-snRNP complex assembly; C:U4/U6 x U5 tri-s			IPR012976 (SMART); IPR002687 (PF.	0,000	0,000	0,025	0,000	0,000									
Solyc01g094330	Variant surface glycoprotein ILTAT 1.23 (AHRD V3.3 *** A0A1D1YEL4_9ARAE)						IPR010839 (PFAM); PTHR13943:SF4	9,372	6,755	16,920	20,091	16,177									
Solyc01g094340	Carboxyltransferase alpha Subunit (AHRD V3.3 *** A0A0G2SJ78_SALMI)		F:GO:0003989; P:G(	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR001095 (PRINTS); IPR001095 (PF	22,471	26,405	26,942	27,006	30,758									
Solyc01g094350	RNA helicase DEAD4	DEAD4	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART); IPR014001 (SM	38,355	39,635	39,067	40,017	36,149									
Solyc01g094360	MYB-related transcription factor (AHRD V3.3 *** A0A059PRS4_SALMI)	R2R3MYB18	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	6,967	4,217	0,525	0,098	0,515									
Solyc01g094370	remorin 2	rem2					IPR005518 (PFAM); IPR005516 (PFA	9,771	9,343	6,078	4,490	4,266									
Solyc01g094380	LOW QUALITY:Protein O-glucosyltransferase 1 (AHRD V3.3 *** A0A0B2PAD6_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:glucosyltransferase activ			IPR006598 (SMART); IPR006598 (PF.	0,227	0,094	0,100	0,171	0,165									
Solyc01g094410	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT4G11610.1)		C:GO:0005829; C:G(	C:cytosol; C:integral component of membrane			IPR000008 (SMART); IPR000008 (PF.	844,900	674,553	194,559	435,895	353,219			0,857	0,007	1,164	0,000		up	up
Solyc01g094420	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						IPR015410 (PFAM); mobidb-lite (MOB	44,182	36,921	44,971	45,461	42,599									
Solyc01g094430	Ripening related protein family (AHRD V3.3 *** G7L3M5_MEDTR)						IPR036908 (G3DSA:2.40.40.GENE3D	0,000	0,021	0,051	0,025	0,024									
Solyc01g094440	Ripening related protein family (AHRD V3.3 *** G7L460_MEDTR)						IPR036908 (G3DSA:2.40.40.GENE3D	0,021	0,000	0,000	0,000	0,048									
Solyc01g094460	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TNY7_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM); G3DSA:3.30.133(	11,443	12,450	2,661	2,625	4,207									
Solyc01g094470	ketose-bisphosphate aldolase class-II family protein (AHRD V3.3 --* AT1G18270.4)							27,988	30,391	22,825	21,621	20,725									
Solyc01g094480	WD40 repeat-like protein (AHRD V3.3 *** I0Z536_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	149,407	123,549	147,398	134,813	134,776									
Solyc01g094485	NAC transcription factor (AHRD V3.3 *-* B3VK71_TOBAC)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM); IPR036093 (G3D	3,069	2,699	4,581	4,009	3,832									
Solyc01g094500	Riboflavin biosynthesis protein RibD (AHRD V3.3 *** W9R4Z5_9ROSA)		F:GO:0008703; F:G(	F:5-amino-6-(5-pho:	EC:3.5.4.26; EC:1.1.	Diaminohydroxyphos	IPR024072 (G3DSA:3.40.430.GENE3I	6,773	6,683	4,162	2,904	4,873									
Solyc01g094510	zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein (AHRD V3.3 --* AT1G67180.7)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,059	0,059	0,144	0,121	0,118									
Solyc01g094520	F-box/kelch-repeat protein (AHRD V3.3 *** A0A059Q2G0_9POAL)		F:GO:0005515	F:protein binding			IPR006652 (SMART); IPR015915 (G3	7,289	8,019	7,293	5,737	6,438									
Solyc01g094530	Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9RDR2_RICCO)		P:GO:0006637; F:G(	P:acyl-CoA metabol	EC:3.1.2.2	Acyl-CoA hydrolase	IPR000595 (SMART); IPR000595 (PF.	15,226	16,113	18,506	19,689	20,238									
Solyc01g094540	Small nuclear ribonucleoprotein-associated protein (AHRD V3.3 *-* K4AZJ5_SOLLC)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus			IPR001163 (SMART); G3DSA:2.30.30	21,701	23,744	18,712	16,289	17,101									
Solyc01g094550	Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9RDR2_RICCO)		P:GO:0006637; F:G(	P:acyl-CoA metabol	EC:3.1.2.2	Acyl-CoA hydrolase	IPR000595 (SMART); IPR003703 (TIG	40,846	63,816	33,117	32,435	35,311	0,670	0,023					up		
Solyc01g094560	60S ribosomal protein L36 (AHRD V3.3 *** K4AZJ7_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000509 (PFAM); IPR038097 (G3D	0,180	0,096	0,093	0,209	0,166									
Solyc01g094570	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G49050.1)		P:GO:0016042	P:lipid catabolic process			IPR002921 (PFAM); IPR029058 (G3D	35,237	33,957	17,407	19,328	23,189									
Solyc01g094580	Beta-amylase (AHRD V3.3 *** K4AZJ9_SOLLC)		P:GO:0000272; F:G(	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001371 (PRIN' BES1	24,178	23,031	24,765	25,374	24,677									
Solyc01g094590	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G23340.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	4,012	2,829	3,712	3,698	3,087									
Solyc01g094600	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RDS2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	1,176	1,141	0,978	1,490	0,871									
Solyc01g094610	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9RDS3_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			IPR005512 (PFAM); G3DSA:1.20.58.2	0,392	0,216	0,122	0,000	0,047									
Solyc01g094620	Mediator of RNA polymerase II transcription subunit 12 (AHRD V3.3 *** MED12_ARATH)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR019035 (SMART); IPR019035 (PF.	57,282	61,095	79,860	78,750	78,970									
Solyc01g094625	NADH dehydrogenase ubiquinone 1 alpha subcomplex assembly factor-like protein (DUF498/DUF598) (AHRD V3.3 --* AT3G60150.1)							0,019	0,019	0,000	0,000	0,000									
Solyc01g094630	pre-mRNA-splicing factor CWC22-like protein (DUF3245) (AHRD V3.3 *** AT3G61370.3)						IPR021641 (PFAM); mobidb-lite (MOB	24,774	30,225	25,744	29,856	28,628									
Solyc01g094640	Phosphatidylinositol N-acetylglucosaminlytransferase subunit P-like protein (AHRD V3.3 *** A0A072TN99_MEDTR)						IPR025486 (PFAM); IPR022212 (PFA	0,697	0,355	1,222	1,159	0,802									
Solyc01g094650	Recombination initiation defects 3, putative isoform 1 (AHRD V3.3 --* A0A061DV47_THECC)		P:GO:0048236; P:G(	P:plant-type sporogenesis; P:chromosome organization involve			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,199	0,303	0,093	0,076	0,117									
Solyc01g094655	Protein PAIR1 (AHRD V3.3 *** A0A151UCR8_CAJCA)		P:GO:0048236; P:G(	P:plant-type sporogenesis; P:chromosome organization involve			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,164	0,235	0,072	0,000	0,141									
Solyc01g094660	Kinase family protein (AHRD V3.3 *** D7LDA2_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity			IPR003613 (SMART); IPR000719 (SM	51,346	45,867	48,887	49,952	46,541									
Solyc01g094680	Signal peptide peptidase-like protein (AHRD V3.3 *** G7LBR2_MEDTR)		F:GO:0004190; C:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR006639 (SMART); IPR003137 (PF.	41,844	58,191	32,485	32,906	33,641									
Solyc01g094690	plasma membrane intrinsic protein 1.2	PIP1.2	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR000425 (TI(	76,954	63,446	66,861	54,463	60,063									
Solyc01g094700	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7LBQ7_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART); PF12710 (PFAM	123,665	96,734	1,252	1,092	1,720									
Solyc01g094710	LOW QUALITY:mitogen-activated protein kinase kinase kinase 6 (AHRD V3.3 --* AT3G07980.3)							0,019	0,000	0,022	0,000	0,000									
Solyc01g094720	Phosphate transporter (AHRD V3.3 *** A0A0B5WYA8_MANES)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D); G3D	67,826	66,067	80,072	76,100	84,541									
Solyc01g094725	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *** Q60D46_SOLDE)						IPR015410 (PFAM); mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc01g094750	Cytochrome P450 family protein (AHRD V3.3 *** B9I8K8_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	5,583	5,689	0,123	0,423	0,117									
Solyc01g094760	Origin recognition complex subunit 5 (AHRD V3.3 *** W9QP90_9ROSA)		C:GO:0000808; C:G(	C:origin recognition complex; C:nucleus; P:DNA replication			G3DSA:3.40.50.300 (GENE3D); PF13	3,985	4,230	2,208	1,168	1,478									
Solyc01g094770	Mesoderm induction early response protein 1, putative isoform 1 (AHRD V3.3 *** A0A061DT69_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	54,815	49,254	79,152	74,722	73,659									
Solyc01g094780	LDLR chaperone MESD (AHRD V3.3 *** A0A1D1YKF8_9ARAE)		P:GO:0006457; C:G(	P:protein folding; C:membrane			G3DSA:3.30.70.260 (GENE3D); mobic	11,085	7,143	9,849	10,071	10,194									
Solyc01g094790	Cysteine synthase (AHRD V3.3 *** K4AZL9_SOLLC)		F:GO:0004124; C:G(	F:cysteine synthase	EC:4.4.1.9; EC:2.5.1	L-3-cyanoalanine syı	IPR005856 (TIGRFAM); G3DSA:3.40.5	69,020	69,157	125,575	144,055	111,989									
Solyc01g094800	ATP-dependent helicase BRM (AHRD V3.3 *** W9QEL4_9ROSA)		F:GO:0005515; F:G(	F:protein binding; F:	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR001650 (SMART); IPR014001 (SM	116,779	98,125	113,081	114,239	118,412									
Solyc01g094810	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A1D1ZAB9_9ARAE)		F:GO:0005524; P:G(	F:ATP binding; P:ubiquitin-dependent protein catabolic process;			SM00212 (SMART); IPR016135 (G3D	58,461	29,939	36,584	30,968	32,680	-0,936	0,000					down		
Solyc01g094820	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** A0A103XI63_CYNCS)		F:GO:0003677	F:DNA binding			IPR001606 (SMART); IPR000949 (SM	4,753	3,868	5,730	5,429	5,793									
Solyc01g094830	Protein DETOXIFICATION (AHRD V3.3 *-* K4AZM3_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM); IPR002528 (TIGF	7,851	6,705	3,992	4,217	4,486									
Solyc01g094835	Serine/threonine-protein kinase (AHRD V3.3 *** M0ZGV5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART); IPR001480 (SM	23,594	16,042	10,248	11,101	12,673									
Solyc01g094840	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061G5W7_THECC)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART); IPR024766 (PF.	3,318	3,397	5,656	5,551	5,134									
Solyc01g094860	Transmembrane protein 8B (AHRD V3.3 *** A0A0B0NPZ1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR021910 (PFAM); PTHR14319:SF3	9,785	12,704	14,362	20,557	16,658					0,517	0,011			up
Solyc01g094870	PLAC8 family protein (AHRD V3.3 *** AT4G23470.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,800	1,728	3,840	3,501	3,155									
Solyc01g094880	Quinoprotein amine dehydrogenase, beta chain-like, RIC1-like guanyl-nucleotide exchange factor (AHRD V3		F:GO:0005515; P:G(	F:protein binding; P:intracellular protein transport; C:RIC1-RGP'			IPR015943 (G3DSA:2.130.10.GENE3I	76,260	62,997	59,235	61,108	58,913									
Solyc01g094890	Ferric reductase oxidase (AHRD V3.3 *** V9HYU6_MANES)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR039261 (G3DSA:3.40.50.GENE3D	0,903	0,826	0,119	0,298	0,118									
Solyc01g094910	ferric-chelate reductase	fro1	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001834 (PRINTS); IPR039261 (G3	1,756	2,255	4,007	4,450	7,032									
Solyc01g094920	receptor-like kinase (AHRD V3.3 *** AT4G00300.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph			IPR024788 (PFAM); G3DSA:2.60.120	189,540	158,482	126,009	230,801	193,307			0,614	0,003	0,874	0,000		up	up

Solyc01g094930	CAAX prenyl protease 1-like protein (AHRD V3.3 *** A0A0B0NSR9_GOSAR)		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bo	IPR032456 (PFAM); G3DSA:3.30.201	59,662	62,769	113,657	122,039	108,817									
Solyc01g094940	Kinase family protein (AHRD V3.3 *** D7KQ62_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	55,163	34,863	24,709	21,019	24,478									
Solyc01g094945	homeobox protein knotted-1-like 4 (AHRD V3.3 --* AT5G11060.1)							0,000	0,000	0,000	0,000	0,024									
Solyc01g094950	Protein BPS1, chloroplastic (AHRD V3.3 *** A0A0B2NV45_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR004320 (PFAM); PTHR31509:SF3	497,669	440,938	445,376	490,741	437,424									
Solyc01g094960	mitogen-activated protein kinase 5	mapk5	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	13,837	16,115	8,962	8,765	10,339									
Solyc01g094965	Simk1 (AHRD V3.3 *** A0A0A9JCU1_ARUDO)							0,000	0,000	0,022	0,000	0,024									
Solyc01g094970	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G61490.4)	PG55-2	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART); IPR000743 (PF	0,077	0,179	0,071	0,050	0,095									
Solyc01g094990	LOW QUALITY:transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:integral component			G3DSA:3.90.550.50 (GENE3D); IPR0	0,042	0,133	0,072	0,098	0,211									
Solyc01g095000	Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *** AT2G46100.1)						IPR018790 (PFAM); PTHR34123:SF1	8,326	10,106	23,732	21,026	28,917									
Solyc01g095010	Diacylglycerol kinase family protein (AHRD V3.3 *** AT2G46090.1)		F:GO:0003951	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR001206 (SMART); IPR001206 (PF	7,983	7,591	17,241	16,391	16,600									
Solyc01g095020	Chorismate synthase (AHRD V3.3 *** A0A0B0NMD4_GOSAR)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cap binding complex			mobidb-lite (MOBIDB_LITE); mobidb-lit	83,778	65,662	101,796	99,219	98,216									
Solyc01g095030	Myb family transcription factor family protein (AHRD V3.3 *** B9I8P3_POPTR)	ARS1	F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB_related	24,935	17,524	16,659	15,258	14,532									
Solyc01g095040	C-terminal binding AN-like protein (AHRD V3.3 *** A0A0B0MUN4_GOSAR)		F:GO:0051287; P:G(	F:NAD binding; P:oxidation-reduction process			G3DSA:3.40.50.720 (GENE3D); G3DS	85,558	72,036	64,242	56,238	60,836									
Solyc01g095050	Negatively light-regulated protein (AHRD V3.3 *** A0A0K9NSD8_ZOSMR)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:cytoplasm; C:plasma			IPR006760 (PFAM); mobidb-lite (MOB	534,063	502,458	488,797	437,982	442,710									
Solyc01g095060	ISCU-like 3 (AHRD V3.3 --* AT4G04080.1)						mobidb-lite (MOBIDB_LITE)	7,115	6,694	8,425	7,482	6,781									
Solyc01g095070	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT1G01490.2)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); mobic	41,940	28,369	10,680	9,332	8,731									
Solyc01g095080	1-aminocyclopropane-1-carboxylic acid synthase-2	ACS2	F:GO:0003824; F:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phosphc			PR00753 (PRINTS); IPR004839 (PFA	0,512	1,091	238,778	443,074	179,415					0,897	0,001			up
Solyc01g095090	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G01270.1)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART); IPR001841 (PF	1,408	0,944	4,758	5,399	4,178									
Solyc01g095100	WRKY transcription factor 22	WRKY22	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF_WRKY	1,960	3,718	0,934	1,350	0,939									
Solyc01g095110	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061DUV4_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	7,088	7,101	5,988	5,368	6,078									
Solyc01g095120	alpha/beta-hydrolases superfamily protein		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity			IPR002410 (PRINTS); IPR000073 (PF	15,891	14,626	18,006	16,114	17,503									
Solyc01g095130	E3 SUMO-protein ligase pli1 (AHRD V3.3 *-* A0A0B2RRT6_GLYSO)		F:GO:0019789	F:SUMO transferase activity			PTHR10782 (PANTHER); IPR027229	1,530	1,016	0,772	0,826	0,777									
Solyc01g095140	Late embryogenesis abundant protein (AHRD V3.3 *** B5TV69_CAMSI)		P:GO:0009269	P:response to desiccation			IPR013990 (SMART); G3DSA:2.60.40	134,615	385,726	58,599	43,307	59,892	1,539	0,009					up		
Solyc01g095150	late embryogenesis-like protein	Lea	P:GO:0009269	P:response to desiccation			IPR013990 (SMART); IPR004864 (PF	476,817	736,809	295,782	318,936	332,003									
Solyc01g095160	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT4G37170.1)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM); IPR002885 (PFA	2,032	2,178	3,056	2,827	2,712									
Solyc01g095170	LOW QUALITY:cell wall protein SITFR88	TFR88	C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM); mobidb-lite (MOB	19,527	19,597	26,433	23,809	21,650									
Solyc01g095180	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61550.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART); IPR001841 (PF	7,305	4,362	6,493	4,511	5,053									
Solyc01g095190	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	0,122	0,114	0,050	0,073	0,094									
Solyc01g095210	Golgin candidate 4-like protein (AHRD V3.3 *** A0A0B0PVX8_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	43,195	35,031	36,794	36,483	35,459									
Solyc01g095220	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 --* AT3G25610.1)							4,122	3,316	2,120	1,901	2,216									
Solyc01g095230	Programmed cell death 7 (AHRD V3.3 *** A0A0B0PWM5_GOSAR)						IPR031974 (PFAM); mobidb-lite (MOB	7,851	5,586	5,751	4,855	4,519									
Solyc01g095240	LOW QUALITY:Membrane-associated kinase regulator-like protein, putative (AHRD V3.3 *** A0A072U9K3_I		F:GO:0000166; F:G(	F:nucleotide bindinc	EC:3.6.1.15	Nucleoside-triphosph	PTHR34576:SF2 (PANTHER); PTHR3	0,804	0,980	0,212	0,243	0,163									
Solyc01g095250	Acidic endochitinase (AHRD V3.3 *** W9R015_9ROSA)		P:GO:0005975	P:carbohydrate metabolic process			G3DSA:3.20.20.80 (GENE3D); IPR00	0,038	0,080	0,000	0,000	0,000									
Solyc01g095260	Acidic endochitinase (AHRD V3.3 *** W9R015_9ROSA)		P:GO:0005975	P:carbohydrate metabolic process			IPR001223 (PFAM); G3DSA:3.20.20.8	0,019	0,000	0,000	0,000	0,000									
Solyc01g095270	DUF2358 family protein (DUF2358) (AHRD V3.3 *** AT2G46220.1)						G3DSA:3.10.450.50 (GENE3D); IPR0	13,598	14,811	29,852	19,348	24,238					-0,621	0,001			down
Solyc01g095280	Protein ABIL1, putative (AHRD V3.3 *** B9RDZ9_RICCO)						IPR028457 (PANTHER); PTHR10460:	23,447	20,737	12,544	11,717	11,879									
Solyc01g095290	Glycosyltransferase (AHRD V3.3 *** K4AZR8_SOLLC)		C:GO:0000139; C:G(	C:Golgi membrane; C:integral component of membrane; F:transf			IPR005069 (PFAM); mobidb-lite (MOB	7,683	5,850	7,254	7,927	6,341									
Solyc01g095300	glycosyl transferase family 1 protein (AHRD V3.3 *** AT4G01210.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; C:integral component of m			G3DSA:3.40.50.2000 (GENE3D); IPR	65,034	39,932	7,869	8,414	10,148	-0,676	0,013					down		
Solyc01g095305	Protein PHOSPHATE STARVATION RESPONSE 2 (AHRD V3.3 --* PHR2_ORYSJ)							301,998	237,621	495,361	444,849	485,849									
Solyc01g095310	Acidic endochitinase (AHRD V3.3 *** A0A199VW52_ANACO)		P:GO:0005975	P:carbohydrate metabolic process			IPR001223 (PFAM); G3DSA:3.20.20.8	0,333	0,326	0,219	0,142	0,376									
Solyc01g095320	BAG family molecular chaperone regulator 6 (AHRD V3.3 *** A0A0B2R655_GLYSO)		F:GO:0051087	F:chaperone binding			IPR003103 (SMART); IPR003103 (PF	9093,904	8023,966	17206,484	14604,995	16948,021									
Solyc01g095350	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 --* A0A072U4F1_MEDTR)						IPR000008 (SMART); IPR000008 (PF	0,021	0,079	0,047	0,047	0,000									
Solyc01g095360	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT4G01200.1)						IPR000008 (SMART); IPR000008 (PF	0,907	0,791	0,386	0,069	0,190									
Solyc01g095370	F-box family protein (AHRD V3.3 *** B9GQF5_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR001810 (PF	10,035	9,369	11,679	7,236	9,422					-0,687	0,002			down
Solyc01g095380	LOW QUALITY:transmembrane protein, putative (DUF679) (AHRD V3.3 --* AT5G46090.1)							0,000	0,000	0,025	0,000	0,000									
Solyc01g095390	Intracellular protein transporter USO1-like protein (AHRD V3.3 *** G7KAQ1_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	11,891	9,525	1,742	3,581	3,386			0,944	0,018	1,027	0,006		up	up
Solyc01g095400	BTB/POZ domain-containing protein (AHRD V3.3 *** W9QSI6_9ROSA)		F:GO:0005515	F:protein binding			IPR000210 (SMART); IPR011705 (SM	57,967	53,245	54,855	47,794	52,813									
Solyc01g095410	Eukaryotic translation initiation factor 1A (AHRD V3.3 *** A0A0B0NM01_GOSAR)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			IPR001253 (SMART); G3DSA:2.40.50	577,912	605,967	629,378	605,007	580,493									
Solyc01g095420	copper ion binding protein (AHRD V3.3 *** AT4G05400.3)		C:GO:0005762	C:mitochondrial large ribosomal subunit			mobidb-lite (MOBIDB_LITE); mobidb-lit	18,855	19,067	29,140	26,109	26,312									
Solyc01g095430	Protein CURVATURE THYLAKOID 1A, chloroplastic (AHRD V3.3 *** CUT1A_ARATH	CURT1	C:GO:0009579	C:thylakoid			IPR025564 (PFAM); IPR033344 (PAN	55,547	103,514	32,552	42,616	75,076	0,926	0,003	1,203	0,000			up	up	
Solyc01g095440	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT4G01140.1)		C:GO:0016021	C:integral component of membrane			IPR010605 (PFAM); IPR010605 (PAN	0,000	0,021	0,000	0,022	0,000									
Solyc01g095450	GDSL esterase/lipase family (AHRD V3.3 *** A0A151QZV0_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	2,631	4,023	0,069	0,198	0,304									
Solyc01g095460	TAF-2 (AHRD V3.3 *** Q40586_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF_bZIP	103,217	122,417	53,684	56,411	72,525									
Solyc01g095470	Aldose 1-epimerase, putative (AHRD V3.3 *** B9RE17_RICCO)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:isomerase activity; F:cart			IPR014718 (G3DSA:2.70.98.GENE3D	10,790	15,710	15,937	24,125	16,303					0,600	0,001			up
Solyc01g095480	Exosome complex exonuclease RRP41, putative (AHRD V3.3 *** B9SWZ0_RICCO)		C:GO:0000176; C:G(	C:nuclear exosome	EC:2.7.7.56	tRNA nucleotidyltrans	IPR015847 (PFAM); IPR027408 (G3D	13,641	12,724	13,268	12,255	12,592									
Solyc01g095490	Ubiquitin-conjugating enzyme E2, putative (AHRD V3.3 *** B9T334_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART); IPR016135 (G3D	11,701	15,264	25,304	25,015	20,286									
Solyc01g095500	Sl Cytokinin Response Factor 5	CRF7	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN_ERF	1,618	1,134	0,191	0,134	0,141									
Solyc01g095510	Mitochondrial carrier protein, putative (AHRD V3.3 *** B9RIM4_RICCO)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transp			IPR002067 (PRINTS); IPR023395 (G3	6,589	5,674	7,512	7,580	5,765									
Solyc01g095520	Arabinogalactan peptide-like protein (AHRD V3.3 *** G7J699_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR009424 (PFAM); IPR009424 (PAN	0,538	0,617	3,383	3,439	3,530									
Solyc01g095530	LOW QUALITY:cytoplasmic tRNA 2-thiolation protein (AHRD V3.3 *** AT3G55570.1)						mobidb-lite (MOBIDB_LITE); PTHR335	343,802	205,687	109,171	138,758	121,667	-0,715	0,016					down		
Solyc01g095540	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT5G41760.2)		C:GO:0000139; F:G(	C:Golgi membrane; F:pyrimidine nucleotide-sugar transmembrar			IPR007271 (PIRSF); IPR007271 (PFA	20,291	16,750	44,730	50,611	40,997									
Solyc01g095550	LOW QUALITY:Protein kinase family protein (AHRD V3.3 *** AT5G41730.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); G3DSA:1.10.5	0,483	0,348	0,149	0,269	0,353									
Solyc01g095560	Cysteine proteinases superfamily protein (AHRD V3.3 --* AT3G48350.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,147	3,914	1,871	2,968	2,423									
Solyc01g095580	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:			IPR004993 (PFAM); IPR031110 (PTH	45,176	23,108	79,877	83,222	69,318	-0,939	0,000					down		
Solyc01g095590	Extra-large G-like protein (AHRD V3.3 *** G7L422_MEDTR)						IPR021480 (PFAM); mobidb-lite (MOB	44,967	41,776	21,717	19,554	23,974									
Solyc01g095600	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9RZB6_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (TIGF	2,540	2,342	2,013	2,820	2,188									
Solyc01g095610	protein trichome birefringence-like 25		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	3,438	2,913	0,884	1,379	1,856									
Solyc01g095620	Glycosyltransferase (AHRD V3.3 *** D7S016_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); G3D	39,593	78,052	5,123	5,918	10,676	1,006	0,001	1,052	0,020			up	up	
Solyc01g095630	WRKY transcription factor 41	WRKY41	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF_WRKY	97,186	62,145	12,184	31,644	33,681			1,462	0,000	1,375	0,000		up	up
Solyc01g095640	Myb family transcription factor (AHRD V3.3 *** A0A0K9P4S6_ZOSMR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB_related	0,270	0,193	0,000	0,072	0,095									
Solyc01g095650	Histone H3 like protein (AHRD V3.3 *-* Q7XIZ8_TURGL)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS); IPR000164 (SM	0,359	0,376	0,119	0,025	0,070									
Solyc01g095670	thylakoid rhodanese-like protein (AHRD V3.3 *** AT4G01050.1)						IPR036873 (G3DSA:3.40.250.GENE3	37,778	53,029	43,148	44,248	57,422			0,409	0,007				up	
Solyc01g095680	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *-* A0A061DSR6_THECC)							5,137	6,885	17,547	16,331	17,405									
Solyc01g095690	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061DSI9_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM); IPR011990 (G3D	1,357	1,204	0,941	1,367	1,602									
Solyc01g095695	acyl-CoA oxidase 2 (AHRD V3.3 --* AT5G65110.2)							0,000	0,000	0,000	0,025	0,000									
Solyc01g095700	regulatory component of ABA receptor3-like		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm			IPR023393 (G3DSA:3.30.530.GENE3	23,251	49,571	4,511	4,850	4,263	1,120	0,000					up		
Solyc01g095710	RNA helicase DEAH-box3	DEAH3	F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART); IPR007502 (SM	24,486	17,980	28,153	30,201	26,253									
Solyc01g095720	Lipase (AHRD V3.3 *** A0A0B0MHI9_GOSAR)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	24,440	10,965	3,407	5,380	4,881	-1,126	0,018					down		
Solyc01g095730	Poly(A) RNA polymerase cid14 (AHRD V3.3 *** W9RAG3_9ROSA)		F:GO:0016779	F:nucleotidyltransferase activity			IPR002934 (PFAM); G3DSA:3.30.460	47,455	45,260	51,460	51,125	50,531									
Solyc01g095740	RNA helicase DEAD5	DEAD5	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART); IPR014001 (SM	32,749	32,679	47,185	37,637	43,840									
Solyc01g095770	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmen			IPR000595 (SMART); G3DSA:1.10.28	0,432	2,180	0,197	0,530	0,470	2,341	0,024					up		
Solyc01g095780	LOW QUALITY:Non-specific lipid-transfer protein (AHRD V3.3 *** A0A022QU64_ERYGU)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS); IPR016140 (PF	0,176	0,422	0,000	0,000	0,000									
Solyc01g095790	Splicing factor 3a, subunit 3 (AHRD V3.3 *-* A0A0K9P946_ZOSMR)		C:GO:0005634	C:nucleus			PF13297 (PFAM); mobidb-lite (MOBID	86,654	73,495	69,439	67,281	70,987									
Solyc01g095800	F-box-like protein (AHRD V3.3 *** A0A072UUB0_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART); IPR032675 (G3	4,933	4,336	4,622	5,726	5,464									
Solyc01g095810	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DTM6_THECC)		F:GO:0030247	F:polysaccharide binding			IPR001841 (SMART); IPR013083 (G3	0,375	0,225	0,584	0,503	0,565									
Solyc01g095840	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DTM6_THECC)		F:GO:0030247	F:polysaccharide binding			IPR001841 (SMART); IPR013083 (G3	0,000	0,000	0,025	0,025	0,000									
Solyc01g095860	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DTM6_THECC)		F:GO:0030247	F:polysaccharide binding			IPR001841 (SMART); IPR013083 (G3	0,063	0,039	0,022	0,095	0,024									
Solyc01g095870	Reduced male fertility, Probable F-box protein (AHRD V3.3 *** A0A0K9NUY5_ZOSMR)		F:GO:0005515	F:protein binding			PTHR15537 (PANTHER); PTHR15537	0,021	0,037	0,000	0,000	0,000									
Solyc01g095890	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9PJE7_ZOSMR)		F:GO:0005515	F:protein binding			IPR000313 (SMART); IPR001965 (SM	33,202	24,043	27,034	27,313	27,848									
Solyc01g095900	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G01320.3)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	53,296	64,864	355,591	435,522	398,742									
Solyc01g095903	aberrant root formation protein (AHRD V3.3 --* AT5G11030.8)							0,142	0,284	2,469	2,928	2,602									
Solyc01g095907	Cytochrome b561 and DOMON domain-containing protein (AHRD V3.3 *** A0A199VLE4_ANACO)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART); PTHR23130:SF	0,000	0,021	0,047	0,050	0,024									
Solyc01g095910	Cytochrome b561 and DOMON domain-containing protein (AHRD V3.3 *-* A0A199VYL9_ANACO)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART); IPR015410 (PF	0,000	0,039	0,097	0,099	0,143									
Solyc01g095920	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 --* A0A199V2I6_ANACO)						G3DSA:3.40.50.150 (GENE3D); IPR0	1,194	0,933	115,110	92,562	99,297									
Solyc01g095930	O-acyltransferase WSD1-like protein (AHRD V3.3 *** A0A0B0P708_GOSAR)		F:GO:0004144; P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR009721 (PFAM); IPR004255 (PFA	44,288	29,498	603,089	603,263	564,892									
Solyc01g095950	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_SOLBU)		F:GO:0003899; F:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA p	G3DSA:3.90.1100.10 (GENE3D); PTH	0,000	0,041	0,332	0,166	0,141									
Solyc01g095960	O-acyltransferase WSD1-like protein (AHRD V3.3 *** A0A0B0P708_GOSAR)		F:GO:0004144; P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR004255 (PFAM); IPR009721 (PFA	0,019	0,000	2,510	2,599	1,238									
Solyc01g095970	dynamin-like protein (AHRD V3.3 *** AT5G42080.4)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS); IPR003130 (SM	55,016	82,964	37,183	40,915	37,415									
Solyc01g095980	Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** AT3G61770.1)		C:GO:0016021	C:integral component of membrane			IPR003832 (PFAM); IPR003832 (PAN	4,297	5,179	5,112	4,758	7,318									
Solyc01g095990	Phosphatidylinositol 3-and 4-kinase family protein (AHRD V3.3 *** D7LEK1_ARALL)		F:GO:0005515	F:protein binding			IPR000626 (SMART); IPR000403 (PF	114,123	93,446	54,580	109,485	88,442			0,693	0,000	1,006	0,000		up	up
Solyc01g095995	Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *** A0A072TWH9_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM); PTHR31852 (PAN	0,000	0,039	0,000	0,000	0,000									
Solyc01g096010	embryo defective 1703 (AHRD V3.3 *** AT3G61780.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	21,981	20,848	54,355	65,037	55,673									
Solyc01g096020	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4AZZ1_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein cata			IPR013083 (G3DSA:3.30.40.GENE3D	9,578	9,590	11,079	10,591	11,151									
Solyc01g096030	UV-stimulated scaffold A-like protein (AHRD V3.3 *** A0A072U659_MEDTR)		P:GO:0009411	P:response to UV			IPR018610 (PFAM); mobidb-lite (MOB	12,681	9,166	10,788	10,805	10,452									
Solyc01g096040	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G01300.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bo	IPR001461 (PRINTS); IPR032799 (PF	202,065	216,803	349,198	353,242	292,911									
Solyc01g096050	bHLH transcription factor_SGN-U238928		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF_bHLH	52,315	91,273	133,938	159,194	116,252									
Solyc01g096060	Exportin-2-like protein (AHRD V3.3 *** A0A0B0N8Q4_GOSAR)		P:GO:0006886; F:G(	P:intracellular protein transport; F:Ran GTPase binding			IPR001494 (SMART); IPR005043 (PF	52,854	49,817	60,023	58,425	55,050									
Solyc01g096070	Auxin Response Factor 18	ARF18	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF_ARF	21,515	17,674	1,990	2,875	2,567									
Solyc01g096080	30S ribosomal protein S16, chloroplastic (AHRD V3.3 --* RR16_SACHY)						PTHR34371 (PANTHER); PTHR34371	7,945	6,132	6,356	6,741	6,276									
Solyc01g096090	Transmembrane protein, putative (AHRD V3.3 *** A0A072U5P8_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	124,107	90,261	222,748	219,739	205,320									
Solyc01g096110	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G46560.2)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	50,158	41,812	62,837	72,156	65,256									
Solyc01g096120	Dof zinc finger protein1	Dof1	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM_Dof	0,056	0,176	0,090	0,100	0,095									
Solyc01g096130	ORMDL family protein (AHRD V3.3 *** AT1G01230.1)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR007203 (PFAM); IPR007203 (PIRS	25,157	17,826	23,921	22,281	22,777									
Solyc01g096140	Aluminum-activated malate transporter		P:GO:0015743	P:malate transport			IPR020966 (PFAM); mobidb-lite (MOB	2,186	1,261	0,548	0,926	0,563									
Solyc01g096150	NC domain-containing protein-like protein (AHRD V3.3 *** AT1G01225.1)						IPR007053 (PFAM); PTHR13943 (PAN	0,637	0,581	1,869	1,551	1,249									
Solyc01g096160	L-fucokinase/GDP-L-fucose pyrophosphorylase (AHRD V3.3 *** AT1G01220.7)		F:GO:0005524; F:G(	F:ATP binding; F:transferase activity, transferring phosphorus-c			PR00959 (PRINTS); IPR006204 (PFA	18,783	19,633	25,331	28,472	25,679									
Solyc01g096170	MAP kinase kinase kinase 5		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	1,589	1,038	2,942	2,000	2,144									
Solyc01g096180	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *** B9SBD0_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spl			IPR000504 (SMART); IPR000504 (PF	12,464	16,240	17,632	14,889	16,414									
Solyc01g096185	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *-* B9SBD0_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spl			IPR012677 (G3DSA:3.30.70.GENE3D	4,747	4,179	6,505	5,978	6,203									
Solyc01g096190	Ca2+-ATPase	LCA1	F:GO:0000166; C:G(	F:nucleotide binding; C:integral component of membrane			PR00119 (PRINTS); IPR004014 (SMA	16,333	23,822	4,765	6,354	7,534									
Solyc01g096193	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2Q7G6_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,584	2,911	1,794	1,531	1,653									
Solyc01g096200	U-box domain-containing protein 43 (AHRD V3.3 *** W9RNX9_9ROSA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prote			IPR003613 (SMART); IPR000225 (SM	144,707	181,296	54,538	62,084	92,201			0,754	0,032				up	
Solyc01g096205	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 --* AT1G65280.2)							0,741	0,502	0,458	0,499	0,706									
Solyc01g096210	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SBC5_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	11,289	8,436	9,799	9,963	9,708									
Solyc01g096220	Ras-related protein RABA3 (AHRD V3.3 *** A0A0B2Q7Y9_GLYSO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00175 (SMAR	20,998	28,323	51,994	53,812	48,084									
Solyc01g096230	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G46620.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART); IPR025753 (PF	19,783	23,114	62,032	57,155	50,438									
Solyc01g096240	plant/protein (AHRD V3.3 *** AT3G61870.1)		C:GO:0009534; C:G(	C:chloroplast thylakoid; C:chloroplast inner membrane; C:integra			IPR025067 (PFAM); PTHR34679:SF2	70,356	107,231	58,492	64,564	96,443	0,635	0,039	0,718	0,000			up	up	
Solyc01g096250	LOW QUALITY:oxidoreductases, acting on NADH or NADPH (AHRD V3.3 *-* AT1G75260.1)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,589	1,926	0,493	0,295	0,281									
Solyc01g096260	NAD-dependent protein deacetylase HST1-like protein (AHRD V3.3 *** AT2G46640.2)						PTHR38366 (PANTHER)	0,199	1,666	0,046	0,000	0,142									
Solyc01g096270	Cytochrome b5 (AHRD V3.3 *** CYB5_BRAOB)		C:GO:0016021; F:G(	C:integral component of membrane; F:heme binding; F:metal ior			IPR001199 (PRINTS); IPR001199 (SM	111,864	97,543	208,708	200,279	200,753									
Solyc01g096280	Cytochrome P450 (AHRD V3.3 *** F4YF83_9APIA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	1,703	0,797	1,644	1,303	1,156									
Solyc01g096290	ubiquitin-ribosomal fusion protein		F:GO:0003735; F:G(	F:structural constituent of ribosome; F:protein binding; C:ribosor			IPR019956 (PRINTS); IPR000626 (SM	124,360	123,002	108,948	92,846	93,866									
Solyc01g096300	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *-* AT4G22290.1)		C:GO:0016021	C:integral component of membrane			IPR040339 (PANTHER); PTHR33709:	1,600	1,376	0,891	1,367	1,429									
Solyc01g096320	Homeobox-leucine zipper protein (AHRD V3.3 *** M4W1Z7_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN_HD-ZIP	6,388	3,680	19,194	18,096	16,641									
Solyc01g096330	LOW QUALITY:UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT3G07020.2)							1,381	1,113	1,207	1,348	1,123									
Solyc01g096340	Small auxin up-regulated RNA2	SAUR2	P:GO:0009733	P:response to auxin			IPR003676 (PFAM); PTHR31374:SF2	19,694	16,216	57,820	69,769	53,280									
Solyc01g096350	CDPK-related protein kinase (AHRD V3.3 *** A0A0B0NV52_GOSAR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	51,590	63,220	71,144	79,440	74,758									
Solyc01g096360	Rho GTPase activating protein 2		P:GO:0007165	P:signal transduction			IPR000095 (SMART); IPR000198 (SM	10,407	8,744	0,855	0,889	0,916									
Solyc01g096370	Basic helix loop helix (BHLH) family transcription factor (AHRD V3.3 *** A0A072TYH1_MEDTR)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF_bHLH	1,115	1,521	0,097	0,048	0,140									
Solyc01g096380	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D); PF13	0,322	0,297	0,384	0,217	0,259									
Solyc01g096390	DNA-directed RNA polymerase subunit (AHRD V3.3 *** K4B027_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p	IPR006592 (SMART); IPR007066 (PF	123,499	95,794	85,247	74,514	84,024									

Solyc01g096400	Transglutaminase family protein (AHRD V3.3 *** G7J0K8_MEDTR)						IPR032698 (PFAM): PTHR31350 (PAI	5,318	5,382	15,658	16,222	17,972									
Solyc01g096410	Phosphatidylinositol-4-phosphate 5-kinase (AHRD V3.3 *** J7K3W0_TOBAC)		F:GO:0005524; F:G(	F:ATP binding; F:1-	EC:2.7.1.68	1-phosphatidylinosito	IPR003409 (SMART): IPR002498 (SM	2,283	2,462	0,193	0,267	0,444									
Solyc01g096420	NADPH:quinone oxidoreductase (AHRD V3.3 *** AT3G27890.1)		F:GO:0016491	F:oxidoreductase activity			IPR029039 (G3DSA:3.40.50.GENE3D	4,476	13,075	2,749	2,178	6,664	1,568	0,001					up		
Solyc01g096430	Maturase K (AHRD V3.3 --* MATK_PAESU)							1,640	2,525	1,132	1,054	1,318									
Solyc01g096435	NADPH:quinone oxidoreductase (AHRD V3.3 *** AT3G27890.1)		F:GO:0016491	F:oxidoreductase activity			IPR029039 (G3DSA:3.40.50.GENE3D	21,496	26,072	18,296	16,318	18,249									
Solyc01g096440	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061EFM5_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	3,033	2,749	1,574	1,770	1,695									
Solyc01g096450	Aspartic proteinase nepenthesin-1-like protein (AHRD V3.3 *** T2DNA5_PHAVU)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR021109 (G3D	40,604	59,779	3,571	2,073	3,075									
Solyc01g096460	LOW QUALITY:U-box domain-containing protein 4 (AHRD V3.3 *** A0A1D1XNU8_9ARAE)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR000225 (PF	12,908	13,006	11,873	10,447	10,317									
Solyc01g096470	Transcription factor (AHRD V3.3 *** G7J0H6_MEDTR)		C:GO:0005634; F:G(	C:nucleus; F:sequence-specific DNA binding; F:transcription rec			PF13837 (PFAM): Trihelix	36,569	22,450	16,750	9,493	15,740	-0,676	0,017			-0,817	0,000	down		down
Solyc01g096475	Thioredoxin-like protein CITRX, chloroplastic (AHRD V3.3 *** CITRX_SOLLC)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): G3DSA:3.40.30.1	8,586	10,445	7,461	9,747	10,173									
Solyc01g096490	protein kinases%3Bubiquitin-protein ligase (AHRD V3.3 *** AT5G13530.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR002110 (PRINTS): IPR002110 (SM	110,586	101,200	152,610	150,164	145,638									
Solyc01g096500	Sphingoid long-chain bases kinase 1 (AHRD V3.3 *** A0A151QX93_CAJCA)		F:GO:0003951	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR001206 (SMART): IPR001206 (PF	93,746	137,858	55,772	52,185	57,538									
Solyc01g096510	LOW QUALITY:VQ motif-containing protein (AHRD V3.3 *** AT2G41180.1)		P:GO:0051091	P:positive regulation of DNA-binding transcription factor activity			IPR008889 (PFAM): mobidb-lite (MOB	4,819	3,727	1,226	1,507	2,356									
Solyc01g096520	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4B040_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR024936 (PII	38,748	39,984	49,917	42,322	50,616									
Solyc01g096530	Trafficking protein particle complex subunit 3 (AHRD V3.3 *** A0A1D1YVK5_9ARAE)		C:GO:0030008; P:G(	C:TRAPP complex; P:Golgi vesicle transport			G3DSA:3.30.1380.20 (GENE3D): IPR(	25,155	26,032	38,128	31,330	32,122									
Solyc01g096540	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *** A0A118JRY8_CYNCS)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal			PF05664 (PFAM): IPR008528 (PANTH	47,952	54,617	44,398	46,508	44,874									
Solyc01g096550	Arginine N-methyltransferase family protein (AHRD V3.3 *** B9GLY6_POPTR)		P:GO:0006479; F:G(	P:protein methylation; F:methyltransferase activity			PF12756 (PFAM): G3DSA:3.40.50.15(	15,203	15,905	16,152	14,250	13,271									
Solyc01g096560	Subtilisin-like protease (AHRD V3.3 *** A0A0B2PRM9_GLYSO)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR010259 (PF	0,494	0,699	0,234	0,124	0,355									
Solyc01g096570	ERI1 exoribonuclease 2 (AHRD V3.3 *** A0A0B0MLH8_GOSAR)		F:GO:0003676	F:nucleic acid binding			IPR013520 (SMART): IPR036397 (G3	50,319	38,092	56,510	48,489	54,490									
Solyc01g096580	ribosomal protein S10p/S20e family protein		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001848 (PRINTS): IPR027486 (SM	60,173	66,550	38,112	36,267	35,570									
Solyc01g096590	ribosomal protein S10p/S20e family protein		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001848 (PRINTS): IPR027486 (SM	47,449	53,653	35,997	33,334	35,235									
Solyc01g096600	THO complex subunit 1 (AHRD V3.3 *** A0A0B0MSX7_GOSAR)		C:GO:0000445; P:G(	C:THO complex part of transcription export complex; P:mRNA e:			IPR021861 (PFAM): mobidb-lite (MOB	53,268	67,951	49,509	46,938	49,558									
Solyc01g096610	UPF0468 protein CG5343 (AHRD V3.3 *** A0A0B2SV55_GLYSO)		C:GO:0031514; C:G(	C:motile cilium; C:ciliary basal body; P:cilium assembly; P:regula			IPR007714 (PFAM): PTHR12458:SF8	15,379	17,162	25,499	26,546	23,764									
Solyc01g096620	MATH and LRR domain-containing protein PFE0570w, putative isoform 2 (AHRD V3.3 *-* A0A061FQQ6_TH		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:circadian rhythm			IPR039928 (PANTHER): PTHR33334:	6,382	5,932	8,740	9,803	8,843									
Solyc01g096630	Dentin sialophosphoprotein-related, putative isoform 1 (AHRD V3.3 --* A0A061E964_THECC)		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:circadian rhythm			mobidb-lite (MOBIDB_LITE): IPR03992	8,610	9,395	13,276	11,457	12,653									
Solyc01g096650	RING/U-box superfamily protein (AHRD V3.3 *** AT5G07040.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	0,176	0,283	0,050	0,025	0,070									
Solyc01g096660	PSII-associated proline-rich protein		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:regulation of protein compl			mobidb-lite (MOBIDB_LITE): mobidb-lit	36,490	65,225	146,589	140,739	181,016	0,864	0,000					up		
Solyc01g096670	Cytochrome P450, putative (AHRD V3.3 *** B9SJN4_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	7,375	8,115	14,776	12,286	14,668									
Solyc01g096680	Microtubule associated family protein (AHRD V3.3 *** B9GX96_POPTR)		P:GO:0000226; F:G(	P:microtubule cytoskeleton organization; F:microtubule binding			G3DSA:1.20.58.1520 (GENE3D): PF0	1,317	1,352	0,144	0,148	0,211									
Solyc01g096690	Kinase family protein (AHRD V3.3 *-* A0A0K9PUI0_ZOSMR)		F:GO:0004713; F:G(	F:protein tyrosine k	EC:2.7.1	Transferring phospho	IPR020635 (SMART): G3DSA:3.30.20	0,038	0,061	0,022	0,025	0,000									
Solyc01g096700	DnaJ domain-containing protein (AHRD V3.3 *** A0A118JUX9_CYNCS)		F:GO:0003677	F:DNA binding			IPR001623 (PRIN' MYB_related	653,827	566,804	495,814	498,926	470,343									
Solyc01g096710	Nuclear transcription factor Y subunit C8 (AHRD V3.3 *** I3TAY5_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YC	74,097	74,856	79,751	83,252	77,498									
Solyc01g096720	zinc induced facilitator-like 1 (AHRD V3.3 *** AT5G13750.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,042	0,240	0,069	0,147	0,209									
Solyc01g096730	zinc induced facilitator-like 1 (AHRD V3.3 *** AT5G13750.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,265	0,881	0,210	0,221	0,212									
Solyc01g096740	Protein zinc induced facilitator-like 1 (AHRD V3.3 *** A0A0B0NBA1_GOSAR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,000	0,062	0,097	0,096	0,094									
Solyc01g096750	Argonaute4d	AGO4d	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR003165 (SMART): IPR014811 (SM	4,120	4,834	1,051	0,891	1,985									
Solyc01g096760	Pre-rRNA-processing protein TSR2, putative (AHRD V3.3 *** A0A061F2C1_THECC)						IPR019398 (PFAM): mobidb-lite (MOB	22,353	24,370	19,805	18,881	17,828									
Solyc01g096780	SAD1/UNC-84 domain protein 1 (AHRD V3.3 *** AT5G04990.1)		C:GO:0016021	C:integral component of membrane			IPR008979 (G3DSA:2.60.120.GENE3I	17,640	15,939	12,099	10,009	10,479									
Solyc01g096790	B3 domain-containing protein (AHRD V3.3 *-* A0A199VWZ9_ANACO)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,021	0,043	0,093	0,072	0,023									
Solyc01g096800	PETER PAN-like protein (AHRD V3.3 *** AT5G61770.3)		P:GO:0000027; C:G(	P:ribosomal large subunit assembly; C:nucleolus; P:translation;			IPR007109 (SMART): IPR007109 (PF	15,020	15,934	13,558	14,099	11,839									
Solyc01g096810	EIL3	EIL3	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus			IPR006957 (PFAM EIL	138,738	142,157	127,979	152,309	146,388									
Solyc01g096820	Calcium/calmodulin dependent protein kinase (AHRD V3.3 *** Q9S792_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			PR00450 (PRINTS): IPR002048 (SMA	0,799	0,783	0,094	0,236	0,139									
Solyc01g096830	Cation-transporting ATPase (AHRD V3.3 *** K4B071_SOLLC)		F:GO:0000166; P:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): PF00702 (PFAM)	56,383	55,092	88,306	92,843	86,289									
Solyc01g096840	QWRF motif protein (DUF566) (AHRD V3.3 *-* AT3G60000.2)		C:GO:0005737; C:G(	C:cytoplasm; C:centrosome; C:nuclear microtubule; P:centrosor			IPR007573 (PFAM): mobidb-lite (MOB	0,273	0,349	0,072	0,116	0,165									
Solyc01g096850	Protein FAR1-RELATED SEQUENCE 3 (AHRD V3.3 *** A0A0B2S126_GLYSO)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	22,950	16,583	21,868	27,042	21,602									
Solyc01g096860	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *-* W9RR61_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' AP2	3,924	4,203	0,025	0,101	0,000									
Solyc01g096865	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9PVT8_ZOSMR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (SMART): IPR036955 (G3	1,130	0,906	0,000	0,000	0,000									
Solyc01g096870	Prolyl-tRNA synthetase, putative (AHRD V3.3 *** B9RIU3_RICCO)		F:GO:0004827; F:G(	F:proline-tRNA ligas	EC:6.1.1.15	Proline--tRNA ligase	IPR002316 (PRINTS): IPR016061 (SM	63,763	75,150	90,924	84,754	108,791									
Solyc01g096880	Major facilitator superfamily protein (AHRD V3.3 *** AT2G26690.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	6,760	5,586	0,362	0,266	0,473									
Solyc01g096890	Cell division control protein 6 6 (AHRD V3.3 *** A0A1D1Y6X9_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,143	8,005	8,704	9,604	9,280									
Solyc01g096900	DNA GYRASE A (AHRD V3.3 *** AT3G10690.1)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:3.6.1.3; EC:5.99.	Adenosinetriphospha	IPR002205 (SMART): IPR035516 (G3	29,111	26,692	32,936	28,800	31,580									
Solyc01g096910	Vacuolar protein sorting-associated protein 36 (AHRD V3.3 *** A0A1D1ZJY1_9ARAE)		C:GO:0000814; F:G(	C:ESCRT II complex; F:phosphatidylinositol-3-phosphate bindin			IPR036388 (G3DSA:1.10.10.GENE3D	15,211	13,609	19,899	18,389	18,895									
Solyc01g096920	Nuclear fragile X mental retardation-interacting protein 1 (AHRD V3.3 *-* A0A1D1YNL7_9ARAE)		F:GO:0003723	F:RNA binding			IPR019496 (PFAM): mobidb-lite (MOB	25,927	22,832	18,619	17,219	16,003									
Solyc01g096930	Phospholipid-transporting ATPase (AHRD V3.3 *** B9RL26_RICCO)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): PF00122 (PFAM)	10,927	13,544	20,583	26,856	21,446									
Solyc01g096940	Receptor-like kinase 17 (AHRD V3.3 *** A5A0Y6_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	6,929	5,425	1,482	1,122	1,648									
Solyc01g096950	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G21060.1)		F:GO:0005515; C:G(	F:protein binding; C:Set1C/COMPASS complex			IPR001680 (SMART): IPR001680 (PF	0,824	0,472	0,934	1,362	0,916									
Solyc01g096960	Heat shock family protein (AHRD V3.3 *-* D7LG79_ARALL)	Hsp49.3	C:GO:0016021	C:integral component of membrane			IPR002068 (PFAM): IPR008978 (G3D	2,891	2,345	3,702	3,592	3,021									
Solyc01g096970	Vacuolar protein sorting-associated protein 9A (AHRD V3.3 --* A0A199ULJ0_ANACO)						IPR037191 (G3DSA:1.20.1050.GENE	3,534	1,611	3,194	3,445	3,112	-1,094	0,019					down		
Solyc01g096980	Heat shock family protein (AHRD V3.3 *-* D7LG79_ARALL)	Hsp39.4	C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,061	0,039	0,172	0,075	0,048									
Solyc01g096990	Vacuolar protein sorting-associated protein 9A (AHRD V3.3 *** A0A1D1ZJE0_9ARAE)		C:GO:0000325; F:G(	C:plant-type vacuole; F:Rho guanyl-nucleotide exchange factor			IPR003123 (SMART): IPR003123 (PF	27,081	23,556	44,047	41,717	41,283									
Solyc01g097000	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR036962 (G3	30,447	27,043	4,337	2,290	2,878									
Solyc01g097010	Poly(RC)-binding protein, putative (AHRD V3.3 *** B9S7H6_RICCO)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR004088 (PF	71,430	73,795	76,596	71,824	76,421									
Solyc01g097020	succinate dehydrogenase subunit (AHRD V3.3 --* AT2G46390.1)		C:GO:0016021	C:integral component of membrane				35,643	36,422	74,971	72,223	64,047									
Solyc01g097030	Mutator-like transposase (AHRD V3.3 *** Q9SR14_ARATH)		F:GO:0008270	F:zinc ion binding			IPR006564 (SMART): IPR007527 (PF	32,298	28,171	32,959	32,951	33,141									
Solyc01g097040	myosin-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *-* AT1G08800.4)		F:GO:0017022	F:myosin binding			IPR007656 (PFAM): mobidb-lite (MOB	18,083	20,844	8,267	8,053	7,769									
Solyc01g097050	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT3G04620.1)		F:GO:0003676	F:nucleic acid binding			IPR002775 (PFAM): IPR036882 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc01g097070	DNA topoisomerase (AHRD V3.3 *** K4B095_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:5.99.1.2	DNA topoisomerase	IPR001878 (SMART): IPR010666 (PF	0,882	0,995	0,118	0,072	0,093									
Solyc01g097080	LOW QUALITY:26S protease regulatory subunit 6A homolog (AHRD V3.3 --* PRS6A_SOLLC)		F:GO:0005085; P:G(	F:guanyl-nucleotide exchange factor activity; P:small GTPase mediated signal transduction				0,241	0,268	0,000	0,047	0,070									
Solyc01g097090	LOW QUALITY:cytochrome P450, family 81, subfamily D, polypeptide 2 (AHRD V3.3 --* AT4G37360.1)							0,079	0,078	0,000	0,000	0,000									
Solyc01g097100	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor superfamily (AHRD V3.3 --* AT5G49180.1)						mobidb-lite (MOBIDB_LITE)	0,443	0,211	0,000	0,000	0,000									
Solyc01g097110	fanconi anemia group D2 protein (AHRD V3.3 *** AT4G14970.3)		P:GO:0006281	P:DNA repair			IPR029448 (PFAM): mobidb-lite (MOB	1,415	1,558	0,241	0,072	0,116									
Solyc01g097120	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *-* AT1G54460.1)						IPR027329 (PFAM): mobidb-lite (MOB	63,676	68,711	34,039	29,530	29,826									
Solyc01g097130	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RNF3_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	14,806	14,213	13,318	12,462	12,272									
Solyc01g097140	Arsenate reductase (AHRD V3.3 *** J7EI21_IPOBA)		F:GO:0004725; C:G(	F:protein tyrosine p	EC:3.1.3.16; EC:3.1.	Protein-serine/threor	IPR001763 (SMART): IPR036873 (G3	20,454	24,054	23,932	21,546	24,026									
Solyc01g097150	Amino acid permease family protein (AHRD V3.3 *-* AT5G05630.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transporter activity; P:transmembrane transport				9,584	6,853	11,315	11,838	10,546									
Solyc01g097155	Amino acid permease family protein (AHRD V3.3 *-* AT1G31830.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			G3DSA:1.20.1740.10 (GENE3D): PTH	2,182	1,434	1,049	1,746	1,133									
Solyc01g097160	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** A0A061F295_THECC)						IPR036188 (G3DSA:3.50.50.GENE3D	15,889	22,579	18,456	21,460	27,972			0,596	0,001				up	
Solyc01g097170	F-box protein with a domain protein (AHRD V3.3 --* AT4G22030.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	30,841	27,783	24,163	22,101	20,543									
Solyc01g097180	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072VMG0_MEDTR)						IPR012881 (PFAM): mobidb-lite (MOB	0,095	0,043	0,071	0,000	0,000									
Solyc01g097190	Ankyrin repeat family protein (AHRD V3.3 *** A0A061F958_THECC)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR019734 (SM	59,441	61,221	115,783	113,175	110,812									
Solyc01g097195	ankyrin repeat family protein (AHRD V3.3 --* AT3G04710.3)							0,040	0,036	0,068	0,075	0,046									
Solyc01g097210	Ankyrin repeat family protein (AHRD V3.3 *-* A0A061F958_THECC)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR011990 (G3	0,037	0,101	0,368	0,290	0,141									
Solyc01g097220	ankyrin repeat family protein (AHRD V3.3 *** AT3G04710.3)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	4,472	2,548	3,232	3,600	2,565									
Solyc01g097230	PRA1 family protein (AHRD V3.3 *-* M1BPP9_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR19317:SF1(	9,660	4,227	8,005	10,755	9,064	-1,164	0,000					down		
Solyc01g097240	Pathogenesis-related protein PR-4 (AHRD V3.3 *** PR4_PRUPE)		P:GO:0042742; P:G(	P:defense response to bacterium; P:defense response to fungu			IPR001153 (PRINTS): IPR036908 (G3	13,148	42,877	198,445	225,146	335,666			0,755	0,000				up	
Solyc01g097250	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** AT4G02550.3)		P:GO:0031347	P:regulation of defense response			IPR024752 (PFAM): mobidb-lite (MOB	15,028	14,449	18,257	18,324	16,946									
Solyc01g097260	Zn-dependent exopeptidases superfamily protein (AHRD V3.3 --* AT1G67420.6)		F:GO:0005525; C:G(	F:GTP binding; C:nucleus; P:ribosome biogenesis			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,515	0,756	0,769	0,838	0,779									
Solyc01g097270	pathogen-induced protein	pi1	F:GO:0008061; P:G(	F:chitin binding; P:defense response to bacterium; P:defense re			IPR001002 (PRINTS): IPR001153 (PF	1,042	2,333	35,869	17,563	18,766					-1,028	0,023			down
Solyc01g097280	Pathogenesis-related protein PR-4 (AHRD V3.3 *** PR4_PRUPE)		F:GO:0008061; P:G(	F:chitin binding; P:defense response to bacterium; P:defense re			IPR001153 (PRINTS): IPR001002 (PF	0,099	0,486	5,774	4,691	3,598									
Solyc01g097290	auxin-regulated IAA16	IAA16	C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated			G3DSA:3.10.20.90 (GENE3D): IPR03:	47,525	34,915	1,698	1,444	1,531									
Solyc01g097300	Prefoldin subunit 4 (AHRD V3.3 *** K4B0B7_SOLLC)		P:GO:0006457; C:G(	P:protein folding; C:prefoldin complex; F:unfolded protein binding			IPR009053 (G3DSA:1.10.287.GENE3I	23,934	23,493	22,090	21,073	20,223									
Solyc01g097310	Sec-independent protein translocase protein TatA (AHRD V3.3 *** A0A0B2P6S1_GLYSO)		C:GO:0005886; F:G(	C:plasma membrane; F:protein transporter activity; P:protein se			PR01506 (PRINTS): IPR006312 (TIGF	15,855	23,789	27,784	30,554	30,306	0,612	0,015					up		
Solyc01g097320	Mediator of RNA polymerase II transcription subunit 14 (AHRD V3.3 *** A0A061F303_THECC)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR013947 (PFAM): mobidb-lite (MOB	41,435	40,272	42,967	39,447	42,583									
Solyc01g097330	BZIP transcription factor (AHRD V3.3 *** Q93YM7_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	14,568	14,220	10,670	12,722	12,967									
Solyc01g097340	GDP-mannose 3',5'-epimerase (AHRD V3.3 *** C6K2K9_SOLLC)	GME1	F:GO:0047918; F:G(	F:GDP-mannose 3,:	EC:5.1.3.18	GDP-mannose 3,5-e	G3DSA:3.40.50.720 (GENE3D): IPR0(	56,816	68,481	36,827	35,398	55,416			0,586	0,000				up	
Solyc01g097350	Calcium-binding EF hand family protein (AHRD V3.3 *** A0A061F999_THECC)		F:GO:0005509	F:calcium ion binding			PTHR34574:SF3 (PANTHER): PTHR3	66,332	107,137	26,771	29,212	36,548	0,717	0,044					up		
Solyc01g097360	Coiled-coil domain-containing protein 14 (AHRD V3.3 *** A0A1D1XHZ9_9ARAE)						mobidb-lite (MOBIDB_LITE): PTHR371	9,698	12,503	12,778	14,615	12,330									
Solyc01g097370	Ammonium transporter (AHRD V3.3 *** K4B0C4_SOLLC)		F:GO:0008519; C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR002229 (PRINTS): IPR024041 (PF	0,000	0,039	0,025	0,076	0,048									
Solyc01g097380	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** A0A061F182_THECC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR023210 (PF	0,102	0,160	0,050	0,022	0,234									
Solyc01g097390	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** A0A061F182_THECC)						IPR036812 (G3DSA:3.20.20.GENE3D	2,348	3,287	0,810	0,961	0,920									
Solyc01g097395	Dimeric alpha-amylase inhibitor (AHRD V3.3 --* T1WIN9_9POAL)						mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,000	0,047	0,046									
Solyc01g097400	Calcium-transporting ATPase (AHRD V3.3 *-* M1BPN9_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR001757 (PRINTS): PR00119 (PRIN	0,100	0,154	0,096	0,555	0,513									
Solyc01g097410	ACA9 (AHRD V3.3 --* A0A0A9NGC7_ARUDO)							0,000	0,000	0,000	0,000	0,069									
Solyc01g097420	Calcium-transporting ATPase (AHRD V3.3 *-* M1BPN9_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR004014 (SMART): IPR004014 (PF	0,100	0,083	0,168	0,661	0,163									
Solyc01g097425	U11/U12 small nuclear ribonucleoprotein (AHRD V3.3 --* AT2G46200.4)							0,040	0,039	0,050	0,264	0,095									
Solyc01g097430	ABC transporter (AHRD V3.3 *** A0A0M3R8G1_9SOLA)	ABCG2	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013525 (PFAM): G3DSA:3.40.50.3	0,076	0,043	0,845	11,196	2,465					3,741	0,000			up
Solyc01g097440	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase-like protein (AHRD V3.3 *** A0A0B0NA55_G(		F:GO:0000224; C:G(	F:peptide-N4-(N-ac	EC:3.5.1.52	Peptide-N(4)-(N-acet	IPR002931 (SMART): G3DSA:3.10.62	43,885	40,021	50,048	54,212	51,944									
Solyc01g097450	PITH domain-containing protein (AHRD V3.3 *** W9S6X8_9ROSA)						IPR010400 (PFAM): IPR037047 (G3D	64,881	60,764	112,531	99,516	96,415									
Solyc01g097460	Ribose 5-phosphate isomerase-related family protein (AHRD V3.3 *** U5GAQ0_POPTR)		F:GO:0004751; P:G(	F:ribose-5-phospha	EC:5.3.1.6	Ribose-5-phosphate	G3DSA:3.30.70.260 (GENE3D): IPR0(	48,758	61,220	103,162	98,945	117,687									
Solyc01g097470	Neurogenic locus notch-like protein (AHRD V3.3 *** A0A072VSF9_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR338	32,020	15,273	4,525	5,457	4,620									
Solyc01g097480	LOW QUALITY:Protein IQ-DOMAIN 14 (AHRD V3.3 *-* W9RI74_9ROSA)		F:GO:0005515	F:protein binding			IPR000048 (PFAM): mobidb-lite (MOB	0,137	0,097	0,000	0,000	0,000									
Solyc01g097490	LOW QUALITY:SUN domain protein 4	SUN4					IPR025064 (PFAM): mobidb-lite (MOB	0,460	0,294	0,125	0,050	0,023									
Solyc01g097500	LSTK-1-like kinase		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	mobidb-lite (MOBIDB_LITE): mobidb-lit	51,017	64,224	83,248	100,988	93,589									
Solyc01g097510	annexin 3		F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR018502 (SM	25,612	35,039	10,999	8,732	9,759									
Solyc01g097520	annexin 5		F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR009118 (PF	62,255	201,840	28,794	24,722	26,215	1,724	0,000					up		
Solyc01g097530	LOW QUALITY:Photosystem II 32 kDa protein (AHRD V3.3 *** G4VY26_9MARC)		P:GO:0009772; F:G(	P:photosynthetic electron transport in photosystem II; F:electron			PTHR33149:SF11 (PANTHER): IPR00	0,179	0,206	0,218	0,101	0,427									
Solyc01g097540	annexin 4	AnnSl4	F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR018502 (SM	15,005	13,864	49,748	47,156	42,223									
Solyc01g097550	annexin 6	AnnSl6	F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR018502 (SMART): IPR037104 (G3	0,000	0,000	0,022	0,000	0,000									
Solyc01g097570	LOW QUALITY:kinase-like protein (AHRD V3.3 --* AT1G66940.4)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,063	0,043	0,624	0,409	0,444									
Solyc01g097600	Pseudouridine synthase family protein (AHRD V3.3 *** AT3G04820.1)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR001656 (PIRSF): G3DSA:3.30.235	18,039	16,533	18,552	18,400	18,247									
Solyc01g097610	F-box family protein, putative (AHRD V3.3 *** A0A061DH99_THECC)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): PTHR45141 (	16,343	15,045	25,305	27,319	24,275									
Solyc01g097620	LOW QUALITY:F-box protein (AHRD V3.3 --* W9SND6_9ROSA)							0,037	0,043	0,100	0,074	0,024									
Solyc01g097630	F-box protein (AHRD V3.3 *** W9SND6_9ROSA)						IPR017451 (TIGRFAM): PTHR44519 (	0,415	1,043	0,262	0,296	0,379									
Solyc01g097640	Ribosome biogenesis protein BMS1 (AHRD V3.3 *** A0A0B2PF71_GLYSO)		F:GO:0005525; C:G(	F:GTP binding; C:nucleus; P:ribosome biogenesis			IPR007034 (SMART): IPR012948 (SM	45,255	42,178	34,582	32,500	30,579									
Solyc01g097650	Serinc-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 *** AT3G24460.2)		C:GO:0016020	C:membrane			IPR005016 (PFAM): IPR005016 (PAN	2,460	2,191	2,886	5,164	4,398					0,840	0,014			up
Solyc01g097670	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JZF1_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR032867 (F	2,479	3,288	5,682	4,413	4,624									
Solyc01g097710	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,508	0,327	0,162	0,097	0,071									
Solyc01g097720	Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)						PR01217 (PRINTS): mobidb-lite (MOB	0,462	0,317	0,047	0,147	0,140									
Solyc01g097730	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YDM4_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,942	3,287	2,238	2,738	2,498									
Solyc01g097735	Mitochondrial transcription termination factor family protein (AHRD V3.3 --* AT5G55580.2)						mobidb-lite (MOBIDB_LITE)	2,895	3,504	2,636	2,528	1,983									
Solyc01g097740	Tetratricopeptide repeat protein 35 (AHRD V3.3 *** W9QKC4_9ROSA)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	32,349	36,861	42,748	40,968	40,443									
Solyc01g097760	60S ribosomal protein L7A-like protein (AHRD V3.3 *** Q2XPW4_SOLTU)		P:GO:0000470; F:G(	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large ribo			IPR018492 (PRINTS): IPR001921 (PF	236,979	267,955	212,187	177,715	188,462									
Solyc01g097770	phototropin 2	phot2	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000014 (SMART): IPR001610 (SM	230,466	176,087	9,586	8,152	21,527			1,160	0,008				up	
Solyc01g097790	Plant/T24G3-80 protein (AHRD V3.3 *** G7I6W7_MEDTR)						IPR008586 (PFAM): IPR008586 (PAN	18,149	15,826	18,575	20,746	16,388									
Solyc01g097800	DNA-damage-repair/toleration protein (DRT102) (AHRD V3.3 *** AT3G04880.1)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:isomerase activity			IPR003500 (PFAM): IPR012100 (PIRS	26,188	21,301	42,802	35,376	36,880									
Solyc01g097810	zeta-carotene desaturase	ZDS	P:GO:0016117; F:G(	P:carotenoid biosyr	EC:1.14.99.3	Acting on paired don	PR00419 (PRINTS): IPR014103 (TIGF	50,194	63,547	188,408	205,776	198,125									
Solyc01g097820	adenine phosphoribosyltransferase-like protein, putative (DUF2358) (AHRD V3.3 *** AT3G04890.1)						IPR018790 (PFAM): G3DSA:3.10.450	1,835	1,527	0,655	0,959	1,528			1,215	0,032				up	
Solyc01g097825	50S ribosomal protein L5, chloroplastic (AHRD V3.3 --* RK5_OLTVI)							0,204	0,058	0,068	0,170	0,140									
Solyc01g097840	MAP kinase kinase kinase 6	MAPKKK6	F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): G3DSA:3.30.20	16,780	26,753	28,446	26,540	32,685	0,698	0,033					up		
Solyc01g097860	Myelin-associated oligodendrocyte basic protein isoform 1 (AHRD V3.3 *** A0A061F284_THECC)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:photosynthetic acclimation			IPR010903 (PFAM): PTHR33975 (PAI	43,108	76,298	14,831	13,890	21,302	0,851	0,007	0,517	0,026			up	up	
Solyc01g097870	40S ribosomal protein S24 (AHRD V3.3 *** K4B0H4_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001976 (PFAM): G3DSA:3.30.70.3	335,859	354,659	130,516	113,763	121,086									

Solyc01g097880	Cytidine/deoxycytidylate deaminase family protein (AHRD V3.3 *** AT5G28050.3)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.140.10 (GENE3D): IPR0(	38,732	53,586	277,878	326,045	237,949									
Solyc01g097890	LOW QUALITY:DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 *** AT5G2804		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAM: GeBP	26,905	30,546	26,773	22,896	23,663									
Solyc01g097900	LOW QUALITY:Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT1G55		C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding				0,096	0,021	0,000	0,022	0,000									
Solyc01g097910	Rubredoxin family protein (AHRD V3.3 *** U5GAX7_POPTR)		F:GO:0005506	F:iron ion binding			IPR024935 (PRINTS): IPR024935 (PF	12,662	16,036	15,138	21,717	27,084			0,838	0,000	0,525	0,014		up	up
Solyc01g097920	Cysteine synthase (AHRD V3.3 *** K4B0H9_SOLLC)		F:GO:0004124; P:G(	F:cysteine synthas	EC:2.5.1.47	Cysteine synthase	G3DSA:3.40.50.1100 (GENE3D): G3D	2,393	2,681	1,162	1,207	1,487									
Solyc01g097930	Cysteine synthase (AHRD V3.3 *** K4B0I0_SOLLC)		F:GO:0004124; P:G(	F:cysteine synthas	EC:2.5.1.47	Cysteine synthase	IPR005859 (TIGRFAM): G3DSA:3.40.!	0,459	0,608	0,097	0,114	0,023									
Solyc01g097940	Cysteine synthase (AHRD V3.3 *-* K4B0H9_SOLLC)		F:GO:0004124; C:G(	F:cysteine synthas	EC:2.5.1.47	Cysteine synthase	G3DSA:3.40.50.1100 (GENE3D): IPR(	0,038	0,000	0,000	0,000	0,000									
Solyc01g097950	Cysteine synthase (AHRD V3.3 *** K4B0I2_SOLLC)		F:GO:0004124; P:G(	F:cysteine synthas	EC:2.5.1.47	Cysteine synthase	IPR005859 (TIGRFAM): IPR005856 (T	4,745	4,965	0,318	0,171	0,331									
Solyc01g097960	Late embryogenesis abundant D-like protein (AHRD V3.3 *** A0A072VMJ1_MEDTR)		C:GO:0005634; C:G(	C:nucleus; C:cytosol			IPR007011 (PFAM): mobidb-lite (MOB	0,000	0,043	0,050	0,000	0,000									
Solyc01g097970	Deoxyuridine 5'-triphosphate nucleotidohydrolase (AHRD V3.3 *** DUT_SOLLC)		F:GO:0004170; P:G(	F:dUTP diphosphata	EC:3.6.1.23; EC:3.6.	dUTP diphosphatase	IPR036157 (G3DSA:2.70.40.GENE3D	3,268	3,790	1,294	1,251	1,505									
Solyc01g097980	CTR1-like protein kinase 2	CTR2	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	64,328	75,892	74,901	68,602	71,466									
Solyc01g097990	LOW QUALITY:Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** G7L0S4_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			G3DSA:3.40.630.30 (GENE3D): IPR0(	2,306	1,785	0,685	0,410	0,354									
Solyc01g098000	Elongation factor 1-beta (AHRD V3.3 *** D7KES3_ARALL)		F:GO:0003746; P:G(	F:translation elongation factor activity; P:translational elongatio			IPR014038 (SMART): IPR014717 (G3	0,019	0,000	0,025	0,000	0,000									
Solyc01g098010	Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** G7L0S4_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR000182 (PFAM): G3DSA:3.40.630	0,721	1,552	0,287	0,146	0,309									
Solyc01g098020	Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** G7L0S4_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR000182 (PFAM): G3DSA:3.40.630	0,757	1,680	0,366	0,371	0,374									
Solyc01g098030	Hydroxyproline-rich glycoprotein family protein, putative isoform 1 (AHRD V3.3 *** A0A061GYH3_THECC)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			mobidb-lite (MOBIDB_LITE): mobidb-lit	55,029	50,999	60,365	47,762	52,152					-0,334	0,042			down
Solyc01g098040	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9REU9_RICCO)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D): PTHR	0,594	0,376	0,311	0,248	0,188									
Solyc01g098050	MADS-box transcription factor family protein (AHRD V3.3 *-* AT1G72350.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN: M-type_MADS	0,019	0,000	0,000	0,000	0,000									
Solyc01g098060	MADS-box transcription factor family protein (AHRD V3.3 *-* AT1G72350.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN: M-type_MADS	0,805	1,363	0,409	0,176	0,422									
Solyc01g098065	MADS-box transcription factor family protein (AHRD V3.3 --* AT1G72350.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR036879 (G3DSA:3.40.1810 GENE	0,000	0,043	0,000	0,000	0,000									
Solyc01g098070	MADS-box transcription factor family protein (AHRD V3.3 *-* AT1G72350.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN: M-type_MADS	0,000	0,000	0,100	0,025	0,073									
Solyc01g098080	BY-2 kinesin-like protein 5 (AHRD V3.3 *** Q9AVP5_TOBAC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	14,404	13,622	12,159	12,591	13,108									
Solyc01g098090	meloidogyne-induced giant cell protein DB214	TOMTRALTBC	F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	95,485	84,374	134,329	131,275	150,317									
Solyc01g098100	60S ribosome subunit biogenesis protein NIP7 homolog (AHRD V3.3 *** K4B0J7_SOLLC)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:ribosome assembly			IPR002478 (SMART): IPR005155 (PF	16,728	21,094	29,943	24,470	22,832									
Solyc01g098110	Esterase/lipase/thioesterase family protein (AHRD V3.3 *** AT1G54570.1)	PES1	F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR022742 (PFAM): IPR007130 (PFA	27,230	33,130	260,898	240,544	278,699									
Solyc01g098130	GNOM-like 1 (AHRD V3.3 --* AT5G39500.2)							0,000	0,000	0,000	0,022	0,023									
Solyc01g098140	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G45600.1)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,366	0,197	92,318	69,053	114,620									
Solyc01g098150	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YF58_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (PFA	5,382	5,710	12,944	14,166	13,579									
Solyc01g098160	Protein kinase superfamily protein (AHRD V3.3 *** AT1G54610.3)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	44,428	51,419	53,675	57,814	53,709									
Solyc01g098170	Protein HASTY 1-like protein (AHRD V3.3 *** A0A0B0PPZ4_GOSAR)		P:GO:0051168	P:nuclear export			IPR013598 (PFAM): PTHR11223 (PAN	49,345	44,381	38,195	40,259	37,228									
Solyc01g098180	Translation initiation factor eIF-2B subunit epsilon (AHRD V3.3 *** A0A0B2P411_GLYSO)		F:GO:0005515; P:G(	F:protein binding; P:biosynthetic process; F:nucleotidyltransfera			IPR003307 (SMART): IPR029044 (G3	68,103	60,006	87,077	80,585	81,605									
Solyc01g098190	(Sodium/potassium)/proton exchanger 4	nhx4	C:GO:0005774; C:G(	C:vacuolar membrane; C:plasma membrane; P:sodium ion trans			IPR004709 (PRINTS): IPR006153 (PF	85,016	75,169	161,964	157,129	182,331									
Solyc01g098200	Vesicle-associated protein 1-1 (AHRD V3.3 *** A0A1D1Y4C8_9ARAE)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR016763 (PIRSF): IPR000535 (PFA	22,599	18,940	34,521	30,801	29,784									
Solyc01g098210	Transmembrane adipocyte-associated 1 (AHRD V3.3 *** A0A0B0NBD1_GOSAR)		P:GO:0002237; P:G(	P:response to molecule of bacterial origin; P:root morphogenesi			IPR018781 (PFAM): IPR018781 (PAN	9,826	7,694	19,919	19,015	16,690									
Solyc01g098220	LOB domain-containing protein, putative (AHRD V3.3 *** B9SI79_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:positive regulation of transcription, DNA-templated			IPR004883 (PFAM: LBD	0,623	0,253	0,000	0,025	0,000									
Solyc01g098230	Mitochondrial import inner membrane translocase subunit tim44, putative (AHRD V3.3 *** B9SF39_RICCO)		C:GO:0005743; P:G(	C:mitochondrial inner membrane; P:protein import into mitochon			IPR007379 (SMART): G3DSA:3.10.45	19,338	21,850	28,252	28,564	26,510									
Solyc01g098240	Protein FRIGIDA, putative (AHRD V3.3 *-* B9REX4_RICCO)		P:GO:0009908; P:G(	P:flower development; P:cell differentiation			IPR012474 (PFAM): PTHR31791:SF1(	1,580	2,691	0,432	0,517	0,706									
Solyc01g098250	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XK41_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	45,873	48,144	38,140	40,056	40,835									
Solyc01g098270	DnaJ domain-containing protein (AHRD V3.3 --* A0A103XIV0_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,060	0,025	0,047	0,046									
Solyc01g098280	LOW QUALITY:DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061F0P5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,876	1,136	1,505	3,283	1,936					1,124	0,010			up
Solyc01g098290	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT3G45090.2)						mobidb-lite (MOBIDB_LITE)	0,000	0,019	0,000	0,025	0,000									
Solyc01g098300	DnaJ heat shock amino-terminal domain protein (AHRD V3.3 *-* G7LDH8_MEDTR)						IPR024593 (PFAM): mobidb-lite (MOB	0,000	0,039	0,000	0,000	0,000									
Solyc01g098320	DNA-directed RNA polymerase II, putative (AHRD V3.3 *** B9ST46_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR014381 (PIRSF): IPR005571 (PFA	9,880	10,159	10,593	11,125	10,785									
Solyc01g098330	LOW QUALITY:DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061F0P5_THECC)						IPR024593 (PFAM): mobidb-lite (MOB	0,019	0,018	0,000	0,047	0,024									
Solyc01g098340	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XK41_CYNCS)						IPR024593 (PFAM): mobidb-lite (MOB	6,872	5,487	4,556	5,294	5,152									
Solyc01g098350	L1_1	CycL1_1	P:GO:0000079; C:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR013763 (SMART): G3DSA:1.10.47	29,846	30,997	23,722	20,699	22,798									
Solyc01g098370	Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *** G7KYV8_MEDTR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	0,588	0,726	0,907	1,552	1,269									
Solyc01g098380	Dihydrodipicolinate reductase, putative (AHRD V3.3 *** B9T529_RICCO)		F:GO:0008839; P:G(	F:4-hydroxy-tetrahy	EC:1.17.1.8	4-hydroxy-tetrahydro	IPR022663 (PFAM): G3DSA:3.40.50.7	24,294	28,715	22,964	21,516	24,726									
Solyc01g098390	Gibberellin receptor GID1A (AHRD V3.3 *** V5JFN9_PETHY)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	10,874	7,830	6,135	5,303	6,530									
Solyc01g098400	Histidine-containing phosphotransfer protein, putative (AHRD V3.3 *** B9REZ5_RICCO)		P:GO:0000160	P:phosphorelay signal transduction system			IPR008207 (PFAM): IPR036641 (G3D	6,678	6,108	3,357	5,322	2,610									
Solyc01g098410	Receptor protein kinase, putative (AHRD V3.3 *** B9RXG1_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	3,459	2,105	0,775	1,367	1,078									
Solyc01g098430	Breast carcinoma-amplified sequence 3 (AHRD V3.3 *** W9SH94_9ROSA)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR022175 (PF	70,499	54,079	106,722	113,184	98,468									
Solyc01g098440	Kinase family protein (AHRD V3.3 *** B9I821_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,222	0,096	0,174	0,075	0,166									
Solyc01g098450	TATA box-binding protein-associated factor RNA polymerase I subunit C, putative (AHRD V3.3 *** A0A061E'		P:GO:0006360	P:transcription by RNA polymerase I			IPR038801 (PANTHER)	20,376	13,646	13,888	17,081	17,418									
Solyc01g098455	Homogentisate 1,2-dioxygenase (AHRD V3.3 *-* Q9M6U1_SOLLC)		F:GO:0004411; P:G(	F:homogentisate 1,	EC:1.13.11; EC:1.13	Acting on single donc	IPR005708 (PFAM): IPR005708 (PAN	3,420	2,730	3,868	2,984	3,295									
Solyc01g098460	Methyltransferase-like protein (AHRD V3.3 *** K4B0N3_SOLLC)		F:GO:0008168	F:methyltransferase activity			IPR010286 (PFAM): IPR017182 (PIRS	27,034	20,363	27,635	26,380	29,578									
Solyc01g098490	Sugar facilitator protein 1	SFP1	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	9,225	8,728	15,174	17,690	16,378									
Solyc01g098500	Sugar facilitator protein 5	SFP5	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI(	9,796	8,958	3,681	3,362	4,142									
Solyc01g098520	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatchec				16,249	29,008	10,799	8,980	10,915	0,861	0,047					up		
Solyc01g098523	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A0B2SBZ1_GLYSO)							0,121	0,163	0,022	0,025	0,023									
Solyc01g098525	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G27950.1)							0,042	0,123	0,044	0,000	0,024									
Solyc01g098527	CTP synthase family protein (AHRD V3.3 *-* AT1G30820.1)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR029062 (G3DSA:3.40.50.GENE3D	4,882	9,027	4,316	3,921	4,313									
Solyc01g098530	CTP synthase family protein (AHRD V3.3 *-* AT1G30820.1)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR017926 (PFAM): IPR029062 (G3D	0,741	0,972	0,480	0,540	0,544									
Solyc01g098540	Sec-independent translocase protein TatB (AHRD V3.3 *-* A0A0B0MGL5_GOSAR)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.2.1.2	Tryptophan synthase	PTHR35512 (PANTHER)	14,318	11,866	13,205	17,564	15,787									
Solyc01g098550	Indole-3-glycerol phosphate lyase (AHRD V3.3 *** W9QCL1_9ROSA)		F:GO:0004834; P:G(	F:tryptophan syntha	EC:4.2.1.2	Tryptophan synthase	IPR013785 (G3DSA:3.20.20.GENE3D	39,942	46,138	68,165	62,910	69,727									
Solyc01g098555	BEACH-DOMAIN HOMOLOG A1 (AHRD V3.3 --* AT1G03060.4)						mobidb-lite (MOBIDB_LITE)	0,000	0,058	0,025	0,000	0,000									
Solyc01g098560	Sugar facilitator protein 8	SFP8	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	11,540	14,526	5,111	5,789	7,949									
Solyc01g098570	LOW QUALITY:FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT1G54740.1)						IPR021410 (PFAM): mobidb-lite (MOB	15,590	6,430	24,553	26,424	29,757	-1,251	0,000					down		
Solyc01g098580	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT3G05170.1)		F:GO:0003824	F:catalytic activity			IPR013078 (SMART): IPR029033 (G3	10,094	16,014	4,679	5,500	6,770									
Solyc01g098610	glutathione synthetase 2	gsh2	F:GO:0004363; F:G(	F:glutathione syntha	EC:6.3.2.3	Glutathione synthase	G3DSA:3.30.470.20 (GENE3D): IPR0;	43,192	48,258	35,790	32,020	37,068									
Solyc01g098630	Mitochondrial inner membrane translocase subunit Tim44 (AHRD V3.3 *** A0A0K9P2C5_ZOSMR)		C:GO:0005739; C:G(	C:mitochondrion; C:ribosome			IPR007379 (SMART): IPR007379 (PF	16,583	16,872	19,827	20,282	18,085									
Solyc01g098640	Thylakoid lumen 18.3 kDa protein (AHRD V3.3 *** A0A061F263_THECC)		F:GO:0003993; C:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR007621 (PFAM): G3DSA:3.10.310	19,239	38,262	7,386	11,136	18,423	1,020	0,004	1,309	0,000			up	up	
Solyc01g098645	GDSL esterase/lipase (AHRD V3.3 *** W9SXJ5_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	9,377	7,334	10,937	11,349	10,853									
Solyc01g098665	Kinesin-like protein (AHRD V3.3 *** K4B0Q4_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (SMART): IPR001752 (PF	0,361	0,336	0,617	0,537	0,426									
Solyc01g098670	Kinesin-like protein (AHRD V3.3 *-* K4B0Q4_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosphate phosphatase		0,341	0,333	0,364	0,510	0,937									
Solyc01g098680	LOW QUALITY:Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A097BR55_GOSBA)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00365 (SMAR	0,000	0,082	0,000	0,000	0,000									
Solyc01g098690	LOW QUALITY:Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A097BR55_GOSBA)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00365 (SMAR	21,054	34,338	8,642	15,633	16,646			0,941	0,007	0,853	0,003		up	up
Solyc01g098700	Branched-chain-amino-acid aminotransferase-like protein (AHRD V3.3 *** G7I8Q0_MEDTR)		F:GO:0003824	F:catalytic activity			IPR001544 (PFAM): G3DSA:3.40.50.3	36,619	38,496	90,190	111,186	89,597									
Solyc01g098710	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT5G43100.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	3,944	6,015	3,079	3,279	4,361									
Solyc01g098720	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT1G72210.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF: bHLH	0,481	1,123	1,272	0,593	0,543									
Solyc01g098725	RING/U-box superfamily protein (AHRD V3.3 *** AT3G05200.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	4,921	4,656	13,088	17,736	10,746									
Solyc01g098730	LOW QUALITY:diacylglycerol kinase 5 (AHRD V3.3 --* AT2G20900.4)							1,381	1,180	4,112	4,644	3,902									
Solyc01g098740	Protein kinase (AHRD V3.3 *** C6ZRT6_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	1,236	2,125	29,379	43,442	31,040					0,570	0,016			up
Solyc01g098750	RING/U-box superfamily protein (AHRD V3.3 *** A0A061F239_THECC)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): IPR013083 (G3	5,960	10,305	8,300	8,864	8,161									
Solyc01g098760	RING/U-box superfamily protein (AHRD V3.3 *-* A0A061F239_THECC)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	99,821	189,571	43,467	38,534	37,828	0,952	0,000					up		
Solyc01g098770	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061F3Y1_THECC)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR032799 (PFA	0,523	0,428	0,247	0,745	0,162									
Solyc01g098780	Signal peptidase subunit (AHRD V3.3 *** AT5G27430.1)		C:GO:0005787; P:G(	C:signal peptidase complex; P:signal peptide processing; F:pep			IPR007653 (PFAM): IPR007653 (PIRS	46,397	50,261	67,214	72,342	63,034									
Solyc01g098790	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT1G20870.2)		C:GO:0005634; P:G(	C:nucleus; P:positive regulation of DNA demethylation			IPR008978 (G3DSA:2.60.40.GENE3D	9,117	6,139	3,462	12,396	6,345			0,862	0,018	1,828	0,000		up	up
Solyc01g098800	Cation calcium exchanger (AHRD V3.3 *** Q2HTM6_MEDTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004837 (PFAM): G3DSA:1.20.142	18,738	12,640	9,638	23,006	14,385					1,249	0,000			up
Solyc01g098805	thiaminC (AHRD V3.3 --* AT2G29630.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,119	0,047	0,119	0,024									
Solyc01g098810	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT1G54850.1)		C:GO:0005730; P:G(	C:nucleolus; P:positive regulation of DNA demethylation			IPR008978 (G3DSA:2.60.40.GENE3D	2,191	2,616	1,440	1,148	1,359									
Solyc01g098813	K(+) efflux antiporter (AHRD V3.3 --* A0A0K9NUN8_ZOSMR)		F:GO:0015299; C:G(	F:solute:proton antiporter activity; C:integral component of membrane; P:proton transmembrane transpc				0,117	0,103	0,022	0,025	0,095									
Solyc01g098817	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-containing protein (AHRD V3.3 --* AT1G09170.8)							0,040	0,000	0,000	0,000	0,023									
Solyc01g098820	Phototropic-responsive NPH3 family protein, putative (AHRD V3.3 *** A0A061FBG1_THECC)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0(	2,855	1,851	0,025	0,045	0,095									
Solyc01g098830	RING/U-box superfamily protein (AHRD V3.3 *** AT3G05250.1)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	8,468	8,377	15,671	15,144	14,856									
Solyc01g098840	Mevalonate kinase (AHRD V3.3 *** K4B0S1_SOLLC)		F:GO:0004496; F:G(	F:mevalonate kinas	EC:2.7.1.36	Mevalonate kinase	PR00959 (PRINTS): IPR013750 (PFA	16,006	24,841	40,122	48,932	43,917									
Solyc01g098850	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G54870.2),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	1,442	5,034	2,544	7,226	0,793									
Solyc01g098860	Glycoprotein membrane GPI-anchored (AHRD V3.3 *** A0A061ELP1_THECC)		C:GO:0016021	C:integral component of membrane			PTHR33976 (PANTHER): PTHR33976	4,872	8,409	1,543	3,864	0,727									
Solyc01g098870	Nucleolar GTPase (AHRD V3.3 *-* A6YTC8_CUCME)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	113,570	100,699	115,948	132,083	116,753									
Solyc01g098880	Seryl-tRNA synthetase, putative (AHRD V3.3 *** B9RKX9_RICCO)		F:GO:0004828; F:G(	F:serine-tRNA ligas	EC:6.1.1.11	Serine--tRNA ligase	IPR002317 (PRINTS): IPR002314 (PF	63,937	76,092	91,163	87,872	83,228									
Solyc01g098890	LOW QUALITY:CLE protein 2							0,000	0,000	0,025	0,000	0,023									
Solyc01g098900	Protein YIPF (AHRD V3.3 *** K4B0S7_SOLLC)		C:GO:0005794; C:G(	C:Golgi apparatus; C:membrane; P:vesicle-mediated transport			IPR006977 (PFAM): mobidb-lite (MOB	31,210	33,980	29,845	30,840	28,979									
Solyc01g098910	Peroxisomal carrier protein (AHRD V3.3 *** B6TAM1_MAIZE)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	75,010	129,315	67,878	94,997	75,117					0,486	0,030			up
Solyc01g098920	Mitochondrial Rho GTPase (AHRD V3.3 *** K4B0S9_SOLLC)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR002048 (SMA	166,879	159,360	221,155	210,515	202,931									
Solyc01g098930	cyclinU3_2	CycU3_2	P:GO:0000079; F:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR013922 (PFAM): G3DSA:1.10.472	1,270	1,890	2,200	2,479	2,216									
Solyc01g098940	Pectinesterase (AHRD V3.3 *** K4B0T1_SOLLC)		F:GO:0004857; F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (PF	0,251	0,335	0,000	0,048	0,000									
Solyc01g098950	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** M1CKC5_SOLTU)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR020831 (PRINTS): IPR020828 (SM	4,417	4,852	8,969	6,977	10,289									
Solyc01g098960	Hexosyltransferase (AHRD V3.3 *** K4B0T3_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR002495 (PFAM): IPR029044 (G3D	0,179	0,870	0,047	0,076	0,070									
Solyc01g098980	MAP kinase kinase kinase 8	MAPKKK8	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,180	1,102	0,122	0,220	0,259									
Solyc01g098985	Kinesin-like protein (AHRD V3.3 *** M1BMZ3_SOLTU)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	1,701	1,241	0,315	0,276	0,448									
Solyc01g098990	DUF1995 domain protein, putative (DUF1995) (AHRD V3.3 *** AT5G27560.4)		C:GO:0009507	C:chloroplast			IPR018962 (PFAM): PTHR35509 (PAN	15,529	24,080	29,164	31,268	38,581	0,661	0,011	0,401	0,024			up	up	
Solyc01g099010	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,021	0,062	0,000	0,000	0,000									
Solyc01g099020	GDSL lipase-like caffeoyltransferase		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	2,712	1,701	3,613	3,311	2,755									
Solyc01g099030	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2PL43_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,431	0,425	0,391	0,310	0,331									
Solyc01g099040	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,241	0,217	11,096	13,318	8,948									
Solyc01g099080	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,197	0,200	0,168	0,363	0,258									
Solyc01g099090	Beta-mannosidase, putative (AHRD V3.3 *** B9RF62_RICCO)		P:GO:0005975; F:G(	P:carbohydrate met	EC:3.2.1.152; EC:3.2	Mannosylglycoprotei	PF18368 (PFAM): IPR006102 (PFAM)	169,548	145,551	259,860	267,391	261,149									
Solyc01g099100	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0R5QM74_SALMI)		F:GO:0003824	F:catalytic activity			IPR025110 (PFAM): IPR000873 (PFA	103,130	105,816	431,917	460,545	415,896									
Solyc01g099110	Metallopeptidase M24 family protein (AHRD V3.3 *** AT3G05350.1)		F:GO:0070006	F:metalloaminopept	EC:3.4.11	Acting on peptide bor	G3DSA:3.90.230.10 (GENE3D): IPR0(	23,299	22,139	37,016	41,662	42,816									
Solyc01g099120	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G54990.1)		C:GO:0005739; C:G(	C:mitochondrion; C:vacuolar membrane; C:endoplasmic reticulu			IPR000073 (PFAM): mobidb-lite (MOB	21,062	17,081	17,633	15,052	14,802									
Solyc01g099140	Vacuole membrane 1 (AHRD V3.3 *** A0A0B0N2I2_GOSAR)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			PTHR10281 (PANTHER): PTHR10281	2,655	2,820	6,404	8,761	6,675									
Solyc01g099150	Desiccation-related protein PCC13-62		F:GO:0016702; F:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	0,517	0,539	27,152	26,089	26,752									
Solyc01g099160	Lipoxygenase (AHRD V1 **** Q9FT17_SOLLC)%3B contains Interpro domain(s) IP	LOX5	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	19,610	20,784	155,285	127,574	164,000									
Solyc01g099163	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT1G15490.4)							0,358	0,386	9,649	6,801	6,871									
Solyc01g099167	Lipoxygenase (AHRD V3.3 *-* M1CAP3_SOLTU)		F:GO:0016702; F:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR013819 (PFAM): G3DSA:1.20.245	0,019	0,000	0,187	0,097	0,235									
Solyc01g099180	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	LOX9	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR013819 (PRINTS): IPR001246 (PF	11,570	5,102	149,968	145,062	116,580	-1,150	0,006					down		
Solyc01g099190	lipoxygenase B	LOX2	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	1800,153	970,469	26785,471	24627,660	21059,168	-0,865	0,017					down		
Solyc01g099200	Lipoxygenase (AHRD V3.3 *** A8W7J7_CAMSI)	LOX7	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR013819 (PRINTS): IPR001246 (PF	12,805	11,709	69,038	52,255	42,894			-0,691	0,009				down	
Solyc01g099210	Lipoxygenase (AHRD V3.3 *** A8W7J7_CAMSI)	LOX13	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	1,626	4,669	0,883	1,817	1,837	1,539	0,012					up		
Solyc01g099220	DNA polymerase (AHRD V3.3 *** K4B0V9_SOLLC)		F:GO:0000166; F:G(	F:nucleotide binding	EC:2.7.7.7	DNA-directed DNA p(	IPR006172 (PRINTS): IPR006172 (SM	41,688	29,837	38,497	41,881	40,137									
Solyc01g099230	Zinc finger family protein, putative (AHRD V3.3 *** A0A061F333_THECC)		C:GO:0005634; C:G(	C:nucleus; C:mitochondrion; P:embryo development ending in se			IPR001876 (SMART): G3DSA:4.10.10	15,510	13,825	16,028	14,196	15,338									
Solyc01g099240	6-phosphogluconate dehydrogenase family protein (AHRD V3.3 *** AT4G29120.1)		F:GO:0016491; F:G(	F:oxidoreductase activity; F:NADP binding; F:NAD binding; P:ox			IPR006115 (PFAM): IPR013328 (G3D	14,866	17,781	15,570	14,729	17,259									
Solyc01g099250	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00365 (SMAR	0,243	0,176	0,099	0,050	0,093									
Solyc01g099260	Chaperone protein DnaJ (AHRD V3.3 *** G7KYP1_MEDTR)		C:GO:0009507	C:chloroplast			IPR001623 (PRINTS): IPR001623 (SM	44,252	35,258	29,261	32,409	31,592									
Solyc01g099270	Microtubule binding protein (AHRD V3.3 *** A6YTD5_CUCME)		C:GO:0005875; C:G(	C:microtubule associated complex; C:preprophase band			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,514	0,339	0,075	0,098	0,094									
Solyc01g099280	Sucrose nonfermenting 4 (AHRD V3.3 *** A0A061FAC2_THECC)		P:GO:0000266; F:G(	P:mitochondrial fiss	EC:2.7.11	Transferring phospho	IPR000644 (SMART): IPR032640 (PF	39,630	38,054	51,306	50,737	48,064									
Solyc01g099290	cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR001373 (PFAM): G3DSA:1.20.131	12,544	9,155	2,320	1,392	1,643									
Solyc01g099300	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0PTV2_GOSAR)						PF17942 (PFAM): PF13589 (PFAM): I	39,390	34,250	41,543	44,010	43,346									
Solyc01g099310	cyclinH1_1	CycH1_1	P:GO:0000079; P:G(	P:regulation of cycli	EC:2.7.11; EC:2.7.1'	Transferring phospho	IPR013763 (SMART): IPR031658 (PF	4,661	4,701	4,501	4,407	3,766									
Solyc01g099330	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G01240.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	0,040	0,281	0,075	0,000	0,047									
Solyc01g099340	Zinc finger protein (AHRD V3.3 *** E9NZV2_PHAVU)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF: C2H2	20,334	15,894	11,283	16,174	11,417									

Solyc01g099350	Acyl-CoA-binding domain-containing protein 4 (AHRD V3.3 *** ACBP4_ARATH)		F:GO:0000062: F:G(	F:fatty-acyl-CoA binding; F:protein binding			PF13415 (PFAM): IPR006652 (PFAM	78,144	89,830	65,134	63,129	63,047									
Solyc01g099360	PWWP (AHRD V3.3 *** A2Q337_MEDTR)		F:GO:0003886: F:G(	F:DNA (cytosine-5-)-methyltransferase activity; F:methyltransfe			IPR000313 (SMART): G3DSA:2.30.30	39,270	36,578	44,671	44,549	43,058									
Solyc01g099370	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G16510.1)		C:GO:0016021	C:integral component of membrane			IPR000008 (SMART): IPR000008 (PF	391,275	337,062	112,400	260,492	192,716			0,775	0,012	1,214	0,000		up	up
Solyc01g099380	U4/U6.U5 tri-snRNP-associated protein 1 (AHRD V3.3 *-* A0A0B2S142_GLYSO)		P:GO:0000398	P:mRNA splicing, via spliceosome			IPR005011 (PFAM): mobidb-lite (MOB	11,130	8,629	11,678	16,162	12,195					0,473	0,031			up
Solyc01g099385	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G16510.1		C:GO:0016021	C:integral component of membrane			IPR000008 (SMART): IPR035892 (G3	2,019	1,503	2,002	1,640	2,185									
Solyc01g099400	WD-repeat protein, putative (AHRD V3.3 *** B9T0U7_RICCO)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	112,171	85,901	122,647	118,327	119,123									
Solyc01g099415	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* A0A1D1ZDN4_9ARAE)		F:GO:0000166: F:G(	F:nucleotide bindinc	EC:3.6.1.15	Nucleoside-triphosphate phosphatase		1,308	1,071	1,613	2,118	1,746									
Solyc01g099420	Catalase (AHRD V3.3 *-* Q6T2D5_SOLTU)		F:GO:0004096: P:G(	F:catalase activity:	EC:1.11.1.7: EC:1.1	Peroxidase: Catalase	IPR037060 (G3DSA:2.40.180.GENE3	2,018	1,871	3,204	2,661	2,810									
Solyc01g099430	ATP-dependent DNA helicase (AHRD V3.3 --* C1N4S4_MICPC)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): PTHR	0,948	0,721	1,519	1,543	1,562									
Solyc01g099440	translation initiation factor 3 (IF-3) family protein (AHRD V3.3 --* AT1G34360.3)							1,207	1,591	1,466	1,059	1,563									
Solyc01g099450	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* W9S050_9ROSA)		C:GO:0016021	C:integral component of membrane			PTHR13710 (PANTHER): PTHR13710	0,700	0,831	0,996	1,218	1,112									
Solyc01g099460	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *** G7I8P0_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR014001 (SMART): IPR001650 (SM	7,089	8,936	3,011	2,769	3,273									
Solyc01g099470	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* A0A0B0MR74_GOSAR)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,141	0,300	0,050	0,025	0,116									
Solyc01g099480	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *-* G7I8P0_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): PTHR	0,812	0,556	0,506	1,217	0,871					1,247	0,043			up
Solyc01g099483	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *-* A0A072VML8_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): PTHR	0,123	0,195	0,194	0,149	0,403									
Solyc01g099485	magnesium transporter NIPA (DUF803) (AHRD V3.3 --* AT4G13800.8)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,123	0,195	0,315	0,072	0,213									
Solyc01g099487	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 --* A0A0B0MR74_GOSAR)		F:GO:0000166: F:G(	F:nucleotide binding: F:nucleic acid binding: F:helicase activity: F:ATP binding: C:nucleus: P:DNA recom				0,077	0,265	0,315	0,217	0,285									
Solyc01g099490	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 --* W9S050_9ROSA)		F:GO:0000166: F:G(	F:nucleotide binding: F:nucleic acid binding: F:helicase activity: F:ATP binding: C:nucleus: P:DNA recom				0,318	0,258	0,240	0,320	0,376									
Solyc01g099500	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *-* A0A072VML8_MEDTR)		F:GO:0000166: F:G(	F:nucleotide bindinc	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): PTHR	0,207	0,486	0,297	0,525	0,332									
Solyc01g099510	Rhamnogalacturonate lyase family protein (AHRD V3.3 --* AT1G09880.4)						mobidb-lite (MOBIDB_LITE)	2,153	1,262	0,812	0,982	1,245									
Solyc01g099520	Rapid alkalinization factor (AHRD V3.3 *** RALF_TOBAC)		F:GO:0005179: C:G(	F:hormone activity: C:extracellular region: C:plasmodesma: P:re			IPR008801 (PFAM): PTHR33136 (PAN	45,870	41,977	22,828	33,481	31,780									
Solyc01g099525	Nucleosome assembly protein 1-like 1 (AHRD V3.3 *-* A0A0B2RAX5_GLYSO)							0,059	0,037	0,050	0,075	0,023									
Solyc01g099530	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XQU8_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	6,528	4,828	7,253	7,471	6,653									
Solyc01g099560	NAD(P)-binding rossmann-fold protein (AHRD V3.3 *** G7LBT9_MEDTR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	0,084	0,037	0,000	0,050	0,023									
Solyc01g099570	Desiccation-related PCC13-62 (AHRD V3.3 *-* A0A0B0N4G5_GOSAR)		C:GO:0016021	C:integral component of membrane			PF13668 (PFAM): PTHR31694 (PANT	0,000	0,019	0,046	0,025	0,023									
Solyc01g099580	Cysteine/Histidine-rich C1 domain family protein, putative (AHRD V3.3 *-* A0A061EYK7_THECC)		C:GO:0016021	C:integral component of membrane			IPR004146 (PFAM): PF13668 (PFAM)	3,368	2,109	22,102	19,073	13,776			-0,684	0,027				down	
Solyc01g099590	glutathione-S-transferase	GSTU6	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:3.40.30.1	63,937	33,787	176,276	150,323	128,291	-0,894	0,000					down		
Solyc01g099600	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061F2B7_THECC)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	57,804	47,250	376,797	328,939	229,009			-0,721	0,001				down	
Solyc01g099620	Respiratory burst oxidase, putative (AHRD V3.3 *** B9RFA3_RICCO)		F:GO:0004601: F:G(	F:peroxidase activit	EC:1.6.3.1: EC:1.11.	NAD(P)H oxidase (H	IPR000778 (PRINTS): IPR002048 (SM	1,195	2,867	4,771	3,762	3,462	1,280	0,014					up		
Solyc01g099630	xyloglucan endotransglucosylase-hydrolase 1	xth1	F:GO:0004553: C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR008264 (PRINTS): IPR000757 (PF	153,697	161,399	4,672	2,742	3,044									
Solyc01g099640	Zeta-carotene desaturase, chloroplastic/chromoplastic (AHRD V3.3 --* ZDS_ONCHC)							0,021	0,018	0,065	0,315	0,188									
Solyc01g099645	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G36290.2)							2,911	3,607	11,737	15,737	9,580									
Solyc01g099650	Formin-like protein (AHRD V3.3 *** K4B0Z9_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (SMART): G3DSA:1.20.58	2,184	3,246	0,022	0,025	0,116									
Solyc01g099660	Heat shock protein 70 (AHRD V3.3 *** Q9M4E8_CUCSA)		F:GO:0005524: C:G(	F:ATP binding: C:nu	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS): IPR013126 (PF	8,166	8,921	30,954	39,334	34,504									
Solyc01g099670	meloidogyne-induced giant cell protein db212	db212	P:GO:0000028: F:G(	P:ribosomal small subunit assembly: F:structural constituent of r			IPR005326 (PFAM): IPR036388 (G3D	77,473	83,716	64,863	60,958	62,371									
Solyc01g099675	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT3G62280.2)						mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,000	0,025	0,023									
Solyc01g099680	Rubber elongation factor protein, putative (AHRD V3.3 *** B9RFA8_RICCO)		C:GO:0005773: C:G(	C:vacuole: C:lipid droplet: P:lipid storage: P:lipid droplet organiz			IPR008802 (PFAM): IPR008802 (PAN	246,235	414,506	267,642	282,671	266,471	0,777	0,017					up		
Solyc01g099690	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4B103_SOLLC)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): IPR023562 (PF	124,979	161,876	414,845	409,562	454,487									
Solyc01g099700	T-box protein (AHRD V3.3 *** AT5G27710.1)						PTHR35759 (PANTHER)	28,054	31,419	41,560	45,429	43,755									
Solyc01g099710	Phospholipid/glycerol acyltransferase family protein (AHRD V3.3 *** B9N4I6_POPTR)		P:GO:0006644: F:G(	P:phospholipid metabolic process: F:transferase activity, transf			IPR000872 (PRINTS): IPR002123 (SM	53,671	55,896	76,534	72,694	68,957									
Solyc01g099715	F-actin capping protein alpha subunit (AHRD V3.3 *** B9I7I3_POPTR)		C:GO:0008290: P:G(	C:F-actin capping protein complex: P:barbed-end actin filament			IPR002189 (PRINTS): IPR002189 (PF	40,654	40,191	57,673	60,135	53,377									
Solyc01g099730	transmembrane protein (AHRD V3.3 *** AT2G41945.1)		C:GO:0016021	C:integral component of membrane			PTHR34459:SF2 (PANTHER): PTHR3	9,910	9,131	17,227	16,695	14,617									
Solyc01g099740	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT5G27720.1)		P:GO:0000398: P:G(	P:mRNA splicing, via spliceosome: P:nuclear-transcribed mRNA			IPR001163 (SMART): IPR001163 (PF	48,214	56,005	53,016	47,621	48,884									
Solyc01g099745	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *** A0A061F3M1_THECC)		C:GO:0016021: F:G(	C:integral component of membrane; F:transferase activity			IPR012429 (PFAM): PTHR31061:SF8	21,085	29,050	33,845	48,764	51,664			0,606	0,000	0,529	0,004		up	up
Solyc01g099760	LeMA-1 putatve Mg-dependent ATPase 1	ma1	F:GO:0005524: C:G(	F:ATP binding: C:cy	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR005937 (TIG	181,622	169,007	254,173	233,735	227,959									
Solyc01g099770	meloidogyne-induced giant cell protein DB141	TOMTRALTAI	F:GO:0005509: C:G(	F:calcium ion binding; C:cytoplasm			IPR018105 (PRINTS): IPR011323 (G3	6124,970	5624,097	5428,553	4877,761	4949,291									
Solyc01g099780	Translationally-controlled tumor protein homolog (AHRD V3.3 *** TCTP_SOLTU)		F:GO:0005509: C:G(	F:calcium ion binding; C:cytoplasm			IPR018105 (PRINTS): IPR011323 (G3	20,501	18,862	16,891	14,682	17,201									
Solyc01g099790	RING/U-box superfamily protein (AHRD V3.3 *** AT3G05545.1)						IPR001841 (SMART): IPR001841 (PF	104,180	122,598	114,606	120,864	121,472									
Solyc01g099800	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G47330.1)							15,059	13,992	42,831	38,344	35,861									
Solyc01g099810	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G02840.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	60,609	54,218	168,883	181,527	166,165									
Solyc01g099820	Hypoxia-responsive family protein (AHRD V3.3 *** G7I8Q8_MEDTR)		C:GO:0031305: P:G(	C:integral component of mitochondrial inner membrane: P:mitocl			IPR007667 (PFAM): PTHR28018:SF1	0,250	0,347	0,069	0,073	0,141									
Solyc01g099830	60S ribosomal protein L22-2 (AHRD V3.3 *** W9QTY3_9ROSA)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR038526 (G3DSA:3.30.1360.GENE	249,939	264,357	183,927	152,001	159,704									
Solyc01g099840	Dormancy/auxin associated protein (AHRD V3.3 *** G7I8R1_MEDTR)						IPR008406 (PFAM): mobidb-lite (MOB	162,540	117,091	75,732	66,527	66,905									
Solyc01g099850	Folate receptor-like protein (AHRD V3.3 *** A0A124SAH4_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR018143 (PFAM): mobidb-lite (MOB	1,195	0,857	1,342	0,824	1,081									
Solyc01g099860	Serine/threonine-protein phosphatase (AHRD V3.3 *** M1CB27_SOLTU)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	15,497	15,035	19,997	24,634	19,373									
Solyc01g099870	Bidirectional sugar transporter SWEET (AHRD V3.3 *-* M1CB29_SOLTU)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D): IPF	0,000	0,021	0,000	0,000	0,000									
Solyc01g099880	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4B122_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D): G3	0,688	0,788	1,041	2,144	1,596									
Solyc01g099890	MCT-1 (AHRD V3.3 *** A0A161G0X0_HORVU)		F:GO:0003723	F:RNA binding			IPR002478 (SMART): PF17832 (PFAM	3,238	3,625	4,647	4,789	4,513									
Solyc01g099900	60S ribosomal protein L18, putative (AHRD V3.3 *** B9RFD6_RICCO)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: C:ribosome			IPR002478 (SMART): IPR021131 (PF	559,070	594,041	491,474	437,868	454,926									
Solyc01g099910	Epoxide hydrolase (AHRD V3.3 *** B3VMR4_NICBE)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR029058 (G3	1,145	1,165	0,141	0,050	0,141									
Solyc01g099920	PAR1 protein (AHRD V3.3 *-* A0A061EYI9_THECC)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			IPR009489 (PFAM): mobidb-lite (MOB	21,528	37,754	59,457	92,894	45,697					0,648	0,002			up
Solyc01g099925	zinc finger protein 6 (AHRD V3.3 --* AT1G67030.1)						mobidb-lite (MOBIDB_LITE)	0,912	0,810	1,426	0,815	1,314									
Solyc01g099930	piezo-type mechanosensitive ion channel component (AHRD V3.3 --* AT2G48060.3)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,381	8,300	14,552	15,797	13,630									
Solyc01g099940	Pectinesterase (AHRD V3.3 *** K4B128_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR006501 (PF	0,118	0,076	0,282	0,265	0,095									
Solyc01g099950	Pectinesterase (AHRD V3.3 *** K4B129_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR012334 (G3	0,057	0,181	0,068	0,025	0,187									
Solyc01g099960	Pectinesterase (AHRD V3.3 *** K4B130_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR012334 (G3	0,976	1,486	2,364	2,466	2,635									
Solyc01g099970	F-box/LRR protein (AHRD V3.3 *** G7KWK1_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR032675 (G3	9,755	12,365	20,151	27,364	23,555					0,445	0,006			up
Solyc01g099980	enolase (DUF1399) (AHRD V3.3 *** AT1G56230.1)						IPR009836 (PFAM): PTHR34365:SF3	38,382	22,412	23,103	18,248	22,626	-0,746	0,033					down		
Solyc01g099990	F-box protein (AHRD V3.3 *** G7KWK0_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR025886 (PFA	1,230	1,251	11,749	11,073	9,303									
Solyc01g100000	F-box protein (AHRD V3.3 *** W9RMP6_9ROSA)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): G3DSA:1.20.128	24,782	32,394	10,458	5,900	13,890					-0,819	0,025			down
Solyc01g100010	F-box protein (AHRD V3.3 *** W9RMP6_9ROSA)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): PTHR32278 (PAN	26,351	16,564	3,163	6,749	6,005					1,086	0,000			up
Solyc01g100020	Phospholipase D (AHRD V3.3 *** I1NJ37_SOYBN)		F:GO:0004630: P:G(	F:phospholipase D :	EC:3.1.4.4	Phospholipase D	IPR001736 (SMART): IPR025202 (PF	5,037	7,463	1,938	1,521	1,762									
Solyc01g100030	deoxyuridine triphosphatase		F:GO:0004170: P:G(	F:dUTP diphosphata	EC:3.6.1.23: EC:3.6.	dUTP diphosphatase	IPR008181 (TIGRFAM): IPR036157 ((	24,982	20,936	9,124	4,632	7,553					-0,970	0,031			down
Solyc01g100040	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G27930.2)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	22,263	33,696	11,581	20,540	17,502			0,591	0,028	0,826	0,000		up	up
Solyc01g100050	TOPLESS 3	TPL3	F:GO:0005515: P:G(	F:protein binding; P:regulation of transcription, DNA-templated			IPR006595 (SMART): IPR006594 (SM	357,125	291,080	440,867	480,134	462,483									
Solyc01g100060	Pre-mRNA splicing factor (AHRD V3.3 *** A8IJK3_CHLRE)		C:GO:0071011	C:precatalytic spliceosome			IPR005037 (PFAM): IPR005037 (PAN	33,822	33,902	48,907	46,099	46,333									
Solyc01g100070	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 --* A0A1D1ZFE6_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,080	0,157	0,191	0,167	0,376									
Solyc01g100080	Single-stranded DNA-binding protein (AHRD V3.3 *** G7I9F0_MEDTR)		F:GO:0003697	F:single-stranded DNA binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	11,104	11,433	12,071	9,104	10,071									
Solyc01g100100	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E1W0_THECC)		C:GO:0016020	C:membrane			IPR001841 (SMART): IPR013083 (G3	0,021	0,222	0,044	0,000	0,000									
Solyc01g100110	Phosphatase 2C family protein (AHRD V3.3 *** A0A061F3G7_THECC)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	119,610	83,767	59,956	57,533	65,536									
Solyc01g100120	Kinesin-like protein (AHRD V3.3 *** B9I798_POPTR)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001715 (SM	0,697	0,421	0,112	0,025	0,071									
Solyc01g100130	RING/U-box protein (AHRD V3.3 *-* AT3G05670.3)		F:GO:0003677: F:G(	F:DNA binding: F:he	EC:3.6.1.15	Nucleoside-triphosph	IPR001965 (SMART): IPR001841 (SM	43,036	46,006	64,371	66,986	58,100									
Solyc01g100140	Dehydration-induced 19-like protein (AHRD V3.3 *-* E3T7S4_GOSHI)						IPR027935 (PFAM): PTHR31875:SF6	8,120	7,543	6,750	5,865	6,612									
Solyc01g100160	Dehydration-induced 19-like protein (AHRD V3.3 *** E3T7S4_GOSHI)						IPR008598 (PFAM): PTHR31875:SF0	20,781	15,986	15,314	15,298	14,996									
Solyc01g100170	Syntaxin (AHRD V3.3 *** B7X6S7_TOBAC)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART): IPR006011 (SM	25,184	32,345	30,058	30,592	28,480									
Solyc01g100180	DNA polymerase III polC-type (AHRD V3.3 *** W9R346_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR013520 (SMART): IPR013520 (PF	5,138	5,047	7,353	6,984	7,173									
Solyc01g100190	Protein misato (AHRD V3.3 *** A0A0B0PN41_GOSAR)						IPR019605 (PFAM): IPR029209 (PFA	17,151	13,163	18,348	15,197	18,241									
Solyc01g100210	Hexosyltransferase (AHRD V3.3 *** K4B155_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR029044 (G3DSA:3.90.550.GENE3	0,037	0,074	0,025	0,050	0,047									
Solyc01g100220	GATA transcription factor, putative (AHRD V3.3 *** B9RZK8_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR000679 (SMAF GATA	1,845	1,950	0,495	0,654	0,591									
Solyc01g100230	DnaJ-like protein (AHRD V3.3 *** D5FNB3_SOYBN)						IPR001623 (PRINTS): IPR001623 (SM	32,015	23,006	72,318	75,301	59,624									
Solyc01g100240	Calmodulin-binding protein (AHRD V3.3 *** AT2G18750.3)		F:GO:0005516	F:calmodulin binding			IPR012416 (PFAM): mobidb-lite (MOB	24,708	24,989	23,587	42,698	35,355			0,581	0,018	0,857	0,001		up	up
Solyc01g100250	trigalactosyldiacylglycerol 1 (AHRD V3.3 *** AT1G19800.6)		C:GO:0043190	C:ATP-binding cassette (ABC) transporter complex			IPR003453 (TIGRFAM): IPR030802 (F	3,679	5,134	8,107	9,782	8,156									
Solyc01g100260	Ppx/GppA phosphatase (AHRD V3.3 *** A0A103YL09_CYNCS)		P:GO:0006357: C:G(	P:regulation of transcription by RNA polymerase II: C:transcripti			IPR003695 (PFAM): G3DSA:3.30.420	21,133	17,820	31,444	31,726	34,152									
Solyc01g100270	3'-5' exonuclease domain-containing family protein (AHRD V3.3 *** U5GFK4_POPTR)		F:GO:0003676: P:G(	F:nucleic acid binding: P:nucleobase-containing compound meta			IPR002562 (SMART): IPR002562 (PF	3,242	3,296	2,910	4,172	4,457									
Solyc01g100280	RNA helicase DEAH-box4	DEAH4	F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR001650 (SMART): IPR014001 (SM	3,633	4,321	1,875	1,734	1,667									
Solyc01g100290	GPI-anchored adhesin-like protein (AHRD V3.3 *** AT5G26910.2)						IPR032795 (PFAM): mobidb-lite (MOB	23,126	31,104	19,560	18,988	18,691									
Solyc01g100310	Calmodulin-binding protein (AHRD V3.3 *** A0A0K9P385_ZOSMR)						IPR012442 (PFAM): mobidb-lite (MOB	4,160	4,667	8,255	6,893	7,320									
Solyc01g100320	Disulfide-isomerase-like protein (AHRD V3.3 *** Q38JJ2_SOLTU)		C:GO:0005783: F:G(	C:endoplasmic reticulum: F:isomerase activity: P:cell redox hon			PR00421 (PRINTS): IPR005788 (TIGF	325,778	310,210	1069,245	1171,718	887,613									
Solyc01g100330	Zinc finger matrin-type 2 (AHRD V3.3 *** A0A0B0MXS7_GOSAR)		P:GO:0000398: F:G(	P:mRNA splicing, via spliceosome: F:nucleic acid binding: C:spli			IPR003604 (SMART): G3DSA:3.30.16	17,273	17,678	25,516	26,462	23,739									
Solyc01g100340	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JRX1_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	2,222	1,513	2,835	2,645	2,310									
Solyc01g100350	GTP-binding protein (AHRD V3.3 *** W9R3Y5_9ROSA)		F:GO:0005525: C:G(	F:GTP binding; C:intracellular; P:intracellular protein transport			IPR006689 (PRINTS): SM00177 (SMA	461,474	393,578	424,548	355,732	378,282									
Solyc01g100360	Dihydrolipoyl dehydrogenase (AHRD V3.3 *** A0A103XB80_CYNCS)		F:GO:0016491: P:G(	F:oxidoreductase activity: P:cell redox homeostasis: F:flavin ad			PR00368 (PRINTS): PR00411 (PRINT	135,134	146,644	208,630	206,751	222,667									
Solyc01g100370	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G62550.1)						IPR006015 (PRINTS): IPR006016 (PF	129,038	161,200	341,793	273,947	317,323									
Solyc01g100390	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)		F:GO:0004427: F:G(	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (PFAM): IPR004131 (TIGF	0,396	1,151	0,288	0,498	0,662									
Solyc01g100400	Pseudouridine synthase family protein (AHRD V3.3 *** AT1G56345.1)		P:GO:0001522: F:G(	P:pseudouridine synthesis: F:RNA binding: F:pseudouridine syn			IPR006145 (PFAM): PTHR45372 (PAN	4,487	4,387	4,197	3,812	4,518									
Solyc01g100410	Iron-sulfur cluster assembly protein IscA (AHRD V3.3 *** G7KQU7_MEDTR)		F:GO:0005198: F:G(	F:structural molecule activity: F:iron-sulfur cluster binding: P:pro			IPR035903 (G3DSA:2.60.300.GENE3	5,883	5,464	12,491	13,440	12,380									
Solyc01g100420	Peptide chain release factor, putative (AHRD V3.3 *** B9RFI5_RICCO)		C:GO:0005737: P:G(	C:cytoplasm: P:translational termination: F:translation release fa			IPR005139 (SMART): IPR005139 (PF	12,826	12,556	29,011	27,510	25,836									
Solyc01g100440	ATP-dependent DNA helicase (AHRD V3.3 *-* AT2G24100.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,642	0,731	0,000	0,000	0,000									
Solyc01g100450	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2SGI8_GLYSO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	2,543	2,310	3,050	3,944	4,002									
Solyc01g100455	myb domain protein 65 (AHRD V3.3 --* AT3G11440.4)							0,793	0,783	0,874	1,332	1,175									
Solyc01g100460	BZIP transcription factor family protein (AHRD V3.3 *** B9GSS6_POPTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR004827 (SMAF bZIP	1,606	1,172	9,192	11,098	7,640									
Solyc01g100470	LOW QUALITY:Endo-1,4-beta-xylanase A (AHRD V3.3 --* A0A1D1ZCC0_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,046									
Solyc01g100480	T-complex protein 1 subunit gamma (AHRD V3.3 --* V7C514_PHAVU)		C:GO:0005783	C:endoplasmic reticulum			mobidb-lite (MOBIDB_LITE): mobidb-lit	23,011	27,636	30,794	31,566	30,782									
Solyc01g100490	chloronerva	chln	F:GO:0030410: P:G(	F:nicotianamine syr	EC:2.5.1.43	Nicotianamine syntha	IPR004298 (PFAM): G3DSA:3.40.50.1	1,347	1,251	3,939	4,825	5,247									
Solyc01g100500	Microfibrillar-associated protein 1 (AHRD V3.3 *** A0A0K9NTB2_ZOSMR)						IPR009730 (PFAM): mobidb-lite (MOB	72,506	65,022	125,527	106,122	111,652									
Solyc01g100510	knotted 4	tkn4	F:GO:0003677: C:G(	F:DNA binding: C:nucleus: P:regulation of transcription, DNA-ter			IPR005539 (SMAF TALE	8,206	10,079	7,591	6,477	6,326									
Solyc01g100520	Clp protease 2 proteolytic subunit	clpp2	F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): G3DSA:3.90.22	100,133	147,516	286,376	285,694	306,912	0,586	0,034					up		
Solyc01g100530	Protein EFR3 B (AHRD V3.3 *** A0A0B0PTG5_GOSAR)		P:GO:0072659	P:protein localization to plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,002	10,162	0,548	0,624	1,111									
Solyc01g100540	HIT zinc finger,PAPA-1-like conserved region, putative (AHRD V3.3 *** A0A061F305_THECC)		P:GO:0006338: C:G(	P:chromatin remodeling; C:Ino80 complex			IPR006880 (SMART): IPR007529 (PF	11,156	12,085	10,535	9,013	10,362									
Solyc01g100570	Nucleolar protein NOP56 (AHRD V3.3 *** A0A061G5W0_THECC)		F:GO:0030515: C:G(	F:snoRNA binding: C:box C/D snoRNP complex: C:small-subunit			IPR012976 (SMART): G3DSA:1.10.24	193,282	180,394	150,216	124,781	130,559									
Solyc01g100580	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RNC6_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	11,774	8,683	9,809	9,888	8,193									
Solyc01g100590	domon-like ligand-binding domain-containing protein		F:GO:0020037	F:heme binding			IPR019020 (SMART): IPR019020 (PF	35,035	49,018	34,699	40,120	37,040									
Solyc01g100600	Kelch repeat protein, putative (AHRD V3.3 *** B9RFJ9_RICCO)		F:GO:0005515	F:protein binding			IPR006652 (SMART): PF13964 (PFAM	17,128	17,020	1,318	0,264	0,472									
Solyc01g100610	Solute carrier family 40 member 3 (AHRD V3.3 *** W9R2S5_9ROSA)		F:GO:0005381: C:G(	F:iron ion transmembrane transporter activity: C:integral compo			IPR009716 (PFAM): PTHR11660:SF5	29,452	29,297	35,107	38,379	42,077									
Solyc01g100620	High mobility group family (AHRD V3.3 *** A0A061F3D5_THECC)		F:GO:0003677	F:DNA binding			SM01014 (SMART): IPR009071 (SMA	2,320	1,751	0,049	0,324	0,023									
Solyc01g100630	Catalase (AHRD V3.3 *-* CATA_SOLAP)		F:GO:0004096: P:G(	F:catalase activity:	EC:1.11.1.7: EC:1.1	Peroxidase: Catalase	IPR018028 (PRINTS): IPR011614 (SM	16,239	12,255	23,229	27,766	26,410									
Solyc01g100640	Catalase (AHRD V3.3 *-* L0SQ20_TOBAC)		F:GO:0004096: P:G(	F:catalase activity:	EC:1.11.1.7: EC:1.1	Peroxidase: Catalase	IPR018028 (PRINTS): IPR037060 (G3	9,357	7,686	12,595	15,044	12,449									
Solyc01g100650	haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** AT1G56500.1)		F:GO:0005515: F:G(	F:protein binding: F:hydrolase activity: P:cell redox homeostasis			IPR006439 (PRINTS): G3DSA:3.40.30	57,918	67,991	88,651	93,590	101,546									
Solyc01g100660	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0S3TVX2_CITUN)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): PTHR331	10,191	14,650	10,204	15,108	12,797					0,570	0,013			up
Solyc01g100690	Transmembrane protein, putative (AHRD V3.3 *** A0A072VMF3_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	15,595	24,826	6,006	7,341	7,566									
Solyc01g100700	IGR motif protein (AHRD V3.3 *** AT3G05810.2)						IPR019083 (SMART): IPR019083 (PF	16,644	17,517	14,687	14,396	13,533									
Solyc01g100720	Importin subunit alpha (AHRD V3.3 *** K4B1A3_SOLLC)		F:GO:0005515: C:G(	F:protein binding: C:nucleus: C:cytoplasm: P:protein import into			IPR000225 (SMART): IPR032413 (PF	124,578	134,453	127,681	120,560	125,011									
Solyc01g100730	rhodanese-like domain protein (AHRD V3.3 *** AT1G09280.1)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm			IPR001763 (SMART): PF17773 (PFAM	14,752	11,125	14,931	15,253	14,026									
Solyc01g100740	Metallopeptidase M24 family protein (AHRD V3.3 *** AT1G09300.1)		F:GO:0004177: F:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR007865 (SMART): IPR007865 (PF	5,511	7,185	9,208	8,805	8,690									
Solyc01g100750	LOW QUALITY:plant/protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G56580.1)						IPR036758 (G3DSA:2.30.240.GENE3	2,154	1,437	0,640	0,868	0,655									
Solyc01g100760	plant/protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G56580.1)						IPR007493 (PFAM): IPR036758 (G3D	10,838	10,870	230,316	388,560	224,192					0,757	0,000			up
Solyc01g100770	LOW QUALITY:plant/protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G56580.1)						IPR036758 (G3DSA:2.30.240.GENE3	29,996	24,997	108,360	123,285	101,491									
Solyc01g100780	Agenet-like domain-containing protein (AHRD V3.3 *** A0A103XFM3_CYNCS)		P:GO:0006306	P:DNA methylation			IPR014002 (SMART): IPR008395 (PF	10,915	9,604	4,981	4,538	5,085									
Solyc01g100790	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y873_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (PFA	0,913	1,026	1,549	1,210	0,944									
Solyc01g100800	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9I6P8_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,900	3,067	2,945	2,506	2,656									
Solyc01g100810	Neutral/alkaline invertase (AHRD V3.3 *** V5N4X0_MANES)		F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetylc	IPR012341 (G3DSA:1.50.10.GENE3D	17,673	13,799	20,350	24,625	22,916									

Solyc01g100820	AP-3 complex subunit mu (AHRD V3.3 *** AP3M_ARATH)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS): IPR001392 (PI	17,898	15,864	22,105	23,903	21,651									
Solyc01g100830	galactinol synthase 1	gols1	P:GO:0006012; F:G(	P:galactose metab	EC:2.4.1.123	Inositol 3-alpha-galac	IPR029044 (G3DSA:3.90.550.GENE3	0,192	0,849	1,482	2,559	0,046									
Solyc01g100840	Trafficking particle complex subunit 4 (AHRD V3.3 *** A0A0B0NT79_GOSAR)		P:GO:0016192; C:G(	P:vesicle-mediated transport; C:TRAPP complex			IPR007233 (SMART): G3DSA:3.30.45	8,467	9,150	10,199	9,920	8,474									
Solyc01g100850	ABC transporter family protein (AHRD V3.3 *** A0A097P9U5_HEVBR)	ABCI2	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	13,522	18,969	14,690	13,798	12,984									
Solyc01g100860	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00178 (SMA	249,791	255,504	300,330	291,721	277,122									
Solyc01g100870	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00177 (SMA	429,276	375,581	349,031	337,534	325,361									
Solyc01g100880	WAT1-related protein (AHRD V3.3 *** K4B1B9_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF1	7,873	5,737	5,316	8,261	6,599									
Solyc01g100890	WAT1-related protein (AHRD V3.3 *-* K4B1C0_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR030184 (PANTHER): IPR030184 (I	0,435	0,627	0,000	0,000	0,024									
Solyc01g100900	WAT1-related protein (AHRD V3.3 *** K4B1C1_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	3,893	2,309	2,390	1,921	3,161									
Solyc01g100910	WAT1-related protein (AHRD V3.3 *** K4B1C2_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	6,084	3,590	1,549	0,679	0,917									
Solyc01g100920	WAT1-related protein (AHRD V3.3 *** K4B1C3_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	10,812	6,999	4,918	4,095	4,640									
Solyc01g100930	GDSL esterase/lipase (AHRD V3.3 *** W9R052_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	25,997	25,104	3,417	2,540	4,890									
Solyc01g100940	LOW QUALITY:starch synthase 2 (AHRD V3.3 --* AT3G01180.1)		P:GO:0010112	P:regulation of systemic acquired resistance			IPR031425 (PFAM): mobidb-lite (MOB	0,755	0,672	0,330	0,368	0,518									
Solyc01g100960	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** M0ZSG9_SOLTU)		F:GO:0004345; P:G(	F:glucose-6-phosph	EC:1.1.1.49	Glucose-6-phosphate	IPR001282 (PRINTS): IPR001282 (TI(	15,113	14,909	36,715	38,933	35,005									
Solyc01g100970	Pyrrolidone-carboxylate peptidase family protein (AHRD V3.3 *** A9PGH9_POPTR)		C:GO:0005829; P:G(	C:cytosol; P:proteo	EC:3.4.19	Acting on peptide bor	IPR016125 (PFAM): IPR036440 (G3D	330,045	302,379	265,878	221,424	255,469									
Solyc01g100980	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G02460.1)	PG7	F:GO:0004650; P:G(	F:polygalacturonas	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,080	0,039	0,047	0,000	0,000									
Solyc01g100990	Zinc finger transcription factor 13	C3H13	F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR003604 (SMAF C3H	12,161	11,782	19,870	17,187	17,157									
Solyc01g101000	Protein kinase (AHRD V3.3 *** R9Q9C7_FRAVE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	364,556	320,753	509,589	545,681	500,976									
Solyc01g101010	F2P16.20 protein, putative isoform 1 (AHRD V3.3 *** A0A061GXF8_THECC)		F:GO:0008420; F:G(	F:RNA polymerase	EC:3.1.3.16	Protein-serine/threor	IPR007308 (PFAM): IPR038534 (G3D	34,893	29,414	55,325	53,178	50,725									
Solyc01g101020	FACT complex subunit SPT16, putative (AHRD V3.3 *** B9RFP6_RICCO)		C:GO:0035101	C:FACT complex			IPR013719 (SMART): IPR013953 (SN	121,539	137,247	156,789	132,023	134,091									
Solyc01g101030	FACT complex subunit SPT16 (AHRD V3.3 *** W9RSN6_9ROSA)		C:GO:0035101	C:FACT complex			IPR013953 (SMART): IPR013719 (SN	10,693	9,196	8,209	6,956	7,788									
Solyc01g101035	Protein with RNI-like/FBD-like domain (AHRD V3.3 --* AT1G56610.3)							0,220	0,064	0,170	0,048	0,117									
Solyc01g101040	ATP-citrate synthase, putative (AHRD V3.3 *** B9RFP8_RICCO)		F:GO:0005524	F:ATP binding			IPR032263 (PFAM): IPR016102 (G3D	174,227	191,778	154,195	146,354	154,346									
Solyc01g101050	Peroxidase (AHRD V3.3 *** K4B1D5_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,072	0,000	0,025	0,024									
Solyc01g101060	S-adenosyl-L-methionine synthetase	sam	F:GO:0004478; F:G(	F:methionine adenc	EC:2.5.1.6	Methionine adenosyl	IPR022630 (PFAM): G3DSA:3.30.300	8614,858	5310,160	1021,927	701,023	935,965	-0,671	0,046			-0,541	0,007	down		down
Solyc01g101070	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TSU1_ACAMN)	ABCG33	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	51,775	44,817	34,824	34,120	40,681									
Solyc01g101080	LOW QUALITY:Polynucleotidyl transferase, Ribonuclease H fold (AHRD V3.3 --* Q2HUC4_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis				0,000	0,018	0,000	0,000	0,000									
Solyc01g101090	putative plant adhesion protein		F:GO:0005096; P:G(	F:GTPase activator activity; P:regulation of GTPase activity			IPR000195 (SMART): G3DSA:1.10.10	40,689	41,171	42,944	41,447	53,203									
Solyc01g101100	Kinase family protein (AHRD V3.3 *** B9N417_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	38,148	27,714	18,715	19,971	22,039									
Solyc01g101110	Serine/threonine-protein kinase haspin (AHRD V3.3 *** A0A146F677_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			SM01331 (SMART): PF12330 (PFAM)	2,361	2,678	1,003	1,047	1,696									
Solyc01g101120	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0PV84_GOSAR)		C:GO:0016021; C:G(	C:integral component of membrane; C:anchored component of r			PR01217 (PRINTS): IPR012946 (SMA	10,719	9,715	2,683	3,474	3,365									
Solyc01g101130	myosin heavy chain, cardiac protein (AHRD V3.3 *** AT5G26770.2)		C:GO:0005635	C:nuclear envelope			IPR038812 (PANTHER)	2,985	4,890	3,493	4,825	5,105									
Solyc01g101140	Endonuclease or glycosyl hydrolase, putative (AHRD V3.3 *** G7KWF4_MEDTR)		C:GO:0005777; P:G(	C:peroxisome; P:regulation of gene expression			IPR025677 (PFAM): IPR021139 (PFA	130,809	131,092	134,709	152,680	139,060									
Solyc01g101150	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RFQ7_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,600	2,385	1,012	1,113	1,203									
Solyc01g101160	PHD finger family protein (AHRD V3.3 *** AT3G17460.1)						mobidb-lite (MOBIDB_LITE): PTHR344	26,391	25,002	33,972	33,557	30,625									
Solyc01g101170	Viridiflorene synthase (AHRD V3.3 *** TPS31_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR036965 (G3D	0,000	0,021	0,147	0,368	0,470									
Solyc01g101180	viridiflorene synthase		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,000	0,018	0,326	0,392	0,662									
Solyc01g101190	Alpha-humulene/(-)-(E)-beta-caryophyllene synthase (AHRD V1 **** HUMS_ARATH)%3B contains Interpro dc		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,018	0,298	0,639	1,416									
Solyc01g101210	viridiflorene synthase		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,059	0,191	0,069	0,118									
Solyc01g101220	Viridiflorene synthase (AHRD V3.3 *-* TPS32_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,021	0,039	0,000	0,000	0,070									
Solyc01g101240	aspartic protease precursor	TOMAPP	F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR033121 (PF	184,448	193,459	130,471	110,038	172,070			0,396	0,048				up	
Solyc01g101250	G-patch domain-containing protein (AHRD V3.3 *** A0A103Y2Y0_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR000467 (SMAF C2H2	32,257	30,585	27,046	23,592	24,335									
Solyc01g101260	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 --* A0A067FYM9_CITSI)						PTHR33511:SF3 (PANTHER): PTHR3	0,739	0,677	0,327	0,221	0,238									
Solyc01g102260	Mads box protein, putative (AHRD V3.3 *** B9S273_RICCO)		F:GO:0000981; F:G(	F:DNA-binding transcription factor activity, RNA polymerase II-s			IPR002100 (PRIN M-type_MADS	2,093	2,049	0,371	0,259	0,538									
Solyc01g102265	RING/U-box superfamily protein (AHRD V3.3 *** AT3G42830.1)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:anaphase-promoting c			IPR024991 (PFAM): IPR013083 (G3D	0,000	0,000	0,025	0,000	0,023									
Solyc01g102270	Jojoba acyl CoA reductase-related male sterility protein (AHRD V3.3 --* AT4G33790.2)							0,777	0,994	2,380	3,052	2,479									
Solyc01g102285	Low temperature and salt responsive protein (AHRD V3.3 *-* Q8H9B8_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR000612 (PANTHER): PTHR21659:	0,315	0,377	0,068	0,100	0,118									
Solyc01g102290	protein RARE-COLD-INDUCIBLE 2B-like		C:GO:0016021	C:integral component of membrane			IPR000612 (PFAM): IPR000612 (PAN	78,409	93,443	83,750	154,526	105,464					0,885	0,000			up
Solyc01g102300	bHLH transcription factor 006	PIF3	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	109,294	49,774	53,350	50,261	49,593	-1,106	0,001					down		
Solyc01g102310	GRIP and coiled-coil domain-containing protein, putative (AHRD V3.3 *-* B9RFR9_RICCO)		F:GO:0016787	F:hydrolase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	103,892	85,841	25,414	25,346	34,009									
Solyc01g102320	LOW QUALITY:F-box family protein (AHRD V3.3 -** AT5G07610.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	0,000	0,000	0,000	0,000	0,024									
Solyc01g102330	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)						IPR036514 (G3DSA:3.40.50.GENE3D	110,298	108,567	30,344	21,410	31,607									
Solyc01g102340	R2R3MYB transcription factor 61	R2R3MYB61	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	28,045	16,357	1,916	4,242	2,513	-0,750	0,027					down		
Solyc01g102350	Pectinacetylesterase family protein (AHRD V3.3 *** AT3G05910.1)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): PTHR21562:SF2	15,267	16,145	7,550	10,121	11,794									
Solyc01g102360	Nitrate transporter protein 1.2-like protein (AHRD V3.3 *** A0A0H3WEV3_CAMSI)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	0,021	0,021	0,000	0,000	0,000									
Solyc01g102370	Flap endonuclease 1 (AHRD V3.3 *** K4B1G5_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:nuclease activity; P:DNA repair			IPR006084 (PRINTS): IPR002421 (SN	30,332	28,094	23,440	19,874	21,222									
Solyc01g102390	Germin-like protein (AHRD V1 ***- O65358_SOLTU)%3B contains Interpro domain(s) IPR014710 RmlC-like		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	1,758	2,894	1,166	1,865	1,790									
Solyc01g102400	Germin-like protein (AHRD V1 ***- O65358_SOLTU)%3B contains Interpro domain(s) IPR014710 RmlC-like		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	3,139	3,053	1,953	1,686	2,115									
Solyc01g102410	Glutamyl-tRNA synthetase (AHRD V3.3 *** G7IAE3_MEDTR)	HEMA/GluTR	F:GO:0004818; F:G(	F:glutamate-tRNA li	EC:6.1.1.17	Glutamate--tRNA liga	IPR000924 (PRINTS): G3DSA:1.20.1(	131,617	138,140	152,794	134,700	154,767									
Solyc01g102420	LOW QUALITY:LisH domain and HEAT repeat-containing protein KIAA1468 (AHRD V3.3 --* A0A1D1YW69_9ARAE)							0,040	0,000	0,000	0,022	0,023									
Solyc01g102435	Transmembrane protein 184B family (AHRD V3.3 *-* A0A151SS00_CAJCA)		C:GO:0016021	C:integral component of membrane			PTHR23423:SF35 (PANTHER): IPR00	0,000	0,019	0,125	0,123	0,071									
Solyc01g102440	Transmembrane protein 184B family (AHRD V3.3 *-* A0A151TXC1_CAJCA)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): IPR0051	0,000	0,019	0,025	0,000	0,023									
Solyc01g102450	organic solute transporter ostalpha protein (DUF300) (AHRD V3.3 *-* AT3G05940.1)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): IPR005178 (PAN	0,021	0,019	0,022	0,025	0,024									
Solyc01g102460	Organic solute transporter ostalpha protein (AHRD V3.3 *-* Q2HUZ5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): mobidb-lite (MOB	4,153	2,268	6,781	6,654	5,282									
Solyc01g102480	Organic solute transporter ostalpha protein (AHRD V3.3 *** Q2HUZ5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): mobidb-lite (MOB	33,234	27,942	32,188	32,223	31,375									
Solyc01g102490	NADPH:adrenodoxin oxidoreductase, mitochondrial (AHRD V3.3 *** M1BK29_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00419 (PRINTS): IPR036188 (G3D	71,391	109,611	58,709	51,390	67,562									
Solyc01g102495	cDNA clone:002-110-H12, full insert sequence (AHRD V3.3 --* B7E9Q4_ORYSJ)							0,362	0,137	0,322	0,506	0,258									
Solyc01g102500	Plant/F18B3-190 protein, putative (AHRD V3.3 *** A0A072TSF8_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR354	11,629	12,723	16,203	17,502	15,091									
Solyc01g102510	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G24710.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	100,813	88,241	80,649	82,671	80,008									
Solyc01g102520	MLO-like protein (AHRD V3.3 *** K4B1I0_SOLLC)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): PTHR31942:SF3	0,198	0,055	0,025	0,000	0,000									
Solyc01g102530	TVP38/TMEM64 family membrane protein (AHRD V3.3 *** A0A0B2S228_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR032816 (PFAM): PTHR12677:SF2	13,022	13,104	13,275	12,768	13,949									
Solyc01g102540	hpoxia-induced protein 242						IPR035192 (PFAM): PF11715 (PFAM)	38,214	36,920	37,497	34,737	35,171									
Solyc01g102550	Nuclear pore complex protein Nup160 (AHRD V3.3 *-* A0A0B2S403_GLYSO),Pfam:PF11715		F:GO:0005515	F:protein binding			PF11715 (PFAM): IPR021717 (PANTH	13,170	10,446	11,177	11,994	11,385									
Solyc01g102570	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *** M1BJV6_SOLTU)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			SM00753 (SMART): IPR000717 (SMA	73,992	74,820	62,456	58,744	63,525									
Solyc01g102580	endo-1,4-beta-glucanase (Cel3)	cel3	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001701 (PFAM): IPR012341 (G3D	135,002	109,396	149,148	169,284	184,583									
Solyc01g102585	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *** M1BJV6_SOLTU)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			IPR000717 (SMART): SM00753 (SMA	15,339	15,708	20,302	21,389	20,169									
Solyc01g102590	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *-* M1BJV6_SOLTU)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			SM00753 (SMART): IPR000717 (SMA	0,466	0,509	0,496	0,460	0,449									
Solyc01g102610	Ferric reduction oxidase 7 (AHRD V3.3 *** W9RRH7_9ROSA)		C:GO:0016020; F:G(	C:membrane; F:oxidoreductase activity; P:oxidation-reduction p			IPR000778 (PRINTS): IPR013112 (PF	61,065	31,390	59,083	53,775	78,719	-0,932	0,038	0,410	0,035			down	up	
Solyc01g102620	Beta oxoacyl-ACP reductase (AHRD V3.3 --* Q9SPC4_BRANA)							0,276	0,496	0,468	0,509	0,307									
Solyc01g102630	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatchec				0,119	0,112	0,050	0,022	0,046									
Solyc01g102633	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		P:GO:0006259; F:G(	P:DNA metabolic process; F:organic cyclic compound binding; F:heterocyclic compound binding				0,057	0,098	0,000	0,025	0,046									
Solyc01g102637	SERINE CARBOXYPEPTIDASE-LIKE 49 (AHRD V3.3 --* AT3G10410.1)							0,061	0,000	0,000	0,025	0,000									
Solyc01g102640	LOW QUALITY:Nuclear pore complex protein Nup98-Nup96 (AHRD V3.3 *-* A0A1D1YSD9_9ARAE)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural con:			IPR007230 (PFAM): IPR036903 (G3D	2,151	2,835	0,936	1,297	1,227									
Solyc01g102650	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G60930.3)							1,491	2,067	0,738	0,970	1,342									
Solyc01g102660	Glutathione S-transferase (AHRD V3.3 *** A5YRT3_CAPAN)	GSTZ2	F:GO:0003824; F:G(	F:catalytic activity; F:protein binding; C:cytoplasm; P:aromatic a			G3DSA:3.40.30.10 (GENE3D): G3DS/	243,820	184,024	500,288	481,954	478,367									
Solyc01g102670	DNA glycosylase (AHRD V3.3 *** A0A118K0P9_CYNCS)		F:GO:0003824; P:G(	F:catalytic activity; P:DNA repair			G3DSA:1.10.340.30 (GENE3D): mobic	11,530	9,067	8,716	10,102	8,675									
Solyc01g102675	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* Q8GY50_ARATH)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR032675 (G3DSA:3.80.10.GENE3D	0,075	0,039	0,044	0,050	0,069									
Solyc01g102680	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* Q8GY50_ARATH)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR032675 (G3DSA:3.80.10.GENE3D	0,180	0,122	0,022	0,050	0,118									
Solyc01g102685	Protein kinase-like protein (AHRD V3.3 *-* A0A0K9NJI5_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,297	0,417	0,245	0,217	0,071									
Solyc01g102690	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IBN2_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	2,308	2,751	1,488	1,364	1,513									
Solyc01g102700	Protein kinase-like protein (AHRD V3.3 *** A0A0K9NJI5_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001245 (PF	34,913	64,431	15,415	31,352	26,722			0,789	0,023	1,023	0,000		up	up
Solyc01g102720	SRPBCC ligand-binding domain superfamily protein		F:GO:0008289	F:lipid binding			IPR002913 (PFAM): IPR023393 (G3D	1,134	0,862	0,025	0,098	0,093									
Solyc01g102730	Cinnamoyl-CoA reductase family protein (AHRD V3.3 *** U5GHC7_POPTR)	CCR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	5,776	8,116	8,567	8,116	8,039									
Solyc01g102740	NAC domain-containing protein, putative (AHRD V3.3 *** B9S056_RICCO)	NAC005	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,122	0,103	0,361	0,174	0,190									
Solyc01g102750	alfin1-like PHD domain-containing protein		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR001965 (SMART): IPR021998 (PF	36,395	32,965	77,788	74,363	59,522									
Solyc01g102760	PHD finger alfin-like protein (AHRD V3.3 *** A0A072UTR5_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR001965 (SMART): IPR019787 (PF	38,664	37,522	49,100	47,954	44,736									
Solyc01g102770	Photosystem II reaction center protein Z (AHRD V3.3 *** PSBZ_SOLBU)		C:GO:0009539; P:G(	C:photosystem II reaction center; P:photosystem II stabilization			IPR036512 (G3DSA:1.10.287.GENE3	0,774	0,872	1,001	1,044	0,994									
Solyc01g102800	Histidyl-tRNA synthetase (AHRD V3.3 *** A0A072VJI1_MEDTR)		F:GO:0004821; F:G(	F:histidine-tRNA liga	EC:6.1.1.21	Histidine--tRNA ligase	G3DSA:3.30.930.10 (GENE3D): IPR0(	44,405	42,692	70,091	71,283	66,958									
Solyc01g102810	DNA polymerase III subunit gamma/tau (AHRD V3.3 *** A0A0B0MH18_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA po	IPR012763 (TIGRFAM): PF13177 (PF	21,720	19,316	4,557	3,970	5,167									
Solyc01g102820	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (AHRD V3.3 *** A9ZN09_H	CMS	P:GO:0008299; F:G(	P:isoprenoid biosyn	EC:2.7.7.6	2-C-methyl-D-erythrit	IPR029044 (G3DSA:3.90.550.GENE3	12,575	19,669	10,592	9,738	13,288	0,672	0,014					up		
Solyc01g102830	NADH dehydrogenase (ubiquinone)s (AHRD V3.3 *** AT1G14450.2)		C:GO:0005747; P:G(	C:mitochondrial respiratory chain complex I; P:electron transpor			IPR012576 (PFAM): IPR012576 (PAN	51,032	52,635	64,510	58,411	63,213									
Solyc01g102840	TIR-NBS-LRR class disease resistance protein (AHRD V3.3 *** A2I7Q5_9ROSI)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	123,755	48,920	25,344	105,623	57,245	-1,315	0,000	1,172	0,000	2,059	0,000	down	up	up
Solyc01g102850	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.2)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	0,021	0,153	0,000	0,022	0,000									
Solyc01g102860	golgin family A protein (AHRD V3.3 *-* AT1G51080.1)		C:GO:0009536	C:plastid			IPR024530 (PFAM): mobidb-lite (MOB	0,019	0,126	0,000	0,022	0,047									
Solyc01g102870	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGJ7_ARATH)		F:GO:0005515	F:protein binding			IPR003591 (SMART): G3DSA:3.30.14	0,498	0,876	0,575	0,685	0,821									
Solyc01g102875	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	0,021	0,119	0,091	0,047	0,071									
Solyc01g102880	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *-* AT5G36930.2)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR003591 (SMA	15,916	26,821	11,481	13,334	14,392	0,777	0,006					up		
Solyc01g102890	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	0,000	0,021	0,047	0,169	0,071									
Solyc01g102900	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	0,000	0,018	0,000	0,000	0,000									
Solyc01g102910	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SN	0,021	0,019	0,072	0,120	0,024									
Solyc01g102925	disease resistance protein (TIR-NBS-LRR class) family protein (AHRD V3.3 --* AT4G09435.2)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,019	0,000	0,000	0,000									
Solyc01g102940	methionine S-methyltransferase (AHRD V3.3 *** AT5G49810.1)		F:GO:0008168; P:G(	F:methyltransferase activity; P:biosynthetic process; F:pyridoxa			IPR015421 (G3DSA:3.40.640.GENE3	22,197	28,536	17,723	23,539	22,090									
Solyc01g102950	Lycopene beta/epsilon cyclase (AHRD V3.3 *** A0A072TS21_MEDTR)		C:GO:0009507	C:chloroplast			IPR036188 (G3DSA:3.50.50.GENE3D	1,556	3,242	1,985	1,398	4,996			1,317	0,000				up	
Solyc01g102960	Heat-shock protein, putative (AHRD V3.3 *** B9S5K5_RICCO)	Hsp21.6A	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;			IPR008978 (G3DSA:2.60.40.GENE3D	152,699	97,074	1358,930	1409,702	1508,246									
Solyc01g102970	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G47620.5)		F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; P:RNA processing			IPR000504 (SMART): IPR003107 (SN	62,753	59,275	49,106	45,460	47,932									
Solyc01g102980	ZF-HD homeobox protein family (AHRD V3.3 *** A0A151SB96_CAJCA)		F:GO:0003677	F:DNA binding			IPR006456 (PFAM ZF-HD	0,176	0,249	0,000	0,000	0,024									
Solyc01g102990	ATP-dependent clp protease ATP-binding subunit clpx, putative (AHRD V3.3 *** B9SPA4_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR003593 (SMART): IPR019489 (SN	27,492	19,614	29,963	28,009	27,935									
Solyc01g103000	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 --* A0A0B2PBN5_GLYSO)							6,112	3,793	7,513	8,327	6,529									
Solyc01g103010	Cullin-associated NEDD8-dissociated protein 1 (AHRD V3.3 *** CAND1_ARATH)		P:GO:0010265	P:SCF complex assembly			IPR011989 (G3DSA:1.25.10.GENE3D	140,122	119,898	150,071	153,401	149,026									
Solyc01g103020	Survival of motor neuron-related-splicing factor 30 (AHRD V3.3 *** W9RZU2_9ROSA)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; C:cytoplasm; P:mRNA processing			IPR002999 (SMART): IPR010304 (PF	43,829	46,699	48,932	44,668	45,925									
Solyc01g103030	Major facilitator superfamily protein (AHRD V3.3 *** AT1G59740.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	0,163	0,955	0,394	1,478	1,013									
Solyc01g103040	Mitotic spindle assembly checkpoint protein MAD1 (AHRD V3.3 *** A0A0B2P2M0_GLYSO)		P:GO:0007094	P:mitotic spindle assembly checkpoint			G3DSA:3.30.457.60 (GENE3D): IPR0(	20,361	18,293	11,077	10,328	10,741									
Solyc01g103050	Auxin Response Factor 1	ARF1	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF ARF	130,652	159,180	67,995	63,596	66,501									
Solyc01g103060	Lipid transfer protein (AHRD V3.3 *** A0A072UG85_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SN	0,019	0,039	0,000	0,097	0,141									
Solyc01g103080	ATP-dependent RNA helicase family protein (AHRD V3.3 *** B9N0I2_POPTR)		F:GO:0003723; F:G(	F:RNA binding; F:RI	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART): IPR014001 (SN	119,315	90,517	86,710	88,397	79,518									
Solyc01g103090	Zinc finger transcription factor 14	C3H14	P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:RNA binding; F:metal ion b			IPR009145 (PRINTS): IPR000571 (SN	30,565	31,281	27,351	23,885	26,062									
Solyc01g103100	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G10310.1)		C:GO:0005829; P:G(	C:cytosol; P:folic acid-containing compound metabolic process;			IPR002347 (PRINTS): IPR002347 (PF	13,155	14,964	13,801	11,724	13,523									
Solyc01g103110	Acyl-CoA N-acyltransferase (AHRD V3.3 *** A0A118K6R4_CYNCS)						IPR007434 (PFAM): G3DSA:3.40.630	9,635	11,592	17,073	17,462	19,128									
Solyc01g103120	Dynamin family protein (AHRD V3.3 *-* B9N0H6_POPTR)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR011993 (G3DSA:2.30.29.GENE3D	2,388	1,959	1,225	1,196	1,107									
Solyc01g103130	Dynamin (AHRD V3.3 *** A0A103XDG1_CYNCS)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR001401 (SN	2,529	1,960	0,807	0,559	0,566									
Solyc01g103140	Chloride channel protein (AHRD V3.3 *** Q40485_TOBAC)		F:GO:0005247; P:G(	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR002251 (PRINTS): IPR001807 (PF	169,871	97,934	282,225	242,813	245,390	-0,767	0,001					down		
Solyc01g103150	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT1G10280.1)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): mobidb-lite (MOB	12,731	9,327	16,508	17,871	18,244									
Solyc01g103160	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YL86_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	23,772	21,096	22,868	20,868	21,227									
Solyc01g103170	lysine ketoglutarate reductase trans-splicing-like protein, putative (DUF707) (AHRD V3.3 *** AT4G18530.3)		C:GO:0016021	C:integral component of membrane			IPR007877 (PFAM): PTHR31210:SF3	28,787	25,552	36,043	34,796	42,813									
Solyc01g103180	FAR1-related sequence 11 (AHRD V3.3 *** AT1G10240.2)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	11,496	10,589	13,084	12,502	12,637									
Solyc01g103185	Cytochrome c oxidase biogenesis protein Cmc1-like protein (AHRD V3.3 *-* AT4G21192.2)		C:GO:0016021	C:integral component of membrane			IPR013892 (PFAM): PTHR34116 (PAN	3,319	3,347	4,425	3,878	3,983									
Solyc01g103190	Cytochrome c oxidase biogenesis protein Cmc1-like protein (AHRD V3.3 *** AT4G21192.2)		C:GO:0005739	C:mitochondrion			IPR013892 (PFAM): IPR013892 (PAN	1,504	1,122	1,397	1,604	1,463									
Solyc01g103200	plasminogen activator inhibitor (AHRD V3.3 *** AT1G57680.3)		C:GO:0016021	C:integral component of membrane			PTHR34116 (PANTHER): PTHR34116	26,537	14,023	16,284	22,997	22,142	-0,891	0,000			0,496	0,032	down		up
Solyc01g103220	Cytochrome c (AHRD V3.3 *** CYC_SOLTU)		F:GO:0009055; F:G(	F:electron transfer activity; F:heme binding			IPR002327 (PRINTS): IPR009056 (PF	151,654	192,756	235,598	221,999	223,823									
Solyc01g103230	Non-lysosomal glucosylceramidase (AHRD V3.3 *** K4B1P9_SOLLC)		F:GO:0004348; P:G(	F:glucosylceramida	EC:3.2.1.45	Glucosylceramidase	IPR012341 (G3DSA:1.50.10.GENE3D	62,343	49,967	24,522	19,048	22,263									
Solyc01g103240	MAP kinase kinase kinase 9	MAPKKK9	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,521	0,884	0,025	0,072	0,046									

Solyc01g103245	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *** W9SKR1_9ROSA)		F:GO:0003677; F:G	F:DNA binding; F:protein binding			IPR019835 (SMART); IPR004343 (SM	0,103	0,106	0,000	0,050	0,000									
Solyc01g103250	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *** W9SKR1_9ROSA)		F:GO:0003677; F:G	F:DNA binding; F:protein binding			IPR004343 (SMART); IPR001965 (SM	17,129	15,022	4,596	3,708	4,907									
Solyc01g103260	LOW QUALITY:F-box/RNI superfamily protein (AHRD V3.3 --* AT1G52650.1)							0,000	0,039	0,000	0,000	0,000									
Solyc01g103275	glutamate receptor 3.4 (AHRD V3.3 --* AT1G05200.7)							0,632	0,727	0,451	0,650	0,448									
Solyc01g103290	NOD26-like intrinsic protein 4-2 (AHRD V3.3 --* AT5G37820.2)						PS51257 (PROSITE_PROFILES)	0,730	0,304	0,466	0,380	0,495									
Solyc01g103295	Gamma-tubulin complex component (AHRD V3.3 --* A0A0R0EVX4_SOYBN)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,596	0,386	0,335	0,512	0,377									
Solyc01g103300	SWIB/MDM2 and Plus-3 and GYF domain-containing protein (AHRD V3.3 *-* AT5G08430.1)		F:GO:0003677; F:G	F:DNA binding; F:metal ion binding			mobidb-lite (MOBIDB_LITE); PTHR138	0,560	0,637	0,649	0,419	0,635									
Solyc01g103310	Binding protein, putative isoform 3 (AHRD V3.3 *-* A0A061DJC6_THECC)		F:GO:0003677; F:G	F:DNA binding; F:protein binding			IPR004343 (SMART); IPR003121 (PF	4,031	4,382	2,990	2,587	2,703									
Solyc01g103330	ATP synthase subunit beta, chloroplastic (AHRD V3.3 --* ATPB_ACUOB)							0,021	0,019	0,096	0,045	0,095									
Solyc01g103335	Binding protein, putative isoform 3 (AHRD V3.3 *** A0A061DJC6_THECC)		F:GO:0003677; F:G	F:DNA binding; F:protein binding			IPR004343 (SMART); IPR036128 (G3	7,772	7,805	9,053	11,296	8,368									
Solyc01g103340	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *-* W9SKR1_9ROSA)		F:GO:0003677	F:DNA binding			IPR004343 (PFAM); PTHR13844 (PAN	1,871	1,499	1,915	2,713	2,239									
Solyc01g103350	Protein kinase superfamily protein (AHRD V3.3 *** AT1G09600.1)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	34,556	30,359	44,710	48,225	41,162									
Solyc01g103360	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G09610.1)		P:GO:0045492	P:xylan biosynthetic process			IPR021148 (PFAM); IPR006514 (TIGF	0,197	0,119	0,000	0,000	0,000									
Solyc01g103370	small GTP-binding protein B	rab1b	F:GO:0003924; F:G	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00175 (SMAR	51,448	59,636	66,350	70,619	68,001									
Solyc01g103380	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)		F:GO:0003924; F:G	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00175 (SMAR	26,085	30,317	27,438	25,320	24,326									
Solyc01g103390	12-oxophytodienoate reductase 2	opr2	F:GO:0010181; F:G	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	2,439	2,970	0,639	0,695	0,982									
Solyc01g103400	transmembrane protein (AHRD V3.3 *** AT1G09645.1)		C:GO:0016021	C:integral component of membrane			PTHR33780:SF2 (PANTHER); PTHR3	3,145	2,719	2,281	2,079	2,149									
Solyc01g103410	KH domain-containing protein (AHRD V3.3 *** W9R1Z3_9ROSA)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR032377 (PF	125,209	106,817	115,511	111,296	108,328									
Solyc01g103415	Ribosomal protein S3 (AHRD V3.3 *-* E5DMB3_9ROSI)		C:GO:0043229; C:G	C:intracellular organelle; C:cytoplasmic part			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,025	0,000									
Solyc01g103420	Regulator of nonsense transcripts 3A (AHRD V3.3 *** A0A151T884_CAJCA)		P:GO:0000184; F:G	P:nuclear-transcribed mRNA catabolic process, nonsense-medi			IPR012677 (G3DSA:3.30.70.GENE3D	71,809	66,405	96,365	97,326	88,744									
Solyc01g103430	Protein kinase (AHRD V3.3 *** Q1SL21_MEDTR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	172,968	165,045	78,032	64,664	80,743									
Solyc01g103440	Phosphoribosylamine-glycine ligase (AHRD V3.3 *** G7K3Z1_MEDTR)		F:GO:0004637; F:G	F:phosphoribosylan	EC:6.3.4.13	Phosphoribosylamine	IPR020560 (SMART); SM01209 (SMA	18,297	22,146	50,809	46,864	45,432									
Solyc01g103450	Heat shock protein 70 (AHRD V3.3 *** Q39641_CUCSA)		F:GO:0005524; P:G	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR013126 (PRINTS); IPR029048 (G3	598,610	673,493	745,001	709,382	811,360									
Solyc01g103457	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *-* Q9FKL3_ARATH)		F:GO:0005515	F:protein binding			IPR000270 (SMART); G3DSA:3.10.20	0,699	0,992	0,122	0,173	0,211									
Solyc01g103460	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHU8_9ROSA)		F:GO:0003676; P:G	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR002562 (SMART); IPR002562 (PF	10,963	11,448	8,896	8,698	8,494									
Solyc01g103470	Cytosolic Fe-S cluster assembly factor nar-1 (AHRD V3.3 *** A0A1D1Z971_9ARAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,088	6,085	0,706	0,445	0,351									
Solyc01g103480	Coatomer subunit delta (AHRD V3.3 *** W9SBM6_9ROSA)		P:GO:0006890; C:G	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			IPR028565 (PFAM); G3DSA:2.60.40.1	200,326	194,665	185,318	175,174	169,911									
Solyc01g103490	MACPF domain-containing protein (AHRD V3.3 *** A0A0B2S5Z8_GLYSO)		C:GO:0005886; P:G	C:plasma membrane; P:plant-type hypersensitive response			IPR020864 (SMART); IPR020864 (PF	12,727	14,925	7,827	8,143	8,137									
Solyc01g103500	Multidrug resistance 3 (AHRD V3.3 *** A0A0B0MAA3_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,430	1,790	0,876	0,682	1,126									
Solyc01g103510	60S ribosomal protein L3 (AHRD V3.3 *** W9S5Y9_9ROSA)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000597 (PFAM); G3DSA:4.10.960	22,812	34,580	32,145	32,439	25,850	0,627	0,022					up		
Solyc01g103530	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4B1S8_SOLLC)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART); IPR000719 (SM	6,180	4,969	1,810	1,327	1,625									
Solyc01g103540	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *-* AT3G13460.4)		F:GO:0003723	F:RNA binding			G3DSA:3.10.590.10 (GENE3D); IPR0	1758,046	1514,591	1578,592	1548,854	1566,531									
Solyc01g103550	LOW QUALITY:Transcription factor, MADS-box (AHRD V3.3 *-* A0A103XMZ4_CYNCS)		F:GO:0000981; F:G	F:DNA-binding transcription factor activity, RNA polymerase II-s			IPR002100 (PRIN M-type_MADS	0,019	0,041	0,000	0,000	0,024									
Solyc01g103560	tRNA pseudouridine synthase (AHRD V3.3 *** K4B1T1_SOLLC)		P:GO:0001522; F:G	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR020095 (G3DSA:3.30.70.GENE3D	10,571	8,637	6,754	7,853	8,112									
Solyc01g103570	Bromodomain-containing factor 2 (AHRD V3.3 *** W9QKA6_9ROSA)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS); IPR001487 (SM	11,482	9,883	6,404	7,631	7,645									
Solyc01g103580	transmembrane protein, putative (DUF679) (AHRD V3.3 *** AT4G24310.1)		P:GO:0010256; C:G	P:endomembrane system organization; C:integral component of			IPR007770 (PFAM); mobidb-lite (MOB	3,957	2,790	3,049	6,502	4,039					1,080	0,002			up
Solyc01g103590	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DWL3_THECC)		F:GO:0016740	F:transferase activity			IPR029068 (G3DSA:3.10.180.GENE3	4,102	8,935	1,900	2,529	2,186	1,152	0,003					up		
Solyc01g103600	Jasmonate ZIM-domain protein 4 (AHRD V3.3 *** T1WMV9_TOBAC)						IPR010399 (SMART); IPR010399 (PF	1,084	1,153	0,865	1,214	0,685									
Solyc01g103605	FBD, F-box and Leucine Rich Repeat domains containing protein (AHRD V3.3 --* AT3G49030.2)							0,445	0,472	0,224	0,344	0,451									
Solyc01g103610	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	5,804	3,512	3,687	4,776	4,972									
Solyc01g103620	Bile acid:sodium symporter (AHRD V3.3 *** A0A103Y361_CYNCS)		C:GO:0016020	C:membrane			IPR038770 (G3DSA:1.20.1530.GENE	5,955	5,310	4,480	5,495	5,188									
Solyc01g103630	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DWL3_THECC)		F:GO:0016740	F:transferase activity			IPR029068 (G3DSA:3.10.180.GENE3	0,040	0,043	0,000	0,000	0,000									
Solyc01g103640	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT4G24320.1)						IPR021099 (PFAM); PTHR31476 (PAN	2,882	3,494	2,690	2,659	2,421									
Solyc01g103650	Embryogenesis-associated EMB8 (AHRD V3.3 *** A0A0B0MZB5_GOSAR)		C:GO:0016021; P:G	C:integral component of membrane; P:cellular lipid metabolic pro			IPR012020 (PIRSF); IPR022742 (PFA	5,127	19,079	5,415	7,697	14,386	1,922	0,000					up		
Solyc01g103660	Embryogenesis-associated EMB8 (AHRD V3.3 *** A0A0B0MZB5_GOSAR)		C:GO:0016021; P:G	C:integral component of membrane; P:cellular lipid metabolic pro			IPR012020 (PIRSF); IPR022742 (PFA	1,746	1,737	0,756	0,440	0,372									
Solyc01g103670	alpha_beta hydrolase fold-1 domain-containing protein		C:GO:0016021; P:G	C:integral component of membrane; P:cellular lipid metabolic pro			IPR022742 (PFAM); IPR029058 (G3D	30,271	22,773	45,418	40,493	43,066									
Solyc01g103680	TSA: Wollemia nobilis Ref_Wollemi_Transcript_7455_2019 transcribed RNA sequence (AHRD V3.3 *** A0A		F:GO:0005509; C:G	F:calcium ion binding; C:endoplasmic reticulum; C:integral comp			IPR012879 (PFAM); mobidb-lite (MOB	166,691	164,161	278,928	254,226	261,308									
Solyc01g103690	ATP-dependent RNA helicase (AHRD V3.3 *-* A0A072V3N4_MEDTR)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART); IPR007502 (SM	17,600	20,170	21,990	22,628	21,802									
Solyc01g103695	ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9SSN0_RICCO)		F:GO:0003723; F:G	F:RNA binding; F:A	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); mobic	24,643	21,372	26,205	30,379	30,060									
Solyc01g103700	WEB family protein (AHRD V3.3 *** A0A0B2SMF5_GLYSO)		P:GO:0009902	P:chloroplast relocation			PTHR32054 (PANTHER); PTHR32054	1,937	2,276	4,732	6,162	4,567									
Solyc01g103710	NIFU-like protein 2 (AHRD V3.3 *** AT5G49940.1)		F:GO:0005506; P:G	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl			IPR034904 (G3DSA:3.30.300.GENE3	22,626	25,162	64,008	67,490	66,066									
Solyc01g103720	Ribosome biogenesis protein BOP1 homolog (AHRD V3.3 *** M1CBT7_SOLTU)		F:GO:0005515; P:G	F:protein binding; P:rRNA processing			IPR001680 (SMART); IPR012953 (SM	138,208	130,742	121,371	115,067	107,894									
Solyc01g103750	ATP phosphoribosyltransferase (AHRD V3.3 *** W9QK95_9ROSA)		P:GO:0000105; F:G	P:histidine biosynth	EC:2.4.2.17	ATP phosphoribosylt	G3DSA:3.40.190.10 (GENE3D); IPR0	54,618	72,241	52,024	48,563	60,934									
Solyc01g103760	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM); mobidb-lite (MOB	16,327	17,739	10,899	11,914	11,164									
Solyc01g103770	Cyclin-C1-1 (AHRD V3.3 --* A0A0K9NU96_ZOSMR)							0,493	0,405	0,427	0,682	0,426									
Solyc01g103780	TCP transcription factor 11	TCP11					IPR017887 (PFAM TCP	62,973	61,161	60,797	69,909	68,375									
Solyc01g103785	Kinase family protein (AHRD V3.3 *** A0A0K9NK70_ZOSMR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	0,960	0,687	0,629	0,679	0,517									
Solyc01g103790	Kinase family protein (AHRD V3.3 *-* A0A0K9NK70_ZOSMR)		F:GO:0004674; F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D); PTHR	0,059	0,036	0,115	0,050	0,000									
Solyc01g103800	40S ribosomal protein S12 (AHRD V3.3 *** K4B1V5_SOLLC)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000530 (PRINTS); IPR004038 (PF	202,692	203,132	112,358	100,663	104,535									
Solyc01g103803	ZF-HD homeobox protein (AHRD V3.3 *** A0A0B2PBF3_GLYSO)		F:GO:0005488	F:binding			G3DSA:1.10.10.60 (GENE3D); IPR00	0,000	0,043	0,000	0,000	0,000									
Solyc01g103850	Ubiquitin-like domain-containing CTD phosphatase (AHRD V3.3 *** W9S7C7_9ROSA)		F:GO:0004721; F:G	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threor	IPR000626 (SMART); IPR004274 (SM	18,590	15,722	20,037	18,871	18,438									
Solyc01g103862	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 *** AT1G58110.2)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			G3DSA:1.20.5.170 (GENE3D); mobidb	13,037	24,955	9,953	7,178	10,114									
Solyc01g103866	COBRA-like protein (AHRD V3.3 *** L0AST8_POPTO)		P:GO:0010215; P:G	P:cellulose microfibril organization; P:cell growth; C:anchored co			IPR006918 (PFAM); IPR006918 (PIRS	0,042	0,018	0,075	0,050	0,000									
Solyc01g103868	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 *** AT1G58110.2)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			G3DSA:1.20.5.170 (GENE3D); mobidb	3,191	3,667	4,458	4,045	4,122									
Solyc01g103890	Magnesium transporter MRS2-like protein (AHRD V3.3 *** G7L8U0_MEDTR)		C:GO:0016020; P:G	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR002523 (PFAM); G3DSA:2.40.128	61,721	67,874	75,227	73,868	72,518									
Solyc01g103900	Phospholipase D (AHRD V3.3 *-* M0ZZP4_SOLTU)		F:GO:0003824	F:catalytic activity			IPR001736 (SMART); G3DSA:3.30.87	0,000	0,000	0,000	0,025	0,024									
Solyc01g103910	Phospholipase D (AHRD V3.3 *** M0ZZP4_SOLTU)		F:GO:0004630; F:G	F:phospholipase D	EC:3.1.4.4	Phospholipase D	IPR000008 (SMART); IPR035892 (G3	0,000	0,000	0,025	0,075	0,023									
Solyc01g103920	Ferredoxin (AHRD V3.3 *** A0A0K0PY61_NICBE)		F:GO:0009055; P:G	F:electron transfer activity; P:electron transport chain; F:2 iron,			IPR001041 (PFAM); IPR012675 (G3D	46,331	51,486	94,428	86,768	153,039			0,694	0,040				up	
Solyc01g103930	Transmembrane 9 superfamily member (AHRD V3.3 *** K4B1W8_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM); PTHR10766:SF8	92,863	87,115	58,407	54,169	56,479									
Solyc01g103940	Kinase family protein (AHRD V3.3 *** B9N888_POPTR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	164,405	153,559	94,033	81,323	86,656									
Solyc01g103945	RNA polymerase II transcription mediator (AHRD V3.3 --* A0A097PNY8_9ROSI)							0,406	0,401	0,218	0,125	0,284									
Solyc01g103950	Thiamine biosynthesis bifunctional ThiED (AHRD V3.3 *-* A0A0B0PE51_GOSAR)		F:GO:0004789; F:G	F:thiamine-phospha	EC:2.7.4.7; EC:2.5.1	Phosphooxymethylpy	IPR022998 (PFAM); IPR013749 (PFA	23,793	25,965	24,494	20,424	23,280									
Solyc01g103960	RNA helicase DEAH-box15	DEAH5	F:GO:0003676; F:G	F:nucleic acid bindi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR001650 (SMART); IPR018982 (SM	12,774	10,171	3,928	3,285	4,542									
Solyc01g103970	RING finger protein (AHRD V3.3 *** A0A0B0MBG4_GOSAR)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR038896 (PANTHER); PTHR22894:	45,796	40,179	50,908	76,107	55,885					0,583	0,000			up
Solyc01g103990	T-complex protein 11 (AHRD V3.3 *** U5GGZ4_POPTR)						IPR008862 (PFAM); mobidb-lite (MOB	276,005	189,199	662,060	650,624	587,170									
Solyc01g104000	Serine hydroxymethyltransferase (AHRD V3.3 *** K4B1X5_SOLLC)		F:GO:0004372; P:G	F:glycine hydroxym	EC:2.1.2.1	Glycine hydroxymeth	IPR015421 (G3DSA:3.40.640.GENE3	54,874	54,400	94,710	107,501	87,553									
Solyc01g104010	LOW QUALITY:BPS1-like protein (AHRD V3.3 *** AT1G22030.1)		C:GO:0016021	C:integral component of membrane			PTHR31509:SF2 (PANTHER); PTHR3	0,155	0,037	0,000	0,025	0,164									
Solyc01g104015	Embryo-specific 3 (AHRD V3.3 *** Q2HUA9_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:2.60.60.20 (GENE3D); IPR01	14,954	12,787	18,163	15,643	16,741									
Solyc01g104030	Potassium channel (AHRD V3.3 *** Q9SSV3_NICPA)		F:GO:0005249; F:G	F:voltage-gated potassium channel activity; F:protein binding; P			IPR002110 (PRINTS); IPR003938 (PF	104,402	80,525	88,948	77,871	90,393									
Solyc01g104040	UDP-glucose glycoprotein glucosyltransferase (AHRD V3.3 *** A0A0G2RIE9_CAMSI)		F:GO:0003980; P:G	F:UDP-glucose:glycoprotein glucosyltransferase activity; P:prot			PF18401 (PFAM); PF18403 (PFAM); F	95,916	97,367	94,513	101,774	105,672									
Solyc01g104050	Kinase family protein (AHRD V3.3 *** B9H3C5_POPTR)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART); IPR006222 (PF	15,498	17,910	13,638	12,675	12,114									
Solyc01g104055	Aminomethyltransferase (AHRD V3.3 *-* A0A151UBV7_CAJCA)		F:GO:0005515	F:protein binding			IPR027266 (G3DSA:3.30.1360.GENE	0,021	0,021	0,000	0,000	0,000									
Solyc01g104060	Aminomethyltransferase (AHRD V3.3 *** A0A151UBV7_CAJCA)		F:GO:0005515	F:protein binding			IPR006222 (PFAM); IPR028896 (PIRS	5,003	7,243	14,042	13,575	14,022									
Solyc01g104070	ARM repeat superfamily protein (AHRD V3.3 *** AT4G27640.1)		P:GO:0006606; F:G	P:protein import into nucleus; F:Ran GTPase binding			IPR001494 (SMART); IPR001494 (PF	80,504	71,570	61,921	57,543	55,522									
Solyc01g104080	Alkaline phytoceramidase (APHC) (AHRD V3.3 *** B7FKE9_MEDTR)		P:GO:0006672; C:G	P:ceramide metabolic process; C:integral component of membra			PTHR34368:SF1 (PANTHER); PTHR3	42,598	45,613	56,118	66,655	57,759									
Solyc01g104090	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YKX6_CYNCS)		F:GO:0005515; F:G	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM); IPR011990 ((	0,837	0,891	1,321	1,054	1,015									
Solyc01g104100	11S globulin seed storage protein 2 (AHRD V3.3 *** A0A0B2RJF9_GLYSO)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS); IPR006045 (SM	0,000	0,041	0,069	0,000	0,000									
Solyc01g104110	11S globulin seed storage protein 2 (AHRD V3.3 *** A0A0B2RJF9_GLYSO)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS); IPR006045 (SM	0,159	0,164	5,619	3,813	2,365			-1,248	0,003				down	
Solyc01g104130	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein (AHRD V3.3 *** G5DX62_SILLA)		F:GO:0016491; P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR027450 (PFAM); IPR037151 (G3D	43,456	17,077	200,098	187,449	167,394	-1,322	0,000					down		
Solyc01g104140	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 *** AT1G60890.1)		F:GO:0005524; F:G	F:ATP binding; F:1-	EC:2.7.1.68	1-phosphatidylinosito	IPR002498 (SMART); IPR003409 (SM	54,240	46,988	93,270	90,976	86,490									
Solyc01g104150	LOW QUALITY:calcium ion-binding protein (AHRD V3.3 --* AT4G37445.1)							0,000	0,060	0,025	0,025	0,000									
Solyc01g104160	arginine/glutamate-rich 1 protein (AHRD V3.3 *** AT1G10890.2)						IPR033371 (PFAM); mobidb-lite (MOB	63,621	59,724	67,413	68,100	65,149									
Solyc01g104170	Ankyrin repeat domain containing protein 2 (AHRD V3.3 *** A0A0A7EAV4_NICBE)		F:GO:0005515	F:protein binding			IPR002110 (SMART); IPR020683 (PF	372,107	387,078	391,957	342,971	400,930									
Solyc01g104180	LOW QUALITY:GNS1/SUR4 membrane protein family (AHRD V3.3 *** AT3G06470.1)		C:GO:0016021	C:integral component of membrane			IPR002076 (PFAM); IPR002076 (PAN	0,000	0,000	0,121	0,100	0,023									
Solyc01g104185	Fatty acyl-CoA reductase (AHRD V3.3 *** K4B1Z5_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			G3DSA:3.40.50.720 (GENE3D); IPR0	0,000	0,000	0,025	0,025	0,000									
Solyc01g104210	GNS1/SUR4 membrane protein family (AHRD V3.3 *** AT3G06470.1)		C:GO:0016021	C:integral component of membrane			IPR002076 (PFAM); PTHR11157:SF1	0,099	0,222	278,251	466,319	313,336					0,749	0,000			up
Solyc01g104220	Transmembrane emp24 domain-containing protein 10 (AHRD V3.3 *** A0A151UBU4_CAJCA)		C:GO:0005789; C:G	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR009038 (SMART); IPR009038 (PF	47,171	39,837	64,911	57,595	55,791									
Solyc01g104230	F-box protein (AHRD V3.3 *** A0A0B2RMW5_GLYSO)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,275	0,303	0,049	0,025	0,000									
Solyc01g104240	Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *** A0A061DX06_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	31,147	14,294	14,768	24,019	19,492	-1,097	0,000			0,700	0,001	down		up
Solyc01g104250	Rhomboid-like protein (AHRD V3.3 *** K4B200_SOLLC)		F:GO:0004252; C:G	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM); IPR035952 (G3D	21,551	18,418	41,196	43,388	39,575									
Solyc01g104260	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DY55_THECC)		F:GO:0016874	F:ligase activity			IPR001841 (SMART); IPR001841 (PF	1,219	1,572	2,813	2,126	2,573									
Solyc01g104270	plant/protein, putative (DUF3411) (AHRD V3.3 *-* AT5G24690.1)		C:GO:0005739; C:G	C:mitochondrion; C:chloroplast inner membrane			IPR021825 (PFAM); mobidb-lite (MOB	46,255	53,310	103,785	97,917	104,242									
Solyc01g104280	GNS1/SUR4 membrane protein (AHRD V3.3 *** A0A103XMP3_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR002076 (PFAM); IPR002076 (PAN	4,443	4,592	7,561	6,761	8,228									
Solyc01g104290	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7K8X4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS); IPR001938 (SM	0,101	0,135	0,276	0,196	0,141									
Solyc01g104300	DUF639 family protein (AHRD V3.3 *** G7IJX0_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR006927 (PFAM); mobidb-lite (MOB	18,453	15,047	33,267	32,633	31,084									
Solyc01g104310	Patatin (AHRD V3.3 *** K4B206_SOLLC)		P:GO:0016042; F:G	P:lipid catabolic process; F:hydrolase activity			IPR002641 (PFAM); G3DSA:3.40.109	38,910	30,663	56,794	51,084	51,044									
Solyc01g104320	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *-* A0A061DXD4_THECC)						IPR006843 (PFAM); PTHR31906:SF1	26,094	32,096	33,801	36,493	37,749									
Solyc01g104340	green ripe	GR	C:GO:0016021	C:integral component of membrane			IPR008496 (PFAM); mobidb-lite (MOB	2,258	2,801	0,480	0,734	0,589									
Solyc01g104345	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT3G47030.1)							0,040	0,076	0,000	0,022	0,023									
Solyc01g104350	Elongation factor 4 (AHRD V3.3 *** A0A0B0NVN0_GOSAR)						PTHR34057 (PANTHER); PTHR34057	10,961	11,370	15,382	18,261	15,470									
Solyc01g104355	Cytochrome c oxidase subunit 1 (AHRD V3.3 --* A0A0H3WI66_9MAGN)						PS51257 (PROSITE_PROFILES)	0,077	0,019	0,000	0,075	0,000									
Solyc01g104370	60S acidic ribosomal protein P1 (AHRD V3.3 *** A0A199VEQ5_ANACO)		P:GO:0002181; F:G	P:cytoplasmic translation; F:structural constituent of ribosome;			PF00428 (PFAM); IPR038716 (G3DSA	122,990	144,653	123,957	121,788	118,797									
Solyc01g104380	Basic blue protein (AHRD V3.3 *** A0A151R4Q3_CAJCA)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	1,929	5,069	0,000	0,000	0,000									
Solyc01g104400	Basic blue protein (AHRD V3.3 *** A0A151R520_CAJCA)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	1,552	2,899	0,187	0,072	0,000									
Solyc01g104410	Sterol glucosyltransferase-like protein (AHRD V3.3 *** A0A072V719_MEDTR)		F:GO:0016740	F:transferase activity			G3DSA:3.40.50.2000 (GENE3D); G3D	9,657	8,878	12,626	12,230	13,364									
Solyc01g104413	Pre-mRNA-processing-splicing factor (AHRD V3.3 --* AT1G80070.1)							1,481	1,586	1,707	1,846	1,679									
Solyc01g104417	LOW QUALITY:GATA transcription factor-like protein (AHRD V3.3 *-* A0A0X7YHI0_SOLTU)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMART); IPR013088 (G3	0,396	0,312	0,601	0,480	0,500									
Solyc01g104420	LOW QUALITY:guanosine nucleotide diphosphate dissociation inhibitor 1 (AHRD V3.3 --* AT2G44100.1)							0,254	0,254	0,194	0,239	0,474									
Solyc01g104430	Nuclear pore complex protein Nup98b (AHRD V3.3 *-* W6JLG1_NICBE)		C:GO:0005643; P:G	C:nuclear pore; P:nucleocytoplasmic transport; F:structural constituent of nuclear pore				4,557	4,057	4,613	5,511	5,226									
Solyc01g104431	Di-glucose binding protein with Kinesin motor domain-containing protein (AHRD V3.3 --* AT2G22610.3)							0,261	0,655	0,122	0,173	0,167									
Solyc01g104432	Thioredoxin reductase (AHRD V3.3 --* C5XZX5_SORBI)		C:GO:0005643; P:G	C:nuclear pore; P:nucleocytoplasmic transport; F:structural constituent of nuclear pore				92,750	109,220	51,568	72,246	78,228			0,598	0,005	0,488	0,031		up	up
Solyc01g104433	Pentatricopeptide repeat-containing protein (AHRD V3.3 --* D7MPU5_ARALL)							2,692	4,973	1,064	1,143	2,279			1,094	0,017				up	
Solyc01g104434	Thioredoxin reductase (AHRD V3.3 --* I1GYQ0_BRADI)							10,640	21,737	7,116	8,507	9,877	1,053	0,025					up		
Solyc01g104435	Outer envelope protein 64, mitochondrial (AHRD V3.3 --* OE64M_ARATH)						mobidb-lite (MOBIDB_LITE)	2,037	1,893	1,177	1,205	1,346									
Solyc01g104436	MATH domain and coiled-coil domain-containing protein At3g58400 (AHRD V3.3 --* MCC28_ARATH)							1,198	1,086	0,941	0,896	1,101									
Solyc01g104437	gibberellin 2-oxidase 7 (AHRD V3.3 --* AT1G50960.1)							0,240	0,269	0,246	0,411	0,423									
Solyc01g104438	LOW QUALITY:GATA transcription factor-like protein (AHRD V3.3 *** A0A0X7YHI0_SOLTU)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMART); IPR013088 (G3	0,234	0,275	0,236	0,366	0,282									
Solyc01g104440	Copine (Calcium-dependent phospholipid-binding protein) family (AHRD V3.3 --* AT5G63970.2)							0,000	0,000	0,000	0,025	0,000									
Solyc01g104442	Ca2+ activated outward rectifying K+ channel 3 (AHRD V3.3 --* AT5G46360.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,855	0,813	0,782	1,080	1,180									
Solyc01g104444	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (AHRD V3.3 --* M4CKM4_BRARP)							1,065	0,606	0,807	1,040	0,940									
Solyc01g104446	GATA transcription factor-like protein (AHRD V3.3 *** A0A0X7YHI0_SOLTU)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMART); IPR013088 (G3	0,038	0,021	0,000	0,048	0,000									
Solyc01g104448	LOW QUALITY:GATA transcription factor-like protein (AHRD V3.3 *-* A0A0X7YHI0_SOLTU)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (PFAM); mobidb-lite (MOB	0,000	0,000	0,025	0,025	0,000									
Solyc01g104460	partner of Y14-MAGO (AHRD V3.3 *** AT1G11400.6)		P:GO:1903259	P:exon-exon junction complex disassembly			IPR015362 (SMART); IPR015362 (PF	17,560	18,295	23,095	20,169	18,711									
Solyc01g104470	Acidic ribosomal protein P0 (AHRD V3.3 *** B9I0W5_POPTR)		P:GO:0000027; C:G	P:ribosomal large subunit assembly; C:intracellular			PF17777 (PFAM); G3DSA:3.90.105.2	156,736	148,568	90,953	94,771	90,870									
Solyc01g104480	C-jun-amino-terminal kinase-interacting protein 3, putative (AHRD V3.3 *** A0A061FHN5_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	49,143	67,126	48,929	51,396	49,407									
Solyc01g104490	Separase, putative (AHRD V3.3 *** B9SSN4_RICCO)		C:GO:0005634; P:G	C:nucleus; P:proteolysis; F:peptidase activity			PF03568 (PFAM); mobidb-lite (MOBID	4,917	5,398	1,565	1,272	1,153									
Solyc01g104500	zinc finger/BTB domain protein, putative (DUF1644) (AHRD V3.3 *** AT1G68140.2)		C:GO:0016021	C:integral component of membrane			IPR012866 (PFAM); mobidb-lite (MOB	31,484	30,832	148,720	133,886	110,694									
Solyc01g104510	WD-40 repeat protein	msi1	F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	41,109	41,978	46,040	42,424	40,950									
Solyc01g104520	At3g54630 (AHRD V3.3 *-* A4FVQ9_ARATH)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,139	0,116	0,068	0,000	0,047									
Solyc01g104525	Kinetochore protein Ndc80 (AHRD V3.3 *-* A0A103Y3D6_CYNCS)							0,656	0,970	1,115	0,644	0,734									
Solyc01g104530	MAP kinase kinase kinase 10	MAPKKK10	F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	79,364	98,661	86,246	88,667	88,685									

Solyc01g104540	C-jun-amino-terminal kinase-interacting protein 3, putative (AHRD V3.3 *** A0A061FHN5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	37,553	38,826	57,474	58,925	55,847									
Solyc01g104550	WRKY transcription factor 9	WRKY9	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,000	0,021	0,000	0,000	0,000									
Solyc01g104560	Protein-protein interaction regulator (AHRD V3.3 *** B9GF79_POPTR)		C:GO:0035145; C:G(	C:exon-exon junction complex; C:catalytic step 2 spliceosome			IPR006786 (PFAM): mobidb-lite (MOB	105,964	108,010	85,634	83,990	85,761									
Solyc01g104570	Kinetochore protein Ndc80 (AHRD V3.3 *** A0A103Y3D6_CYNCS)						IPR038273 (G3DSA:1.10.418.GENE3	10,165	8,300	4,642	3,247	4,731									
Solyc01g104580	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G01080.1)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	11,652	9,294	6,373	4,568	5,505									
Solyc01g104590	ribosomal protein L3	rpl3	F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000597 (PFAM): G3DSA:4.10.960	807,962	821,016	609,181	515,215	558,108									
Solyc01g104600	COP9 signalosome complex subunit 8 (AHRD V3.3 *** A0A1D1XKQ8_9ARAE)		P:GO:0000338; C:G(	P:protein deneddylation; C:COP9 signalosome; P:COP9 signalc			IPR033464 (PFAM): G3DSA:1.25.40.9	15,005	15,114	24,111	25,990	23,371									
Solyc01g104620	Class II aaRS and biotin synthetases superfamily protein (AHRD V3.3 --* AT3G62120.3)							2,206	0,938	9,685	7,639	6,472	-1,205	0,038					down		
Solyc01g104630	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GM92_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,905	9,639	9,063	8,813	7,480									
Solyc01g104640	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G15570.3)		F:GO:0003723; F:G(	F:RNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): PF13	41,257	36,126	35,612	25,113	32,184					-0,501	0,001			down
Solyc01g104650	Transcription factor (AHRD V3.3 *-* D6MJX4_9ASPA)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	21,303	25,206	229,184	140,912	141,331			-0,701	0,000	-0,697	0,000		down	down
Solyc01g104660	Plant/F1M20-13 protein (AHRD V3.3 *** A0A072UZK1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR008511 (PFAM): mobidb-lite (MOB	42,507	33,551	123,815	126,758	105,599									
Solyc01g104670	Tubby-like F-box protein (AHRD V3.3 *** K4B241_SOLLC)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS): IPR001810 (PF	115,816	107,659	84,060	97,941	90,045									
Solyc01g104680	Ran protein/TC4 protein ran2a	ran2a						7,977	8,596	14,348	12,967	10,543									
Solyc01g104685	GTP-binding nuclear protein (AHRD V3.3 *** Q38JH1_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002041 (PRINTS): SM00173 (SMA	250,181	237,573	337,297	285,701	297,746									
Solyc01g104700	Ran protein/TC4 protein ran2b	ran2b	F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	124,680	126,383	194,460	184,934	175,719									
Solyc01g104710	thionin-like protein (AHRD V3.3 -** AT1G25275.2)						PTHR37183 (PANTHER)	18,749	20,511	13,681	13,907	18,433									
Solyc01g104720	thionin-like protein (AHRD V3.3 -** AT1G25275.1)						PTHR37183 (PANTHER)	501,952	369,032	811,288	770,169	712,452									
Solyc01g104725	organic solute transporter ostalpha protein (DUF300) (AHRD V3.3 --* AT4G21570.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				3,998	4,358	3,227	4,087	3,502									
Solyc01g104730	organic solute transporter ostalpha protein (DUF300) (AHRD V3.3 *-* AT1G11200.1)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): PTHR23423:SF1	9,104	5,132	10,551	12,062	9,678	-0,794	0,037					down		
Solyc01g104750	WAT1-related protein (AHRD V3.3 *** K4B247_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	0,354	0,325	0,188	0,269	0,283									
Solyc01g104770	transcription factor (AHRD V3.3 *** AT1G76870.3)	Actina					G3DSA:1.10.10.60 (GENE3D): PF138	2,807	3,221	0,982	1,031	1,292									
Solyc01g104775	Actin (AHRD V3.3 *** ACT_GOSHI)		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): IPR004000 (SM	203,498	226,930	180,380	151,695	155,143									
Solyc01g104780	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061DXK2_THECC)		F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ior			IPR008217 (PFAM): PTHR31851:SF6	2,266	3,841	1,950	0,922	1,919									
Solyc01g104790	NADPH-dependent 7-cyano-7-deazaguanine reductase (AHRD V3.3 *-* A0A1D1YW23_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	12,727	12,024	13,629	11,778	12,834									
Solyc01g104795	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 --* AT5G22140.1)						IPR007110 (PROSITE_PROFILES)	0,063	0,021	0,050	0,025	0,023									
Solyc01g104820	Vacuolar iron transporter family protein (AHRD V3.3 *-* A0A061FJ80_THECC)		F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ior			IPR008217 (PFAM): IPR008217 (PAN	0,000	0,043	0,000	0,000	0,024									
Solyc01g104830	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061G788_THECC)		P:GO:0000041; F:G(	P:transition metal ion transport; F:iron ion transmembrane trans			IPR008217 (PFAM): mobidb-lite (MOB	0,019	0,000	0,000	0,000	0,000									
Solyc01g104840	Glycine-rich RNA-binding protein (AHRD V3.3 *-* A0A0B0N033_GOSAR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR000504 (SMART): IPR000504 (PF	165,543	160,594	143,898	125,414	131,081									
Solyc01g104850	Carboxypeptidase (AHRD V3.3 *** K4B257_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	37,368	25,659	6,319	9,122	10,984			0,791	0,037				up	
Solyc01g104860	Peroxidase (AHRD V3.3 *** K4B258_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	10,419	6,524	0,243	0,170	0,360									
Solyc01g104870	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT1G03050.1)		F:GO:0005545; C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART): IPR008942 (G3	0,205	0,221	0,051	0,025	0,072									
Solyc01g104880	Phosphatidylserine decarboxylase proenzyme 2 (AHRD V3.3 *** K4B260_SOLLC)		F:GO:0004609; F:G(	F:phosphatidylserin	EC:4.1.1.65	Phosphatidylserine d	IPR002048 (SMART): IPR002048 (PF	28,757	39,778	24,859	21,853	23,742									
Solyc01g104890	Ribosomal L29 family protein (AHRD V3.3 --* AT5G02610.2)							8,664	5,881	9,751	7,202	8,827									
Solyc01g104900	NAC domain protein, (AHRD V3.3 *** A0A061E1M1_THECC)	NAC006	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	3,007	3,482	0,534	0,730	0,447									
Solyc01g104910	Loricrin-like protein (AHRD V3.3 *** A0A072UZF2_MEDTR)						PTHR31827:SF33 (PANTHER): PTHR	194,722	107,336	243,119	207,586	202,487	-0,831	0,008					down		
Solyc01g104915	Two pore calcium channel protein 1 (AHRD V3.3 --* TPC1_WHEAT)							0,137	0,503	0,410	0,371	0,493									
Solyc01g104920	AAA-type ATPase family protein (AHRD V3.3 *** AT4G04910.1)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:1.10.8.6	176,761	245,621	110,502	114,160	112,094									
Solyc01g104930	26S protease regulatory subunit (AHRD V3.3 --* A0A0K9P0X4_ZOSMR)		F:GO:0016887; P:G(	F:ATPase activity; I	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): PTHF	0,819	1,070	0,561	0,754	0,659									
Solyc01g104935	Vesicle-fusing ATPase family protein (AHRD V3.3 *-* B9H2U6_POPTR)		F:GO:0016887; P:G(	F:ATPase activity; I	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR23078:SF11 (PANTHER): IPR03	0,040	0,083	0,047	0,000	0,000									
Solyc01g104940	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** S1RTT0_THECC)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	0,059	0,037	0,000	0,025	0,023									
Solyc01g104950	LEXYL2	xyl2	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR026891 (SM	64,568	60,187	17,935	36,783	35,443			0,979	0,000	1,038	0,001		up	up
Solyc01g104970	Receptor-like kinase (AHRD V3.3 *** A0A0K9PIY0_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:signaling receptor binding; F:ATP bir			IPR000719 (SMART): IPR032675 (G3	9,392	22,164	6,593	8,805	9,741	1,266	0,000					up		
Solyc01g104980	F-box/kelch-repeat protein (AHRD V3.3 *** W9S379_9ROSA)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR001810 (SM	2,956	2,361	3,082	2,617	3,533									
Solyc01g104990	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *** AT1G30550.2)		P:GO:0001510; F:G(	P:RNA methylation; F:methyltransferase activity; P:7-methylgua			IPR019012 (PFAM): G3DSA:3.40.50.1	2,631	1,629	1,823	1,646	1,624									
Solyc01g105000	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G02600.2)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	0,019	0,000	0,000	0,000	0,000									
Solyc01g105010	Lipid transfer protein (AHRD V3.3 *** G7KE52_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	17,826	17,544	10,718	11,027	10,779									
Solyc01g105020	Protein phosphatase 2C family protein (AHRD V3.3 *-* AT4G33500.1)		F:GO:0003824	F:catalytic activity			IPR001932 (SMART): IPR036457 (G3	17,581	25,374	16,579	20,320	28,834			0,793	0,000				up	
Solyc01g105040	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT3G58520.1)						IPR021099 (PFAM): mobidb-lite (MOB	4,945	4,624	7,613	7,618	7,351									
Solyc01g105050	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1AY18_SOLTU)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	101,048	251,094	60,141	65,500	142,079	1,342	0,001	1,236	0,000			up	up	
Solyc01g105060	Beta-hydroxyacyl-ACP dehydratase (AHRD V3.3 *** F2VYC9_HELAN)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:hydro-lyase activity			IPR013114 (PFAM): G3DSA:3.10.129	0,158	0,000	0,209	0,504	0,308									
Solyc01g105070	LECEVI16G peroxidase precursor	cevi16	F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	5,902	7,387	4,083	5,094	5,497									
Solyc01g105080	LOW QUALITY:Leucine-rich repeat protein kinase family protein, putative (AHRD V3.3 *** A0A061E1I7_THE		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,042	0,039	0,050	0,025	0,000									
Solyc01g105090	CRS1 / YhbY (CRM) domain-containing protein (AHRD V3.3 *** A0A0K9PB57_ZOSMR)		F:GO:0003723	F:RNA binding			IPR001890 (SMART): IPR035920 (G3	17,720	13,260	12,317	12,835	12,302									
Solyc01g105100	Endoplasmic reticulum vesicle transporter protein (AHRD V3.3 *** AT1G36050.2)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:endoplasmic reticulum to Golgi vesi			IPR012936 (PFAM): IPR039542 (PFA	59,471	63,023	84,212	85,911	80,557									
Solyc01g105120	Dentin sialophosphoprotein-related, putative isoform 3 (AHRD V3.3 *** A0A061E394_THECC)		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:circadian rhythm			mobidb-lite (MOBIDB_LITE): mobidb-lit	242,348	209,653	202,392	250,393	246,310									
Solyc01g105130	Dbj:BAA96220.1 (AHRD V3.3 *** A0A061E1G9_THECC)						G3DSA:1.20.1600.10 (GENE3D): PTH	14,060	15,031	13,896	13,124	12,663									
Solyc01g105140	Serine/arginine rich splicing factor, putative (AHRD V3.3 *** B9SZR9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR003954 (SMART): IPR000504 (SM	107,667	98,408	154,573	140,413	141,880									
Solyc01g105150	Potassium transporter (AHRD V3.3 *** M1AY13_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): IPR003855 (TIGF	24,410	27,781	28,502	28,551	28,685									
Solyc01g105160	P-type ATP-ase 1 (AHRD V3.3 *** AT4G33520.2)		F:GO:0000166; F:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): G3DSA:2.70.150	22,366	23,037	20,792	22,774	24,002									
Solyc01g105165	Cation-transporting P-type ATPase (AHRD V3.3 *-* A0A103Y3F8_CYNCS)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	35,301	41,310	59,172	54,857	63,028									
Solyc01g105180	Protein DA1-related 1 (AHRD V3.3 *** A0A199UXH9_ANACO)		F:GO:0043130	F:ubiquitin binding			IPR022087 (PFAM): PTHR24209:SF1	2,885	8,215	1,196	1,678	1,716	1,533	0,000					up		
Solyc01g105190	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT1G79540.1)							0,101	0,160	0,121	0,139	0,332									
Solyc01g105220	alternative oxidase 2	aox1a	F:GO:0009916; P:G(	F:alternative oxidas	EC:1.1.3	Acting on diphenols a	IPR002680 (PIRSF): IPR038659 (G3D	2,761	2,736	3,460	3,478	3,589									
Solyc01g105225	Protein DA1-related 1 (AHRD V3.3 *** DAR1_ARATH)		F:GO:0043130	F:ubiquitin binding			IPR022087 (PFAM): PTHR24209:SF1	0,100	0,039	0,050	0,098	0,024									
Solyc01g105230	Calmodulin-binding transcription activator (AHRD V3.3 *** Q8S389_BRANA)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR005559 (SMAF CAMTA	85,136	109,948	83,466	87,991	84,518									
Solyc01g105240	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9SZ50_RICCO)		P:GO:0016579; F:G(	P:protein deubiquitii	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM): G3DSA:3.90.70.1	10,920	9,890	17,501	18,613	16,816									
Solyc01g105270	LeTH2tobamovirus multiplication 1 homolog 2	th2	C:GO:0009705; C:G(	C:plant-type vacuole membrane; C:integral component of memb			IPR009457 (PFAM): IPR040226 (PAN	8,020	7,845	10,414	11,807	11,432									
Solyc01g105280	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G34750.3)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	28,014	44,598	42,867	47,228	45,975									
Solyc01g105290	1,8-cineole synthase (AHRD V3.3 *** AT5G64230.1)		C:GO:0016021	C:integral component of membrane			PTHR31060:SF4 (PANTHER): IPR038	45,419	47,369	25,975	27,782	28,450									
Solyc01g105300	Metacaspase-1 (AHRD V3.3 *-* A0A0B2R4L3_GLYSO)		F:GO:0016787	F:hydrolase activity			G3DSA:3.40.50.12660 (GENE3D): PF	1,417	2,287	0,782	1,050	0,608									
Solyc01g105310	metacaspase 2,Pfam:PF00656		F:GO:0016787	F:hydrolase activity			PF00656 (PFAM): G3DSA:3.40.50.12(	1,484	0,992	3,832	3,232	5,225									
Solyc01g105320	Metacaspase 1, putative (AHRD V3.3 *** A0A061E359_THECC),Pfam:PF00656		F:GO:0004197; P:G(	F:cysteine-type enc	EC:3.4.22	Acting on peptide bor	IPR005735 (TIGRFAM): PF00656 (PF	1,459	1,009	3,070	3,113	3,072									
Solyc01g105330	Methyl-CpG-binding domain-containing protein 8 (AHRD V3.3 *-* A0A199UGF7_ANACO)		F:GO:0003677	F:DNA binding			IPR013087 (SMART): G3DSA:3.30.16	17,097	13,888	21,704	21,507	21,286									
Solyc01g105340	Chaperone protein DnaJ (AHRD V3.3 *** W9QNE7_9ROSA)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS): IPR001623 (SM	606,333	557,723	988,557	875,131	926,208									
Solyc01g105350	Glycosyltransferase (AHRD V3.3 *** K4B2A5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	1,629	2,205	3,478	4,888	3,933									
Solyc01g105360	Glycosyltransferase (AHRD V3.3 *** M1AXT7_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	2,326	7,502	2,158	1,770	4,540	1,712	0,001					up		
Solyc01g105370	Phospho-2-dehydro-3-deoxyheptonate aldolase (AHRD V3.3 *-* K4B2A9_SOLLC)		F:GO:0003849; F:G(	F:3-deoxy-7-phospl	EC:3.6.1.3; EC:1.13.	Adenosinetriphospha	IPR004136 (PFAM): IPR003439 (PFA	8,981	16,522	51,724	83,135	87,750	0,907	0,043	0,759	0,000	0,688	0,002	up	up	up
Solyc01g105390	Phospho-2-dehydro-3-deoxyheptonate aldolase (AHRD V3.3 *** K4B2A9_SOLLC)		F:GO:0003849; P:G(	F:3-deoxy-7-phospl	EC:2.5.1.54	3-deoxy-7-phosphoh	IPR013785 (G3DSA:3.20.20.GENE3D	3,269	4,415	8,600	6,978	8,865									
Solyc01g105410	Phosphate-induced protein 1 (AHRD V3.3 *** A0A103YKN4_CYNCS)						IPR006766 (PFAM): IPR006766 (PAN	167,536	195,705	45,625	63,574	69,061									
Solyc01g105420	Phospho-2-dehydro-3-deoxyheptonate aldolase (AHRD V3.3 *-* M1AXT4_SOLTU)		F:GO:0003849; P:G(	F:3-deoxy-7-phospl	EC:2.5.1.54	3-deoxy-7-phosphoh	IPR013785 (G3DSA:3.20.20.GENE3D	22,744	28,991	59,412	56,292	66,004									
Solyc01g105430	abscisic aldehyde oxidase 3 (AHRD V3.3 --* AT2G27150.6)							0,213	0,138	0,097	0,170	0,071									
Solyc01g105435	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)		F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF	0,788	1,212	0,511	0,318	0,419									
Solyc01g105440	LOW QUALITY:Cytochrome b6-f complex iron-sulfur subunit, chloroplastic (AHRD V3.3 --* UCRIA_WHEAT)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,274	0,142	0,050	0,075	0,094									
Solyc01g105450	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	ABCG3	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	1,851	6,012	0,849	0,936	1,683	1,720	0,010					up		
Solyc01g105460	1,4-dihydroxy-2-naphthoate polyprenyltransferase (AHRD V3.3 *** A0A0K9PHB6_Z ABC4		F:GO:0004659; C:G(	F:prenyltransferase activity; C:integral component of membrane			IPR026046 (PIRSF): IPR000537 (PFA	4,411	4,942	7,263	7,647	9,373									
Solyc01g105470	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT1G63880.2)							0,180	0,101	0,121	0,048	0,047									
Solyc01g105480	TBP-associated factor 4B (AHRD V3.3 --* AT1G27720.9)							0,037	0,019	0,050	0,022	0,047									
Solyc01g105490	myosin 2 (AHRD V3.3 --* AT5G43900.3)							0,282	0,447	0,267	0,147	0,303									
Solyc01g105493	Integrase-type DNA-binding superfamily protein (AHRD V3.3 --* AT5G13910.1)							0,697	0,761	0,987	0,631	0,655									
Solyc01g105495	HYPERSENSITIVE TO PI STARVATION 4 (AHRD V3.3 --* AT1G58250.2)							6,365	4,994	3,799	3,937	4,380									
Solyc01g105497	ureide permease 2 (AHRD V3.3 --* AT2G03530.5)							3,726	2,190	2,536	2,972	2,211									
Solyc01g105500	Endo-1,4-beta-xylanase (AHRD V3.3 *** A0A151U7N8_CAJCA)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001000 (SMART): IPR001000 (PF	8,328	6,392	0,025	0,395	0,191									
Solyc01g105510	LMBR1-like membrane protein (AHRD V3.3 *** AT5G65290.1)		C:GO:0016021	C:integral component of membrane			IPR006876 (PFAM): mobidb-lite (MOB	25,924	18,464	17,385	15,256	17,191									
Solyc01g105520	DNA helicase (AHRD V3.3 *** I1Q0P7_ORYGL)		F:GO:0003677; F:G(	F:DNA binding; F:ATP binding; P:DNA replication initiation			IPR001208 (PRINTS): IPR003593 (SM	8,958	7,284	3,903	3,498	4,450									
Solyc01g105530	DNA helicase (AHRD V3.3 *-* A0A0A9SCZ0_ARUDO)		F:GO:0003677; F:G(	F:DNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	IPR031327 (PANTHER): PTHR11630:	3,761	2,552	3,313	2,775	2,753									
Solyc01g105540	2-oxoglutarate/malate translocator, chloroplastic (AHRD V3.3 *** A0A0B0P714_GOSAR)		F:GO:0005215; P:G(	F:transporter activity; P:sodium ion transport; C:membrane; P:tr			IPR001898 (PFAM): IPR001898 (TIGF	22,284	27,596	25,686	26,306	29,371									
Solyc01g105545	2-oxoglutarate/malate translocator, chloroplastic (AHRD V3.3 *-* A0A0B0P714_GOSAR)		F:GO:0005215; P:G(	F:transporter activity; P:sodium ion transport; C:membrane; P:tr			IPR001898 (PFAM): mobidb-lite (MOB	13,201	14,592	13,456	14,142	13,868									
Solyc01g105550	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc01g105560	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase	riba	F:GO:0003935; F:G(	F:GTP cyclohydrola	EC:3.5.4.25; EC:4.1.	GTP cyclohydrolase	IPR000422 (PFAM): IPR036144 (G3D	172,429	270,063	135,519	169,136	158,446									
Solyc01g105570	U2 small nuclear ribonucleoprotein auxiliary factor-like protein (AHRD V3.3 *-* AT5G64010.1)		P:GO:0009414; P:G(	P:response to water deprivation; P:stomatal closure			PTHR35770 (PANTHER)	11,785	11,969	18,119	17,288	18,002									
Solyc01g105590	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	0,000	0,018	0,000	0,000	0,000									
Solyc01g105600	Phage capsid scaffolding protein (GPO) serine peptidase (AHRD V3.3 --* G7KAI6_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33735 (PANTHER): PTHR33735	0,561	0,631	1,559	2,429	1,435									
Solyc01g105605	sodium hydrogen exchanger 5 (AHRD V3.3 --* AT1G54370.1)							0,000	0,000	0,065	0,025	0,000									
Solyc01g105610	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E293_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination			IPR001841 (SMART): IPR013083 (G3	0,000	0,096	0,000	0,050	0,073									
Solyc01g105620	RING/U-box superfamily protein, putative (AHRD V3.3 *-* A0A061E293_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination			IPR001841 (SMART): IPR013083 (G3	1,878	2,731	4,798	6,121	6,119									
Solyc01g105630	Calmodulin, putative (AHRD V3.3 *** B9S4P7_RICCO)		F:GO:0005509	F:calcium ion binding			PR00450 (PRINTS): IPR002048 (SMA	0,675	1,838	0,438	0,249	0,353									
Solyc01g105650	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,690	3,897	0,068	0,025	0,073	2,503	0,000					up		
Solyc01g105660	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	359,466	275,775	972,787	877,876	870,253									
Solyc01g105670	Calcium-dependent protein kinase (AHRD V3.3 *** G3M0D5_HEVBR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	37,743	29,195	56,299	50,828	51,153									
Solyc01g105680	Phototropic-responsive NPH3 family protein (AHRD V3.3 *-* AT5G64330.2)		P:GO:0016567	P:protein ubiquitination			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,451	3,756	1,337	1,502	1,357									
Solyc01g105700	Conserved peptide upstream open reading frame 37 (AHRD V3.3 *** B3H738_ARATH)						PTHR35281 (PANTHER): PTHR35281	31,574	29,057	17,435	13,987	14,852									
Solyc01g105710	peptidyl-prolyl isomerase FKBP12		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer:	G3DSA:3.10.50.40 (GENE3D): IPR00	423,736	336,181	158,187	116,898	131,850					-0,433	0,007			down
Solyc01g105720	LOW QUALITY:Peptide upstream ORF protein (AHRD V3.3 *** G7J561_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33597 (PANTHER): PTHR33597	238,683	134,483	31,538	33,233	25,611									
Solyc01g105750	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072UVS4_MEDTR)						IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,021	0,075	0,022	0,024									
Solyc01g105760	LOW QUALITY:hydroxyproline-rich glycoprotein family protein (AHRD V3.3 -** AT5G09520.1)						mobidb-lite (MOBIDB_LITE): PTHR33(	0,019	0,000	0,000	0,025	0,000									
Solyc01g105770	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072UVS4_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,310	0,232	0,538	0,636	0,934									
Solyc01g105775	Carbonic anhydrase (AHRD V3.3 --* V7B641_PHAVU)							0,600	0,503	0,629	0,636	0,539									
Solyc01g105780	Chaperone DnaJ-domain protein (AHRD V3.3 *-* G7KBK7_MEDTR)						IPR001623 (SMART): IPR001623 (PF	43,496	45,032	46,202	40,550	42,425									
Solyc01g105790	abscisic acid responsive element-binding factor 1 (AHRD V3.3 --* AT1G49720.3)							0,000	0,039	0,000	0,000	0,000									
Solyc01g105800	MADS box transcription factor (AHRD V1 **-- Q2NNB9_ELAGV)%3B contains Interpro domain(s) IPR00210(		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	1,576	1,073	0,071	0,050	0,000									
Solyc01g105810	GDP dissociation inhibitor	gdi1	F:GO:0005093; P:G(	F:Rab GDP-dissociation inhibitor activity; P:small GTPase medi			IPR018203 (PRINTS): IPR000806 (PF	0,021	0,058	0,000	0,000	0,000									
Solyc01g105820	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_COF		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	20,330	24,115	22,796	21,598	24,359									
Solyc01g105823	Cysteine proteinases superfamily protein (AHRD V3.3 --* AT4G33620.1)		F:GO:0008233	F:peptidase activity			mobidb-lite (MOBIDB_LITE): PTHR453	0,218	0,287	0,280	0,197	0,304									
Solyc01g105827	Ulp1 protease family protein (AHRD V3.3 *-* B9HEB6_POPTR)		F:GO:0008233	F:peptidase activity			G3DSA:3.40.395.10 (GENE3D): PTHF	0,021	0,019	0,000	0,025	0,000									
Solyc01g105860	(R)-limonene synthase (AHRD V1 ***- B9T537_RICCO)%3B contains Interpro domain(s) IPR005630 Terpen		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,000	0,019	0,000	0,000	0,000									
Solyc01g105870	(E)-beta-ocimene synthase (AHRD V1 **** Q5CD81_CITUN)%3B contains Interpro domain(s) IPR005630 Te		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,059	0,000	0,000	0,000									
Solyc01g105880	Monoterpenoid synthase 2	MTS2	F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,413	1,458	0,051	0,025	0,140									
Solyc01g105890	Monoterpene synthase 1	MTS1	F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR036965 (G3D	0,155	1,015	0,240	0,117	0,166									
Solyc01g105920	(E)-beta-ocimene synthase		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,058	0,101	0,047	0,144	0,048									
Solyc01g105930	Beta-phellandrene synthase (AHRD V3.3 *-* Q1XBU4_SOLLC)		F:GO:0010333	F:terpene synthase activity			IPR001906 (PFAM): IPR036965 (G3D	0,000	0,041	0,000	0,000	0,023									
Solyc01g105940	Linalool synthase (AHRD V3.3 *-* Q1XBU5_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,019	0,147	0,247	0,167	0,213									
Solyc01g105950	Linalool synthase (AHRD V3.3 *-* Q1XBU5_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3	0,000	0,000	0,025	0,022	0,000									
Solyc01g105960	(E)-beta-ocimene synthase		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR005630 (PFA	0,021	0,000	0,000	0,000	0,024									
Solyc01g105970	Magnesium-dependent phosphatase 1 (AHRD V3.3 *** A0A0B0NEK9_GOSAR)		F:GO:0016791	F:phosphatase activity			IPR023214 (G3DSA:3.40.50.GENE3D	151,768	120,927	194,007	180,260	192,181									
Solyc01g105980	vacuole protein (AHRD V3.3 *** AT4G33625.1)		C:GO:0005774; C:G(	C:vacuolar membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	18,949	16,253	19,403	18,950	17,388									
Solyc01g105990	Protein EXECUTER 1, chloroplastic (AHRD V3.3 *** A0A0B0P9A3_GOSAR)		P:GO:0010343; C:G(	P:singlet oxygen-mediated programmed cell death; C:thylakoid r			IPR021894 (PFAM): mobidb-lite (MOB	52,965	43,909	70,816	73,380	75,216									
Solyc01g106000	nicotinamidase 1 (AHRD V3.3 *** AT2G22570.1)		F:GO:0003824	F:catalytic activity			IPR036380 (G3DSA:3.40.50.GENE3D	32,324	24,656	43,045	36,750	35,206									
Solyc01g106010	Fructose-1,6-bisphosphatase (AHRD V3.3 *** W0D846_CAMSI)		P:GO:0005975; F:G(	P:carbohydrate met	EC:3.1.3.23; EC:3.1.	Sugar-phosphatase;	IPR028343 (PRINTS): G3DSA:3.40.19	21,167	19,985	19,983	19,787	23,782									
Solyc01g106020	RNA-binding KH domain protein (AHRD V3.3 *** G7JV44_MEDTR)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR036612 (G3	17,410	24,990	17,736	15,352	20,091									
Solyc01g106030	GATA transcription factor, putative (AHRD V3.3 *** B9S9L8_RICCO)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:i			IPR010399 (SMAF GATA	25,214	21,868	38,863	35,643	36,025									

Solyc01g106040	GATA transcription factor, putative (AHRD V3.3 *** B9SN00_RICCO)		F:GO:0003700; F:GC	F:DNA-binding transcription factor activity; F:protein binding; P:r			IPR010399 (SMAF GATA	8,123	6,295	2,397	2,091	2,122									
Solyc01g106050	Dynamin, putative (AHRD V3.3 *** B9T3E4_RICCO)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS); IPR003130 (SM	21,198	21,099	23,605	26,891	26,757									
Solyc01g106055	Receptor-like kinase (AHRD V3.3 *** A0A072UI92_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); G3DS	7,769	7,977	9,288	7,645	8,924									
Solyc01g106060	Class I glutamine amidotransferase (AHRD V3.3 *** G7K286_MEDTR)		C:GO:0005829; P:GC	C:cytosol; P:glutamine metabolic process			IPR017926 (PFAM); IPR029062 (G3D	35,498	46,904	58,198	51,197	51,385									
Solyc01g106070	LOW QUALITY:HVA22-like protein (AHRD V3.3 *** M1AQ42_SOLTU)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR003604 (SMART); IPR013087 (SM	0,021	0,057	0,173	0,267	0,284									
Solyc01g106080	Aldehyde dehydrogenase (AHRD V3.3 *** Q2HV89_MEDTR)		F:GO:0004491; P:GC	F:methylmalonate-s	EC:1.2.1.27	Methylmalonate-semi	IPR016163 (G3DSA:3.40.309.GENE3	65,713	64,971	149,741	145,668	139,829									
Solyc01g106090	PsbP-domain protein 1 (AHRD V3.3 *** A0A0F7GZA5_9ROSI)		F:GO:0005509; C:GC	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR016123 (G3DSA:3.40.1000.GENE	7,079	8,204	30,099	34,522	32,200									
Solyc01g106105	LOW QUALITY:F-box family protein with a domain of Uncharacterized protein function, putative (AHRD V3.3		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR005174 (PFAM); PTHR33127:SF5	0,057	0,000	0,000	0,000	0,000									
Solyc01g106120	F-box protein PP2 (AHRD V3.3 *-* A0A059PC27_CICAR)						IPR025886 (PFAM); PTHR32278 (PAN	7,155	7,198	7,926	8,876	8,412									
Solyc01g106130	LOW QUALITY:F-box protein (AHRD V3.3 *** G7I272_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR005174 (PFAM); mobidb-lite (MOB	0,021	0,000	0,000	0,047	0,000									
Solyc01g106150	LOW QUALITY:Interferon-related developmental regulator family protein (AHRD V3.3 *** B9GNQ1_POPTR)						IPR011989 (G3DSA:1.25.10.GENE3D	0,452	0,574	0,296	0,507	0,236									
Solyc01g106160	Clade XVIII lectin receptor kinase (AHRD V3.3 *** K4B2I4_SOLLC)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	0,040	0,019	0,000	0,000	0,000									
Solyc01g106170	AGAMOUS-like MADS-box transcription factor (AHRD V3.3 *-* Q84LE8_GINBI)		F:GO:0000977; P:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN M-type_MADS	0,021	0,021	0,000	0,000	0,000									
Solyc01g106173	PDI-like 2-3 (AHRD V3.3 --* AT2G32920.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,566	0,498	0,962	1,486	0,826									
Solyc01g106175	myb domain protein 115 (AHRD V3.3 --* AT5G40360.1)							6,093	6,537	10,035	14,066	11,933					0,492	0,025			up
Solyc01g106177	MADS-box transcription factor (AHRD V3.3 *** G7IS85_MEDTR)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM); PTHR11945 (PAN	3,307	2,899	3,678	3,532	4,102									
Solyc01g106180	LOW QUALITY:CK25 (AHRD V3.3 *** Q1W1G0_TOBAC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,043	0,025	0,000	0,000									
Solyc01g106190	heat shock protein (AHRD V3.3 *** AT5G09580.1)						PTHR13734 (PANTHER); PTHR13734	7,548	5,980	7,848	9,059	7,598									
Solyc01g106195	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 --* AT2G37520.1)						mobidb-lite (MOBIDB_LITE)	0,902	0,764	1,019	0,769	0,828									
Solyc01g106200	Oligopeptide transporter, putative (AHRD V3.3 *** B9RX59_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (TIGRFAM); IPR004813 (F	1,859	1,053	1,522	1,436	1,747									
Solyc01g106205	myosin-M heavy protein (AHRD V3.3 --* AT3G54060.2)							0,258	0,094	0,212	0,100	0,216									
Solyc01g106210	Heat shock protein 70 (AHRD V3.3 *** B9HN74_POPTR)		F:GO:0005524; P:GC	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR013126 (PRINTS); G3DSA:3.30.42	158,755	150,168	251,364	228,272	226,634									
Solyc01g106230	B3 domain-containing protein (AHRD V3.3 *** W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,317	0,405	0,288	0,170	0,116									
Solyc01g106260	Heat shock protein 70 (AHRD V3.3 *** B9HN74_POPTR)		F:GO:0005524; P:GC	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR013126 (PRINTS); IPR012725 (TI(	53,519	59,888	75,203	69,230	64,970									
Solyc01g106270	LOW QUALITY:DNA polymerase V (AHRD V3.3 *-* A0A0B0NGE1_GOSAR)		F:GO:0003677; C:GC	F:DNA binding; C:nucleolus; C:cytosol; P:regulation of transcription, DNA-templated; F:transcription fact				0,000	0,021	0,000	0,000	0,000									
Solyc01g106280	PSTVd RNA-biding protein	Virp1	F:GO:0005515	F:protein binding			IPR001487 (PRINTS); IPR001487 (SM	502,851	472,583	299,448	580,946	419,232			0,482	0,026	0,959	0,000		up	up
Solyc01g106290	LOW QUALITY:Lipid binding protein (AHRD V3.3 --* B6TCG2_MAIZE)							37,908	23,434	12,068	30,111	22,555	-0,669	0,034	0,897	0,017	1,317	0,000	down	up	up
Solyc01g106300	cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 -** AT2G32210.1)		C:GO:0016021	C:integral component of membrane			IPR028144 (PFAM); PTHR31568:SF3	0,135	0,425	0,148	0,683	0,000									
Solyc01g106310	cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 -** AT2G32210.1)		C:GO:0016021	C:integral component of membrane			IPR028144 (PFAM); mobidb-lite (MOB	4,417	3,201	14,853	17,248	14,147									
Solyc01g106320	Octicosapeptide/Phox/Bem1p family protein (AHRD V3.3 *** AT5G64430.1)		F:GO:0005515	F:protein binding			IPR000270 (SMART); G3DSA:3.10.20	242,074	222,071	264,286	262,707	249,752									
Solyc01g106330	fatty acid amide hydrolase (AHRD V3.3 *** AT5G64440.1)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR036928 (G3DSA:3.90.1300.GENE	142,292	114,687	15,903	13,278	17,150									
Solyc01g106340	fatty acid amide hydrolase (AHRD V3.3 *** AT5G64440.1)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR023631 (PFAM); IPR036928 (G3D	16,503	15,250	2,037	2,418	2,041									
Solyc01g106350	fatty acid amide hydrolase (AHRD V3.3 *** AT5G64440.1)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR023631 (PFAM); IPR036928 (G3D	3,323	3,697	0,941	0,963	0,964									
Solyc01g106360	Fatty acid amide hydrolase (AHRD V3.3 *** A0A097PM41_SOLTU)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR023631 (PFAM); IPR036928 (G3D	129,615	114,480	145,643	129,882	137,659									
Solyc01g106370	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT5G64470.2)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	19,479	14,144	15,529	16,858	15,456									
Solyc01g106375	transcriptional factor B3 family protein (AHRD V3.3 --* AT1G26680.6)							1,853	2,563	2,467	2,983	3,109									
Solyc01g106390	Glutamyl-tRNA reductase (AHRD V3.3 *** K4B2K7_SOLLC)	HEMA/GluTR	F:GO:0008883; P:GC	F:glutamyl-tRNA rec	EC:1.2.1.7	Glutamyl-tRNA reduc	IPR006151 (PFAM); G3DSA:3.40.50.7	37,491	18,765	18,653	35,801	24,329	-0,974	0,012			0,943	0,000	down		up
Solyc01g106400	Methionine sulfoxide reductase, putative (AHRD V3.3 *** B9RX37_RICCO)		P:GO:0006979; P:GC	P:response to oxida	EC:1.8.4.12	Peptide-methionine (	IPR002579 (PFAM); IPR002579 (TIGF	0,299	0,389	0,071	0,097	0,259									
Solyc01g106420	Major facilitator superfamily protein (AHRD V3.3 *** AT2G22730.3)		C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM); mobidb-lite (MOB	6,866	6,972	7,412	8,856	7,675									
Solyc01g106430	Inorganic pyrophosphatase (AHRD V3.3 *** A0A124SF20_CYNCS)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:3.6.1.1	Inorganic diphosphat	IPR036649 (G3DSA:3.90.80.GENE3D	65,755	83,481	34,017	31,955	47,793			0,487	0,003				up	
Solyc01g106440	S-acyltransferase (AHRD V3.3 *** K4B2L2_SOLLC)		F:GO:0005515	F:protein binding			IPR002110 (SMART); IPR020683 (PF	17,683	14,059	18,102	18,082	18,046									
Solyc01g106460	bHLH transcription factor 007		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,000	0,120	0,000	0,000	0,000									
Solyc01g106470	Tunicamycin induced 1 (AHRD V3.3 *** A0A097PPU7_SOLLC)		F:GO:0003899; C:GC	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA pc	PTHR34454 (PANTHER); PTHR34454	17,751	16,911	38,111	41,489	38,981									
Solyc01g106480	glyoxisomal malate dehydrogenase	gmdh	P:GO:0005975; P:GC	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR015955 (G3DSA:3.90.110.GENE3	64,820	126,888	32,482	29,572	44,928	0,996	0,000	0,465	0,009			up	up	
Solyc01g106500	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT1G09970.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART); IPR032675 (G3	23,283	55,595	37,281	47,027	43,300	1,277	0,040					up		
Solyc01g106510	LOW QUALITY:F-box protein (AHRD V3.3 *** A0A1D1YUP5_9ARAE)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR005174 (PFAM); PTHR33127:SF5	0,019	0,132	0,000	0,045	0,000									
Solyc01g106540	neurofilament heavy protein (AHRD V3.3 *** AT4G17000.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,389	0,330	0,025	0,022	0,024									
Solyc01g106560	At4g33690-like protein (AHRD V3.3 *** A0A068F6W6_BRANA)		C:GO:0009507	C:chloroplast			mobidb-lite (MOBIDB_LITE); mobidb-lit	10,809	12,103	13,759	11,287	12,217									
Solyc01g106570	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2SPP5_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM); PTHR12064 (PAN	25,598	23,931	27,095	25,981	26,764									
Solyc01g106580	transmembrane protein (AHRD V3.3 *** AT5G65810.1)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D); PTHF	60,816	46,129	20,104	17,670	18,685									
Solyc01g106590	TRICHOME BIREFRINGENCE-LIKE 13 (AHRD V3.3 *** AT2G14530.1)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR029962 (PAN	8,290	8,188	6,213	6,252	6,146									
Solyc01g106600	Pathogenesis-related protein 1 (AHRD V3.3 *** E2GEU1_9ROSI)		C:GO:0005615	C:extracellular space			IPR001283 (PRINTS); IPR014044 (SM	0,021	0,000	0,098	0,000	0,023									
Solyc01g106610	LEPR1A1A	pr1a1	C:GO:0005615; P:GC	C:extracellular space; P:defense response; P:response to biotic			IPR002413 (PRINTS); IPR001283 (PF	0,000	0,000	1,663	0,616	0,401									
Solyc01g106650	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4B2N2_SOLLC)		F:GO:0004553; C:GC	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR016455 (PIRSF); G3DSA:2.60.120	0,101	0,082	0,000	0,047	0,000									
Solyc01g106680	Transmembrane protein, putative (AHRD V3.3 *** G8A0T5_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	83,755	75,839	70,339	61,061	63,751									
Solyc01g106690	DUF1005 family protein (AHRD V3.3 *** G7J413_MEDTR)						IPR010410 (PFAM); IPR010410 (PAN	101,677	61,583	40,310	109,766	67,467	-0,697	0,016	0,740	0,010	1,447	0,000	down	up	up
Solyc01g106700	Transcription factor, MADS-box (AHRD V3.3 *** A0A103YHS3_CYNCS)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN M-type_MADS	0,568	0,760	2,482	4,132	1,869									
Solyc01g106720	Transcription factor, MADS-box (AHRD V3.3 *** A0A103YIE3_CYNCS)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN M-type_MADS	0,000	0,018	0,000	0,000	0,000									
Solyc01g106740	Aspartate--tRNA ligase (AHRD V3.3 *** A0A0B2QN00_GLYSO)		F:GO:0003676; F:GC	F:nucleic acid binding; F:aminoacyl-tRNA ligase activity; F:ATP			IPR002312 (PRINTS); IPR004365 (PF	38,505	39,716	66,876	67,944	65,604									
Solyc01g106750	Transmembrane protein, putative (AHRD V3.3 *** G7JJ78_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,256	0,504	0,000	0,000	0,024									
Solyc01g106770	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0K0XR78_TOBAC)		F:GO:0004674; F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR024585 (SMART); IPR003152 (SM	153,895	104,864	153,351	163,870	158,677									
Solyc01g106780	Pyruvate kinase (AHRD V3.3 *** K4B2P5_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS); IPR001697 (TI(	31,511	34,627	21,444	21,998	21,425									
Solyc01g106790	Tubulin alpha-6 chain, putative (AHRD V3.3 *** A0A072VQC5_MEDTR)		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:integral component of men			mobidb-lite (MOBIDB_LITE); mobidb-lit	5,311	4,099	5,563	5,103	6,439									
Solyc01g106800	amino acid transporter 1	aap1	C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM); PTHR22950:SF2	4,687	4,125	2,859	3,694	3,304									
Solyc01g106805	Amino acid permease (AHRD V3.3 *** A0A0A0L0I6_CUCSA)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM); PTHR22950 (PAN	4,125	3,396	2,717	3,911	3,651									
Solyc01g106810	ATP phosphoribosyltransferase regulatory subunit (AHRD V3.3 *** AT4G33780.1)		P:GO:0009787; P:GC	P:regulation of abscisic acid-activated signaling pathway; P:nec			mobidb-lite (MOBIDB_LITE); PTHR354	4,203	2,917	3,998	4,093	4,342									
Solyc01g106820	Sterol regulatory element-binding protein site 2 protease, putative (AHRD V3.3 *** B9S7Z4_RICCO)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity; P:response to heat; P:respo			mobidb-lite (MOBIDB_LITE); mobidb-lit	28,643	23,163	87,091	105,987	107,388									
Solyc01g106830	Phytosulfokines 3 (AHRD V3.3 *** W9QZQ5_9ROSA)		C:GO:0005576; F:GC	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM); IPR009438 (PAN	0,103	0,054	0,025	0,221	0,118									
Solyc01g106860	Serine/threonine-protein kinase TOR (AHRD V3.3 *-* TOR_ARATH)		F:GO:0004674	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR026683 (PTHR11139:PANTHER);	0,256	0,098	0,119	0,197	0,047									
Solyc01g106870	Receptor-like kinase (AHRD V3.3 *** A0A072UI92_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); IPR0(	20,375	16,993	22,940	24,311	19,461									
Solyc01g106880	Ribosomal RNA small subunit methyltransferase E (AHRD V3.3 *** A0A0B2P1K7_GLYSO)		P:GO:0006364; F:GC	P:rRNA processing; F:methyltransferase activity			IPR006700 (PFAM); IPR029026 (G3D	6,244	8,445	21,389	20,572	18,459									
Solyc01g106900	Magnesium transporter MRS2-3 (AHRD V3.3 *** W9QFB3_9ROSA)		C:GO:0016020; P:GC	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:2.40.128.330 (GENE3D); IPR(	84,450	70,658	96,777	84,843	94,500									
Solyc01g106905	Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 --* AT3G09970.2)							0,237	0,304	0,050	0,048	0,072									
Solyc01g106910	At4g33800-like protein (AHRD V3.3 *** A0A068F5X7_BRANA)		P:GO:0009690	P:cytokinin metabolic process			mobidb-lite (MOBIDB_LITE); PTHR333	0,063	0,037	0,000	0,000	0,000									
Solyc01g106920	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM); IPR029949 (PTH	1,720	3,090	0,548	0,612	0,993									
Solyc01g106930	cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 *-* AT2G32190.1)		C:GO:0005886	C:plasma membrane			IPR028144 (PFAM); mobidb-lite (MOB	0,000	0,018	0,000	0,025	0,047									
Solyc01g106940	Myb transcription factor (AHRD V3.3 *-* A0A072VG04_MEDTR)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR005818 (SMAF MYB_related	13,793	10,602	18,159	15,818	16,235									
Solyc01g106943	Myosin heavy chain-like protein (AHRD V3.3 *-* G7JZT3_MEDTR)						PTHR35712 (PANTHER)	1,714	1,394	1,212	1,248	1,697									
Solyc01g106947	Exocyst complex component SEC3A (AHRD V3.3 --* A0A1D1XZ59_9ARAE)							1,378	0,259	0,922	1,090	0,869									
Solyc01g106950	myosin heavy chain-like protein (AHRD V3.3 *** AT2G14680.3)						PTHR35712 (PANTHER)	0,472	0,565	0,284	0,369	0,639									
Solyc01g106960	rhamnogalacturonan xylosyltransferase 1 (AHRD V3.3 --* AT4G01770.2)							0,298	0,018	0,289	0,217	0,142									
Solyc01g106970	F-box family protein (AHRD V3.3 *** A0A061EZ38_THECC)						PTHR33127:SF11 (PANTHER); PTHR:	0,000	0,019	0,000	0,000	0,000									
Solyc01g107000	Endo-1,4-beta-xylanase C (AHRD V3.3 *** A0A199V4M1_ANACO)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001000 (SMART); IPR001000 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc01g107010	DNA/RNA polymerases superfamily protein (AHRD V3.3 *** AT1G49980.8)		F:GO:0003684; F:GC	F:damaged DNA bir	EC:2.7.7.7	DNA-directed DNA pc	PIRSF036603 (PIRSF); IPR017961 (F	23,844	34,044	41,891	43,571	43,318									
Solyc01g107040	Ribosomal RNA large subunit methyltransferase N (AHRD V3.3 *** A0A1D1ZB43_9ARAE)		F:GO:0008173; P:GC	F:RNA methyltransferase activity; P:tRNA methylation; F:iron-su			IPR007197 (PFAM); PF13394 (PFAM)	35,641	32,444	34,913	33,027	31,118									
Solyc01g107050	HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT5G67150.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM); IPR023213 (G3D	0,474	0,438	0,000	0,022	0,093									
Solyc01g107060	LOW QUALITY:3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 2 (AHRD V3.3 --* HSDD2_ARATH)						mobidb-lite (MOBIDB_LITE)	0,623	0,317	0,050	0,025	0,047									
Solyc01g107070	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM); IPR023213 (G3D	4,488	4,565	3,437	5,744	4,340					0,746	0,033			up
Solyc01g107080	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	1,906	1,270	3,680	2,141	2,320									
Solyc01g107090	LOW QUALITY:beta-1,4-xylosidase (AHRD V3.3 *** AT3G19615.1)						PTHR38370 (PANTHER)	14,833	2,399	1,925	4,005	3,508	-2,596	0,000			1,053	0,045	down		up
Solyc01g107100	LOW QUALITY:beta-1,4-xylosidase (AHRD V3.3 *** AT3G19615.1)						PTHR38370 (PANTHER)	8,198	3,838	0,982	1,069	2,062	-1,069	0,022					down		
Solyc01g107120	DUF936 family protein (AHRD V3.3 *** G7JEV5_MEDTR)						IPR010341 (PFAM); mobidb-lite (MOB	0,203	0,174	0,171	0,265	0,190									
Solyc01g107130	Vacuolar sorting receptor homolog (AHRD V3.3 *** P93027_ARATH)		F:GO:0005509	F:calcium ion binding			IPR001881 (SMART); G3DSA:2.10.25	136,228	142,239	242,502	234,172	237,744									
Solyc01g107150	Zinc finger protein-like 1 like (AHRD V3.3 *** A0A0B2PGN2_GLYSO)		P:GO:0009737; C:GC	P:response to abscisic acid; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	39,376	40,213	50,056	51,628	47,434									
Solyc01g107160	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G19590.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	19,678	17,374	17,838	18,811	17,231									
Solyc01g107170	Zinc finger protein (AHRD V3.3 *** A0T3Q5_SOLTU)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	36,927	14,945	118,347	230,410	106,316	-1,280	0,007			0,965	0,000	down		up
Solyc01g107180	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** B9HMY5_POPTR)		F:GO:0005515; P:GC	F:protein binding; P:positive gravitropism			IPR000210 (PFAM); G3DSA:3.30.710	33,967	27,057	30,087	18,229	31,228					-0,718	0,000			down
Solyc01g107190	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)						IPR004883 (PFAM LBD	19,636	15,841	11,930	18,191	13,575					0,609	0,010			up
Solyc01g107200	QWRF motif protein (DUF566) (AHRD V3.3 *** AT1G49890.1)						IPR007573 (PFAM); mobidb-lite (MOB	7,716	6,409	3,410	2,895	2,895									
Solyc01g107210	Transcriptional adapter 1 (AHRD V3.3 *** A0A0B0NLB4_GOSAR)		C:GO:0070461	C:SAGA-type complex			IPR024738 (PFAM); mobidb-lite (MOB	11,216	9,352	18,163	14,696	14,810									
Solyc01g107215	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT2G14080.2)							0,936	1,048	1,260	1,391	1,131									
Solyc01g107220	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,062	0,000	0,000	0,000									
Solyc01g107240	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT4G33905.1)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM); IPR007248 (PAN	2,914	2,238	1,723	1,854	1,836									
Solyc01g107250	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9P218_ZOSMR)		F:GO:0005515	F:protein binding			IPR001611 (PFAM); IPR032675 (G3D	16,848	23,810	8,196	10,222	10,962									
Solyc01g107260	myosin-2 heavy chain-like protein (AHRD V3.3 *** AT1G49870.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,651	0,491	0,097	0,127	0,023									
Solyc01g107270	40S ribosomal protein S24 (AHRD V3.3 *-* A0A0D3F2R2_9ORYZ)		F:GO:0004642; P:GC	F:phosphoribosylfor	EC:6.3.5.3	Phosphoribosylformy	SM01211 (SMART); IPR036921 (G3D	4,856	5,420	2,825	2,387	2,406									
Solyc01g107273	Phosphoribosylformylglycinamidine synthase, putative (AHRD V3.3 *-* B9SDY9_RICCO)		F:GO:0004642; P:GC	F:phosphoribosylfor	EC:6.3.5.3	Phosphoribosylformy	PF18076 (PFAM); PTHR10099 (PANT	0,295	0,181	0,047	0,000	0,070									
Solyc01g107277	Phosphoribosylformylglycinamidine synthase, putative (AHRD V3.3 *-* B9SDY9_RICCO)		F:GO:0004642; P:GC	F:phosphoribosylfor	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase		0,392	0,381	0,193	0,270	0,189									
Solyc01g107280	Late embryogenesis abundant protein Lea5, putative (AHRD V3.3 *** A0A061E251_THECC)						IPR004926 (PFAM); mobidb-lite (MOB	2,621	1,652	0,495	0,537	0,260									
Solyc01g107290	RING-H2 finger protein		F:GO:0016874	F:ligase activity			IPR001841 (SMART); IPR001841 (PF	214,044	129,190	44,193	93,420	80,815			0,868	0,001	1,080	0,000		up	up
Solyc01g107300	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G33920.1)		F:GO:0004722; P:GC	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART); IPR001932 (PF	39,272	31,497	24,592	36,115	37,871			0,620	0,007	0,555	0,027		up	up
Solyc01g107320	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YFW6_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	11,911	9,758	36,273	37,234	34,633									
Solyc01g107330	SWIB_MDM2 domain protein		F:GO:0005515	F:protein binding			IPR019835 (SMART); IPR036885 (G3	22,453	30,867	23,360	21,898	27,610									
Solyc01g107340	Copper ion binding protein, putative (AHRD V3.3 *** B9SG43_RICCO)		C:GO:0005886	C:plasma membrane			PR01217 (PRINTS); mobidb-lite (MOB	7,261	10,642	6,882	6,343	5,223									
Solyc01g107350	glutamyl-tRNA (Gln) amidotransferase subunit A (DUF620) (AHRD V3.3 *** AT3G19540.1)						IPR006873 (PFAM); mobidb-lite (MOB	14,874	11,667	2,404	2,798	4,162									
Solyc01g107360	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *-* K4B9A4_SOLLC)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	25,685	24,861	49,784	46,115	42,055									
Solyc01g107370	Gibberellin-regulated protein (AHRD V3.3 *** K0E174_POPTO)		C:GO:0016021	C:integral component of membrane			IPR003854 (PFAM); PTHR23201 (PAN	0,021	0,062	0,022	0,025	0,071									
Solyc01g107380	MAR-binding filament-like protein 1 isoform 1 (AHRD V3.3 *** A0A061E182_THECC)						IPR008479 (PFAM); mobidb-lite (MOB	61,898	58,762	101,107	121,856	108,364									
Solyc01g107390	GH3 (AHRD V3.3 *** E2FHL1_9ROSI)	GH3					IPR004993 (PFAM); IPR004993 (PAN	32,165	38,955	55,751	153,572	54,304					1,465	0,000			up
Solyc01g107395	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *-* A0A061F4Q5_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); PTHR33127:SF1	0,021	0,021	0,047	0,000	0,000									
Solyc01g107400	IAA-amido synthetase						PTHR31901:SF9 (PANTHER); IPR004	5,282	5,965	56,183	90,203	40,086					0,689	0,014			up
Solyc01g107410	PHD-finger family homeodomain protein		F:GO:0003677	F:DNA binding			IPR001965 (SMAF HB-PHD	36,171	31,091	24,768	25,872	21,446									
Solyc01g107415	TIP41 (AHRD V3.3 *-* M9TER4_PERCU)						IPR007303 (PFAM); PTHR21021 (PAN	1,939	1,292	2,328	1,976	2,596									
Solyc01g107420	TIP41-like family protein (AHRD V3.3 *-* AT4G34270.1)						IPR007303 (PFAM); PTHR21021 (PAN	0,207	0,244	0,074	0,269	0,143									
Solyc01g107450	caspase-6 protein (AHRD V3.3 *** AT2G15000.7)						mobidb-lite (MOBIDB_LITE); PTHR331	19,960	25,029	27,265	26,824	25,322									
Solyc01g107460	LOW QUALITY:neuronal PAS domain protein (AHRD V3.3 *** AT5G64190.2)						PTHR31439 (PANTHER); PTHR31439	0,277	0,158	0,000	0,000	0,140									
Solyc01g107470	FAD-binding Berberine family protein (AHRD V3.3 --* AT1G30710.1)						IPR008011 (PFAM); PTHR36758 (PAN	4,710	5,360	3,889	3,472	4,159									
Solyc01g107490	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT3G19500.1)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,804	0,786	0,025	0,048	0,000									
Solyc01g107500	DNA repair protein REV1 (AHRD V3.3 --* A0A0A0K6E9_CUCSA)		F:GO:0003684; C:GC	F:damaged DNA binding; C:nucleus; F:nucleotidyltransferase ac			mobidb-lite (MOBIDB_LITE)	2,677	4,437	2,357	1,922	2,410									
Solyc01g107510	DNA repair protein REV1 (AHRD V3.3 *** K4B2W7_SOLLC)		F:GO:0003684; F:GC	F:damaged DNA binding; F:nucleotidyltransferase activity; P:err			IPR001357 (SMART); IPR001126 (PF	62,866	114,864	57,231	56,318	56,610	0,894	0,017					up		
Solyc01g107520	Plant basic secretory family protein (AHRD V3.3 *** B9GHT3_POPTR)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity			IPR007541 (PFAM); IPR007541 (PAN	0,159	0,094	0,050	0,000	0,000									
Solyc01g107550	Methylthioribose kinase (AHRD V3.3 *** MTK_ARATH)		P:GO:0009086; F:GC	P:methionine biosyr	EC:2.7.1.1	S-methyl-5-thioribose	IPR009212 (PIRSF); G3DSA:3.30.200	74,915	71,459	127,237	131,237	129,108									
Solyc01g107560	Glycosyltransferase (AHRD V3.3 *** K4B2X2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR(	4,039	2,175	2,179	1,891	2,270									
Solyc01g107580	Pseudouridine synthase family protein (AHRD V3.3 *** AT3G19440.1)		P:GO:0001522; F:GC	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR006145 (PFAM); PTHR44832:SF1	3,357	3,320	2,967	2,943	2,724									
Solyc01g107590	Cinnamyl alcohol dehydrogenase (AHRD V3.3 *** C1IC55_GOSHI)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART); IPR013154 (PF	34,212	39,415	4,937	4,342	6,063									
Solyc01g107600	UNC-50 family protein (AHRD V3.3 *** AT2G15240.1)		C:GO:0030173	C:integral component of Golgi membrane			IPR007881 (PFAM); IPR007881 (PAN	13,749	14,496	19,003	17,202	15,891									
Solyc01g107610	PRKR-interacting 1 (AHRD V3.3 *-* A0A0B0P818_GOSAR)						IPR009548 (PFAM); mobidb-lite (MOB	19,225	20,498	25,107	21,120	23,058									
Solyc01g107620	Reticulon-like protein (AHRD V3.3 *** M1CF80_SOLTU)		C:GO:0005789; C:GC	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM); PTHR10994:SF1	6,482	6,382	7,531	8,708	7,215									
Solyc01g107625	AAA-type ATPase family protein / ankyrin repeat family protein (AHRD V3.3 --* AT3G24530.2)							0,596	0,518	0,749	1,263	0,804									
Solyc01g107640	Protein TIC 21, chloroplastic (AHRD V3.3 *** A0A0B2PGL4_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR022051 (PFAM); IPR022051 (PAN	70,159	84,007	139,818	124,740	139,609									
Solyc01g107650	Ovary receptor kinase 1 (AHRD V3.3 *** S4WIP5_SOLCH)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:3.30.200	0,604	1,083	0,072	0,070	0,071									

Solyc01g107660	Stress enhanced protein 1, chloroplastic (AHRD V3.3 *** STEP1_ARATH)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:response to wounding; C:i		PTHR14154:SF18 (PANTHER); PTHR	19,285	32,107	28,888	33,523	43,699	0,762	0,005	0,592	0,004			up	up	
Solyc01g107670	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9NH19_ZOSMR)		F:GO:0005515	F:protein binding		PR00019 (PRINTS); IPR003591 (SMA	51,392	20,884	22,829	23,627	25,308	-1,271	0,000					down		
Solyc01g107675	Chloroplast envelope membrane protein (AHRD V3.3 --* CEMA_OENGL)						0,604	0,567	0,656	0,473	0,447									
Solyc01g107680	ATP-dependent clp protease ATP-binding subunit clpx (AHRD V3.3 *-* E5GBA0_CUCME)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding		PTHR11262:SF15 (PANTHER); IPR00	0,913	0,678	0,535	0,468	0,592									
Solyc01g107690	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* A0A1D1XQW5_9ARAE)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding		G3DSA:3.40.50.300 (GENE3D); IPR0	5,527	3,814	2,980	2,854	3,085									
Solyc01g107695	Kynurenine formamidase (AHRD V3.3 *-* A0A0B0P1F0_GOSAR)		F:GO:0004061; P:G(	F:arylformamidase : EC:3.5.1.9	Arylformamidase	IPR007325 (PFAM); IPR011989 (G3D	27,139	22,789	73,194	71,170	64,526									
Solyc01g107700	Kynurenine formamidase (AHRD V3.3 *** A0A1D1Y8U0_9ARAE)		F:GO:0004061; P:G(	F:arylformamidase : EC:3.5.1.9	Arylformamidase	IPR037175 (G3DSA:3.50.30.GENE3D	34,071	38,259	78,529	76,628	73,984									
Solyc01g107710	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)					IPR009646 (PFAM); mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc01g107720	Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)					IPR009646 (PFAM); PTHR31656 (PAI	0,000	0,000	0,000	0,025	0,000									
Solyc01g107730	D-type cyclin-2	cycd3c2	C:GO:0005634	C:nucleus		IPR013763 (SMART); IPR004367 (SM	4,214	2,716	0,000	0,000	0,000									
Solyc01g107740	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT4G34150.1)					IPR000008 (SMART); IPR000008 (PF	25,806	23,136	25,749	53,365	33,682			0,384	0,044	1,052	0,000		up	up
Solyc01g107750	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (AH		F:GO:0004725; P:G(	F:protein tyrosine p EC:3.1.3.16; EC:3.1. Protein-serine/threor		IPR014020 (SMART); IPR029021 (G3	107,347	98,383	146,324	150,277	143,009									
Solyc01g107760	Cysteine protease, putative (AHRD V3.3 *** B9RYC1_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity		IPR000668 (PRINTS); IPR000668 (SM	0,136	0,138	0,050	0,025	0,023									
Solyc01g107770	Glycosyltransferase (AHRD V3.3 *** M1CFS3_SOLTU)		F:GO:0035251	F:UDP-glucosyltransferase activity		G3DSA:3.40.50.2000 (GENE3D); PTH	0,021	0,000	0,000	0,000	0,000									
Solyc01g107780	Glycosyltransferase (AHRD V3.3 *** K4B2Z4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D); IPR(	3,114	7,704	5,028	5,910	9,473	1,333	0,001					up		
Solyc01g107790	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PL83_ZOSMR)		C:GO:0016021	C:integral component of membrane		IPR032675 (G3DSA:3.80.10.GENE3D	0,061	0,278	0,000	0,000	0,000									
Solyc01g107800	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G71690.1)		P:GO:0045492	P:xylan biosynthetic process		IPR021148 (PFAM); IPR006514 (TIGF	25,783	26,682	30,095	27,146	27,475									
Solyc01g107810	Glycosyltransferase (AHRD V3.3 *** K4B2Z7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D); IPR(	1,688	2,011	0,372	0,191	0,236									
Solyc01g107820	TOMATO WOUND-INDUCED 1	TWI1	F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D); G3C	91,207	188,764	55,400	85,230	92,887			0,741	0,008				up	
Solyc01g107830	Glycosyltransferase (AHRD V3.3 *** K4B2Z9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D); G3C	13,969	15,297	436,332	489,759	297,475			-0,556	0,032				down	
Solyc01g107850	Glycosyltransferase (AHRD V3.3 *-* M1DUE9_SOLTU)		C:GO:0043231; F:G(	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl		G3DSA:3.40.50.2000 (GENE3D)	0,826	0,577	3,372	5,045	2,188									
Solyc01g107853	Glycosyltransferase (AHRD V3.3 *-* M1DUE9_SOLTU)		C:GO:0043231; F:G(	C:intracellular membrane-bounded organelle; F:quercetin 3-O-glucosyltransferase activity; F:quercetin 7			0,858	0,978	6,305	6,307	3,206			-0,979	0,003				down	
Solyc01g107857	Glycosyltransferase (AHRD V3.3 *** C1JIE1_9SOLA)		F:GO:0016757	F:transferase activity, transferring glycosyl groups		G3DSA:3.40.50.2000 (GENE3D); PTH	0,937	1,768	41,074	37,409	20,250			-1,022	0,000				down	
Solyc01g107860	CBS domain-containing family protein (AHRD V3.3 *** B9GHB5_POPTR)		C:GO:0009507; P:G(	C:chloroplast; P:cell redox homeostasis		IPR000644 (SMART); G3DSA:3.10.58	44,904	86,561	60,726	69,430	66,520	0,971	0,015					up		
Solyc01g107870	Polyadenylate-binding protein (AHRD V3.3 *** K4B303_SOLLC)		F:GO:0003723	F:RNA binding		IPR000504 (SMART); IPR002004 (SM	697,093	683,462	721,989	652,740	675,742									
Solyc01g107880	RING/U-box superfamily protein (AHRD V3.3 *** AT4G34100.2)		F:GO:0008270	F:zinc ion binding		IPR011016 (SMART); IPR013083 (G3	131,207	131,186	125,201	125,432	128,940									
Solyc01g107890	Filament-like plant protein (AHRD V3.3 *-* A0A072UQ33_MEDTR)					IPR008587 (PFAM); mobidb-lite (MOB	105,688	59,677	1,947	0,828	1,719	-0,795	0,034					down		
Solyc01g107900	O-acyltransferase WSD1 (AHRD V3.3 *** A0A0B0P2X1_GOSAR)		F:GO:0004144; P:G(	F:diacylglycerol O-a EC:2.3.1.2	Diacylglycerol O-acy	IPR004255 (PFAM); IPR009721 (PFA	44,318	41,651	87,062	83,351	82,711									
Solyc01g107910	Caffeoyl CoA O-methyltransferase (AHRD V3.3 *** A0A0S2UWA5_PETHY)		F:GO:0008171	F:O-methyltransferase activity		G3DSA:3.40.50.150 (GENE3D); IPR(	10,744	13,514	4,487	5,794	5,406									
Solyc01g107920	LOW QUALITY:Harbinger transposase-derived nuclease (AHRD V3.3 *** A0A103YKF9_CYNCS)		C:GO:0016021	C:integral component of membrane		IPR027806 (PFAM); PTHR22930 (PAI	1,025	1,780	3,159	4,255	3,307									
Solyc01g107930	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G34040.1)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin protein ligase activity		IPR001841 (SMART); IPR001841 (PF	19,358	18,496	25,707	25,742	25,907									
Solyc01g107933	Photosystem II reaction center protein K (AHRD V3.3 --* PSBK_PINTH)						0,000	0,000	0,000	0,000	0,023									
Solyc01g107937	Protein kinase superfamily protein (AHRD V3.3 --* AT3G01085.3)						0,407	0,450	0,149	0,431	0,256									
Solyc01g107940	RING/U-box superfamily protein (AHRD V3.3 *** AT2G15530.7)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin protein ligase activity		IPR001841 (SMART); IPR001841 (PF	22,460	22,580	17,181	18,281	17,995									
Solyc01g107950	bHLH transcription factor 008		F:GO:0046983	F:protein dimerization activity		IPR011598 (SMAF bHLH	0,961	0,518	0,000	0,000	0,000									
Solyc01g107960	bHLH transcription factor 009		F:GO:0046983	F:protein dimerization activity		IPR036638 (G3DS bHLH	0,000	0,060	0,000	0,000	0,000									
Solyc01g107961	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0H3YC60_SALMI)		F:GO:0046983	F:protein dimerization activity		PTHR11514 (PANTHER); PTHR11514	0,056	0,058	0,000	0,000	0,000									
Solyc01g107962	Basic helix-loop-helix transcription factor (AHRD V3.3 --* A0A0H3YBU1_SALMI)		F:GO:0046983	F:protein dimerization activity		IPR036638 (G3DSA:4.10.280.GENE3	0,075	0,000	0,000	0,000	0,000									
Solyc01g107964	Basic helix-loop-helix transcription factor (AHRD V3.3 *-* A0A0H3YC60_SALMI)		F:GO:0046983	F:protein dimerization activity		PTHR11514 (PANTHER); PTHR11514	0,000	0,019	0,000	0,000	0,000									
Solyc01g107970	bHLH transcription factor 077		F:GO:0046983	F:protein dimerization activity		IPR011598 (PFAM bHLH	0,000	0,019	0,000	0,000	0,000									
Solyc01g107980	U-box domain-containing family protein (AHRD V3.3 *** B9HS21_POPTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination		IPR003613 (SMART); IPR011989 (G3	25,245	18,601	9,602	13,758	11,814									
Solyc01g107990	PI-PLC X domain-containing protein (AHRD V3.3 *** A0A0B2PDX2_GLYSO)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi		IPR017946 (G3DSA:3.20.20.GENE3D	20,963	17,004	11,657	9,986	10,296									
Solyc01g108000	Kinase family protein (AHRD V3.3 *** D7L9X7_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART); G3DSA:1.10.51	1,129	1,188	0,440	0,613	0,330									
Solyc01g108010	Endonuclease or glycosyl hydrolase (AHRD V3.3 *** A0A061E1S3_THECC)		C:GO:0005777; P:G(	C:peroxisome; P:regulation of gene expression		IPR021139 (PFAM); IPR025605 (PFA	33,390	42,383	55,693	58,293	56,212									
Solyc01g108020	Thioredoxin (AHRD V3.3 *** A0A103YKE9_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoreds		PR00421 (PRINTS); G3DSA:3.40.30.1	17,026	15,200	28,613	24,174	28,651									
Solyc01g108030	3-methylcrotonyl-CoA carboxylase (AHRD V3.3 *** AT4G34030.1)		F:GO:0016874	F:ligase activity		G3DSA:3.90.226.10 (GENE3D); IPR0:	54,519	55,875	110,675	130,791	116,530									
Solyc01g108035	Dynamin-related protein 3A (AHRD V3.3 *-* A0A0B2RN44_GLYSO)		F:GO:0000166; P:G(	F:nucleotide binding; P:mitochondrial fission; F:GTPase activity		G3DSA:1.20.120.1240 (GENE3D); IPI	8,021	6,022	4,707	6,080	5,374									
Solyc01g108040	Dynamin-related protein 3A (AHRD V3.3 *-* A0A1D1XWG2_9ARAE)		F:GO:0000166; P:G(	F:nucleotide binding; P:mitochondrial fission; F:GTPase activity		G3DSA:1.20.120.1240 (GENE3D)	4,646	4,595	3,524	4,013	3,502									
Solyc01g108043	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103XM66_CYNCS)		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	1,199	0,943	1,005	1,201	1,248									
Solyc01g108047	GATA transcription factor-like protein (AHRD V3.3 *** A0A0X7YHI0_SOLTU)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans		IPR000679 (PFAM); IPR039355 (PAN	14,072	15,192	13,201	13,498	13,313									
Solyc01g108050	Dynamin-related protein 3A (AHRD V3.3 --* A0A1D1YF72_9ARAE)		P:GO:0000266; F:G(	P:mitochondrial fiss EC:3.6.1.15	Nucleoside-triphosphate phosphatase		6,563	8,053	6,850	7,219	6,315									
Solyc01g108060	Methylcrotonyl-CoA carboxylase beta chain, putative (AHRD V3.3 *-* A0A072UYJ8_MEDTR)		F:GO:0004485; C:G(	F:methylcrotonoyl-C EC:6.4.1.4	Methylcrotonoyl-CoA	G3DSA:3.90.226.10 (GENE3D); IPR0:	0,932	1,553	0,675	0,733	0,586									
Solyc01g108070	Class I glutamine amidotransferase-like superfamily protein isoform 1 (AHRD V3.3 *** A0A061E0X3_THECC		C:GO:0005634; C:G(	C:nucleus; C:cytosol; F:protein deglycase activity; P:protein de		IPR029062 (G3DSA:3.40.50.GENE3D	8,787	12,145	7,710	7,398	8,574									
Solyc01g108080	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT2G36360.4)					bZIP	0,000	0,000	0,000	0,025	0,000									
Solyc01g108087	Abscisic acid responsive elements-binding factor 2 (AHRD V3.3 *** H6SFS2_BRANA)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		mobidb-lite (MOBIDB_LITE); mobidb-lit	38,391	23,574	53,647	49,398	41,852	-0,676	0,006					down		
Solyc01g108090	spire, putative (DUF1685) (AHRD V3.3 *-* AT2G15590.2)					IPR012881 (PFAM); PTHR31865:SF1	0,038	0,058	0,000	0,000	0,000									
Solyc01g108100	Cold regulated gene 27, putative isoform 1 (AHRD V3.3 *** A0A061DZZ1_THECC)					mobidb-lite (MOBIDB_LITE); PTHR336	6,215	5,447	3,437	4,863	5,459									
Solyc01g108110	Alpha 1,3 fucosyltransferase (AHRD V3.3 *** Q5DTC8_MEDSA)		P:GO:0006486; F:G(	P:protein glycosylation; F:fucosyltransferase activity; C:membra		IPR001503 (PFAM); IPR038577 (G3D	10,339	9,010	14,075	13,615	12,618									
Solyc01g108120	B3 domain-containing protein (AHRD V3.3 *-* W9R6M5_9ROSA)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	11,522	13,751	14,379	14,860	14,930									
Solyc01g108130	B3 domain-containing protein (AHRD V3.3 *** A0A0B2REX2_GLYSO)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	10,303	7,980	6,766	11,784	8,655					0,800	0,000			up
Solyc01g108140	B3 domain-containing protein (AHRD V3.3 *** W9RY77_9ROSA)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	2,068	2,023	1,074	0,949	1,112									
Solyc01g108150	Zinc-binding alcohol dehydrogenase 2 (AHRD V3.3 *** A0A143FQT2_9FABA)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR002347 (PRINTS); IPR002347 (PF	116,833	104,175	136,538	136,510	136,589									
Solyc01g108160	Autophagy-related protein 2 (AHRD V3.3 *** A0A0K0XR15_TOBAC)		P:GO:0030242	P:autophagy of peroxisome		IPR026854 (PFAM); IPR015412 (PFA	50,304	39,260	62,865	75,367	64,583									
Solyc01g108170	BEST plant protein match is: (TAIR:plant.1) protein, putative (AHRD V3.3 *** G7JLA4_MEDTR)					PTHR31722:SF5 (PANTHER); PTHR3	0,019	0,000	0,025	0,000	0,047									
Solyc01g108180	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2RYJ5_GLYSO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding		IPR002885 (PFAM); IPR032867 (PFA	18,382	17,664	16,720	15,044	15,119									
Solyc01g108190	Calcium-binding EF-hand (AHRD V3.3 *** A0A118JV88_CYNCS)		F:GO:0005509	F:calcium ion binding		PR01697 (PRINTS); IPR002048 (SMA	6,025	7,298	9,348	14,661	11,096					0,654	0,003			up
Solyc01g108200	Protein disulfide-isomerase SCO2 (AHRD V3.3 *** SCO2_ARATH)		F:GO:0016853	F:isomerase activity		IPR037477 (PANTHER)	1,086	2,163	0,889	1,695	1,957			1,122	0,043				up	
Solyc01g108210	Cytochrome P450 family ABA 8'-hydroxylase (AHRD V3.3 *** G7JL85_MEDTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR001128 (PRINTS); IPR002401 (PF	5,971	10,795	3,184	2,951	3,919									
Solyc01g108220	Unknown protein (AHRD V3.3)						2,724	4,821	0,946	1,320	1,338									
Solyc01g108230	LAG1 longevity assurance-like protein (AHRD V3.3 *** G7JL86_MEDTR)		C:GO:0016021	C:integral component of membrane		IPR006634 (SMART); IPR016439 (PIF	9,391	10,889	6,902	7,743	7,266									
Solyc01g108240	Ethylene Response Factor D.3	ERF_D_3	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg		IPR001471 (PRIN ERF	6,225	6,280	2,049	3,079	2,401									
Solyc01g108260	TP53RK-binding protein (AHRD V3.3 *** A0A151S6M7_CAJCA)		C:GO:0005634; C:G(	C:nucleus; C:cytosol		IPR036504 (G3DSA:3.30.2380.GENE	23,453	24,519	19,167	21,699	21,146									
Solyc01g108270	Leucine-rich repeat family protein / protein kinase family protein (AHRD V3.3 *** A0A0K9PIB6_ZOSMR)		F:GO:0005515	F:protein binding		IPR013210 (PFAM); IPR024788 (PFA	0,058	0,019	0,075	0,051	0,000									
Solyc01g108280	Protein kinase superfamily protein (AHRD V3.3 *** AT4G33950.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART); G3DSA:1.10.51	52,863	47,496	60,871	56,250	57,853									
Solyc01g108290	SWIB/MDM2 domain-containing protein		F:GO:0005515	F:protein binding		IPR019835 (SMART); IPR003121 (PF	24,361	24,130	26,788	25,170	23,463									
Solyc01g108300	Myb family transcription factor		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.6(G2-like	64,346	46,948	47,409	45,576	44,610									
Solyc01g108320	Peroxidase (AHRD V3.3 *** K4B348_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,080	0,041	0,000	0,000	0,046									
Solyc01g108330	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7J5T0_MEDTR)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE); mobidb-lit	2,707	2,276	0,118	0,097	0,069									
Solyc01g108340	peptidyl-prolyl cis-trans isomerase CYP40-like		P:GO:0000413; F:G(	P:protein peptidyl-p EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS); IPR019734 (SN	42,653	37,504	18,888	17,860	19,264									
Solyc01g108350	Plastocyanin-like domain protein (AHRD V3.3 *** G7JMH4_MEDTR)		F:GO:0009055	F:electron transfer activity		IPR008972 (G3DSA:2.60.40.GENE3D	0,021	0,216	0,000	0,000	0,000									
Solyc01g108360	Blue copper protein (AHRD V3.3 *** A0A199VY96_ANACO)		F:GO:0009055	F:electron transfer activity		IPR008972 (G3DSA:2.60.40.GENE3D	0,021	0,037	0,000	0,000	0,000									
Solyc01g108390	Proteinase inhibitor (AHRD V3.3 *** A0A0R4WFE3_TOBAC)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc		IPR000864 (PFAM); G3DSA:3.30.10.1	0,946	2,258	0,047	0,025	0,094	1,281	0,045					up		
Solyc01g108400	CDPK-related kinase (AHRD V3.3 *** AT3G50530.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART); G3DSA:1.10.23	4,247	13,032	105,828	158,849	109,199	1,641	0,000			0,589	0,000	up		up
Solyc01g108410	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XM66_CYNCS)		F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated; I		IPR011990 (G3DSA:1.25.40.GENE3D	30,055	22,953	46,090	57,825	49,673									
Solyc01g108420	LOW QUALITY:mitogen-activated protein kinase kinase kinase 3 (AHRD V3.3 --* AT1G53570.7)						8,259	6,794	13,441	12,687	12,944									
Solyc01g108430	Nucleic acid binding protein, putative (AHRD V3.3 *** B9S791_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:nuc		IPR003604 (SMART); IPR013085 (PF	12,536	15,201	18,593	17,918	16,483									
Solyc01g108440	LOW QUALITY:calmodulin-binding protein (DUF1645) (AHRD V3.3 *** AT2G15760.1)		C:GO:0005886	C:plasma membrane		IPR012442 (PFAM); mobidb-lite (MOB	4,236	9,245	0,984	0,886	0,891									
Solyc01g108450	Carboxypeptidase (AHRD V3.3 *** K4B360_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor		IPR001563 (PRINTS); IPR001563 (PF	16,152	47,064	0,336	0,120	0,072									
Solyc01g108460	Carboxypeptidase (AHRD V3.3 *** K4B361_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor		IPR001563 (PRINTS); IPR001563 (PF	0,042	0,076	0,025	0,025	0,000									
Solyc01g108470	Carboxypeptidase (AHRD V3.3 *** K4B362_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor		IPR001563 (PRINTS); IPR029058 (G3	0,000	0,021	0,000	0,000	0,000									
Solyc01g108480	Carboxypeptidase (AHRD V3.3 *** K4B363_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor		IPR001563 (PRINTS); IPR001563 (PF	0,379	0,320	0,075	0,047	0,164									
Solyc01g108490	Carboxypeptidase (AHRD V3.3 *** K4B364_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor		IPR001563 (PRINTS); IPR029058 (G3	78,939	68,597	7,101	11,646	15,502			1,122	0,006				up	
Solyc01g108500	RNA-binding protein (AHRD V3.3 *** A0A0K9NR72_ZOSMR)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART); IPR012677 (G3	1044,232	866,283	339,694	270,616	252,494			-0,431	0,009				down	
Solyc01g108510	Sulfotransferase (AHRD V3.3 *** K4B366_SOLLC)		F:GO:0008146	F:sulfotransferase activity		IPR000863 (PFAM); G3DSA:3.40.50.3	173,673	130,365	57,792	45,527	44,091			-0,393	0,023	-0,341	0,030		down	down
Solyc01g108520	Acetyl esterase IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR029058 (G3DSA:3.40.50.GENE3D	0,019	0,101	0,025	0,164	0,000									
Solyc01g108530	Acetyl esterase IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR013094 (PFAM); IPR029058 (G3D	14,722	14,448	36,033	40,391	42,271									
Solyc01g108540	Acetyl esterase IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR013094 (PFAM); IPR029058 (G3D	7,802	6,022	16,915	17,563	17,266									
Solyc01g108550	LOW QUALITY:E3 ubiquitin-protein ligase ATL9 (AHRD V3.3 --* ATL9_ARATH)					mobidb-lite (MOBIDB_LITE)	0,061	0,098	0,046	0,101	0,023									
Solyc01g108560	Acetyl esterase IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR029058 (G3DSA:3.40.50.GENE3D	1,865	2,195	3,913	2,681	2,416									
Solyc01g108570	Gibberellin receptor GID1L2 IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR029058 (G3DSA:3.40.50.GENE3D	4,313	4,552	2,575	1,524	2,125									
Solyc01g108580	Gibberellin receptor GID1L2 IPR013094 Alpha_beta hydrolase fold-3		F:GO:0016787	F:hydrolase activity		IPR029058 (G3DSA:3.40.50.GENE3D	29,141	27,846	33,865	28,398	28,753									
Solyc01g108600	presequence protease 2 (AHRD V3.3 *** AT1G49630.3)		F:GO:0003824; P:G(	F:catalytic activity; P:proteolysis; F:metal ion binding		IPR013578 (SMART); IPR013578 (PF	108,718	154,698	138,383	144,706	183,357			0,402	0,043				up	
Solyc01g108610	Cyclin-dependent kinase inhibitor (AHRD V3.3 *** A0A103YKD7_CYNCS)		F:GO:0004861; C:G(	F:cyclin-dependent protein serine/threonine kinase inhibitor acti		IPR003175 (PIRSF); IPR003175 (PFA	0,552	0,401	0,049	0,000	0,047									
Solyc01g108620	Transmembrane 53 (AHRD V3.3 *** A0A0B0NXX7_GOSAR)					IPR008547 (PFAM); mobidb-lite (MOB	22,392	27,629	14,152	16,653	21,426			0,596	0,035				up	
Solyc01g108630	nii1 nitrite reductase	nii1	F:GO:0016491; P:G(	F:oxidoreductase activity; F:heme binding; F:iron-sulfur cluster I		IPR006066 (PRINTS); G3DSA:3.30.41	8,188	18,380	8,416	19,396	13,989	1,193	0,000			1,205	0,016	up		up
Solyc01g108640	LOW QUALITY:GDSL esterase/lipase (AHRD V3.3 *** A0A199UQJ3_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds		IPR036514 (G3DSA:3.40.50.GENE3D	0,694	1,014	1,742	1,721	1,506									
Solyc01g108650	LOW QUALITY:embryo defective 1273 (AHRD V3.3 *** AT1G49510.3)		C:GO:0016021	C:integral component of membrane		PTHR36000:SF2 (PANTHER); PTHR3(	4,371	4,671	8,254	9,290	10,150									
Solyc01g108660	N-acetyl-gamma-glutamyl-phosphate reductase (AHRD V3.3 *** S8C8Q1_9LAMI)		F:GO:0003942; P:G(	F:N-acetyl-gamma-(EC:1.2.1.38	N-acetyl-gamma-gluta	IPR000534 (SMART); IPR000534 (PF	41,768	44,811	49,111	46,242	55,082									
Solyc01g108670	Kinesin motor family protein (AHRD V3.3 *** U5GJ60_POPTR)		F:GO:0003777; F:G(	F:microtubule motor EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	1,615	1,897	0,094	0,195	0,141									
Solyc01g108700	LOW QUALITY:transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)					PTHR37705 (PANTHER)	0,021	0,057	0,022	0,000	0,023									
Solyc01g108710	transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)					PTHR37705 (PANTHER)	0,037	0,019	0,022	0,025	0,023									
Solyc01g108720	methyl esterase 4 (AHRD V3.3 --* AT2G23580.2)						0,000	0,021	1,360	1,207	1,582									
Solyc01g108730	methyl esterase 1 (AHRD V3.3 *-* AT2G23620.1)					IPR029058 (G3DSA:3.40.50.GENE3D	0,021	0,000	5,667	8,025	5,635									
Solyc01g108740	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:G(	P:jasmonic acid me EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM); IPR029058 (G3D	0,021	0,061	0,097	0,251	0,118									
Solyc01g108745	Polyneuridine-aldehyde esterase-like protein (AHRD V3.3 *** A0A075F1V8_TOBAC)					IPR000073 (PFAM); IPR029058 (G3D	1,954	1,549	2,925	3,955	3,291									
Solyc01g108765	Methylketone synthase Ib (AHRD V3.3 *** E0YCS5_SOLLC)		F:GO:0052689	F:carboxylic ester h EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,019	0,018	0,000	0,000	0,046									
Solyc01g108780	methylketone synthase 1a		P:GO:0009694; P:G(	P:jasmonic acid me EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM); IPR029058 (G3D	8,709	5,527	6,526	5,171	4,811									
Solyc01g108790	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *-* A0A072TX02_MEDTR)		F:GO:0016787	F:hydrolase activity		G3DSA:3.90.226.40 (GENE3D); mobic	2,545	2,257	0,696	0,837	1,058									
Solyc01g108800	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072TKX0_MEDTR)		F:GO:0003860	F:3-hydroxyisobuty EC:3.1.2.4	3-hydroxyisobutyryl-(	G3DSA:3.90.226.10 (GENE3D); G3DS	1,234	0,843	0,620	0,438	0,633									
Solyc01g108820	Methyl esterase 10, putative (AHRD V3.3 *** A0A061DMV1_THECC)		P:GO:0009694; P:G(	P:jasmonic acid me EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,019	0,000	0,000	0,025	0,000									
Solyc01g108830	Methyl esterase (AHRD V3.3 *-* A0A072UEL6_MEDTR)		P:GO:0009694; P:G(	P:jasmonic acid me EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,181	0,064	0,122	0,000	0,046									
Solyc01g108840	Receptor protein kinase, putative (AHRD V3.3 *** B9T5F6_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART); G3DSA:3.30.20	75,184	46,322	39,723	58,488	57,440	-0,671	0,007	0,530	0,001	0,560	0,001	down	up	up
Solyc01g108850	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A068EUD3_COCNU)		F:GO:0005515	F:protein binding		IPR003591 (SMART); IPR032675 (G3	0,171	1,217	0,025	0,045	0,047									
Solyc01g108860	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A061E0N9_TH		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PR00682 (PRINTS); IPR026992 (PFA	2,047	5,041	0,612	2,478	1,063	1,322	0,021			2,012	0,000	up		up
Solyc01g108870	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT3G19010.4)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR027443 (G3DSA:2.60.120.GENE3	0,000	0,018	3,270	6,027	1,629					0,894	0,042			up
Solyc01g108880	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G19000.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PR00682 (PRINTS); IPR027443 (G3D	3,456	4,500	162,159	291,427	108,990					0,851	0,004			up
Solyc01g108890	BAT2 domain protein (AHRD V3.3 *** AT2G15860.1)					mobidb-lite (MOBIDB_LITE); mobidb-lit	51,348	42,605	39,324	35,125	43,106									
Solyc01g108900	pollen leucine rich repeat domain-extensin					PR01217 (PRINTS); IPR032675 (G3D	0,059	0,174	0,970	4,208	0,643					2,110	0,000			up
Solyc01g108910	Maternal effect embryo arrest protein, putative (AHRD V3.3 *** G7JNK2_MEDTR)		P:GO:0010183; F:G(	P:pollen tube guidance; F:mediator complex binding		mobidb-lite (MOBIDB_LITE); mobidb-lit	12,610	23,973	21,518	25,850	42,138	0,952	0,010	0,967	0,000			up	up	
Solyc01g108935	B3 domain-containing protein (AHRD V3.3 *-* W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding		IPR003340 (SMART); IPR003340 (PF	0,098	0,059	0,000	0,000	0,024									
Solyc01g108940	B3 domain-containing protein (AHRD V3.3 *-* W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	2,061	1,720	0,884	0,666	0,892									
Solyc01g108950	B3 domain-containing protein (AHRD V3.3 -** A0A0B2PAD4_GLYSO)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	0,538	0,262	0,047	0,022	0,000									
Solyc01g108970	B3 domain-containing protein (AHRD V3.3 --* M8BW15_AEGTA)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus		IPR015300 (G3DSA:2.40.330.GENE3	7,918	4,742	5,316	4,687	3,710									
Solyc01g108973	Sorting nexin-16 (AHRD V3.3 *-* W9R163_9ROSA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:phosphatidylinositol binding			3,851	1,867	1,323	1,424	1,200									
Solyc01g108975	Germacrene A oxidase (AHRD V3.3 --* GAO_SAUCO)					mobidb-lite (MOBIDB_LITE); mobidb-lit	2,629	1,523	2,387	2,165	1,815									
Solyc01g108977	AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT5G60140.1)		F:GO:0003676	F:nucleic acid binding		PTHR31920:SF15 (PANTHER); PTHR:	0,000	0,000	0,000	0,000	0,023									
Solyc01g108990	Receptor-like protein 12 (AHRD V3.3 --* M7Z494_TRIUA)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus		mobidb-lite (MOBIDB_LITE); mobidb-lit	0,685	0,288	0,502	0,464	0,448									
Solyc01g109010	Sorting nexin-16 (AHRD V3.3 *-* A0A0B2RCD7_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:phosphatidylinositol bindi		PTHR22999:SF23 (PANTHER); PTHR:	8,270	7,264	8,429	8,498	7,446									
Solyc01g109020	Lipase, GDSL (AHRD V3.3 *-* A0A124SDS7_CYNCS)		P:GO:0006629; F:G(	P:lipid metabolic process; F:lipase activity; F:hydrolase activity		PTHR22835:SF262 (PANTHER); PTHI	0,042	0,000	0,025	0,000	0,000									
Solyc01g109030	transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G31640.1)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus		IPR015300 (G3DSA:2.40.330.GENE3	0,021	0,000	0,000	0,000	0,000									
Solyc01g109040	Cytochrome b6-f complex subunit 7 (AHRD V3.3 *** W9R158_9ROSA)		C:GO:0009512	C:cytochrome b6f complex		IPR012595 (PFAM); PTHR34951 (PAI	28,204	59,429	10,006	14,079	27,982	1,102	0,001	1,478	0,000			up	up	

Solyc01g109050	glycosyl hydrolase family protein 43 (AHRD V3.3 *** AT3G49880.1)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR023296 (G3DSA:2.115.10.GENE3I	1,134	1,227	0,725	0,634	0,494									
Solyc01g109060	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RZG0_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	3,539	3,968	3,766	3,422	4,402									
Solyc01g109070	LOW QUALITY:CSL zinc finger domain-containing protein (AHRD V3.3 *** AT2G15910.3)		P:GO:0002098; C:G(	P:tRNA wobble uridine modification; C:nucleus; C:cytosol; P:pe	IPR007872 (PFAM): IPR036671 (G3D	12,945	17,565	14,732	11,746	12,378									
Solyc01g109080	Serine/threonine-protein kinase SMG1 (AHRD V3.3 *** A0A0B2PF15_GLYSO)		P:GO:0000184; F:G(	P:nuclear-transcribe EC:2.7.11 Transferring phospho	IPR000403 (SMART): IPR003152 (SM	74,400	56,131	65,164	82,320	75,664									
Solyc01g109085	phragmoplast orienting kinesin 1 (AHRD V3.3 --* AT3G17360.3)					0,000	0,000	0,025	0,000	0,000									
Solyc01g109090	LOW QUALITY:mRNA, clone: RTFL01-34-C05 (AHRD V3.3 -** E4MXL5_EUTHA)				PTHR36346 (PANTHER)	8,006	5,221	10,277	7,512	7,216									
Solyc01g109100	LOW QUALITY:phytochrome interacting factor 3-like 5 (AHRD V3.3 --* AT2G20180.6)		F:GO:0043531	F:ADP binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,072	0,050	0,095									
Solyc01g109110	Guanine nucleotide-binding protein alpha-2 subunit (AHRD V3.3 *** A0A151THZ4_CAJCA)		F:GO:0003924; P:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR001019 (PRINTS): IPR001019 (SM	145,053	111,799	48,637	129,059	106,375			1,125	0,000	1,408	0,000		up	up
Solyc01g109120	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G18950.1)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR001680 (SM	0,355	0,566	1,819	11,765	2,637					2,690	0,000			up
Solyc01g109130	Proteasome assembly chaperone 2 (AHRD V3.3 *** K4B3C7_SOLLC)		C:GO:0000502; C:G(	C:proteasome complex; C:nucleus; C:cytosol; P:proteasome as	IPR016562 (PIRSF): IPR019151 (PFA	15,605	13,347	37,687	36,528	33,660									
Solyc01g109140	divinyl ether synthase	des	F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR002403 (PRINTS): IPR036396 (G3	0,019	0,060	0,804	0,302	0,211									
Solyc01g109150	cytochrome P450 CYP74C4		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR002403 (PRINTS): IPR001128 (PF	0,140	0,062	0,000	0,000	0,000									
Solyc01g109160	CYP74C4	CYP74C4	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR036396 (G3DSA:1.10.630.GENE3I	0,040	0,059	0,047	0,216	0,023									
Solyc01g109170	WCOR413-like plant cold acclimation protein		C:GO:0016021	C:integral component of membrane	IPR008892 (PFAM): PTHR33596:SF1	0,040	0,000	0,000	0,069	0,187									
Solyc01g109180	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0G2SJ83_SALMI)		F:GO:0003824	F:catalytic activity	IPR000873 (PFAM): G3DSA:3.40.50.1	42,184	34,818	0,523	0,263	0,348									
Solyc01g109190	LOW QUALITY:nuclear factor Y, subunit A10 (AHRD V3.3 --* AT5G06510.6)					1,021	0,041	0,025	0,148	0,142									
Solyc01g109210	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT3G04310.2)					5,081	1,766	1,143	1,682	1,736	-1,488	0,000					down		
Solyc01g109220	Mitochondrial import receptor subunit TOM6 homolog (AHRD V3.3 *** TOM6_ARATH)		C:GO:0005742	C:mitochondrial outer membrane translocase complex	IPR034554 (PANTHER)	1,403	1,504	1,373	1,157	0,920									
Solyc01g109230	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** A0A061E4Q7_THECC)		P:GO:0035556	P:intracellular signal transduction	IPR004146 (PFAM): G3DSA:3.30.60.9	0,773	0,955	0,577	1,005	0,983									
Solyc01g109250	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** I3SPG4_MEDTR)				IPR025322 (PFAM): PTHR33052:SF2	12,089	9,194	2,279	2,184	2,682									
Solyc01g109260	Plastid division PDV2-like protein (AHRD V3.3 *** A0A0B0MUD2_GOSAR)	PDV2	P:GO:0010020	P:chloroplast fission	mobidb-lite (MOBIDB_LITE): mobidb-lit	12,496	13,117	15,922	15,984	14,486									
Solyc01g109270	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G66600.9)				IPR025757 (PFAM): IPR006869 (PFA	0,000	0,019	0,000	0,000	0,000									
Solyc01g109280	RING/U-box superfamily protein (AHRD V3.3 *** AT2G16090.4)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART): IPR013083 (G3	25,680	27,995	39,781	43,288	36,410									
Solyc01g109290	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	IPR025714 (PFAM): G3DSA:3.40.50.1	9,156	9,659	9,964	8,570	8,419									
Solyc01g109300	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	HDR	P:GO:0019288; F:G(	P:isopentenyl dipho EC:1.17.1; EC:1.17. Acting on CH or CH2	G3DSA:3.40.1010.20 (GENE3D): IPR(	238,004	280,117	545,587	522,188	543,831									
Solyc01g109310	Protein DETOXIFICATION (AHRD V3.3 *** K4B3E4_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (PFAM): IPR002528 (TIGF	3,350	4,549	9,200	7,374	8,594									
Solyc01g109320	Protein DETOXIFICATION (AHRD V3.3 *** K4B3E5_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (PFAM): PTHR11206 (PAN	0,115	0,197	9,229	11,011	8,440									
Solyc01g109330	cytochrome c biogenesis protein-like protein		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	IPR007816 (PFAM): PTHR31566:SF0	1,488	2,124	3,838	4,787	4,651									
Solyc01g109340	RING/U-box superfamily protein (AHRD V3.3 *** AT2G23780.3)		P:GO:0006511; C:G(	P:ubiquitin-dependent protein catabolic process; C:integral com	IPR001841 (SMART): IPR013083 (G3	39,830	35,803	5,437	3,666	4,999									
Solyc01g109350	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT3G18860.1)		F:GO:0043130; P:G(	F:ubiquitin binding; P:proteasome-mediated ubiquitin-dependent	IPR020472 (PRINTS): IPR001680 (SM	124,114	117,118	141,825	133,865	137,648									
Solyc01g109360	Tyrosyl-tRNA synthetase (AHRD V3.3 *** P93363_TOBAC)		F:GO:0004831; F:G(	F:tyrosine-tRNA lig: EC:6.1.1.1 Tyrosine--tRNA ligas	IPR014729 (G3DSA:3.40.50.GENE3D	119,473	130,197	114,694	132,131	116,081									
Solyc01g109370	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** B2LWM5_RICCO)		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR002123 (SMART): IPR032098 (PF	7,121	4,717	2,487	1,970	2,511									
Solyc01g109380	UPF0496 protein (AHRD V3.3 *** A0A061E8F5_THECC)		C:GO:0016021	C:integral component of membrane	IPR007749 (PFAM): PTHR31113:SF1	9,999	7,992	3,396	6,108	4,748					0,841	0,009			up
Solyc01g109390	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)		F:GO:0005504; P:G(	F:fatty acid binding; P:systemic acquired resistance	IPR016140 (SMART): G3DSA:1.10.11	0,449	3,343	0,050	0,000	0,023									
Solyc01g109400	Flavoprotein wrbA (AHRD V3.3 *** A0A0B0P664_GOSAR)		F:GO:0003955; F:G(	F:NAD(P)H dehydrc EC:1.6.5.2 NAD(P)H dehydroger	IPR005025 (PFAM): IPR029039 (G3D	20,762	22,914	15,403	17,512	16,557									
Solyc01g109410	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit		F:GO:0003955; C:G(	F:NAD(P)H dehydrc EC:1.6.5.2 NAD(P)H dehydroger	IPR029039 (G3DSA:3.40.50.GENE3D	153,539	154,059	203,270	214,868	197,062									
Solyc01g109420	Flavoprotein wrbA (AHRD V3.3 *** A0A0B0MNA5_GOSAR)		F:GO:0003955; F:G(	F:NAD(P)H dehydrc EC:1.6.5.2 NAD(P)H dehydroger	IPR010089 (TIGRFAM): IPR029039 ((	0,021	0,021	0,000	0,045	0,118									
Solyc01g109430	PPPDE putative thiol peptidase family protein				IPR008580 (SMART): IPR008580 (PF	0,258	0,250	0,071	0,025	0,024									
Solyc01g109440	LOW QUALITY:G-box-binding factor 1 (AHRD V3.3 --* W9RBL5_9ROSA)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,018	0,025	0,148	0,187									
Solyc01g109450	PfkB family carbohydrate kinase (AHRD V3.3 *** A0A072UMB6_MEDTR)		F:GO:0019200; P:G(	F:carbohydrate kina EC:2.7.1.83 Pseudouridine kinase	IPR011611 (PFAM): PTHR43085 (PAN	6,918	5,991	8,921	9,018	8,380									
Solyc01g109460	Polyol monosaccharide transporter 4	PMT4	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): IPR003663 (TI(	30,288	245,372	39,925	51,199	105,331	3,037	0,000	1,393	0,034			up	up	
Solyc01g109470	Dehydration-responsive protein RD22, putative (AHRD V3.3 *** B9RBD8_RICCO)		C:GO:0016020	C:membrane	IPR004873 (SMART): IPR004873 (PF	0,057	0,103	0,025	0,047	0,000									
Solyc01g109480	LOW QUALITY:BURP domain protein RD22 (AHRD V3.3 --* RD22_ARATH)				PTHR33731 (PANTHER): PTHR33731	0,042	0,057	0,122	0,189	0,047									
Solyc01g109490	Cysteinyl-tRNA synthetase, putative (AHRD V3.3 --* B9RP10_RICCO)		F:GO:0000166; F:G(	F:nucleotide binding; F:aminoacyl-tRNA ligase activity; F:cysteine-tRNA ligase activity; F:ATP binding; (		0,240	0,232	0,074	0,126	0,117									
Solyc01g109495	Dehydration-responsive protein RD22 (AHRD V3.3 *** K7XKT0_SOLTU)				IPR004873 (PFAM): PTHR31236:SF4	0,140	0,099	0,065	0,050	0,023									
Solyc01g109500	Dehydration-responsive protein RD22, putative (AHRD V3.3 *** B9RBD8_RICCO)				IPR004873 (SMART): IPR004873 (PF	2,618	6,408	0,419	0,285	0,470									
Solyc01g109505	pleckstrin homology (PH) domain-containing protein (AHRD V3.3 --* AT4G17140.3)					0,019	0,019	0,000	0,000	0,000									
Solyc01g109510	SWI/SNF complex subunit SWI3D (AHRD V3.3 *** W9R169_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding; F:zinc ion binding	IPR000433 (SMART): IPR001005 (SM	75,230	60,605	72,382	68,199	73,324									
Solyc01g109520	Rab family GTPase (AHRD V3.3 *** D8RRT7_SELML)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	160,483	175,130	249,868	228,323	229,605									
Solyc01g109540	Coatomer subunit gamma (AHRD V3.3 *** K4B3G7_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:structural molecule activity; F:ATP b	IPR000719 (SMART): G3DSA:3.30.20	259,835	267,982	227,549	216,350	219,113									
Solyc01g109550	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT3G18870.1)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (SMART): IPR003690 (PF	0,118	0,351	0,094	0,097	0,117									
Solyc01g109560	Guanine nucleotide-binding protein subunit beta (AHRD V3.3 *** GBB_SOLTU)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction	IPR020472 (PRINTS): IPR001632 (PF	1,522	1,526	1,496	1,548	1,577									
Solyc01g109570	Beta-1,3-glucanase 12 (AHRD V3.3 *** K9MBD2_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:prote	IPR001632 (PRINTS): IPR020472 (PF	131,055	169,040	57,691	62,576	68,790									
Solyc01g109580	Adenylyl cyclase-associated protein (AHRD V3.3 *** K4B3H1_SOLLC)		P:GO:0000902; F:G(	P:cell morphogenesis; F:actin binding; P:cytoskeleton organizati	IPR006599 (SMART): IPR013912 (PF	9,369	12,835	0,991	0,991	1,040									
Solyc01g109590	Kinase family protein (AHRD V3.3 *** D7MF07_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	83,681	58,435	20,063	33,609	22,860					0,744	0,000			up
Solyc01g109600	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A1D1XPT6_9ARAE)				G3DSA:3.30.710.10 (GENE3D): mobi(	56,942	46,513	61,587	46,454	54,512					-0,404	0,005			down
Solyc01g109610	Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** G7JG61_MEDTR)		F:GO:0004617; P:G(	F:phosphoglycerate EC:1.1.1.95 Phosphoglycerate de	PTHR42938:SF7 (PANTHER): PTHR4:	1,016	0,780	0,071	0,000	0,047									
Solyc01g109620	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 *** NDHI_ARAHI)		C:GO:0016020; F:G(	C:membrane; F:oxidoreductase activity, acting on NAD(P)H; F:4	G3DSA:3.30.70.3270 (GENE3D): IPR(	91,912	85,581	139,607	126,376	137,785									
Solyc01g109630	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT2G21710.1)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (SMART): IPR003690 (PF	10,067	8,380	9,690	8,941	10,499									
Solyc01g109640	AP-3 complex subunit sigma (AHRD V3.3 *** AP3S_ARATH)		F:GO:0008565; P:G(	F:protein transporter activity; P:protein transport; C:AP-3 adapt(	IPR016635 (PIRSF): G3DSA:3.30.450	4,653	5,384	5,572	6,490	5,808									
Solyc01g109650	Lrr receptor protein kinase, putative (AHRD V3.3 *** B9RBF5_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	4,661	4,576	5,078	6,950	5,695									
Solyc01g109660	meloidogyne-induced giant cell protein DB275		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	749,083	790,777	439,728	299,225	417,362					-0,552	0,001			down
Solyc01g109680	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G06670.6)				mobidb-lite (MOBIDB_LITE): mobidb-lit	9,967	16,593	21,177	25,255	24,297	0,760	0,008					up		
Solyc01g109690	MYB transcription factor (AHRD V3.3 *** F2WZH1_VITPS)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	0,280	0,415	0,000	0,025	0,000									
Solyc01g109700	bHLH transcription factor 010		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	15,775	14,711	4,187	5,321	5,182									
Solyc01g109710	protein response to dessication 2		C:GO:0005886; F:G(	C:plasma membrane; F:hydrolase activity	IPR014729 (G3DSA:3.40.50.GENE3D	31,970	77,898	49,487	55,917	56,003	1,307	0,007					up		
Solyc01g109720	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G18360.1)		F:GO:0003824	F:catalytic activity	IPR000639 (PRINTS): IPR000073 (PF	1,250	3,341	0,590	0,979	1,037	1,442	0,010					up		
Solyc01g109730	LOW QUALITY:Eukaryotic initiation factor 4A (AHRD V3.3 --* IF4A_WHEAT)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		0,000	0,183	0,025	0,000	0,000									
Solyc01g109760	LOW QUALITY:Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *-* A0A0K9NWX1_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D): G3D	3,928	4,233	6,338	6,384	5,587									
Solyc01g109770	RER1 family protein		C:GO:0016021	C:integral component of membrane	IPR004932 (PIRSF): IPR004932 (PFA	71,053	75,006	58,137	58,189	54,225									
Solyc01g109780	F-box protein (AHRD V3.3 *-* A0A0B2RZB4_GLYSO)		P:GO:0010099	P:regulation of photomorphogenesis	PTHR36062:SF1 (PANTHER): IPR037	16,808	15,060	36,029	37,224	38,923									
Solyc01g109790	ADP-glucose pyrophosphorylase large subunit 1	AGPase L1	P:GO:0005978; F:G(	P:glycogen biosynt! EC:2.7.7.27 Glucose-1-phosphate	G3DSA:2.160.10.10 (GENE3D): IPR0	89,880	99,865	4,958	3,895	5,611									
Solyc01g109800	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *-* G7J762_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR33640:SF3 (PANTHER): PTHR3:	6,634	6,450	2,589	3,265	2,335									
Solyc01g109810	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7JHE9_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR33640:SF3 (PANTHER): PTHR3:	3,273	3,915	2,387	2,648	1,938									
Solyc01g109820	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT4G05350.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:ligase activ	IPR001841 (PFAM): IPR013083 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc01g109830	Bifunctional dihydrofolate reductase-thymidylate synthase (AHRD V3.3 *** K4B3J6_SOLLC)		F:GO:0004146; F:G(	F:dihydrofolate redu EC:2.1.1.45; EC:1.5. Thymidylate synthase	IPR000398 (PRINTS): IPR023451 (PF	55,167	73,981	83,532	69,915	74,646									
Solyc01g109850	Diaminopimelate decarboxylase family protein (AHRD V3.3 *** B9HRK5_POPTR)		F:GO:0008836; P:G(	F:diaminopimelate c EC:4.1.1.2 Diaminopimelate dec	IPR002986 (PRINTS): IPR000183 (PF	145,146	165,732	112,701	107,358	118,534									
Solyc01g109860	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT2G18180.2)				PR00180 (PRINTS): IPR011074 (SMA	2,155	2,653	0,378	0,754	0,707									
Solyc01g109870	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT2G21520.1)		C:GO:0016021	C:integral component of membrane	PR00180 (PRINTS): IPR001251 (SMA	72,644	64,409	106,771	107,447	103,319									
Solyc01g109880	BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	195,397	143,867	288,266	308,789	250,977									
Solyc01g109890	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *** AT4G39150.3)				IPR001623 (PRINTS): IPR001623 (SM	67,435	94,594	70,414	64,687	75,860									
Solyc01g109900	Aspartate carbamoyltransferase (AHRD V3.3 *** A0A0B0NCD8_GOSAR)		P:GO:0010039; P:G(	P:response to iron ion; P:response to acidic pH; C:Casparian s	mobidb-lite (MOBIDB_LITE): PTHR352	1,678	1,530	0,535	0,262	0,306									
Solyc01g109910	RING/U-box superfamily protein (AHRD V3.3 *** AT4G39140.5)				IPR001841 (SMART): IPR013083 (G3	37,678	46,990	49,101	55,411	53,772									
Solyc01g109920	LOW QUALITY:Dehydrin protein (AHRD V3.3 *** V9M5C3_MANES)		P:GO:0009415	P:response to water	IPR000167 (PFAM): mobidb-lite (MOB	21,813	30,931	30,252	58,238	27,374					0,950	0,002			up
Solyc01g109930	inositol monophosphatase family protein (AHRD V3.3 *** AT4G39120.2)		P:GO:0046854	P:phosphatidylinositol phosphorylation	IPR000760 (PRINTS): IPR000760 (PF	21,775	25,403	36,444	36,534	39,286									
Solyc01g109940	26S proteasomal subunit RPT4a		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata	IPR003593 (SMART): G3DSA:2.40.50	107,618	110,724	152,865	143,474	140,507									
Solyc01g109950	Kinase, putative (AHRD V3.3 *** B9RH93_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:2.60.12	0,019	0,059	0,000	0,000	0,000									
Solyc01g109960	SUMO-activating enzyme 2 (AHRD V3.3 *** AT2G21470.1)		F:GO:0016881; P:G(	F:acid-amino acid ligase activity; P:protein sumoylation; F:SUM	IPR028077 (PFAM): IPR000594 (PFA	17,471	17,447	26,612	26,427	25,432									
Solyc01g109970	SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 *** AT2G16390.2)		F:GO:0005524	F:ATP binding	IPR001650 (SMART): IPR014001 (SM	1,623	0,896	1,897	1,287	1,390									
Solyc01g109980	BEL1-related homeotic protein 30 (AHRD V3.3 *** Q8LLD8_SOLTU)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR001356 (SMAF TALE	28,048	17,149	22,575	24,701	24,557	-0,681	0,048					down		
Solyc01g109990	RNA-binding family protein, putative (AHRD V3.3 *** A0A061DYQ5_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	45,331	39,301	45,880	47,473	44,840									
Solyc01g110000	Beta-galactosidase (AHRD V3.3 *** A0A0V0ITW0_SOLCH)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS): IPR031330 (PF	105,128	39,431	18,296	36,297	18,855	-1,385	0,001			0,987	0,000	down		up
Solyc01g110010	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XXP7_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	3,137	3,972	2,837	3,631	2,986									
Solyc01g110020	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein (AHRD V3.3 *** AT4G		F:GO:0003682	F:chromatin binding	IPR001025 (SMART): IPR001025 (PF	36,141	29,541	36,616	31,800	33,170									
Solyc01g110030	Transducin/WD40 repeat protein (AHRD V3.3 *** A0A072TQH3_MEDTR)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR015943 (G3	11,731	12,562	14,106	14,531	13,513									
Solyc01g110060	Purple acid phosphatase (AHRD V3.3 *** A0A0V0IAA9_SOLCH)		F:GO:0003993; F:G(	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR004843 (PFAM): IPR029052 (G3D	1,804	3,698	1,546	2,312	3,061	1,062	0,023	0,980	0,010			up	up	
Solyc01g110070	Transposon-like element Lyt2-2 DNA (AHRD V3.3 *** D5MNY6_SOLLC)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding	IPR006564 (SMART): IPR018289 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc01g110090	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** AT3G14250.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART): IPR002867 (PF	0,000	0,043	0,022	0,076	0,024									
Solyc01g110100	RING/U-box superfamily protein (AHRD V3.3 *** AT3G53690.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART): IPR013083 (G3	4,057	3,785	2,332	4,803	4,227			0,845	0,031	1,031	0,001		up	up
Solyc01g110110	Cysteine proteinase (AHRD V3.3 *** C0KIY3_SOLLC)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (SM	0,198	0,222	0,162	0,241	0,234									
Solyc01g110120	V-type proton ATPase subunit a (AHRD V3.3 *** K4B3M5_SOLLC)		C:GO:0000220; F:G(	C:vacuolar proton-transporting V-type ATPase, V0 domain; F:pr	IPR026028 (PIRSF): IPR002490 (PFA	339,872	282,156	422,668	411,017	417,834									
Solyc01g110130	DNA helicase (AHRD V3.3 *** K4B3M6_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:3.6.1.15 Nucleoside-triphosph	IPR008047 (PRINTS): IPR001208 (PF	32,344	31,108	27,011	18,521	24,871					-0,539	0,030			down
Solyc01g110140	Calcium-transporting ATPase (AHRD V3.3 --* A0A0J8EL09_BETVU)				SRS	0,078	0,000	0,000	0,000	0,000									
Solyc01g110150	LOW QUALITY:prostatic spermine-binding-like protein (AHRD V3.3 *** AT4G34630.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	6,643	9,691	14,702	14,725	13,022									
Solyc01g110160	Ribosomal RNA small subunit methyltransferase H (AHRD V3.3 *** A0A1D1Y2V6_9ARAE)				PTHR36348 (PANTHER)	1,409	2,099	0,527	0,512	1,080									
Solyc01g110180	B-box zinc finger family protein (AHRD V3.3 *** AT4G39070.1)	BBX25	F:GO:0008270	F:zinc ion binding	IPR000315 (SMAF DBB	0,058	0,060	0,022	0,000	0,023									
Solyc01g110190	Kinesin-related protein (AHRD V3.3 *** D3YBF5_TRIRP)		F:GO:0003777; F:G(	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	5,251	12,870	2,376	2,176	2,229	1,319	0,000					up		
Solyc01g110230	LOW QUALITY:Protein Mei2 (AHRD V3.3 *-* A0A0U9HRM8_KLEFL)		F:GO:0003676	F:nucleic acid binding	IPR007201 (PFAM): IPR012677 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc01g110250	LOW QUALITY:ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 --* AT1G72700.3)					0,000	0,021	0,000	0,000	0,000									
Solyc01g110260	Protein Mei2 (AHRD V3.3 *-* A0A0U9HRM8_KLEFL)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	0,040	0,019	0,000	0,000	0,000									
Solyc01g110270	CRS1/YhbY domain protein (AHRD V3.3 *-* G7JIN8_MEDTR)		F:GO:0003723	F:RNA binding	IPR001890 (SMART): IPR001890 (PF	9,204	10,950	14,833	13,345	15,831									
Solyc01g110280	Protein DETOXIFICATION (AHRD V3.3 *** K4B3P1_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (PFAM): PTHR42893:SF9	3,817	3,313	4,124	4,601	5,110									
Solyc01g110290	Squalene synthase (AHRD V3.3 *** D0VFU8_SOLLC)		F:GO:0004310; P:G(	F:farnesyl-diphosph EC:2.5.1.29; EC:2.5. Geranylgeranyl diph(	IPR006449 (TIGRFAM): IPR008949 ((	63,277	96,120	56,693	58,239	54,303									
Solyc01g110300	BAR and SH3 domain-containing protein		F:GO:0005515	F:protein binding	IPR001452 (SMART): IPR001452 (PF	49,530	49,257	54,491	52,534	50,228									
Solyc01g110310	GATA transcription factor (AHRD V3.3 *** K4B3P4_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ion	IPR000679 (SMAF GATA	53,996	42,081	43,505	61,647	53,414					0,505	0,000			up
Solyc01g110330	N-acetyltransferase ESCO2 (AHRD V3.3 *** A0A1D1YG22_9ARAE)		P:GO:0000070; P:G(	P:mitotic sister chromatid segregation; P:sister chromatid cohe	IPR028005 (PFAM): IPR028009 (PFA	0,040	0,018	0,000	0,000	0,000									
Solyc01g110340	Endoglucanase (AHRD V3.3 *** M0ZU30_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	2,776	3,094	1,069	1,091	1,247									
Solyc01g110350	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G50420.2)				PTHR36388 (PANTHER)	5,402	4,368	4,619	4,440	3,659									
Solyc01g110360	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4B3P9_SOLLC)		F:GO:0004332; P:G(	F:fructose-bisphosp EC:4.1.2.13 Fructose-bisphospha	IPR000741 (PFAM): IPR013785 (G3D	197,542	487,708	35,716	37,265	115,209	1,330	0,000	1,685	0,000			up	up	
Solyc01g110370	Zinc finger, B-box (AHRD V3.3 *** A0A118K2C5_CYNCS)	BBX19	F:GO:0008270	F:zinc ion binding	IPR000315 (SMAF DBB	13,799	12,527	12,964	17,461	15,238									
Solyc01g110380	Kinesin-like protein (AHRD V3.3 *** K4B3Q1_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	59,087	52,465	49,618	52,854	48,839									
Solyc01g110385	NADH dehydrogenase 1 beta subcomplex subunit 9 (AHRD V3.3 *** A0A0K9P2C4_ZOSMR)		C:GO:0005747; P:G(	C:mitochondrial respiratory chain complex I; P:mitochondrial ele	IPR033034 (PANTHER)	82,273	90,383	169,766	157,664	157,417									
Solyc01g110400	30S ribosomal protein S31 (AHRD V3.3 *** A0A061DYK3_THECC),Pfam:PF17067		C:GO:0005840	C:ribosome	IPR030826 (TIGRFAM): IPR030826 (F	9,452	10,192	10,822	9,526	10,532									
Solyc01g110410	ubiquitin fusion degradation 1 (AHRD V3.3 *** AT2G21270.5)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process	G3DSA:3.10.330.10 (GENE3D): G3DS	95,393	95,062	126,460	135,885	129,084									
Solyc01g110440	arginine decarboxylase	TOMARGDECA	P:GO:0006527; P:G(	P:arginine catabolic EC:4.1.1.19 Arginine decarboxyla	IPR002985 (PRINTS): IPR000183 (PF	44,223	61,179	46,503	63,520	56,496									
Solyc01g110450	NADP dependent sorbitol 6-phosphate dehydrogenase family protein (AHRD V3.3 *** B9HRF0_POPTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020471 (PRINTS): IPR023210 (PF	139,403	135,043	185,355	139,421	161,836					-0,408	0,011			down
Solyc01g110460	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** B9H0Y7_POPTR)		F:GO:0003865; P:G(	F:3-oxo-5-alpha-ste EC:1.3.99.5 3-oxo-5-alpha-steroi(	IPR001104 (PFAM): IPR039698 (PAN	12,294	14,057	8,557	11,604	9,569									
Solyc01g110470	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN98_SOLTU)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR010409 (SMAF BBR-BPC	8,551	7,874	10,382	8,999	8,610									
Solyc01g110480	BZIP transcription factor (AHRD V3.3 *** G7JJX7_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	183,636	196,812	121,009	150,778	165,352					0,447	0,020			up
Solyc01g110490	Zinc finger transcription factor 15	C3H15	P:GO:0008033; F:G(	P:tRNA processing; F:tRNA dihydrouridine synthase activity; F:z	IPR013785 (G3DS C3H	43,316	39,322	43,058	40,136	40,731									
Solyc01g110500	ENTH/VHS family protein (AHRD V3.3 *** A0A061GXX0_THECC)				IPR013809 (SMART): IPR008942 (G3	0,119	0,043	0,046	0,222	0,094									
Solyc01g110510	ENTH/VHS family protein (AHRD V3.3 *** A0A061GXX0_THECC)				IPR013809 (SMART): IPR013809 (PF	0,254	0,206	0,464	0,540	0,498									
Solyc01g110530	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4B3R6_SOLLC)		F:GO:0003755	F:peptidyl-prolyl cis EC:5.2.1.8 Peptidylprolyl isomer	IPR000297 (PFAM): G3DSA:3.10.50.4	58,437	62,848	31,927	26,389	31,944									
Solyc01g110540	protein Aucsia-2		C:GO:0000276; F:G(	C:mitochondrial proton-transporting ATP synthase complex, cou	IPR008386 (PFAM): PTHR36028 (PAN	17,286	20,224	20,495	16,277	18,285									
Solyc01g110550	ribosome-binding factor A family protein (AHRD V3.3 *** AT4G34730.3)		P:GO:0006364	P:rRNA processing	IPR000238 (TIGRFAM): IPR000238 (F	9,136	13,759	13,852	14,734	19,434	0,618	0,049	0,486	0,017			up	up	
Solyc01g110560	Small auxin up-regulated RNA3	SAUR3	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	5,221	2,898	3,312	1,589	3,348					-1,059	0,014			down
Solyc01g110570	Small auxin up-regulated RNA4	SAUR4	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	0,215	0,214	0,000	0,000	0,000									
Solyc01g110580	Small auxin up-regulated RNA5	SAUR5	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	0,019	0,039	0,000	0,000	0,000									
Solyc01g110590	Small auxin up-regulated RNA6	SAUR6	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374:SF2	0,021	0,000	0,000	0,000	0,000									
Solyc01g110605	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G34760.1)		P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374:SF2	0,105	0,060	0,000	0,000	0,000									
Solyc01g110630	Small auxin up-regulated RNA9	SAUR9	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31929:SF1	0,021	0,021	0,000	0,025	0,070									

Solyc01g110640	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_MORIN)							0,392	0,841	1,098	1,518	1,083									
Solyc01g110643	DNA mismatch repair protein mutL (AHRD V3.3 --* A0A0B2SBZ1_GLYSO)							0,772	0,946	1,538	2,774	2,247					0,846	0,046			up
Solyc01g110647	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *-* A0A061E6C2_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,059	0,021	0,000	0,025	0,046									
Solyc01g110660	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G21210.2)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	1,128	0,985	0,776	0,778	0,567									
Solyc01g110670	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G21210.2)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	1,371	1,412	0,850	0,916	1,200									
Solyc01g110680	Small auxin up-regulated RNA12	SAUR12	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	3,112	2,536	1,703	2,677	2,097									
Solyc01g110682	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatchec				2,401	2,613	3,779	3,885	4,452									
Solyc01g110684	K-box region and MADS-box transcription factor family protein (AHRD V3.3 --* AT5G65070.6)							0,940	0,488	0,828	1,206	0,945									
Solyc01g110686	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatchec				0,474	0,485	0,489	0,762	0,967									
Solyc01g110688	CTP synthase (AHRD V3.3 --* A0A068U755_COFCA)							1,275	0,906	1,260	1,806	1,963									
Solyc01g110710	Small auxin up-regulated RNA10	SAUR10	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,116	0,062	0,050	0,000	0,046									
Solyc01g110720	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G21210.2)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	0,040	0,000	0,022	0,025	0,000									
Solyc01g110730	Auxin responsive SAUR protein (AHRD V3.3 *** A0A118K004_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,143	0,174	0,150	0,173	0,163									
Solyc01g110735	SAUR-like auxin-responsive protein family (AHRD V3.3 *-* AT5G18030.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	2,629	1,858	2,712	3,749	4,328									
Solyc01g110760	respiratory burst oxidase protein F (AHRD V3.3 --* AT1G64060.1)							0,199	0,119	0,316	0,300	0,258									
Solyc01g110780	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G38840.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	0,019	0,000	0,000	0,050	0,023									
Solyc01g110800	Small auxin up-regulated RNA19	SAUR19	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,058	0,064	0,000	0,025	0,094									
Solyc01g110810	Surfeit locus 1 cytochrome c oxidase biogenesis protein (AHRD V3.3 --* AT1G48510.4)							2,060	1,836	1,620	2,079	2,025									
Solyc01g110820	RNA binding protein, putative (AHRD V3.3 *** B9SHJ5_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	9,862	8,381	9,338	8,558	8,892									
Solyc01g110840	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein (AHRD V3.3 --* AT5G50780.3)							0,063	0,043	0,025	0,050	0,000									
Solyc01g110843	SAUR-like auxin-responsive protein family (AHRD V3.3 *** A0A061DYL9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF2	0,019	0,039	0,022	0,022	0,000									
Solyc01g110847	SAUR-like auxin-responsive protein family (AHRD V3.3 *** A0A061DYL9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF2	0,021	0,000	0,000	0,000	0,000									
Solyc01g110860	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G34770.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,195	0,204	0,122	0,123	0,117									
Solyc01g110870	SAUR-like auxin-responsive protein family (AHRD V3.3 *** A0A061DYL9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,101	0,021	0,047	0,096	0,071									
Solyc01g110880	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G38840.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF2	0,114	0,000	0,215	0,100	0,259									
Solyc01g110890	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G34770.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF2	0,060	0,000	0,000	0,025	0,046									
Solyc01g110910	Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,160	0,119	0,271	0,383	0,280									
Solyc01g110913	Auxin responsive SAUR protein (AHRD V3.3 *** A0A118K004_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,306	0,158	0,022	0,141	0,000									
Solyc01g110917	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G38840.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	1,041	1,098	0,890	0,969	1,179									
Solyc01g110920	Small auxin up-regulated RNA26	SAUR26	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	4,600	4,742	1,424	1,503	1,623									
Solyc01g110925	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 --* B9RG65_RICCO)							0,180	0,297	0,097	0,190	0,165									
Solyc01g110930	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT5G18030.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,316	0,334	0,217	0,122	0,165									
Solyc01g110940	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G38840.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF1	0,098	0,041	0,072	0,069	0,023									
Solyc01g110950	LOW QUALITY:DWNN domain, a CCHC-type zinc finger (AHRD V3.3 *-* AT5G47430.3)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR014891 (SMART): IPR014891 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc01g110960	Prefoldin chaperone subunit family protein, putative (AHRD V3.3 *** A0A061F1S1_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,000	8,759	1,316	0,880	0,872									
Solyc01g110970	Auxin responsive SAUR protein (AHRD V3.3 *-* A0A103Y0W3_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929:SF2	0,103	0,116	0,000	0,000	0,000									
Solyc01g110990	RNA helicase DEAH-box6	DEAH6	F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR022967 (SMART): IPR001650 (SM	64,510	71,447	56,244	63,819	63,959									
Solyc01g110995	4-coumarate:CoA ligase 1 (AHRD V3.3 --* AT1G51680.3)	4CL						0,536	0,497	0,777	0,859	0,757									
Solyc01g111000	Auxin responsive SAUR protein (AHRD V3.3 *** A0A118K2C1_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	1,808	1,106	1,242	1,592	1,366									
Solyc01g111010	X-intrinsic protein 1.6	XIP1.6	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAI	0,697	0,757	0,459	0,317	0,281									
Solyc01g111020	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T729_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	78,791	129,689	83,440	89,078	116,911	0,745	0,008	0,483	0,031			up	up	
Solyc01g111070	Chalcone synthase, putative (AHRD V3.3 *** B9STD8_RICCO)	CHS	P:GO:0009058; F:G(	P:biosynthetic process; F:transferase activity, transferring acyl			IPR001099 (PFAM): IPR011141 (PIRS	0,040	0,018	0,000	0,048	0,000									
Solyc01g111080	Unknown protein (AHRD V3.3)							1,130	1,276	4,150	6,129	4,202									
Solyc01g111090	ER lumen protein retaining receptor family protein (AHRD V3.3 *** AT4G38790.1)		P:GO:0006621; C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS): IPR000133 (PF	24,376	23,178	27,878	29,728	27,389									
Solyc01g111100	Alkaline and neutral invertase		F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetylc	IPR012341 (G3DSA:1.50.10.GENE3D	3,788	6,680	0,193	0,050	0,047									
Solyc01g111110	Oxidoreductase/transition metal ion-binding protein (AHRD V3.3 -** A2Q3C9_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33306:SF7 (PANTHER): PTHR3:	16,043	8,754	4,890	3,494	3,101									
Solyc01g111120	triosephosphate isomerase (AHRD V3.3 *** AT2G21170.3)		F:GO:0004807; P:G(	F:triose-phosphate	EC:5.3.1.1	Triose-phosphate isc	IPR000652 (PFAM): IPR013785 (G3D	140,378	180,296	191,896	161,959	194,156									
Solyc01g111130	bHLH transcription factor 011		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	16,631	14,344	20,043	19,922	18,008									
Solyc01g111140	Protein XAP5 CIRCADIAN TIMEKEEPER (AHRD V3.3 *** XCT_ORYSJ)		C:GO:0005634	C:nucleus			IPR007005 (PFAM): mobidb-lite (MOB	35,842	32,854	26,335	22,880	26,750									
Solyc01g111145	Proline-rich protein (AHRD V3.3 *-* O82066_SOLTU)						PR01217 (PRINTS): PF01190 (PFAM)	288,936	253,459	0,951	0,791	0,615									
Solyc01g111150	Translocon-associated protein subunit alpha (AHRD V3.3 *** W9QKE0_9ROSA)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR005595 (PFAM): PTHR12924 (PAI	78,309	87,662	154,238	156,842	138,445									
Solyc01g111170	diageotropica	cyp	P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR029000 (G3	1690,918	1757,401	1091,211	908,309	1078,030									
Solyc01g111190	magnesium transporter NIPA (DUF803) (AHRD V3.3 *-* AT3G23870.4)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM): PTHR12570:SF1	3,366	3,466	2,744	3,372	3,435									
Solyc01g111200	Translation initiation factor (AHRD V3.3 *** E5GC13_CUCME)		F:GO:0003743	F:translation initiation factor activity			IPR010433 (PFAM): mobidb-lite (MOB	128,268	158,856	116,289	116,739	110,132									
Solyc01g111210	Amidase, putative (AHRD V3.3 *** B9SQJ8_RICCO)		F:GO:0016740	F:transferase activity			IPR023631 (PFAM): PF01190 (PFAM)	18,160	14,004	2,176	2,325	2,894									
Solyc01g111220	Amidase family protein (AHRD V3.3 *** B9H162_POPTR)						IPR023631 (PFAM): IPR036928 (G3D	7,175	5,619	0,271	0,244	0,283									
Solyc01g111230	Dirigent protein (AHRD V3.3 *** K4B3Y5_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAI	80,027	34,221	0,843	0,137	0,494	-1,196	0,000					down		
Solyc01g111235	Dirigent protein (AHRD V3.3 *** M0ZMW5_SOLTU)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495:SF7	0,259	0,259	0,044	0,000	0,000									
Solyc01g111240	Translocase of chloroplast (AHRD V3.3 *-* A0A0K9PF83_ZOSMR)		F:GO:0005525; F:G(	F:GTP binding; F:hydrolase activity, acting on acid anhydrides			IPR024283 (PFAM): IPR006703 (PFAI	232,406	208,775	195,094	181,579	201,286									
Solyc01g111250	1-phosphatidylinositol phosphodiesterase-related family protein (AHRD V3.3 *** B9H168_POPTR)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR000909 (SMART): IPR000909 (PF.	1,670	6,325	62,350	101,001	57,815	1,938	0,045			0,699	0,000	up		up
Solyc01g111260	1-phosphatidylinositol phosphodiesterase-related family protein (AHRD V3.3 *** B9H168_POPTR)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR000909 (SMART): IPR000909 (PF.	152,133	129,784	50,797	42,758	49,767									
Solyc01g111270	Armadillo repeat only protein (AHRD V3.3 *** A0A072UNA0_MEDTR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	35,595	15,547	11,409	5,023	9,654	-1,164	0,000			-1,180	0,007	down		down
Solyc01g111280	cold shock domain protein 1 (AHRD V3.3 *** AT4G36020.2)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR002059 (PRINTS): IPR001878 (SM	9,295	5,463	3,389	2,289	2,589									
Solyc01g111300	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							118,268	123,679	86,798	76,809	77,483									
Solyc01g111310	SILAX2	LAX2	P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): PTHR22950:SF3	2,311	2,796	0,143	0,243	0,143									
Solyc01g111320	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UM98_MEDTR)						IPR001938 (PRINTS): IPR001938 (SM	10,270	8,914	7,726	6,741	6,629									
Solyc01g111330	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UXB7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS): IPR001938 (SM	1,476	1,778	0,072	0,125	0,069									
Solyc01g111340	Endo-1,4-beta-xylanase A (AHRD V3.3 *** W9QKK9_9ROSA)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001000 (PRINTS): IPR001000 (SM	7,010	11,982	41,045	36,554	29,933			-0,458	0,022				down	
Solyc01g111350	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9P7P6_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM): G3DSA:1.20.125	361,104	321,508	1069,285	1127,171	914,566									
Solyc01g111360	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4B3Z8_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR029000 (G3	24,540	23,306	75,996	58,965	53,565			-0,507	0,023				down	
Solyc01g111370	Choline transporter-related family protein (AHRD V3.3 *** B9HR78_POPTR)		C:GO:0016021	C:integral component of membrane			IPR007603 (PFAM): mobidb-lite (MOB	26,897	21,149	28,459	31,592	27,384									
Solyc01g111380	Actin-depolymerizing factor (AHRD V3.3 *** A0A151TUH5_CAJCA)		F:GO:0003779; C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymei			IPR002108 (SMART): IPR002108 (PF.	15,740	12,288	5,323	5,458	6,276									
Solyc01g111400	Subtilisin-like protease (AHRD V3.3 *** W9QT04_9ROSA)		F:GO:0004252; P:G(	F:serine-type endo|	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	123,702	76,769	102,230	73,207	87,963	-0,660	0,023			-0,479	0,006	down		down
Solyc01g111410	Protein prenyltransferase alpha subunit repeat-containing protein 1 (AHRD V3.3 *** W9RT57_9ROSA)		F:GO:0008318; P:G(	F:protein prenyltransferase activity; P:protein prenylation			IPR002088 (PFAM): G3DSA:1.25.40.1	18,294	18,191	21,231	21,893	22,476									
Solyc01g111420	Ribosomal protein L1p/L10e family (AHRD V3.3 *** AT3G58660.1)		P:GO:0000470; F:G(	P:maturation of LSU-rRNA; F:RNA binding; C:90S preribosome			IPR016095 (G3DSA:3.40.50.GENE3D	45,083	45,800	32,338	25,812	27,682									
Solyc01g111430	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061DY90_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	0,861	1,438	0,527	0,640	0,682									
Solyc01g111440	Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)		C:GO:0005886	C:plasma membrane			IPR009686 (PFAM): mobidb-lite (MOB	125,974	235,107	123,998	138,420	137,655	0,923	0,040					up		
Solyc01g111450	LEY14339 proteasome, alpha subunit	psr5	F:GO:0004298; P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000426 (SMART): IPR000426 (PF.	74,403	84,401	116,474	113,672	106,603									
Solyc01g111455	Proteasome subunit alpha type (AHRD V3.3 *-* A0A151RN76_CAJCA)		F:GO:0004298; C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bonds (peptidases)		1,747	1,751	2,007	2,043	1,860									
Solyc01g111460	Proteasome subunit alpha type (AHRD V3.3 *-* K4B407_SOLLC)		F:GO:0004298; C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	1,926	2,190	2,396	2,137	2,399									
Solyc01g111470	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061FPD8_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	11,170	8,196	8,242	9,109	9,498									
Solyc01g111500	R2R3MYB transcription factor 7	R2R3MYB7	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,814	1,115	0,712	0,868	1,011									
Solyc01g111510	Ascorbate peroxidase (AHRD V3.3 *** J9Z324_CAPFR)	APX4	F:GO:0004601; P:G(	F:peroxidase activil	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS): IPR002016 (PF	185,340	244,102	223,686	211,600	300,938			0,425	0,008				up	
Solyc01g111520	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G20080.5)		F:GO:0008289	F:lipid binding			IPR000008 (PRINTS): IPR000008 (SM	150,739	192,965	130,892	119,450	128,283									
Solyc01g111530	E3 ubiquitin-protein ligase (AHRD V3.3 *** G7JNF2_MEDTR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			IPR000569 (SMART): G3DSA:3.30.21	245,600	258,182	263,894	265,346	265,812									
Solyc01g111540	Beta-galactosidase (AHRD V3.3 *** M1A6P4_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): PF17834 (PFAI	1,194	0,936	0,050	0,073	0,047									
Solyc01g111550	minichromosome maintenance 10 (AHRD V3.3 *** AT2G20980.1)		F:GO:0003690; F:G(	F:double-stranded DNA binding; F:single-stranded DNA binding;			IPR015408 (PFAM): G3DSA:2.40.50.1	2,469	2,136	0,352	0,122	0,236									
Solyc01g111560	Rac-like GTP-binding protein (AHRD V3.3 *** Q1PCH8_SOLCH)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	44,559	36,909	23,836	28,301	27,254									
Solyc01g111570	Kinase family protein (AHRD V3.3 *** B9H1A0_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	78,601	55,135	4,804	2,820	3,031									
Solyc01g111580	BZIP transcription factor (AHRD V3.3 *** B7FIL7_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	32,657	26,743	23,061	25,427	22,648									
Solyc01g111590	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G16780.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,466	0,864	0,373	0,335	0,518									
Solyc01g111600	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT4G35060.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	52,832	64,769	32,006	30,583	31,589									
Solyc01g111610	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT4G35070.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR013083 (G3DSA:3.30.40.GENE3D	0,748	0,706	0,075	0,025	0,095									
Solyc01g111620	high-affinity nickel-transport family protein (AHRD V3.3 *** AT2G16800.1)		C:GO:0016021	C:integral component of membrane			PTHR33876 (PANTHER): PTHR33876	22,040	34,071	33,406	29,376	36,925	0,655	0,031					up		
Solyc01g111630	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *-* AT4G34200.1)		F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0(	182,295	256,161	133,564	137,122	288,644			1,108	0,000				up	
Solyc01g111640	SKP1-like protein (AHRD V3.3 *** C3V9V9_CITMA)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR001232 (SMART): IPR016072 (PF.	3,089	5,324	0,647	1,395	0,688									
Solyc01g111650	Skp1 (AHRD V3.3 *** Q49HP3_CAPAN)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR001232 (SMART): IPR016072 (PF.	130,462	131,764	184,924	162,032	163,938									
Solyc01g111660	plasma membrane intrinsic protein 2.8	PIP2.8	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	3,588	3,713	0,572	1,118	1,784			1,609	0,003				up	
Solyc01g111670	transmembrane protein, putative (DUF1279) (AHRD V3.3 *** AT2G20940.2)		C:GO:0016021	C:integral component of membrane			IPR009688 (PFAM): PTHR21377 (PAI	5,806	6,760	9,409	8,948	8,624									
Solyc01g111680	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A0A7RAT3_9ROSI)						SM00212 (SMART): IPR016135 (G3D	38,820	31,577	34,680	36,095	36,222									
Solyc01g111690	Trafficking protein particle complex subunit 2-like protein (AHRD V3.3 *** A0A0B2QQK3_GLYSO)		C:GO:0005622; P:G(	C:intracellular; P:endoplasmic reticulum to Golgi vesicle-mediate			IPR006722 (PFAM): G3DSA:3.30.450	7,795	7,974	6,674	6,106	6,651									
Solyc01g111700	26S proteasome non-ATPase regulatory subunit 3 (AHRD V3.3 *** G7J5U6_MEDTR)		C:GO:0000502; F:G(	C:proteasome complex; F:enzyme regulator activity; P:regulatio			IPR000717 (SMART): SM00753 (SMA	0,240	0,460	0,100	0,099	0,117									
Solyc01g111710	PCI superfamily protein		C:GO:0000502; F:G(	C:proteasome complex; F:enzyme regulator activity; P:regulatio			SM00753 (SMART): IPR000717 (SMA	115,258	116,346	146,142	145,373	136,194									
Solyc01g111720	Translation initiation factor if-3, putative (AHRD V3.3 *** B9RJ84_RICCO)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			IPR019815 (PFAM): IPR019814 (PFAI	35,447	31,333	53,953	48,775	44,723									
Solyc01g111730	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G38520.2)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	55,469	53,505	67,455	65,156	66,466									
Solyc01g111740	bZIP transcription factor, putative (DUF630 and DUF632) (AHRD V3.3 *-* AT4G39790.1)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM): IPR006868 (PFAI	15,576	11,484	5,148	3,008	3,901					-0,764	0,028			down
Solyc01g111750	Chaperone DnaJ (AHRD V3.3 *** A0A0B0PUN1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR021788 (PFAM): mobidb-lite (MOB	2,876	3,377	8,396	8,935	9,313									
Solyc01g111760	ATP synthase subunit beta vacuolar, putative (AHRD V3.3 *-* B9R8F3_RICCO)		P:GO:0046034; P:G(	P:ATP metabolic process; P:proton transmembrane transport			IPR004100 (PFAM): G3DSA:3.40.50.1	262,371	244,649	282,001	289,896	286,837									
Solyc01g111765	Sept9 (DUF616) (AHRD V3.3 *** AT4G38500.1)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): mobidb-lite (MOB	30,069	26,746	33,743	29,957	29,617									
Solyc01g111780	transportin 1 (AHRD V3.3 *** AT2G16950.2)		P:GO:0006606; F:G(	P:protein import into nucleus; F:Ran GTPase binding			IPR001494 (SMART): PF13513 (PFAI	115,934	107,117	122,793	119,783	120,164									
Solyc01g111790	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9IFU5_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR002554 (PFAM): IPR011989 (G3D	0,260	0,219	0,195	0,269	0,284									
Solyc01g111800	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR002293 (PIRSF): G3DSA:1.20.174	1,431	1,123	1,617	1,220	1,316									
Solyc01g111810	L18 ribosomal protein Heart Stopper (AHRD V3.3 *** A0A0I9RJ77_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005484 (PFAM): IPR036967 (G3D	13,925	17,427	11,422	10,640	11,497									
Solyc01g111820	LOW QUALITY:Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 --* AT5G36740.5)						PTHR34569 (PANTHER): PTHR34569	0,056	0,095	0,000	0,050	0,000									
Solyc01g111830	Methyltransferase (AHRD V3.3 *** K4B445_SOLLC)		P:GO:0006694; F:G(	P:steroid biosynthetic process; F:methyltransferase activity			IPR013705 (PFAM): IPR013216 (PFAI	144,086	123,058	30,723	30,635	41,624									
Solyc01g111840	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM): G3DSA:1.20.125	7,706	6,339	4,847	4,827	3,978									
Solyc01g111860	Transducin/WD-like repeat-protein (AHRD V3.3 *** A0A072VRM2_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	19,158	20,058	22,979	21,499	20,958									
Solyc01g111870	Serine/threonine-protein kinase ATR, putative (AHRD V3.3 *** B9S5G9_RICCO)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phosphc	IPR003152 (SMART): IPR012993 (SM	8,964	7,749	3,735	3,866	4,041									
Solyc01g111880	MAP kinase kinase kinase 11	MAPKKK11	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	1,811	2,251	1,424	2,146	2,234									
Solyc01g111890	F-box family protein (AHRD V3.3 *** B9HR17_POPTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR032675 (G3	34,135	28,123	18,271	18,265	19,874									
Solyc01g111900	O-methyltransferase, putative (AHRD V3.3 *** B9SUX6_RICCO)		F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity			IPR036388 (G3DSA:1.10.10.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc01g111910	RNA polymerase II-associated protein 1, putative (AHRD V3.3 *** A0A061DXN5_THECC)		P:GO:0006366	P:transcription by RNA polymerase II			IPR013929 (PFAM): IPR013930 (PFAI	53,900	39,499	67,749	69,623	65,366									
Solyc01g111920	F-box protein SKIP23 (AHRD V3.3 *** W9RTM3_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	45,603	31,542	41,500	49,059	42,137									
Solyc01g111930	DNA repair DEAD helicase RAD3/XP-D subfamily protein (AHRD V3.3 --* AT2G05635.2)							0,081	0,101	0,050	0,025	0,023									
Solyc01g111937	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9SR08_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.2010 (GENE3D): IPR(	4,983	5,425	0,897	0,791	0,988									
Solyc01g111940	Coiled-coil domain-containing protein 124 (AHRD V3.3 *** A0A199VGP5_ANACO)						IPR010422 (PFAM): mobidb-lite (MOB	36,240	37,964	72,057	70,334	62,557									
Solyc01g111950	Proline-rich receptor-like protein kinase PERK1 (AHRD V3.3 *** W9RKU6_9ROSA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	0,619	0,849	0,653	1,489	1,036									
Solyc01g111960	GDSL esterase/lipase family (AHRD V3.3 *** A0A151QLH4_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,042	0,021	0,125	0,325	0,118									
Solyc01g111970	L-ascorbate oxidase-like protein (AHRD V3.3 *** W9RW65_9ROSA)		F:GO:0005507; F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	14,405	16,298	76,464	128,185	82,730					0,747	0,005			up
Solyc01g111980	Amino acid transporter, putative (AHRD V3.3 *** B9SQZ7_RICCO)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): PTHR22950 (PAI	158,055	428,884	39,473	66,332	72,091	1,459	0,036			0,750	0,020	up		up
Solyc01g111990	Alanine--tRNA ligase (AHRD V3.3 *** A0A0R0JGB6_SOYBN)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:6.1.1.7	Alanine--tRNA ligase	IPR002318 (PRINTS): IPR012947 (SM	31,301	35,705	53,975	53,933	67,758									
Solyc01g112000	expansin-like protein precursor 1	EXLA1	C:GO:0005576; P:G(	C:extracellular region; P:sexual reproduction			IPR007118 (PRINTS): IPR005795 (PF	148,635	134,786	43,804	56,644	80,292			0,871	0,040				up	
Solyc01g112010	Pre-rRNA-processing protein esf2 (AHRD V3.3 *-* A0A0B2SES6_GLYSO)		F:GO:0003723	F:RNA binding			IPR039119 (PANTHER)	3,998	2,925	2,217	1,066	1,941					-1,043	0,016			down
Solyc01g112020	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A0G2T442_9ROSI)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	52,362	61,292	71,996	64,969	65,143									
Solyc01g112040	LOW QUALITY:Cyclic nucleotide-gated ion channel 1 (AHRD V3.3 --* B6U0R1_MAIZE)							0,942	1,128	0,946	0,663	1,205									
Solyc01g112050	DUF630 family protein, putative (DUF630 and DUF632) (AHRD V3.3 *** AT1G21740.1)		P:GO:0071249	P:cellular response to nitrate			IPR006868 (PFAM): IPR006867 (PFAI	65,736	70,757	47,954	56,733	59,574									
Solyc01g112060	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G35250.1)		F:GO:0050446; P:G(	F:azobenzene reduc	EC:1.7.1.6	Azobenzene reductas	G3DSA:3.40.50.720 (GENE3D): IPR0(	17,311	35,801	18,008	19,206	39,361	1,075	0,000	1,127	0,000			up	up	
Solyc01g112070	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G20550.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF): IPR019378 (PFA	1,943	1,428	1,194	2,216	2,169									
Solyc01g112080	LysM domain GPI-anchored protein (AHRD V3.3 *** G8A1U1_MEDTR)		F:GO:0008061; C:G(	F:chitin binding; C:plasmodesma; C:integral component of memt			IPR018392 (SMART): IPR036779 (G3	17,122	20,861	4,972	5,535	7,461									
Solyc01g112090	Protein DETOXIFICATION (AHRD V3.3 *** K4B470_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	2,154	2,680	0,571	0,645	0,542									
Solyc01g112120	Flavin-containing monooxygenase (AHRD V3.3 *** M1BLU2_SOLTU)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.:	Flavin-containing mo	IPR020946 (PFAM): IPR036188 (G3D	24,174	12,416	128,652	144,008	128,221	-0,933	0,015					down		

Solyc01g112130	Flavin-containing monooxygenase (AHRD V3.3 *** M1B691_SOLTU)		F:GO:0004499; F:GC	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.'	Flavin-containing mo	IPR036188 (G3DSA:3.50.50.GENE3D	3,535	2,924	27,120	28,662	27,236									
Solyc01g112140	Flavin-containing monooxygenase (AHRD V3.3 *** M1B691_SOLTU)		F:GO:0004499; F:GC	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.'	Flavin-containing mo	IPR036188 (G3DSA:3.50.50.GENE3D	6,001	8,721	1,574	1,704	2,065									
Solyc01g112150	SEC1-family transport family protein (AHRD V3.3 *** B9MYY5_POPTR)		P:GO:0006904	P:vesicle docking involved in exocytosis			IPR027482 (G3DSA:3.40.50.GENE3D	49,099	59,235	65,039	61,226	59,479									
Solyc01g112160	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT4G38370.1)		C:GO:0005829	C:cytosol			PIRSF000709 (PIRSF): IPR013078 (F	5,564	5,829	9,381	8,200	8,466									
Solyc01g112165	F-box family protein (AHRD V3.3 --* AT5G39250.2)							0,019	0,041	0,000	0,000	0,070									
Solyc01g112170	Calcium-dependent protein kinase 23 isoform 1 (AHRD V3.3 *** A0A061G9K4_THECC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	11,313	10,981	14,015	13,416	12,740									
Solyc01g112175	RNA polymerase II transcriptional coactivator (AHRD V3.3 --* G7JC59_MEDTR)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR009044 (G3DSA:2.30.31.GENE3D	1,877	1,637	1,367	2,027	1,582									
Solyc01g112180	integral membrane hemolysin-III-like protein (AHRD V3.3 *-* AT4G38280.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	17,159	13,787	24,697	24,092	22,855									
Solyc01g112190	Plant regulator RWP-RK family protein (AHRD V3.3 *** AT4G35270.4)		F:GO:0005515	F:protein binding			IPR000270 (SMAF Nin-like	12,480	9,033	1,036	1,879	1,593									
Solyc01g112200	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9MYZ7_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	2,922	3,454	3,293	2,977	2,894									
Solyc01g112210	Hexosyltransferase (AHRD V3.3 *** M1B698_SOLTU)	GAUT3	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	34,355	24,795	26,762	24,707	23,850									
Solyc01g112220	Kinase family protein (AHRD V3.3 *** U5GGQ9_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	8,716	15,638	6,741	4,983	7,180									
Solyc01g112230	Metallothionein-like protein (AHRD V3.3 *** Q9FUJ8_SESIN)		F:GO:0008270	F:zinc ion binding			IPR000316 (PRINTS): IPR000316 (PF	22,621	26,572	2,575	5,304	0,395									
Solyc01g112240	Ribonuclease S-5 (AHRD V3.3 --* RNS5_PYRPY)							7,113	6,636	9,581	10,185	8,879									
Solyc01g112245	Alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (AHRD V3.3 *** Q9ST97_TOBA(		P:GO:0006486; F:GC	P:protein glycosylation; F:acetylglucosaminyltransferase activit			IPR004139 (PFAM): IPR029044 (G3D	19,890	19,828	29,358	31,190	27,799									
Solyc01g112250	Calcium-dependent protein kinase family protein (AHRD V3.3 *** AT2G17290.2)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): IPR002048 (SM	72,711	69,153	83,515	86,398	80,209									
Solyc01g112260	Phosphoenolpyruvate carboxylase (AHRD V3.3 --* A7DX51_9POAL)						PTHR35714 (PANTHER): PTHR35714	113,442	61,645	7,699	8,153	11,974	-0,854	0,001					down		
Solyc01g112270	LOW QUALITY:pantothenate kinase (AHRD V3.3 *** AT4G35360.3)						IPR002791 (PFAM): PTHR12280:SF3	0,079	0,105	0,093	0,145	0,211									
Solyc01g112280	partialaminoacylase-1	ctd3	F:GO:0004046; C:GC	F:aminoacylase act	EC:3.5.1.14	N-acyl-aliphatic-L-am	IPR002933 (PFAM): G3DSA:3.30.70.1	150,152	104,264	144,865	104,256	124,630					-0,471	0,005			down
Solyc01g112290	glutamate tRNA synthetase (AHRD V3.3 *-* AT5G64050.1)		F:GO:0000049; F:GC	F:tRNA binding; F:g	EC:6.1.1.17	Glutamate--tRNA liga	IPR000924 (PRINTS): IPR014729 (G3	116,949	126,712	186,062	175,440	190,579									
Solyc01g112300	Chloride channel protein (AHRD V3.3 *-* A0A0V0ITC5_SOLCH)		F:GO:0005247; P:GC	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR001807 (PRINTS): IPR014743 (G3	6,770	6,200	7,920	7,176	7,609									
Solyc01g112303	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT4G21330.1)							0,021	0,021	0,000	0,025	0,070									
Solyc01g112305	U-box domain-containing protein 54 (AHRD V3.3 --* PUB54_ARATH)							0,000	0,021	0,025	0,000	0,047									
Solyc01g112310	Chloride channel protein (AHRD V3.3 *** A0A0V0ITC5_SOLCH)		F:GO:0005247; P:GC	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR000644 (SMART): IPR001807 (PF	5,661	5,044	7,345	7,465	7,283									
Solyc01g112320	FAR1-related sequence 5 (AHRD V3.3 *** AT4G38180.1)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	29,538	22,697	40,360	41,254	39,684									
Solyc01g112340	Brefeldin A-inhibited guanine nucleotide-exchange protein (AHRD V3.3 *-* G7KFH4_MEDTR)		F:GO:0005086; P:GC	F:ARF guanyl-nucleotide exchange factor activity; P:regulation (			IPR032629 (PFAM): PTHR10663:SF1	28,071	21,583	30,727	33,199	31,237									
Solyc01g112350	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (AHRD V3.3 *** A0A0B2R8L7_GLYSO)		F:GO:0005086; P:GC	F:ARF guanyl-nucleotide exchange factor activity; P:regulation (			IPR000904 (SMART): IPR015403 (PF	97,606	87,323	124,447	127,521	117,900									
Solyc01g112370	LOW QUALITY:DUF3128 family protein (AHRD V3.3 *** G7J0G9_MEDTR)						IPR021475 (PFAM): IPR021475 (PAN	0,000	0,000	0,000	0,022	0,000									
Solyc01g112380	LOW QUALITY:Unknown protein (AHRD V3.3)							0,138	0,179	0,068	0,047	0,047									
Solyc01g113450	LOW QUALITY:DEAD-box ATP-dependent RNA helicase 29 (AHRD V3.3 --* RH29_ORYSI)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,056	0,130	0,000	0,000	0,000									
Solyc01g113620	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.4)		F:GO:0005515; F:GC	F:protein binding; F:ADP binding			PR00364 (PRINTS): IPR035897 (G3D	7,072	5,132	3,344	3,345	3,746									
Solyc01g150007	Serine/threonine-protein kinase (AHRD V3.3 *-* M1DYE5_SOLTU)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	PTHR32444 (PANTHER): PTHR32444	0,000	0,000	0,000	0,048	0,000									
Solyc02g005060	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR015894 (PFAM): G3DSA:3.40.50.3	1,611	1,415	0,967	0,473	0,654									
Solyc02g005070	arginine-rich cyclin 1 (AHRD V3.3 --* AT2G26430.4)						mobidb-lite (MOBIDB_LITE)	2,369	1,565	1,406	0,879	0,960									
Solyc02g005100	LOW QUALITY:Unknown protein (AHRD V3.3)							2,419	3,010	3,198	4,145	3,737									
Solyc02g005110	Homeobox leucine-zipper protein (AHRD V3.3 --* Q8H963_ZINVI)		F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA binding; F:DNA binding; F:DNA-binding tr				6,375	5,747	1,615	1,464	1,782									
Solyc02g005140	GPI-anchored adhesin-like protein, putative (Protein of unknown function, DUF547) (AHRD V3.3 --* AT1G16750.1)							0,077	0,021	0,000	0,000	0,023									
Solyc02g005180	Sugar facilitator protein 2	SFP2	C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	12,895	13,099	11,083	12,447	12,812									
Solyc02g005185	COP1-interactive protein 1 (AHRD V3.3 --* AT5G41790.2)							0,021	0,060	0,025	0,048	0,023									
Solyc02g005200	RNA binding protein (AHRD V3.3 *** AT3G08010.1)		F:GO:0003723	F:RNA binding			IPR009472 (PFAM): PTHR34556:SF2	30,952	31,659	161,954	265,819	194,196					0,718	0,000			up
Solyc02g005210	cofactor assembly of complex C (AHRD V3.3 *** AT3G26710.1)		C:GO:0016021	C:integral component of membrane			IPR021919 (PFAM): IPR021919 (PAN	26,701	29,841	72,687	80,912	73,969									
Solyc02g005280	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061E854_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,257	1,631	1,954	2,133	1,859									
Solyc02g005290	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *-* A0A0K9P1Y7_ZOSMR)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAN GeBP	14,382	14,644	13,393	14,697	13,982									
Solyc02g005310	DNA glycosylase (AHRD V3.3 *** A0A103X5G9_CYNCS)		F:GO:0003824; P:GC	F:catalytic activity; P:base-excision repair			G3DSA:1.10.340.30 (GENE3D): IPR0(	1,469	0,975	1,377	1,273	1,080									
Solyc02g005315	dynamin-like protein (AHRD V3.3 --* AT5G42080.4)		F:GO:0016853	F:isomerase activity				0,019	0,018	0,000	0,000	0,000									
Solyc02g005320	ARM repeat superfamily protein (AHRD V3.3 --* AT5G18980.3)							4,529	2,821	4,616	6,190	4,913									
Solyc02g005340	Oligopeptide transporter, putative (AHRD V3.3 *** B9T1I2_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM): IPR004813 (TIGF	7,479	5,591	7,011	4,894	6,635									
Solyc02g005350	succinyl-CoA ligase alpha 2 subunit	scoa2	F:GO:0003824; F:GC	F:catalytic activity; F:cofactor binding			PR01798 (PRINTS): IPR003781 (SMA	8,903	9,329	14,001	20,365	13,658					0,544	0,005			up
Solyc02g005360	Transposon protein, putative, CACTA, En/Spm sub-class, expressed (AHRD V3.3 *-* Q2QSV4_ORYSJ)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,000	0,046									
Solyc02g005370	LOW QUALITY:Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *-* W9QQU0_9ROSA)		C:GO:0000932; P:GC	C:P-body; P:deadenylation-independent decapping of nuclear-tr			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc02g005423	Pectinesterase (AHRD V3.3 *-* K4CWJ9_SOLLC)		F:GO:0030599; P:GC	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Carboxylesterase		0,000	0,018	0,000	0,022	0,023									
Solyc02g005430	Conglutin beta 7 (AHRD V3.3 --* CONB7_LUPAN)							0,000	0,043	0,075	0,101	0,093									
Solyc02g005480	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19910.1)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	37,570	35,313	34,328	32,284	33,619									
Solyc02g005490	60S acidic ribosomal protein family (AHRD V3.3 *** AT5G24510.1),Pfam:PF00428		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translationa			PF00428 (PFAM): IPR038716 (G3DSA	0,019	0,082	0,000	0,000	0,023									
Solyc02g005510	Transcriptional coactivator/pterin dehydratase (AHRD V3.3 *** AT1G29810.1)		P:GO:0006729; F:GC	P:tetrahydrobiopteri	EC:4.2.1.96	4a-hydroxytetrahydrc	IPR036428 (G3DSA:3.30.1360.GENE	16,786	19,133	21,566	22,180	23,380									
Solyc02g005517	PIF1-like helicase (AHRD V3.3 *-* A0A072TJC6_MEDTR)		P:GO:0000723; F:GC	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	0,158	0,043	0,165	0,099	0,236									
Solyc02g005530	PIF1-like helicase (AHRD V3.3 *-* A0A072TSL1_MEDTR)						G3DSA:2.40.50.140 (GENE3D): mobic	0,059	0,037	0,047	0,025	0,048									
Solyc02g005600	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase-like protein (AHRD V3.3 *-* A0A072U6X5_MEDTR)		P:GO:0016579; F:GC	P:protein deubiquitii	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM): G3DSA:3.90.70.1	0,000	0,000	0,000	0,048	0,000									
Solyc02g010600	Ribosomal protein S12 (AHRD V3.3 *** A0A060DDV2_9GENT)		F:GO:0003735; P:GC	F:structural constituent of ribosome; P:translation; C:small ribos			IPR006032 (PRINTS): G3DSA:2.40.5(	0,000	0,021	0,025	0,050	0,000									
Solyc02g011680	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151SIU7_CAJCA)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	1,369	1,919	2,142	2,178	2,022									
Solyc02g011690	LOW QUALITY:Cyclin-dependent kinases regulatory subunit 2 (AHRD V3.3 --* CKS2_ARATH)							0,000	0,000	0,025	0,000	0,000									
Solyc02g011700	Plasma membrane ATPase (AHRD V3.3 *-* B9HCD3_POPTR)		F:GO:0005524; C:GC	F:ATP binding; C:pl	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	G3DSA:1.20.1110.10 (GENE3D): PTH	0,000	0,000	0,025	0,000	0,000									
Solyc02g011710	NADH dehydrogenase subunit (AHRD V3.3 *-* M1R1Z2_SOLCA)		C:GO:0009507; C:GC	C:chloroplast; C:thylakoid; C:membrane; F:oxidoreductase activ			PR01434 (PRINTS): IPR001750 (PFA	0,000	0,000	0,000	0,050	0,000									
Solyc02g011740	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_TOBAC)		F:GO:0008137; P:GC	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR003918 (PANTHER): IPR003918 (I	0,000	0,041	0,022	0,050	0,023									
Solyc02g011750	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLLC)		F:GO:0008137; P:GC	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM): IPR022997 (PTH	0,019	0,081	0,044	0,022	0,046									
Solyc02g011760	Photosystem I iron-sulfur center (AHRD V3.3 *-* PSAC_SOYBN)		C:GO:0005739; F:GC	C:mitochondrion; F:electron transfer activity; C:photosystem I; (			G3DSA:3.30.70.20 (GENE3D): IPR01	0,000	0,043	0,000	0,000	0,000									
Solyc02g011800	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 *-* NU1C_NICSY)		C:GO:0016020; P:GC	C:membrane; P:oxidation-reduction process			IPR001694 (PFAM): IPR001694 (PAN	0,019	0,206	0,100	0,143	0,093									
Solyc02g011810	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_TOBAC)		F:GO:0016651; F:GC	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindii			IPR001135 (PFAM): IPR038290 (G3D	0,019	0,000	0,025	0,025	0,023									
Solyc02g011815	30S ribosomal protein S15, chloroplastic (AHRD V3.3 *-* RR15_SOLLC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.287.10 (GENE3D): IPR0(	0,019	0,021	0,000	0,126	0,048									
Solyc02g011930	Protein Ycf2 (AHRD V3.3 *-* YCF2_IPOPU)		F:GO:0005524; C:GC	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,050	0,046									
Solyc02g011960	Protein Ycf2 (AHRD V3.3 *-* YCF2_VITVI)		F:GO:0005524; C:GC	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc02g011980	50S ribosomal protein L23, chloroplastic (AHRD V3.3 *-* A0A190LKY7_9MAGN)		P:GO:0000027; F:GC	P:ribosomal large subunit assembly; F:structural constituent of ribosome; C:mitochondrion; P:translatior				0,059	0,139	0,000	0,000	0,071									
Solyc02g011990	Photosystem II protein D1 (AHRD V3.3 *** F1KC16_9ASTE)		P:GO:0009772; F:GC	P:photosynthetic electron transport in photosystem II; F:electroi			IPR036854 (G3DSA:1.20.85.GENE3D	0,247	0,306	0,273	0,628	0,878									
Solyc02g012000	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_SOLTU)		F:GO:0005524; P:GC	F:ATP binding; P:ATP synthesis coupled proton transport			IPR000194 (PFAM): G3DSA:3.40.50.3	0,158	0,633	0,072	0,197	0,070									
Solyc02g012010	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_ATRBE)		F:GO:0005524; P:GC	F:ATP binding; P:ATP metabolic process; P:proton transmembra			G3DSA:3.40.50.300 (GENE3D): IPR0(	0,019	0,236	0,000	0,022	0,023									
Solyc02g012020	ATP synthase subunit b, chloroplastic (AHRD V3.3 *** ATPF_NICTO)		F:GO:0015078; P:GC	F:proton transmembrane transporter activity; P:ATP synthesis c			IPR002146 (PFAM): PTHR34264:SF3	0,000	0,043	0,025	0,025	0,000									
Solyc02g014030	Kinase, putative (AHRD V3.3 *-* B9SYC3_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	15,305	38,975	1,828	1,874	3,902	1,369	0,032					up		
Solyc02g014040	Protein kinase (AHRD V3.3 *** C6ZRU2_SOYBN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	0,101	0,128	0,051	0,000	0,046									
Solyc02g014050	Kinase family protein (AHRD V3.3 *-* U5GGQ9_POPTR)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): PTHF	0,000	0,018	0,000	0,051	0,000									
Solyc02g014060	Kinase, putative (AHRD V3.3 *-* B9SYC3_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,000	0,000	0,025	0,000	0,000									
Solyc02g014070	Protein kinase (AHRD V3.3 *-* C6ZRU2_SOYBN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,215	0,163	0,022	0,000	0,047									
Solyc02g014073	Malectin/receptor-like protein kinase family protein, putative (AHRD V3.3 --* A0A061EN67_THECC)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; C:plasma membrane; C:plasmodesma; P:protein autophosphor				0,059	0,062	0,000	0,000	0,046									
Solyc02g014077	phosphoglucan, water dikinase (AHRD V3.3 --* AT4G24450.3)							0,000	0,000	0,000	0,025	0,000									
Solyc02g014090	Peptidoglycan-binding LysM domain-containing protein (AHRD V3.3 *** AT5G23130.1)						IPR018392 (SMART): IPR036779 (G3	27,747	31,996	23,697	24,780	23,027									
Solyc02g014095	Elongation factor Ts, mitochondrial (AHRD V3.3 --* EFTS_ORYSJ)							0,141	0,061	0,150	0,075	0,119									
Solyc02g014130	Tudor/PWWP/MBT domain-containing protein (AHRD V3.3 *** AT5G23150.3)						PR01217 (PRINTS): IPR006569 (SMA	90,724	73,106	87,577	88,934	89,545									
Solyc02g014140	Xyloglucan galactosyltransferase KATAMARI1-like protein (AHRD V3.3 *** W9QKN8_9ROSA)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc			IPR004263 (PFAM): IPR004263 (PAN	0,000	0,000	0,025	0,025	0,000									
Solyc02g014150	Photosystem II stability/assembly factor HCF136 (AHRD V3.3 *** G7JPH8_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	29,649	66,121	34,636	39,659	69,290	1,184	0,000	0,997	0,000			up	up	
Solyc02g014170	RING/U-box superfamily protein (AHRD V3.3 --* AT2G38195.1)						IPR001841 (SMART): PF13920 (PFAN	34,830	31,063	39,777	43,314	37,734									
Solyc02g014180	Sacsin (AHRD V3.3 *-* A0A0B0NEN2_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	40,787	29,903	39,383	50,153	41,914					0,350	0,040			up
Solyc02g014183	LOW QUALITY:BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THE		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,000	0,023									
Solyc02g014187	Sacsin (AHRD V3.3 *-* A0A0B0NEN2_GOSAR)						PTHR15600 (PANTHER): PTHR15600	3,586	3,079	3,546	4,143	4,031									
Solyc02g014190	Protein binding protein, putative (AHRD V3.3 *** B9SMC2_RICCO)						PTHR15600 (PANTHER): PTHR15600	56,293	35,868	45,786	64,680	55,663									
Solyc02g014230	Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 --* A0A072VF16_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	5,851	8,856	4,775	5,158	5,176									
Solyc02g014240	NBS-LRR resistance protein (AHRD V3.3 *-* B6E013_SOLBU)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	7,177	11,519	6,234	7,122	6,900									
Solyc02g014250	RB protein (AHRD V3.3 *** M1EX66_9SOLN)		F:GO:0043531	F:ADP binding			PTHR23155:SF863 (PANTHER): PTHF	1,600	2,354	1,037	1,720	1,533									
Solyc02g014255	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 --* AT1G30140.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc02g014300	Pectinesterase (AHRD V3.3 *** K4B4M9_SOLLC)		F:GO:0004857; F:GC	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (TIC	0,000	0,021	0,025	0,050	0,024									
Solyc02g014310	glycine rich protein X55695		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	367,182	408,619	331,370	267,546	278,962									
Solyc02g014350	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G19740.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:3.40.50	35,993	36,349	46,742	49,099	45,559									
Solyc02g014355	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT1G50140.5)		F:GO:0005524	F:ATP binding			PF17862 (PFAM): G3DSA:3.40.50.30(	8,704	9,647	12,075	11,924	12,092									
Solyc02g014360	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT4G14850.1)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	9,632	10,206	11,610	10,447	10,991									
Solyc02g014370	LOW QUALITY:SKP1-like 20 (AHRD V3.3 --* AT2G45950.5)							0,389	0,078	0,744	0,467	0,121									
Solyc02g014380	Protein odr-4 (AHRD V3.3 *** A0A0B0P6V2_GOSAR)		P:GO:0008104; C:GC	P:protein localization; C:integral component of membrane			IPR029454 (PFAM): IPR029454 (PAN	31,335	30,925	35,218	31,715	33,054									
Solyc02g014430	Equilibrative nucleoside transporter (AHRD V3.3 *** A0A103XTG7_CYNCS)		F:GO:0005337; C:GC	F:nucleoside transmembrane transporter activity; C:integral con			IPR002259 (PFAM): IPR002259 (PIRS	0,019	0,036	0,000	0,022	0,047									
Solyc02g014450	TBC1 domain family member-like protein (AHRD V3.3 *-* A0A0K9P002_ZOSMR)		F:GO:0005096; C:GC	F:GTPase activator activity; C:cell; P:intracellular protein transc			IPR000195 (PFAM): G3DSA:1.10.8.27	1,865	1,781	0,360	0,325	0,542									
Solyc02g014455	Microtubule-associated protein (AHRD V3.3 *** E1U7Y5_NICBE)		F:GO:0005096; P:GC	F:GTPase activator activity; P:intracellular protein transport; F:I			IPR000195 (PFAM): G3DSA:1.10.472	11,678	10,281	4,103	2,555	4,378									
Solyc02g014460	WD40 repeat-containing protein (AHRD V3.3 *** A0A103XDG9_CYNCS)		F:GO:0005515; P:GC	F:protein binding; P:cellular response to DNA damage stimulus			IPR001680 (SMART): IPR015943 (G3	15,332	16,669	31,101	30,284	34,969									
Solyc02g014470	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GF41_THECC)		P:GO:0006629; F:GC	P:lipid metabolic prc	EC:3.1.1.32; EC:3.1.	Phospholipase A(1);	IPR002921 (PFAM): G3DSA:3.40.50.1	0,099	0,140	0,489	0,657	0,331									
Solyc02g014480	LOW QUALITY:FORMS APLOID AND BINUCLEATE CELLS 1A (AHRD V3.3 --* AT1G34260.4)							0,117	0,055	0,444	0,944	0,400									
Solyc02g014490	Glycerophosphoryl diester phosphodiesterase family protein (AHRD V3.3 *** D7MPL3_ARALL)		P:GO:0006629; F:GC	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR030395 (PFAM): IPR017946 (G3D	0,235	0,506	1,325	1,517	1,224									
Solyc02g014520	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151U6C2_CAJCA)		F:GO:0005515	F:protein binding			G3DSA:3.90.1410.10 (GENE3D): IPR(	31,291	30,814	33,867	32,183	34,627									
Solyc02g014530	Glycerophosphoryl diester phosphodiesterase family protein (AHRD V3.3 *** D7MPL3_ARALL)		P:GO:0006629; F:GC	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR030395 (PFAM): IPR017946 (G3D	0,114	0,105	0,022	0,049	0,000									
Solyc02g014545	RNA-binding KH domain-containing protein (AHRD V3.3 --* AT5G08420.1)							0,000	0,000	0,000	0,100	0,000									
Solyc02g014560	calcium-binding EF hand family protein (AHRD V3.3 *** AT4G32060.1)		F:GO:0005509; P:GC	F:calcium ion binding; P:mitochondrial calcium ion transmembrai			IPR002048 (SMART): G3DSA:1.10.23	0,021	0,079	0,000	0,000	0,000									
Solyc02g014640	LOW QUALITY:U1 small nuclear ribonucleoprotein 70 kDa (AHRD V3.3 --* A0A151TI67_CAJCA)							0,040	0,000	0,000	0,000	0,000									
Solyc02g014660	LOW QUALITY:L-fucokinase/GDP-L-fucose pyrophosphorylase (AHRD V3.3 --* AT1G01220.8)							0,000	0,021	0,000	0,000	0,000									
Solyc02g014670	BTB/POZ domain protein (AHRD V3.3 *** AT3G19920.2)		C:GO:0016021	C:integral component of membrane			IPR038920 (PANTHER): PTHR31060::	1,135	2,992	0,864	2,386	0,140									
Solyc02g014690	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 --* AT2G46150.1)							0,000	0,000	0,000	0,000	0,023									
Solyc02g014700	LOW QUALITY:histidine kinase 2 (AHRD V3.3 --* AT5G35750.1)							0,000	0,000	0,050	0,000	0,000									
Solyc02g014720	Metal-dependent phosphohydrolase (AHRD V3.3 *-* AT1G17330.1)						G3DSA:1.10.472.50 (GENE3D): PTHF	48,629	52,470	53,846	56,343	52,518									
Solyc02g014730	Cytochrome P450 (AHRD V3.3 *** A0A103YA00_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	2,142	1,769	0,511	0,801	1,202									
Solyc02g014740	DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 *-* AT4G00390.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAN GeBP	0,000	0,021	0,000	0,000	0,000									
Solyc02g014750	DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 *-* AT4G00390.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAN GeBP	0,197	0,076	0,025	0,022	0,000									
Solyc02g014770	RNA helicase DEAH-box7	DEAH7	F:GO:0005524	F:ATP binding			IPR001650 (SMART): IPR014001 (SN	19,027	18,031	18,065	18,183	18,263									
Solyc02g014790	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GC	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc02g014820	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLBU)		F:GO:0005524; C:GC	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc02g014830	Carboxypeptidase (AHRD V3.3 *** K4B4T2_SOLLC)		F:GO:0004185; P:GC	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide boi	IPR001563 (PRINTS): IPR029058 (G3	0,096	0,229	0,000	0,022	0,023									
Solyc02g014840	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT2G31470.1)							9,952	8,977	3,853	8,671	7,413			0,940	0,003	1,168	0,000		up	up
Solyc02g014843	Pectate lyase (AHRD V3.3 --* H9W0I9_PINTA)							0,019	0,094	0,075	0,238	0,117									
Solyc02g014845	LOW QUALITY:PIF1-like helicase (AHRD V3.3 *-* A0A072TJC6_MEDTR)		P:GO:0000723; F:GC	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	0,000	0,000	0,000	0,022	0,000									
Solyc02g014847	Replication protein A 70 kDa DNA-binding subunit B (AHRD V3.3 --* RFA1B_ARATH)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D): G3DS	0,834	1,252	0,783	1,455	1,688									
Solyc02g014850	LOW QUALITY:synaptosomal-associated protein SNAP25-like 29 (AHRD V3.3 --* AT5G07880.2)							0,153	0,018	0,140	0,025	0,116									
Solyc02g014860	DnaJ domain-containing protein (AHRD V3.3 *** A0A124SD50_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR001623 (SMART): IPR001623 (PF	39,883	59,602	125,846	96,575	135,547	0,607	0,029					up		
Solyc02g014870	Thioredoxin-like protein 4A (AHRD V3.3 *** A0A151RDS9_CAJCA)		P:GO:0000398; C:GC	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			IPR004123 (SMART): IPR004123 (PF	12,971	13,265	21,279	17,887	18,404									
Solyc02g020880	60S ribosomal protein L12 (AHRD V3.3 --* RL12_PRUAR)							0,322	0,433	0,339	0,503	0,447									
Solyc02g020890	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *-* A0A0K9PU50_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR008547 (PFAM): IPR032675 (G3D	3,432	4,390	7,645	13,114	11,279			0,556	0,023	0,778	0,000		up	up
Solyc02g020910	Myosin-related family protein (AHRD V3.3 *** B9H5P2_POPTR)		F:GO:0003774; F:GC	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR001609 (SN	89,494	78,362	74,445	73,800	72,274									
Solyc02g020920	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_CYNDA)							0,101	0,037	0,025	0,000	0,023									
Solyc02g020940	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4B4U4_SOLLC)		P:GO:0006006; F:GC	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR020828 (SN	54,536	107,151	15,347	22,022	56,139	1,002	0,003	1,865	0,000			up	up	
Solyc02g020960	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *** PSAA_ATRBE)		C:GO:0009522; P:GC	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,040	0,000	0,125	0,247	0,047									

Solyc02g020980	4-alpha-glucanotransferase (AHRD V3.3 *** Q6R608_SOLTU)		F:GO:0004134: P:G(	F:4-alpha-glucanotr	EC:2.4.1.25	4-alpha-glucanotrans	IPR003385 (PFAM): G3DSA:3.20.20.8	76,162	88,670	118,469	119,493	135,386									
Solyc02g021000	YGGT family protein-like (AHRD V3.3 *-* Q5JJV4_ORYSJ)		C:GO:0016020	C:membrane			IPR003425 (PFAM): PTHR33219:SF1	19,226	18,228	6,824	7,720	11,033			0,688	0,002				up	
Solyc02g021010	NagB/RpiA/CoA transferase-like superfamily protein (AHRD V3.3 --* AT1G48970.2)							12,116	15,066	12,955	12,489	13,158									
Solyc02g021020	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SMD1_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	16,643	15,520	13,732	15,689	15,496									
Solyc02g021050	BTB/POZ domain protein, putative (DUF177) (AHRD V3.3 *** AT3G19810.2)						IPR003772 (PFAM): PTHR34374 (PAN	10,376	11,820	28,498	25,828	27,633									
Solyc02g021063	Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,569	0,946	0,495	0,366	0,589									
Solyc02g021100	Methyl-CpG-binding domain protein 4-like protein (AHRD V3.3 *** MBD4L_ARATH)		F:GO:0003824: P:G(	F:catalytic activity; P:DNA repair			G3DSA:1.10.340.30 (GENE3D): mobic	34,469	29,041	39,622	40,727	37,143									
Solyc02g021140	Superoxide dismutase (AHRD V3.3 *** K4B4W4_SOLLC)		F:GO:0004784: P:G(	F:superoxide dismu	EC:1.15.1.1	Superoxide dismutas	IPR001189 (PRINTS): IPR019831 (PF	32,802	44,199	54,809	51,998	63,793									
Solyc02g021160	Unknown protein (AHRD V3.3)							0,019	0,000	0,000	0,000	0,000									
Solyc02g021170	LOW QUALITY:cyclic nucleotide gated channel 9 (AHRD V3.3 --* AT4G30560.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,075	0,018	0,000	0,000	0,000									
Solyc02g021210	Phototropic-responsive NPH3 family protein (AHRD V3.3 *-* U5FHY7_POPTR)						IPR027356 (PFAM): PTHR32370:SF2	0,117	0,124	0,731	0,236	0,428									
Solyc02g021220	Subtilisin-like protease (AHRD V3.3 *** W9R4Z9_9ROSA)		F:GO:0004252: P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	84,804	58,243	66,737	74,334	65,500									
Solyc02g021230	Glycosyltransferase (AHRD V3.3 *** A0A067KPV4_JATCU)		C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane; F:transf			IPR005069 (PFAM): PTHR44478 (PAN	6,065	5,452	16,337	20,002	17,330									
Solyc02g021240	oligopeptide transporter 1	opt1	C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	51,442	50,564	83,195	97,974	83,826									
Solyc02g021260	AP2/B3-like transcriptional factor family protein, putative (AHRD V3.3 *-* A0A061DGP3_THECC)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,179	0,120	2,413	0,976	1,327									
Solyc02g021270	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RY36_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,034	3,274	2,410	2,410	2,874									
Solyc02g021277	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G27110.4)							0,122	0,136	0,025	0,000	0,023									
Solyc02g021290	LOW QUALITY:Photosystem II 32 kDa protein (AHRD V3.3 *-* G4VY79_9MARC)		P:GO:0009772: F:G(	P:photosynthetic electron transport in photosystem II; F:electro			IPR000484 (PANTHER): PTHR33149:	0,509	0,850	0,688	1,615	2,085			1,595	0,005	1,235	0,033		up	up
Solyc02g021340	Ser/Thr-rich T10 in DGCR region (AHRD V3.3 *** A0A0B0NE22_GOSAR)						IPR008551 (PFAM): PTHR17985:SF1	12,074	11,667	21,902	21,659	22,455									
Solyc02g021350	Nucleosome assembly protein family (AHRD V3.3 *** A9RDJ7_PHYPA)		C:GO:0005634: P:G(	C:nucleus; P:nucleosome assembly			G3DSA:3.30.1120.90 (GENE3D): IPR(	0,000	0,000	0,458	1,419	0,166									
Solyc02g021360	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *** K4B4Y6_SOLLC)		F:GO:0008017: C:G(	F:microtubule binding; C:katanin complex; P:microtubule severin			IPR020472 (PRINTS): IPR001680 (SM	29,676	26,522	20,781	23,618	22,503									
Solyc02g021400	40S ribosomal protein S28 (AHRD V3.3 *-* W9SEX7_9ROSA)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.50.140 (GENE3D): IPR0(	74,734	86,819	65,623	58,846	56,715									
Solyc02g021410	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NPK0_ZOSMR)		P:GO:0006812: F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	0,139	0,287	0,096	0,139	0,141									
Solyc02g021420	villin 4 (AHRD V3.3 *** AT4G30160.4)		F:GO:0051015: P:G(	F:actin filament binding; P:actin filament bundle assembly			IPR007122 (PRINTS): IPR003128 (SM	80,691	76,834	82,613	90,507	85,344									
Solyc02g021430	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT2G34620.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR003690 (PF	0,825	2,503	0,468	0,572	0,801	1,612	0,007					up		
Solyc02g021440	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A067KSM5_JATCU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR004041 (PF	308,718	319,997	189,202	174,220	196,710									
Solyc02g021450	Myosin heavy chain-related family protein (AHRD V3.3 *** B9I192_POPTR)						mobidb-lite (MOBIDB_LITE): PTHR383	0,000	0,000	0,000	0,025	0,000									
Solyc02g021470	cullin	CUL4	P:GO:0006511: F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR019559 (SMART): IPR016158 (SM	47,292	43,671	59,330	63,925	63,854									
Solyc02g021475	Cullin 4 (AHRD V3.3 *-* A9LK40_SOLLC)		P:GO:0006511: C:G(	P:ubiquitin-dependent protein catabolic process; C:cullin-RING u			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,878	7,827	11,972	12,871	12,023									
Solyc02g021480	Magnesium transporter CorA-like family protein (AHRD V3.3 *** AT1G29820.2)		C:GO:0016020: P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:1.20.58.340 (GENE3D): IPR0(	23,805	20,825	23,015	21,330	24,216									
Solyc02g021550	Eukaryotic translation initiation factor 4E (AHRD V3.3 *** Q00LS7_NICBE)		F:GO:0003743: C:G(	F:translation initiation factor activity; C:cytoplasm; P:translation			IPR023398 (G3DSA:3.30.760.GENE3	33,274	32,931	48,022	42,503	40,950									
Solyc02g021560	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT3G15010.2)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	89,339	91,381	112,219	101,248	107,584									
Solyc02g021590	Receptor protein kinase, putative (AHRD V3.3 *** B9T7R3_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PFAM): IPR001611 (PFA	34,616	28,962	16,729	15,866	19,888									
Solyc02g021600	F-box/kelch-repeat protein (AHRD V3.3 *** A0A0B2SR15_GLYSO)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR001810 (SM	14,608	15,035	9,374	9,428	11,095									
Solyc02g021620	Cation-chloride cotransporter 1 (AHRD V3.3 *** CCC1_ORYSJ)		P:GO:0006811: F:G(	P:ion transport; F:cation:chloride symporter activity; C:integral c			IPR004842 (TIGRFAM): G3DSA:1.20.	38,135	28,069	26,000	27,534	25,096									
Solyc02g021640	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT1G30440.1)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR027356 (PF	27,919	25,689	12,381	11,333	13,169									
Solyc02g021650	UV damaged DNA binding protein 1	DDB1	F:GO:0003676: F:G(	F:nucleic acid binding; F:protein binding; C:nucleus; P:DNA repa			IPR015943 (G3DSA:2.130.10.GENE3	91,645	84,767	143,891	144,388	141,908									
Solyc02g021660	Kinase, putative (AHRD V3.3 *-* B9SRU2_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200	0,000	0,000	0,093	0,246	0,047									
Solyc02g021670	Protein kinase (AHRD V3.3 *-* C6ZRS5_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	0,021	0,021	0,168	0,261	0,023									
Solyc02g021680	WRKY transcription factor 35	WRKY35	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	1,557	1,981	9,861	14,423	7,229					0,553	0,045			up
Solyc02g021690	Alpha N-terminal protein methyltransferase 1 (AHRD V3.3 *-* W9QEM5_9ROSA)		P:GO:0006480: F:G(	P:N-terminal protein amino acid methylation; F:methyltransferas			G3DSA:3.40.50.150 (GENE3D): IPR0(	10,356	9,299	11,219	9,597	10,386									
Solyc02g021700	Alpha N-terminal protein methyltransferase 1 (AHRD V3.3 *** W9QEM5_9ROSA)		P:GO:0006480: F:G(	P:N-terminal protein amino acid methylation; F:methyltransferas			IPR008576 (PIRSF): IPR008576 (PFA	28,989	24,885	27,867	26,094	26,862									
Solyc02g021760	Zinc finger transcription factor 16	C3H16	F:GO:0003723: F:G(	F:RNA binding; F:metal ion binding			IPR000571 (SMART): G3DSA:4.10.10	22,375	19,704	21,979	21,511	22,601									
Solyc02g021770	LOW QUALITY:Cytochrome c oxidase subunit 1 (AHRD V3.3 *** K4B525_SOLLC)		F:GO:0004129: P:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR000883 (PRINTS): IPR000883 (PF	0,021	0,021	0,051	0,170	0,024									
Solyc02g022830	DNA primase/helicase (AHRD V3.3 *** A0A0B2Q2W6_GLYSO)		F:GO:0003678: F:G(	F:DNA helicase act	EC:3.6.1.15	Nucleoside-triphosph	IPR006171 (SMART): IPR006171 (PF	20,081	20,283	20,050	18,733	19,551									
Solyc02g022850	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20840.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			G3DSA:3.40.462.20 (GENE3D): IPR0	2,794	25,202	1,142	0,695	1,402	3,196	0,000					up		
Solyc02g022870	Maternal effect embryo arrest protein (AHRD V3.3 *** A0A072VFX6_MEDTR)						PTHR35480 (PANTHER)	36,456	36,204	38,051	40,215	41,535									
Solyc02g022880	purple acid phosphatase 25 (AHRD V3.3 --* AT4G36350.1)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE)	6,276	6,177	6,186	7,184	6,506									
Solyc02g022890	Fatty acid 2-hydroxylase (AHRD V3.3 *** A0A1D1ZHT2_9ARAE)		F:GO:0005506: P:G(	F:iron ion binding; P:lipid biosynthetic process; C:integral compo			PTHR12863:SF7 (PANTHER): PTHR1	2,476	3,187	2,316	2,064	3,251									
Solyc02g022900	fatty acid hydroxylase 2 (AHRD V3.3 --* AT4G20870.2)						PS51257 (PROSITE_PROFILES)	1,029	0,762	0,876	0,533	1,039									
Solyc02g022920	ethylene-responsive nuclear protein	ern1	C:GO:0005634: C:G(	C:nucleus; C:integral component of membrane			PTHR36381 (PANTHER)	5,788	5,523	13,176	9,933	10,914									
Solyc02g022930	3-hydroxyisobutyrate dehydrogenase (AHRD V3.3 *** K4B541_SOLLC)		F:GO:0008442: F:G(	F:3-hydroxyisobutyı	EC:1.1.1.31	3-hydroxyisobutyrate	G3DSA:3.40.50.720 (GENE3D): IPR0	18,555	14,387	6,857	5,375	7,079									
Solyc02g022934	Branched-chain-amino-acid aminotransferase 6 (AHRD V3.3 --* BCAT6_ARATH)						mobidb-lite (MOBIDB_LITE)	2,206	1,907	2,401	2,063	2,820									
Solyc02g023930	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT5G45840.2)							1,498	0,728	2,104	2,444	1,346									
Solyc02g023950	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT4G20940.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR001611 (PF	6,658	5,463	1,261	0,943	1,171									
Solyc02g023970	Obg-like ATPase 1 (AHRD V3.3 *** K4B546_SOLLC)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR004396 (TI	129,502	131,334	172,322	160,891	160,362									
Solyc02g023980	N-acetyl-D-glucosamine kinase (AHRD V3.3 *** A0A0B0P7N8_GOSAR)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			G3DSA:3.30.420.40 (GENE3D): G3DS	24,550	23,911	25,018	23,305	24,270									
Solyc02g023990	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G20760.2)						IPR002347 (PRINTS): IPR002347 (PF	1,527	2,708	1,146	1,597	1,840									
Solyc02g023997	WPP domain-associated protein (AHRD V3.3 *-* WAP_ARATH)		C:GO:0005739	C:mitochondrion			IPR037490 (PANTHER): PTHR33883:	4,597	4,217	3,891	4,484	3,769									
Solyc02g024000	WPP domain-associated protein (AHRD V3.3 *** WAP_SOLLC)						IPR037490 (PANTHER): PTHR33883:	21,957	16,405	18,786	20,349	18,543									
Solyc02g024010	transmembrane protein (AHRD V3.3 *** AT4G21740.1)		C:GO:0016021	C:integral component of membrane			PTHR37189 (PANTHER)	4,325	3,247	3,642	4,387	3,872									
Solyc02g024020	Calcium-dependent ARF-type GTPase activating protein family (AHRD V3.3 *** AT4G21160.4)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR000008 (SM	30,844	25,297	42,579	41,928	40,948									
Solyc02g024050	Ferredoxin--NADP reductase (AHRD V3.3 *** K4B553_SOLLC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001709 (PRINTS): IPR035442 (PI	11,333	13,541	19,233	24,277	18,916									
Solyc02g024060	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* Q8GY50_ARATH)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,198	0,812	0,025	0,214	0,234									
Solyc02g024070	Homeobox leucine-zipper protein (AHRD V3.3 *** Q8H963_ZINVI)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (SMAF HD-ZIP	9,401	8,627	1,842	1,485	1,804									
Solyc02g024075	TIR-NBS-LRR class disease resistance protein (AHRD V3.3 --* AT4G16890.5)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,000	0,025	0,000									
Solyc02g026080	B3 domain-containing protein (AHRD V3.3 *-* W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,344	0,196	0,000	0,000	0,000									
Solyc02g027080	Disease resistance protein BS2 (AHRD V3.3 *** Q9SNW0_9SOLA)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	16,968	10,668	10,954	14,197	12,084									
Solyc02g030080	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT5G11240.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	158,808	122,963	94,822	85,324	81,586									
Solyc02g030095	Zinc finger protein LSD1 (AHRD V3.3 *-* F8RP38_PEA)		P:GO:0000303: P:G(	P:response to superoxide; P:response to hypoxia; P:response t			IPR005735 (TIGRFAM): IPR005735 (F	0,019	0,021	0,000	0,000	0,000									
Solyc02g030100	Vacuolar protein sorting-associated protein 54 (AHRD V3.3 *** W9SA63_9ROSA)		C:GO:0000938: P:G(	C:GARP complex; P:retrograde transport, endosome to Golgi			mobidb-lite (MOBIDB_LITE): IPR0397	14,446	12,772	12,860	13,337	13,561									
Solyc02g030105	Vacuolar protein sorting-associated protein 54 (AHRD V3.3 *** W9SA63_9ROSA)		C:GO:0000938: P:G(	C:GARP complex; P:retrograde transport, endosome to Golgi			IPR012501 (PFAM): mobidb-lite (MOB	0,021	0,000	0,000	0,025	0,024									
Solyc02g030120	Subtilisin-like protease (AHRD V3.3 *** A0A0B0N731_GOSAR)		F:GO:0004252: P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	0,556	0,901	0,025	0,072	0,070									
Solyc02g030130	Subtilisin-like protease (AHRD V3.3 *-* A0A0B0N731_GOSAR)		F:GO:0004252: P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,294	0,559	0,046	0,025	0,073									
Solyc02g030170	DWARF1/DIMINUTO	dwf1	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR006094 (PFAM): IPR016169 (G3D	846,096	742,407	461,507	387,489	414,802									
Solyc02g030180	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G19860.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc02g030185	LOW QUALITY:HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2R0F0_ORYSJ)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): PTHR23272:SF5	0,019	0,000	0,000	0,000	0,000									
Solyc02g030210	AP2-like ethylene-responsive transcription factor family (AHRD V3.3 *** A0A151TTV5_CAJCA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN AP2	22,618	18,831	21,395	20,436	20,887									
Solyc02g030215	INO80 complex subunit D-like protein (AHRD V3.3 --* AT2G31600.6)							0,156	0,202	0,072	0,049	0,071									
Solyc02g030220	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)						PR01217 (PRINTS): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc02g030230	UDP-glucose 4-epimerase, putative (AHRD V3.3 *** B9SV82_RICCO)		F:GO:0003978: P:G(	F:UDP-glucose 4-e	EC:5.1.3.2	UDP-glucose 4-epim	IPR016040 (PFAM): G3DSA:3.90.25.1	22,272	19,766	50,695	52,797	45,485									
Solyc02g030250	Coatomer epsilon subunit (AHRD V3.3 *** AT1G30630.1)		F:GO:0005198: F:G(	F:structural molecule activity; F:protein binding; P:retrograde ve			IPR006822 (PIRSF): PF04733 (PFAM	53,855	58,012	70,017	75,313	67,126									
Solyc02g030260	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G38350.1)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,076	0,000	0,048	0,000									
Solyc02g030270	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 *** G7K2U8_MEDTI		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,018	0,000	0,000	0,046									
Solyc02g030280	LOW QUALITY:Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *-* A0A072VHI8		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,039	0,000	0,048	0,000									
Solyc02g030290	LOW QUALITY:Nbs-lrr resistance protein, putative (AHRD V3.3 *-* A0A061FET6_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): PF18052 (PFAM)	0,019	0,000	0,025	0,047	0,000									
Solyc02g030300	Serine/threonine-protein kinase (AHRD V3.3 *** U5GTQ6_POPTR)		F:GO:0004674: F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR003609 (SMART): IPR001480 (SM	0,000	0,096	0,025	0,072	0,072									
Solyc02g030310	LOW QUALITY:C3HC4 type zinc finger protein (AHRD V3.3 *-* E2IPA5_BRACM)						PTHR10579:SF49 (PANTHER): PTHR	0,000	0,000	0,000	0,022	0,000									
Solyc02g030380	Serine/threonine-protein kinase (AHRD V3.3 *-* K4B581_SOLLC)		F:GO:0016740	F:transferase activity			IPR001480 (SMART): IPR036426 (G3	0,021	0,202	0,025	0,000	0,116									
Solyc02g030383	Serine/threonine-protein kinase (AHRD V3.3 *-* K4B581_SOLLC)		F:GO:0004674: F:G(	F:protein serine/thr	EC:2.7.11	Transferring phosphorus-containing groups		0,000	0,000	0,000	0,000	0,023									
Solyc02g030450	Protein ROOT HAIR DEFECTIVE 3 homolog (AHRD V3.3 *** K4B594_SOLLC)		F:GO:0005525	F:GTP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	22,648	19,903	45,681	49,544	48,715									
Solyc02g030460	LOW QUALITY:Sh4 homologue protein (AHRD V3.3 *** B6ZKM2_9POAL)						PF13837 (PFAM): Trihelix	0,000	0,036	0,000	0,000	0,000									
Solyc02g030470	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SA73_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,037	0,000	0,000	0,000	0,000									
Solyc02g030480	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9R8D9_RICCO)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.90.18	0,688	0,229	0,049	0,025	0,000									
Solyc02g030500	Calcium-transporting ATPase (AHRD V3.3 *-* M1AEH0_SOLTU)		F:GO:0005388: F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PTHR24093 (PANTHER): PTHR24093	0,080	0,240	0,025	0,000	0,024									
Solyc02g030505	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0000166	F:nucleotide binding			IPR006068 (PFAM): G3DSA:1.20.111	0,203	0,694	0,093	0,148	0,354									
Solyc02g030510	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0000166	F:nucleotide binding			IPR023299 (G3DSA:3.40.1110.GENE	0,021	0,096	0,000	0,025	0,046									
Solyc02g030530	Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *** A0A061EH36_T		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	0,000	0,079	0,000	0,025	0,000									
Solyc02g030605	Ninja-family protein (AHRD V3.3 *-* A0A199VX64_ANACO)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): mobidb-lite (MOB	0,037	0,057	0,000	0,000	0,000									
Solyc02g030610	Ninja-family protein (AHRD V3.3 *-* A0A1D1YDC3_9ARAE)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): IPR031307 (PAN	0,000	0,018	0,000	0,000	0,000									
Solyc02g030655	Ninja-family protein (AHRD V3.3 *-* A0A1D1YDC3_9ARAE)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): PTHR31413:SF1	0,037	0,057	0,000	0,000	0,000									
Solyc02g031680	LOW QUALITY:50S ribosomal protein L34 (AHRD V3.3 --* AT1G29040.5)							0,000	0,018	0,000	0,000	0,000									
Solyc02g031700	F-box protein 7 (AHRD V3.3 --* AT1G21760.2)						mobidb-lite (MOBIDB_LITE)	0,115	0,154	0,096	0,195	0,191									
Solyc02g031710	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT3G12920.1)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	10,904	55,549	9,370	12,682	8,241	2,373	0,000					up		
Solyc02g031740	Phloem protein 2 (AHRD V3.3 *** D0R6I7_MALDO)						IPR025886 (PFAM): PTHR32278:SF8	14,747	13,094	5,441	5,806	5,570									
Solyc02g031750	Phloem protein 2-like protein (AHRD V3.3 *** A0A103Y5W1_CYNCS)						IPR025886 (PFAM): PTHR32278 (PAN	0,318	0,199	0,094	0,316	0,187									
Solyc02g031760	LOW QUALITY:Lipase (AHRD V3.3 --* A0A0D3FTP8_9ORYZ)							0,040	0,000	0,022	0,000	0,024									
Solyc02g031770	ATP synthase mitochondrial F1 complex assembly factor 1 (AHRD V3.3 *** W9RFR7_9ROSA)		C:GO:0005739: P:G(	C:mitochondrion; P:protein-containing complex assembly			IPR010591 (PFAM): IPR010591 (PAN	5,395	6,228	6,425	5,761	6,441									
Solyc02g031780	proline transporter 2 (AHRD V3.3 --* AT3G55740.1)							5,546	5,494	0,846	1,258	1,073									
Solyc02g031790	Receptor-like protein kinase (AHRD V3.3 *** RPK1_IPONI)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	8,914	10,225	5,540	4,694	2,934			-0,921	0,023				down	
Solyc02g031830	polyadenylate-binding protein 1-B-binding protein (AHRD V3.3 *** AT4G19950.1)		C:GO:0016021	C:integral component of membrane			PTHR33133 (PANTHER): PTHR33133	17,010	18,163	15,057	18,637	16,453									
Solyc02g031840	Potassium transporter (AHRD V3.3 *** M1BIK3_SOLTU)		F:GO:0015079: C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (TIGRFAM): IPR003855 (F	39,538	33,243	90,160	105,195	83,311									
Solyc02g031850	Protein kinase family protein (AHRD V3.3 *-* O64768_ARATH)		F:GO:0004672: P:G(	F:protein kinase activity; P:protein phosphorylation			G3DSA:1.10.510.10 (GENE3D): IPR0(	9,849	11,451	13,007	10,992	12,806									
Solyc02g031860	MAP kinase kinase kinase 12	MAPKKK12	F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR000270 (SM	183,214	158,138	194,379	205,391	199,783									
Solyc02g031900	Kinase family protein (AHRD V3.3 *-* D7LHR9_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	233,527	202,321	355,773	315,920	331,364									
Solyc02g031920	Pathogen-related protein (AHRD V3.3 *** A0A151SPD2_CAJCA)						G3DSA:3.10.450.50 (GENE3D): PTHR	2,555	4,510	3,199	1,878	1,896									
Solyc02g031930	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 --* AT5G19100.1)							0,080	0,085	0,100	0,000	0,024									
Solyc02g031940	Pathogen-like protein (AHRD V3.3 *** A0A172WBY3_NICBE)						mobidb-lite (MOBIDB_LITE): PTHR317	5,733	10,629	9,434	7,252	6,268									
Solyc02g031950	pathogenesis-related family protein (AHRD V3.3 *** AT1G78780.5)						G3DSA:3.10.450.50 (GENE3D): mobic	232,667	224,254	962,662	1314,029	837,576									
Solyc02g031960	Pectate lyase (AHRD V3.3 *-* M1BHN6_SOLTU)		F:GO:0030570	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR007524 (PFAM): PTHR31683 (PAN	4,193	1,276	19,035	19,078	14,773	-1,695	0,000					down		
Solyc02g031970	50S ribosomal protein L7/L12 (AHRD V3.3 *** A0A0B2SQD1_GLYSO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR008932 (PFAM): IPR014719 (G3D	21,541	20,013	51,680	46,537	45,261									
Solyc02g031975	Mannose-binding lectin superfamily protein (AHRD V3.3 --* AT1G52130.2)							0,911	0,693	3,364	2,158	2,456									
Solyc02g031980	urease accessory protein D	ured	P:GO:0006807: F:G(	P:nitrogen compound metabolic process; F:nickel cation binding			IPR002669 (PFAM): IPR002669 (PAN	12,873	9,036	22,757	23,035	19,747									
Solyc02g031990	LOW QUALITY:VQ motif-containing protein, putative (AHRD V3.3 *-* A0A061DVP3_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	0,223	0,843	0,435	1,026	1,194									
Solyc02g032000	MADS-box transcription factor family protein (AHRD V3.3 *-* AT4G36590.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN M-type_MADS	0,000	0,039	0,000	0,000	0,000									
Solyc02g032020	ECA1 gametogenesis family protein (DUF784) (AHRD V3.3 --* AT4G07515.1)							0,040	0,083	0,000	0,025	0,046									
Solyc02g032030	Dirigent protein (AHRD V3.3 *** K4B5E9_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAN	0,101	0,078	0,225	0,025	0,192									
Solyc02g032040	Dirigent protein (AHRD V3.3 *** K4B5F0_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495:SF7	0,000	0,000	0,000	0,025	0,000									
Solyc02g032070	LOW QUALITY:B3 domain-containing protein (AHRD V3.3 *-* W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,000	0,000	0,000	0,025	0,000									
Solyc02g032080	LOW QUALITY:B3 DNA binding domain-containing protein (AHRD V3.3 *-* A0A103XWU7_CYNCS)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,075	0,000	0,000									
Solyc02g032100	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)		F:GO:0005385: C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM): IPR003689 (F	5,944	3,944	6,195	6,030	3,715			-0,737	0,016				down	
Solyc02g032120	Zinc finger family protein (AHRD V3.3 *** B9GY13_POPTR)		F:GO:0003677	F:DNA binding			IPR013087 (SMART): G3DSA:3.30.16	22,631	20,606	41,217	38,139	37,784									
Solyc02g032140	Ninja-family protein (AHRD V3.3 *-* A0A199VX64_ANACO)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): mobidb-lite (MOB	0,461	0,292	0,000	0,000	0,000									
Solyc02g032150	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G10955.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,000	0,000									
Solyc02g032190	Nuclear transcription factor Y protein (AHRD V3.3 *-* I3TAW1_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YB	0,190	0,078	0,000	0,000	0,000									
Solyc02g032200	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.3)		F:GO:0005515: P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	60,987	44,699	36,095	39,152	43,534									
Solyc02g032210	LOW QUALITY:B3 domain protein (DUF313) (AHRD V3.3 *** AT2G24670.1)						IPR005508 (PFAM): IPR015300 (G3D	0,021	0,060	0,150	0,242	0,117									
Solyc02g032230	LOW QUALITY:disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G27180.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,000	0,000	0,025	0,000									
Solyc02g032260	LOW QUALITY:NBS-LRR disease resistance protein (AHRD V3.3 *-* Q1WGB0_ORYSI)		F:GO:0043531	F:ADP binding			PTHR43886 (PANTHER)	0,000	0,000	0,047	0,000	0,000									
Solyc02g032270	LOW QUALITY:B3 domain-containing protein (AHRD V3.3 *** A0A0B2RZ88_GLYSO)						IPR005508 (PFAM): IPR015300 (G3D	0,000	0,000	0,022	0,047	0,024									
Solyc02g032300	Enhancer of polycomb-like protein (AHRD V3.3 *** K4B5H6_SOLLC)		P:GO:0006357: C:G(	P:regulation of transcription by RNA polymerase II; C:Piccolo N			IPR019542 (PFAM): PTHR14898:SF5	16,922	13,211	15,732	17,156	16,622									

Solyc02g032303	Duplicated homeodomain-like superfamily protein (AHRD V3.3 --* AT1G14350.2)						0,080	0,041	0,125	0,097	0,141									
Solyc02g032310	Calcineurin B (AHRD V3.3 *** Q8L7F6_PEA)		F:GO:0005509	F:calcium ion binding		IPR002048 (SMART): IPR002048 (PF.	0,019	0,000	0,000	0,000	0,000									
Solyc02g032330	3-beta-hydroxysteroid-dehydrogenase/decarboxylase		F:GO:0003854; P:G(	F:3-beta-hydroxy-d(EC:1.1.1.145	3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D): IPR0(	29,330	26,674	27,551	25,254	27,056									
Solyc02g032335	Serine/threonine-protein kinase (AHRD V3.3 --* A0A0Q3EFL8_BRADI)						1,636	3,048	1,206	1,273	1,508									
Solyc02g032337	RING/U-box superfamily protein (AHRD V3.3 --* AT3G15740.1)					IPR001841 (SMART): IPR013083 (G3	0,000	0,018	0,049	0,000	0,000									
Solyc02g032340	RING/U-box superfamily protein (AHRD V3.3 --* AT3G20395.1)		C:GO:0005886	C:plasma membrane		IPR001841 (SMART): IPR013083 (G3	0,000	0,018	0,000	0,000	0,000									
Solyc02g032360	Desiccation-related protein PCC13-62 (AHRD V3.3 --* A0A061DRH0_THECC)						0,038	0,145	0,126	0,122	0,070									
Solyc02g032370	RING/U-box superfamily protein (AHRD V3.3 --* AT5G45290.1)					IPR001841 (SMART): IPR013083 (G3	0,076	0,021	0,147	0,121	0,048									
Solyc02g032380	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,436	0,500	0,368	0,628	0,472									
Solyc02g032400	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					PTHR34418:SF1 (PANTHER): PTHR3·	0,397	0,300	0,235	0,414	0,236									
Solyc02g032410	LOW QUALITY:P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-containing protein (AHRD V3.3 --* AT1G63640.5)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,097	0,098	0,047	0,069	0,047									
Solyc02g032420	LOW QUALITY:purple acid phosphatase 14 (AHRD V3.3 --* AT2G46880.2)						0,038	0,018	0,075	0,000	0,000									
Solyc02g032430	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT5G45290.1)					IPR001841 (SMART): IPR001841 (PF.	0,000	0,000	0,000	0,000	0,024									
Solyc02g032450	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					mobidb-lite (MOBIDB_LITE): mobidb-lit	26,789	27,366	29,793	33,227	29,443									
Solyc02g032460	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					mobidb-lite (MOBIDB_LITE): PTHR344	6,303	5,409	6,432	8,056	6,786									
Solyc02g032480	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					PTHR34418:SF1 (PANTHER): PTHR3·	4,867	4,406	5,581	6,707	5,901									
Solyc02g032490	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)					PTHR34418 (PANTHER): PTHR34418	3,525	3,003	3,869	5,485	4,408									
Solyc02g032510	BTB/POZ domain-containing protein (AHRD V3.3 *** AT4G08455.1)		F:GO:0005515	F:protein binding		IPR000210 (SMART): G3DSA:1.25.40	18,425	17,186	44,494	46,308	41,960									
Solyc02g032520	LOW QUALITY:Apyrase (AHRD V3.3 *-* APY_SOLTU)		F:GO:0016787	F:hydrolase activity		IPR000407 (PFAM): G3DSA:3.30.420	0,000	0,000	0,000	0,045	0,000									
Solyc02g032525	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		F:GO:0003677; F:G(	F:DNA binding; F:catalytic activity; F:DNA-directed DNA polyme		IPR015410 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc02g032580	Apyrase (AHRD V3.3 *-* APY_SOLTU)		F:GO:0016787	F:hydrolase activity		G3DSA:3.30.420.40 (GENE3D): IPR0(	0,000	0,021	0,000	0,000	0,000									
Solyc02g032600	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT4G18540.2)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane		PTHR33927 (PANTHER): PTHR33927	0,000	0,000	0,000	0,025	0,000									
Solyc02g032620	LOW QUALITY:Late embryogenesis abundant protein, group 2 (AHRD V3.3 --* AT2G44060.2)						0,000	0,021	0,000	0,000	0,000									
Solyc02g032650	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** A0A072U6S8_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding		PR00364 (PRINTS): IPR000157 (SMA	1,874	2,848	1,373	1,356	1,505									
Solyc02g032660	Protein DETOXIFICATION (AHRD V3.3 *** K4B5L0_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo		IPR002528 (TIGRFAM): IPR002528 (F	6,247	5,590	2,234	0,930	2,377					-1,243	0,039			down
Solyc02g032685	Unknown protein (AHRD V3.3)						0,058	0,118	0,022	0,000	0,000									
Solyc02g032720	Ninja-family protein (AHRD V3.3 *-* A0A199VX64_ANACO)		P:GO:0007165	P:signal transduction		IPR032308 (PFAM): mobidb-lite (MOB	0,000	0,000	0,071	0,000	0,023									
Solyc02g032730	LOW QUALITY:ABI five binding protein 3 (AHRD V3.3 --* AT3G29575.4)		F:GO:0003723; P:G(	F:RNA binding; P:regulation of cellular process		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc02g032780	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* AT1G04380.2)						0,040	0,348	0,050	0,072	0,259									
Solyc02g032790	LOW QUALITY:Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *** ,		F:GO:0003676	F:nucleic acid binding		IPR000504 (PFAM): IPR012677 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc02g032800	LOW QUALITY:Senescence regulator (AHRD V3.3 *** A0A103XFA1_CYNCS)					IPR007608 (PFAM): PTHR33083 (PAN	7,742	11,381	4,677	2,683	4,491					-0,799	0,013			down
Solyc02g032820	Protein kinase (AHRD V3.3 *** Q9AR92_MEDSA)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F		IPR002048 (SMART): IPR000719 (SM	0,101	0,217	0,000	0,047	0,093									
Solyc02g032830	Peroxidase (AHRD V3.3 *** K4B5M7_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc02g032840	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 --* A0A061FTS5_THECC)					mobidb-lite (MOBIDB_LITE): PTHR333	1,076	1,487	0,050	0,050	0,046									
Solyc02g032850	Phytoalexin-deficient 4-1 protein (AHRD V3.3 *** Q2TNK3_SOLTU)		P:GO:0006629	P:lipid metabolic process		IPR029058 (G3DSA:3.40.50.GENE3D	24,178	35,976	25,099	27,220	28,685									
Solyc02g032860	5'-adenylylsulfate reductase (AHRD V3.3 *** A0A072V4H5_MEDTR)		F:GO:0016671; P:G(	F:oxidoreductase activity, acting on a sulfur group of donors, di		IPR002500 (PFAM): IPR004508 (TIGF	10,727	17,650	30,509	32,174	34,633									
Solyc02g032870	Tyrosyl-DNA phosphodiesterase 2 (AHRD V3.3 *** W9R361_9ROSA)		F:GO:0003697; C:G(	F:single-stranded DNA binding; C:cytoplasm; P:double-strand br		IPR001876 (SMART): IPR036691 (G3	17,560	14,194	12,588	9,071	10,070									
Solyc02g032877	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 --* A0A151SWQ3_CAJCA)					IPR019557 (PFAM): PTHR44194 (PAN	0,000	0,021	0,025	0,022	0,000									
Solyc02g032910	Glycine rich protein (AHRD V3.3 *** Q43498_SOLLC)						2,896	2,069	2,579	3,211	2,926									
Solyc02g032920	U3 small nucleolar RNA-associated protein 6-like protein (AHRD V3.3 *** W9R9F9_9ROSA)		P:GO:0000462; F:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSU		IPR003107 (SMART): IPR011990 (G3	17,659	21,871	18,080	21,337	18,352									
Solyc02g032930	B-cell receptor-associated 31-like (AHRD V3.3 *** A0A061GGS0_THECC)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte		G3DSA:1.20.5.110 (GENE3D): IPR00(	50,428	44,768	135,745	139,357	115,891									
Solyc02g032940	Aspartic proteinase (AHRD V3.3 *** A0A0B0NH67_GOSAR)		F:GO:0004190; P:G(	F:aspartic-type end EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	5,339	5,509	1,847	2,576	1,692									
Solyc02g032950	WRKY transcription factor 16	WRKY16	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans		IPR003657 (SMAF WRKY	0,269	1,328	0,049	0,289	0,255									
Solyc02g032970	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** A0A0B0PX39_GOSAR)		F:GO:0004222; F:G(	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): G3DSA:1.10.8.6	57,860	67,757	73,976	71,391	77,584									
Solyc02g033030	Histone H1 (AHRD V3.3 --* A0A151SYJ4_CAJCA)		F:GO:0003677; P:G(	F:DNA binding; P:DNA packaging; P:regulation of nucleobase-co		PTHR11467:SF62 (PANTHER): PTHR	3,127	2,771	1,199	1,037	1,133									
Solyc02g033040	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYNCS)					IPR017451 (TIGRFAM): IPR006527 (F	0,764	0,542	0,025	0,075	0,140									
Solyc02g033050	LOW QUALITY:chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding		IPR014001 (SMART): IPR001650 (SM	0,019	0,058	0,000	0,000	0,023									
Solyc02g033060	TSA: Wollemia nobilis Ref_Wollemi_Transcript_5463_1093 transcribed RNA sequence (AHRD V3.3 *** A0A(		P:GO:0009555	P:pollen development		IPR016621 (PFAM): PTHR35732 (PAN	0,949	1,220	0,606	0,408	1,361									
Solyc02g033070	LOW QUALITY:MEF2BNB-like protein (AHRD V3.3 *** AT2G39170.1)					IPR019320 (PFAM): mobidb-lite (MOB	0,097	0,142	0,119	0,101	0,164									
Solyc02g033110	PLATZ transcription factor family protein (AHRD V3.3 *** A0A061EE86_THECC)		F:GO:0008270	F:zinc ion binding		IPR006734 (PFAM): PTHR31065:SF9	0,000	0,019	0,000	0,000	0,000									
Solyc02g036140	LOW QUALITY:PLATZ transcription factor family protein (AHRD V3.3 *** A0A061EE86_THECC)		F:GO:0008270	F:zinc ion binding		IPR006734 (PFAM): mobidb-lite (MOB	0,019	0,037	0,000	0,000	0,000									
Solyc02g036250	LOW QUALITY:Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** ,		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane		IPR003406 (PFAM): PTHR31042 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc02g036260	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G22120.6)		C:GO:0016020	C:membrane		IPR003864 (PFAM): IPR027815 (PFA	0,233	0,442	0,025	0,050	0,000									
Solyc02g036270	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): IPR003593 (SMA	4,807	7,491	4,291	4,637	4,783									
Solyc02g036280	Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)		F:GO:0043531	F:ADP binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,360	0,602	0,357	0,341	0,705									
Solyc02g036290	malonyl-CoA decarboxylase family protein (AHRD V3.3 *-* AT4G04320.2)		P:GO:0006633; F:G(	P:fatty acid biosyntl EC:4.1.1.9	Malonyl-CoA decarbc	G3DSA:3.40.630.150 (GENE3D): IPR(	1,675	1,170	1,955	1,907	1,773									
Solyc02g036300	malonyl-CoA decarboxylase family protein (AHRD V3.3 *-* AT4G04320.2)		P:GO:0006633; F:G(	P:fatty acid biosyntl EC:4.1.1.9	Malonyl-CoA decarbc	IPR007956 (PFAM): G3DSA:3.40.630	2,063	1,679	2,540	2,797	1,886									
Solyc02g036310	Malonyl-CoA decarboxylase (AHRD V3.3 *-* A0A103Y230_CYNCS)		P:GO:0006633; F:G(	P:fatty acid biosyntl EC:4.1.1.9	Malonyl-CoA decarbc	IPR038351 (G3DSA:1.20.140.GENE3	2,182	1,734	2,425	2,495	2,238									
Solyc02g036320	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me		G3DSA:1.20.1130.20 (GENE3D): IPR(	0,019	0,055	0,076	0,201	0,047									
Solyc02g036330	26S protease regulatory subunit, putative (AHRD V3.3 *** B9RXE9_RICCO)		F:GO:0005524	F:ATP binding		IPR003593 (SMART): G3DSA:1.10.8.6	44,588	43,970	63,754	67,745	60,022									
Solyc02g036350	1-aminocyclopropane-1-carboxylate oxidase EF501822	ACO6	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR027443 (G3DSA:2.60.120.GENE3	1197,397	1348,411	937,129	666,870	957,832					-0,488	0,045			down
Solyc02g036360	LOW QUALITY:Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repeat-containing		F:GO:0005515	F:protein binding		IPR019734 (SMART): IPR000270 (SM	18,561	28,176	27,644	28,076	28,318	0,629	0,019					up		
Solyc02g036370	Myb family transcription factor		F:GO:0003677	F:DNA binding		IPR001005 (SMAF MYB_related	13,206	7,880	23,193	21,385	16,003			-0,538	0,012				down	
Solyc02g036380	Autophagy protein 5 (AHRD V3.3 *** K4B5T1_SOLLC)		C:GO:0005737; P:G(	C:cytoplasm; P:autophagy		IPR007239 (PFAM): G3DSA:3.10.20.9	24,946	28,344	34,865	29,870	30,194									
Solyc02g036430	NAC domain protein, (AHRD V3.3 *** A0A061EDT4_THECC)	NAC007	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated		IPR036093 (G3DS NAC	0,021	0,094	0,025	0,025	0,000									
Solyc02g036440	LEM3 (Ligand-effect modulator 3) family protein (AHRD V3.3 *** D7KWI0_ARALL)		C:GO:0016020	C:membrane		IPR005045 (PIRSF): IPR005045 (PFA	0,021	0,000	0,025	0,025	0,000									
Solyc02g036450	Ras-related GTP-binding protein (AHRD V3.3 *** Q40570_TOBAC)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	26,046	22,248	34,057	32,080	30,284									
Solyc02g036460	OO_Ba0013J05-OO_Ba0033A15.14 protein (AHRD V3.3 *** D0ABF7_9ORYZ)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,025	0,000	0,000									
Solyc02g036470	Transporter protein (AHRD V3.3 *** A0A0B0N017_GOSAR)		C:GO:0016021	C:integral component of membrane		IPR000620 (PFAM): PTHR22911:SF6	11,467	8,850	14,081	14,713	16,270									
Solyc02g036480	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane		IPR004864 (PFAM): mobidb-lite (MOB	7,205	22,722	1,950	5,449	5,155			1,394	0,003	1,480	0,008		up	up
Solyc02g037490	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT5G16340.1)		F:GO:0003824	F:catalytic activity		IPR025110 (PFAM): G3DSA:3.40.50.1	0,357	0,214	0,000	0,000	0,000									
Solyc02g037495	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT5G16340.1)		F:GO:0003824	F:catalytic activity		IPR000873 (PFAM): IPR025110 (PFA	12,293	47,985	576,056	584,836	514,707	1,988	0,001					up		
Solyc02g037510	Cationic amino acid transporter, putative (AHRD V3.3 *** B9SI71_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmer		IPR002293 (PFAM): G3DSA:1.20.174	15,213	16,844	14,454	16,781	16,701									
Solyc02g037530	auxin response factor 8B	ARF8B	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran		IPR003340 (SMAF ARF	65,315	62,885	25,462	19,814	31,589									
Solyc02g037540	Disease resistance protein (AHRD V3.3 *** W9R405_9ROSA)		F:GO:0005515; F:G(	F:protein binding; F:ADP binding		PR00364 (PRINTS): IPR032675 (G3D	0,042	0,142	0,075	0,072	0,166									
Solyc02g037550	Auxin efflux carrier family protein (AHRD V3.3 *** AT1G76520.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport		IPR004776 (PFAM): PTHR31651 (PAN	0,176	0,250	0,000	0,000	0,000									
Solyc02g037590	LOW QUALITY:Mannose-binding lectin superfamily protein (AHRD V3.3 --* AT1G60110.3)						3,031	2,272	3,980	3,512	3,396									
Solyc02g037595	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)					G3DSA:2.40.50.140 (GENE3D): PTHF	1,075	2,264	0,619	1,303	1,457									
Solyc02g037640	LOW QUALITY:DNA helicase homolog, putative (AHRD V3.3 *-* Q1EPC6_MUSAC)		P:GO:0000723; F:G(	P:telomere mainten EC:3.6.1.15	Nucleoside-triphosph	IPR010285 (PFAM): G3DSA:3.40.50.3	0,019	0,156	0,025	0,146	0,000									
Solyc02g038640	Maturase K (AHRD V3.3 --* E5G0M6_9ASPA)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,332	0,939	0,075	0,897	0,654									
Solyc02g038660	Tetratricopeptide repeat protein 5 (AHRD V3.3 *** W9RAT0_9ROSA)		F:GO:0005515	F:protein binding		IPR019734 (SMART): IPR001440 (PF.	0,021	0,000	0,046	0,000	0,000									
Solyc02g038670	Tetratricopeptide repeat 5 (AHRD V3.3 *** A0A0B0NMW4_GOSAR)		F:GO:0005515	F:protein binding		G3DSA:1.10.287.950 (GENE3D): IPR(	0,082	0,039	0,049	0,000	0,000									
Solyc02g038680	LOW QUALITY:Tetratricopeptide repeat 5 (AHRD V3.3 *** A0A0B0NMW4_GOSAR)		F:GO:0005515	F:protein binding		IPR032076 (PFAM): IPR011990 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc02g038690	Histone H2B (AHRD V3.3 *** K4B5W3_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti		IPR000558 (PRINTS): IPR000558 (SM	1,464	1,805	0,517	0,391	0,279									
Solyc02g038710	photosystem II reaction center protein I (AHRD V3.3 *** ATCG00080.1)		C:GO:0009539; P:G(	C:photosystem II reaction center; P:photosynthesis		IPR003686 (PFAM): PTHR35772:SF1	0,060	0,000	0,000	0,000	0,000									
Solyc02g038720	LOW QUALITY:Acyl carrier protein (AHRD V3.3 *** K4B5W6_SOLLC)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:phosphopantetheine bindin(		IPR020806 (SMART): IPR009081 (PF.	0,000	0,019	0,000	0,000	0,000									
Solyc02g038740	3-hydroxy-3-methylglutaryl coenzyme A reductase (AHRD V3.3 *** K4B5W7_SOLLC)		F:GO:0004420; P:G(	F:hydroxymethylglut EC:1.1.1.34	Hydroxymethylglutary	IPR002202 (PRINTS): IPR023282 (G3	11,843	12,413	13,815	11,997	12,156									
Solyc02g038750	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G34260.1)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR001680 (PF.	26,491	25,557	42,527	41,550	38,179									
Solyc02g038760	AT hook motif DNA-binding family protein (AHRD V3.3 *-* A0A0K9NSQ5_ZOSMR)		F:GO:0003680	F:AT DNA binding		IPR017956 (SMART): G3DSA:3.30.13	27,018	25,067	29,594	25,973	28,317									
Solyc02g038770	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G13228.1)		F:GO:0008270; C:G(	F:zinc ion binding; C:endomembrane system; P:protein ubiquitin		IPR001841 (SMART): IPR013083 (G3	0,000	0,000	0,025	0,000	0,047									
Solyc02g043810	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT5G57200.1)		F:GO:0005545; C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla		IPR013809 (SMART): IPR011417 (PF.	0,979	1,145	1,374	1,451	1,805									
Solyc02g043815	LOW QUALITY:Polyprotein, 3'-partial, putative (AHRD V3.3 *-* Q0KIP3_SOLDE)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding		IPR001878 (SMART): G3DSA:4.10.60	0,021	0,037	0,025	0,050	0,071									
Solyc02g043860	Insulin-degrading enzyme (AHRD V3.3 *** W9RZP1_9ROSA)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding		IPR032632 (PFAM): G3DSA:3.30.830	70,592	62,593	87,105	89,310	89,970									
Solyc02g043864	Insulin-degrading enzyme (AHRD V3.3 *-* A0A072UY22_MEDTR)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding		G3DSA:3.30.830.10 (GENE3D): PTHF	0,019	0,021	0,000	0,000	0,000									
Solyc02g043880	LOW QUALITY:Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *-* AT4G23000.2)		C:GO:0016020	C:membrane		PTHR34211:SF1 (PANTHER): PTHR3·	0,000	0,018	0,000	0,000	0,000									
Solyc02g043900	LOW QUALITY:UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT1G16570.2)						0,000	0,021	0,000	0,000	0,000									
Solyc02g043910	LOW QUALITY:SET domain protein 25 (AHRD V3.3 --* AT5G42400.8)						0,000	0,000	0,046	0,022	0,000									
Solyc02g043950	LOW QUALITY:BnaC09g16530D protein (AHRD V3.3 --* A0A078E240_BRANA)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc02g043967	secretory carrier 3 (AHRD V3.3 --* AT1G61250.2)					mobidb-lite (MOBIDB_LITE)	0,021	0,021	0,000	0,000	0,000									
Solyc02g043970	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G06170.2)						0,040	0,061	0,022	0,117	0,071									
Solyc02g044000	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A118JUD2_CYNCS)	ABCC19				IPR003871 (PFAM): G3DSA:2.40.50.1	0,040	0,041	0,047	0,025	0,023									
Solyc02g044003	LOW QUALITY:BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 --* A0A061FD65_THE(		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM): mobidb-lite (MOB	0,000	0,019	0,000	0,000	0,000									
Solyc02g044020	Ribosomal RNA large subunit methyltransferase N (AHRD V3.3 *-* A0A0B0PAE8_GOSAR)		F:GO:0003824	F:catalytic activity		IPR013785 (G3DSA:3.20.20.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc02g044030	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *-* A0A072TGP1_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:protein refolding		IPR001844 (PRINTS): IPR000008 (PF	0,257	0,200	0,169	0,075	0,162									
Solyc02g044040	Dihydroorotate dehydrogenase family protein (AHRD V3.3 *-* G7KQB6_MEDTR)		F:GO:0003824	F:catalytic activity		IPR013785 (G3DSA:3.20.20.GENE3D	0,264	0,195	0,147	0,097	0,211									
Solyc02g044050	LOW QUALITY:Multidrug resistance protein ABC transporter family protein (AHRD \	ABCC20	F:GO:0003677; F:G(	F:DNA binding; F:DI EC:3.6.1.3; EC:2.7.7	Adenosinetriphospha	IPR007645 (PFAM): G3DSA:3.40.50.3	0,254	0,243	0,050	0,214	0,141									
Solyc02g049070	4-coumarate:CoA ligase (AHRD V3.3 --* O81139_POPTM)	4CL	C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast envelope; C:ir		mobidb-lite (MOBIDB_LITE): PTHR367	15,501	19,612	25,836	25,056	28,375									
Solyc02g049080	LOW QUALITY:L-2-hydroxyglutarate dehydrogenase, mitochondrial (AHRD V3.3 --* L2HDH_ARATH)						0,040	0,039	0,000	0,025	0,000									
Solyc02g050180	heat-inducible transcription repressor (DUF639) (AHRD V3.3 *-* AT1G48840.1)		C:GO:0016021	C:integral component of membrane		IPR006927 (PFAM): mobidb-lite (MOB	4,298	3,218	2,278	2,098	2,186									
Solyc02g050187	polygalacturonase inhibitor (DUF639) (AHRD V3.3 *-* AT5G23390.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,115	0,041	0,025	0,172	0,119									
Solyc02g050190	LOW QUALITY:Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q2RB37_ORYSJ)					IPR025312 (PFAM): PTHR33499:SF7	0,000	0,018	0,000	0,000	0,000									
Solyc02g050200	Breast cancer type 2 susceptibility-like protein (AHRD V3.3 *** W9RBD4_9ROSA)		P:GO:0000724	P:double-strand break repair via homologous recombination		G3DSA:2.40.50.140 (GENE3D): IPR0	6,317	5,468	4,606	3,541	4,734									
Solyc02g050205	Prolyl oligopeptidase family protein (AHRD V3.3 *-* AT1G50380.2)		F:GO:0004252; F:G(	F:serine-type endor EC:3.4.21	Acting on peptide bor	G3DSA:2.130.10.120 (GENE3D): IPR(	28,982	25,928	29,167	30,627	28,737									
Solyc02g050207	Prolyl oligopeptidase family protein (AHRD V3.3 *-* AT1G50380.2)		F:GO:0004252; F:G(	F:serine-type endor EC:3.4.21	Acting on peptide bor	PF13650 (PFAM): G3DSA:2.130.10.1:	6,490	6,437	7,325	8,557	7,924									
Solyc02g050210	Breast cancer type 2 susceptibility (AHRD V3.3 *** A0A0B0P9I0_GOSAR)		P:GO:0000724	P:double-strand break repair via homologous recombination		G3DSA:2.40.50.140 (GENE3D): IPR0	4,453	3,450	2,329	2,121	2,627									
Solyc02g050240	Prolyl oligopeptidase family protein (AHRD V3.3 *-* AT1G50380.2)		F:GO:0004252; P:G(	F:serine-type endor EC:3.4.21	Acting on peptide bor	IPR002470 (PRINTS): IPR001375 (PF	23,729	23,326	26,957	26,063	25,970									
Solyc02g050280	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD		F:GO:0005524; F:G(	F:ATP binding; F:metal ion binding		IPR014001 (SMART): IPR038718 (G3	28,339	23,951	29,545	29,542	28,655									
Solyc02g050283	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072VR89_MEDTR)					IPR025558 (PFAM)	0,000	0,019	0,000	0,025	0,046									
Solyc02g050287	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD		F:GO:0004386; F:G(	F:helicase activity; EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART): IPR001650 (PF.	4,526	4,759	5,208	4,975	5,323									
Solyc02g050290	LOW QUALITY:Cytochrome c biogenesis FN (AHRD V3.3 *-* A0A0C5ART5_HYONI)		F:GO:0015232; P:G(	F:heme transporter activity; P:heme transport; C:membrane; P:(		IPR003569 (PRINTS): PTHR30009 (P.	0,021	0,019	0,000	0,025	0,023									
Solyc02g050300	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_ABIFI)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,024									
Solyc02g050330	Late embryogenesis abundant protein At1g64065 (AHRD V3.3 --* Y1465_ARATH)						5,060	4,842	1,907	1,460	1,557									
Solyc02g055370	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G31650.2)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	0,416	0,213	0,125	0,125	0,285									
Solyc02g055390	LOW QUALITY:SPOC domain / Transcription elongation factor S-II protein (AHRD V3.3 --* AT5G25520.7)		F:GO:0016779	F:nucleotidyltransferase activity		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,159	0,018	0,022	0,025	0,000									
Solyc02g055440	E3 ubiquitin-protein ligase, putative (DUF177) (AHRD V3.3 *** AT3G19800.2)					IPR003772 (PFAM): PTHR37734 (PAN	10,735	23,439	2,074	3,365	9,850	1,155	0,000	2,231	0,000			up	up	
Solyc02g055460	Protein disulfide-isomerase (AHRD V3.3 *** A0A0B2RKB0_GLYSO)		C:GO:0005623; C:G(	C:cell; C:integral component of membrane; P:cell redox homeos		G3DSA:3.40.30.10 (GENE3D): PTHR1	19,694	17,047	25,360	27,781	24,481									
Solyc02g055465	Phospholipase A1-II 5 (AHRD V3.3 --* A0A199V7Q2_ANACO)		C:GO:0005623; P:G(	C:cell; P:cell redox homeostasis		PTHR18929 (PANTHER): PTHR18929	0,628	0,742	0,629	0,914	0,848									
Solyc02g055467	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 --* AT5G43740.2)						3,153	4,444	3,961	3,535	3,772									
Solyc02g055530	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TUG3_ACAMN)	ABCG68	C:GO:0016020	C:membrane		IPR013525 (PFAM): PTHR19241 (PAN	0,019	0,000	0,000	0,000	0,048									
Solyc02g055550	exocyst subunit exo70 family protein D1 (AHRD V3.3 --* AT1G72470.1)						2,633	2,088	2,011	3,052	2,102									
Solyc02g055565	High mobility group family protein (AHRD V3.3 *-* D7LH08_ARALL)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus		IPR036910 (G3DSA:1.10.30.GENE3D	8,384	6,212	7,144	7,800	7,304									
Solyc02g060570	Ubiquitin 1 (AHRD V3.3 *** E9P1L2_MUSAC)		F:GO:0005515	F:protein binding		IPR000626 (SMART): G3DSA:3.10.20	0,037	0,225	0,000	0,000	0,000									
Solyc02g060580	Ubiquilin-1 (AHRD V3.3 *** A0A0B2NTN2_GLYSO)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc02g060590	ubiquitin family protein (AHRD V3.3 *-* AT2G17200.1)		F:GO:0005515	F:protein binding		IPR000626 (SMART): IPR000626 (PF.	0,057	0,021	0,000	0,000	0,000									
Solyc02g060595	Ubiquitin-like superfamily protein (AHRD V3.3 --* AT5G57860.4)						0,019	0,000	0,000	0,000	0,000									
Solyc02g061610	Ubiquitin 1 (AHRD V3.3 *** E9P1L2_MUSAC)		F:GO:0005515	F:protein binding		IPR000626 (SMART): G3DSA:3.10.20	0,056	0,121	0,000	0,000	0,000									
Solyc02g061620	Phenylalanyl-tRNA synthetase alpha chain, putative (AHRD V3.3 *-* G7JG63_MEDTR)		F:GO:0000049; F:G(	F:tRNA binding; F:p EC:6.1.1.2	Phenylalanine--tRNA	G3DSA:3.30.930.10 (GENE3D)	0,000	0,043	0,075	0,022	0,023									
Solyc02g061630	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 3, chloroplastic (AHRD V3.3 --* NU3C_AETGR)						0,037	0,018	0,000	0,000	0,000									
Solyc02g061640	ubiquitin family protein (AHRD V3.3 *-* AT2G17200.1)		F:GO:0005515	F:protein binding		IPR000626 (SMART): G3DSA:3.10.20	0,000	0,019	0,000	0,000	0,000									
Solyc02g061665	Starch branching enzyme I (AHRD V3.3 --* Q18PQ3_IPOBA)						0,019	0,018	0,000	0,000	0,000									
Solyc02g061670	Ubiquitin 1 (AHRD V3.3 *** E9P1L2_MUSAC)		F:GO:0005515	F:protein binding		IPR000626 (PFAM): G3DSA:3.10.20.9	0,021	0,097	0,000	0,000	0,000									

Solyc02g061680	Ubiquitin 1 (AHRD V3.3 *** E9P1L2_MUSAC)		F:GO:0005515	F:protein binding			IPR000626 (SMART): IPR000626 (PF.	0,037	0,058	0,000	0,000	0,000									
Solyc02g061705	S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61420.4)							0,019	0,000	0,000	0,000	0,000									
Solyc02g061710	Ubiquitin 1 (AHRD V3.3 *-* E9P1L2_MUSAC)						mobidb-lite (MOBIDB_LITE): IPR01549	0,037	0,041	0,000	0,000	0,000									
Solyc02g061720	ubiquitin family protein (AHRD V3.3 *** AT2G17200.1)		F:GO:0005515	F:protein binding			IPR000626 (SMART): IPR000626 (PF.	0,021	0,019	0,000	0,000	0,000									
Solyc02g061740	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *-* A0A061DL75_THECC)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D): IPF	0,019	0,000	0,000	0,000	0,000									
Solyc02g061745	Protein DETOXIFICATION (AHRD V3.3 *** K4B666_SOLLC)		P:GO:0006855: F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): IPR002528 (TIGF	2,287	2,894	1,074	1,115	1,270									
Solyc02g061760	Protein DETOXIFICATION (AHRD V3.3 *** K4B666_SOLLC)		P:GO:0006855: F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): PTHR42893:SF8	2,543	3,042	0,941	1,125	1,226									
Solyc02g061770	chitinase 2	chi2	F:GO:0004568: P:GC	F:chitinase activity;	EC:3.2.1.14	Chitinase	G3DSA:3.30.20.10 (GENE3D): IPR01(	0,076	0,682	1,779	2,668	1,542									
Solyc02g061780	NAC domain-containing protein (AHRD V3.3 *** A0A059ZXJ7_BOENI)	NAC008	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	1,150	1,118	2,999	7,042	5,096					1,232	0,001			up
Solyc02g061790	RNA polymerase II transcriptional coactivator (AHRD V3.3 *** G7JC59_MEDTR)		F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR009044 (G3DSA:2.30.31.GENE3D	22,120	16,056	33,680	29,056	29,991									
Solyc02g061800	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4B670_SOLLC)		P:GO:0000413: F:GC	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomera	IPR002130 (PRINTS): IPR000504 (SM	0,419	0,300	0,090	0,120	0,164									
Solyc02g061810	S-acyltransferase (AHRD V3.3 *** K4B671_SOLLC)		C:GO:0005783: C:GC	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883 (PAN	8,504	6,659	8,559	8,014	7,773									
Solyc02g061820	ankyrin repeat protein (AHRD V3.3 *** AT5G66055.1)		F:GO:0005515	F:protein binding			IPR002110 (SMART): PIRSF000654 (	10,611	12,627	35,498	35,830	36,826									
Solyc02g061840	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT4G35785.2)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	49,179	59,548	87,955	77,022	78,348									
Solyc02g061850	Phospholipase D (AHRD V3.3 *** K4B675_SOLLC)		F:GO:0004630: F:GC	F:phospholipase D	EC:3.1.4.4	Phospholipase D	IPR001736 (SMART): IPR000008 (SM	0,674	0,590	3,182	3,244	2,985									
Solyc02g061860	LOW QUALITY:Ubiquitin-like superfamily protein (AHRD V3.3 --* AT5G25270.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc02g061870	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 *-* B9SK58_F	NAC009	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,215	0,080	0,025	0,000	0,000									
Solyc02g061900	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 *** B9SVG2_I	NAC010	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,197	0,380	0,050	0,051	0,000									
Solyc02g061910	NAC domain-containing protein (AHRD V3.3 *-* A0A059ZXJ2_BOENI)	NAC011	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,019	0,021	0,050	0,047	0,024									
Solyc02g061920	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *** A0A151RZV3		C:GO:0000943	C:retrotransposon nucleocapsid			PF14223 (PFAM): mobidb-lite (MOBID	0,037	0,000	0,000	0,000	0,000									
Solyc02g061940	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** G7JXJ8_MEDTR)						IPR024752 (PFAM): mobidb-lite (MOB	3,407	3,051	4,535	3,898	4,015									
Solyc02g061950	Methyltransferase family protein, putative (AHRD V3.3 *** G7JXM7_MEDTR)		F:GO:0016740	F:transferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0'	5,835	4,696	8,248	7,493	8,155									
Solyc02g061960	RNA-binding protein Lupus La (AHRD V3.3 *** A0A103Y5K4_CYNCS)		F:GO:0003729: C:GC	F:mRNA binding; C:cytoplasm; P:response to abscisic acid; P:re			IPR006630 (SMART): IPR006630 (PF.	135,269	122,643	190,982	177,466	167,010									
Solyc02g061980	RNA-binding protein Lupus La (AHRD V3.3 *** A0A103YGQ1_CYNCS)		P:GO:0001101: F:GC	P:response to acid chemical; F:RNA binding; P:response to hor			IPR006630 (SMART): IPR006630 (PF.	75,935	72,732	89,653	88,179	85,434									
Solyc02g061990	Bzip transcription factor (AHRD V3.3 *** A0A087GK23_ARAAL)		F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			mobidb-lite (MOBIL bZIP	0,364	0,273	0,022	0,000	0,047									
Solyc02g062000	Zinc finger, FYVE/PHD-type (AHRD V3.3 *** A0A103XCA5_CYNCS)		F:GO:0046872	F:metal ion binding			IPR000306 (SMART): IPR000306 (PF.	95,263	110,465	130,655	128,841	126,765									
Solyc02g062010	LOW QUALITY:calpain-type cysteine protease family (AHRD V3.3 --* AT1G55350.6)							1,654	1,221	1,083	1,110	1,222									
Solyc02g062020	ROP GTPases family protein		F:GO:0003924: F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	8,161	11,671	8,624	8,398	9,661									
Solyc02g062030	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506: F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,096	0,191	0,253	0,050	0,048									
Solyc02g062040	RING/U-box superfamily protein (AHRD V3.3 *** AT4G35840.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	12,609	10,537	16,508	13,412	14,488									
Solyc02g062050	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151T1T1_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid			IPR009686 (PFAM): IPR013103 (PFAI	0,021	0,124	0,025	0,050	0,000									
Solyc02g062060	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 *-* B9SK58_F	NAC012	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,019	0,000	0,000	0,000	0,000									
Solyc02g062090	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 --* B9T476_R	NAC014	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,059	0,103	0,000	0,050	0,000									
Solyc02g062100	Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)		C:GO:0005886	C:plasma membrane			IPR009686 (PFAM): PTHR21068 (PAN	39,068	41,666	22,962	30,567	32,655			0,505	0,046				up	
Solyc02g062110	Ferredoxin--NADP reductase (AHRD V3.3 *-* K4B6A3_SOLLC)		P:GO:0016192: F:GC	P:vesicle-mediated transport; F:oxidoreductase activity; C:Mon			IPR001709 (PRINTS): IPR019150 (PF	38,386	62,879	50,997	48,501	48,703	0,737	0,031					up		
Solyc02g062120	Membrane fusion protein Use1 (AHRD V3.3 *-* AT3G55600.2)		C:GO:0016021	C:integral component of membrane			IPR019150 (PFAM): IPR019150 (PAN	1,472	1,004	1,536	2,061	1,412									
Solyc02g062130	Ferredoxin--NADP reductase (AHRD V3.3 *** K4B6A3_SOLLC)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR001709 (PRINTS): IPR035442 (PII	1,053	1,012	1,324	1,086	1,535									
Solyc02g062140	Armadillo repeat only (AHRD V3.3 *** W0TQK6_ACAMN)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	43,418	60,011	32,415	31,256	31,286									
Solyc02g062150	Pectinesterase (AHRD V3.3 *** K4B6A5_SOLLC)		F:GO:0030599: P:GC	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM): IPR012334 (G3D	0,000	0,060	0,000	0,000	0,000									
Solyc02g062160	Chaperone DnaJ-like protein (AHRD V3.3 *-* A0A1C6ZYA6_MEDSA)						IPR001623 (PRINTS): IPR001623 (SM	2,069	2,513	1,706	1,238	2,218									
Solyc02g062180	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein (AHRD V3.3 *** A8MRW3_ARATH)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027450 (PFAM): IPR037151 (G3D	14,069	10,701	12,963	12,813	11,964									
Solyc02g062190	tryptophan aminotransferase related 2 (AHRD V3.3 *** AT4G24670.2)		F:GO:0016846	F:carbon-sulfur lyase activity			IPR037029 (G3DSA:2.10.25.GENE3D	0,000	0,124	1,363	3,026	0,617					1,154	0,002			up
Solyc02g062230	Small auxin up-regulated RNA32	SAUR32	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF3	0,366	0,654	0,148	0,365	0,353									
Solyc02g062240	Small nuclear ribonucleoprotein (AHRD V3.3 *** G7LBD3_MEDTR)		P:GO:0000387: C:GC	P:spliceosomal snRNP assembly; C:spliceosomal complex			IPR001163 (SMART): IPR001163 (PF.	6,286	6,549	4,009	2,606	3,401									
Solyc02g062250	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *-* K4B6B4_SOLLC)		F:GO:0003755	F:peptidyl-prolyl cis-	EC:5.2.1.8	Peptidylprolyl isomer	IPR000297 (PFAM): G3DSA:3.10.50.4	38,381	43,429	57,459	60,368	54,668									
Solyc02g062270	RNA binding protein, putative (AHRD V3.3 *** B9SZV1_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	106,876	95,242	91,598	89,634	93,912									
Solyc02g062300	BURP domain protein RD22 (AHRD V3.3 *-* RD22_ARATH)		C:GO:0016021	C:integral component of membrane			IPR004873 (SMART): IPR004873 (PF.	2,253	1,530	1,940	1,838	2,355									
Solyc02g062310	BURP domain protein RD22 (AHRD V3.3 *-* RD22_ARATH)						IPR004873 (SMART): IPR004873 (PF	0,901	2,420	0,000	0,025	0,000									
Solyc02g062320	BURP domain protein RD22 (AHRD V3.3 *** RD22_ARATH)		C:GO:0016020: C:GC	C:membrane; C:integral component of membrane			IPR004873 (SMART): IPR004873 (PF.	4,544	2,644	0,000	0,025	0,023									
Solyc02g062330	Kinesin-like protein (AHRD V3.3 *** M1AVJ1_SOLTU)		F:GO:0003777: F:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,365	0,307	0,342	0,290	0,451									
Solyc02g062340	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4B6C3_SOLLC)		F:GO:0004332: P:GC	F:fructose-bisphos	EC:4.1.2.13	Fructose-bisphospha	IPR000741 (PFAM): IPR013785 (G3D	84,052	216,818	16,821	23,866	79,879	1,394	0,000	2,242	0,000			up	up	
Solyc02g062350	DnaJ, mitochondrial (AHRD V3.3 *** A0A0B0PT99_GOSAR)		C:GO:0009706: C:GC	C:chloroplast inner membrane; C:integral component of membra			IPR021788 (PFAM): IPR021788 (PAN	16,592	22,550	45,806	43,235	45,871									
Solyc02g062355	Vacuolar iron transporter family protein (AHRD V3.3 *-* A0A061E3E8_THECC)		C:GO:0016020: F:GC	C:membrane; F:transition metal ion transmembrane transporter			IPR008217 (PANTHER): PTHR31851:	0,019	0,000	0,000	0,025	0,000									
Solyc02g062370	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *-* W9SN42_9ROSA)		F:GO:0003677: F:GC	F:DNA binding; F:protein binding			IPR004343 (SMART): IPR019835 (SM	26,376	34,221	24,782	27,975	28,304									
Solyc02g062375	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *-* W9SN42_9ROSA)		F:GO:0005515	F:protein binding			IPR003169 (SMART): IPR035445 (G3	22,687	35,758	23,633	22,929	25,418	0,682	0,022					up		
Solyc02g062385	GATA transcription factor (AHRD V3.3 *** K4B6C7_SOLLC)		F:GO:0003700: C:GC	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ior			IPR000679 (SMART): IPR016679 (PIF	0,078	0,220	0,124	0,285	0,376									
Solyc02g062390	Dehydrin (AHRD V3.3 *** E7BXD9_JATCU)		P:GO:0009415	P:response to water			IPR000167 (PFAM): mobidb-lite (MOB	9,339	7,879	191,538	226,913	157,521									
Solyc02g062400	expression of terpenoids 1		F:GO:0003677: C:GC	F:DNA binding; C:nucleus; P:positive regulation of transcription,			IPR006511 (TIGRI SRS	0,000	0,000	0,000	0,000	0,023									
Solyc02g062410	Nuclear migration nudC (AHRD V3.3 *** A0A0B0N407_GOSAR)		C:GO:0005737: P:GC	C:cytoplasm; P:protein folding; P:developmental process; F:unfc			IPR007052 (PFAM): IPR008978 (G3D	0,040	0,081	0,000	0,022	0,000									
Solyc02g062420	green ripe-like 2	GRL2	C:GO:0016021	C:integral component of membrane			IPR008496 (PFAM): IPR008496 (PAN	7,502	5,455	12,995	14,647	11,560									
Solyc02g062430	D-2-hydroxyglutarate dehydrogenase (AHRD V3.3 *** G7KGB4_MEDTR)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR006094 (PFAM): IPR016169 (G3D	19,784	17,172	37,168	35,407	36,006									
Solyc02g062460	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *-* B9GL08_POPTR)		F:GO:0046872: F:GC	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR027443 (G3DSA:2.60.120.GENE3I	13,201	32,015	29,302	47,974	27,118					0,716	0,004			up
Solyc02g062463	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	72,797	169,565	171,841	284,211	176,636					0,730	0,000			up
Solyc02g062500	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,000	0,061	0,051	0,075	0,095									
Solyc02g062510	Peroxidase (AHRD V3.3 *** K4B6D9_SOLLC)		F:GO:0004601: P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,345	0,181	0,094	0,072	0,023									
Solyc02g062515	Photosynthetic NDH subcomplex B 2 (AHRD V3.3 --* A0A0F7GZL7_9ROSI)		F:GO:0003824: P:GC	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			mobidb-lite (MOBIDB_LITE)	0,239	0,136	0,218	0,169	0,191									
Solyc02g062520	Pseudouridine synthase family protein (AHRD V3.3 *** AT3G52260.2)		P:GO:0001522: F:GC	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			G3DSA:3.30.2350.10 (GENE3D): IPR(	8,623	8,407	10,901	11,564	9,782									
Solyc02g062530	thiamine-phosphate synthase (AHRD V3.3 *** AT5G49410.2)						mobidb-lite (MOBIDB_LITE): PTHR351	14,809	18,819	17,888	17,353	18,341									
Solyc02g062540	Thioredoxin domain-containing protein, putative (AHRD V3.3 *** B9S6A8_RICCO)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	21,990	19,931	16,422	15,569	14,900									
Solyc02g062550	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:3.40.50	4,489	18,587	4,558	4,410	5,896	2,069	0,003					up		
Solyc02g062560	Tobacco mosaic virus resistance-1	Tm-1	F:GO:0003824	F:catalytic activity			IPR009215 (PFAM): IPR013785 (G3D	2,135	2,638	0,267	0,614	0,402									
Solyc02g062570	Phosphatidic acid phosphatase family protein, putative (AHRD V3.3 *** A0A061DFN2_THECC)		P:GO:0006487: P:GC	P:protein N-linked g	EC:3.6.1.43	Dolichyldiphosphatas	G3DSA:1.20.144.10 (GENE3D): IPR0(	1,923	1,519	1,895	1,674	1,677									
Solyc02g062580	Phosphatidic acid phosphatase 2 (AHRD V3.3 *** X5I2G6_NICBE)		P:GO:0006487: P:GC	P:protein N-linked g	EC:3.6.1.43	Dolichyldiphosphatas	IPR000326 (PFAM): G3DSA:1.20.144	1,717	3,148	1,831	2,218	3,079									
Solyc02g062590	Hexosyltransferase (AHRD V3.3 *** K4B6E7_SOLLC)		P:GO:0006012: F:GC	P:galactose metabc	EC:2.4.1.123	Inositol 3-alpha-galac	IPR029044 (G3DSA:3.90.550.GENE3I	0,021	0,167	0,000	0,000	0,070									
Solyc02g062600	Gamma carbonic anhydrase-like protein (AHRD V3.3 *** I3SYK2_MEDTR)						IPR001451 (PFAM): G3DSA:2.160.10	30,484	33,790	68,986	67,708	68,003									
Solyc02g062610	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G36530.2)	PPHL1	C:GO:0009507: P:GC	C:chloroplast; P:chl	EC:3.1.1.14; EC:3.1.	Chlorophyllase; Carb	IPR000073 (PRINTS): IPR029058 (G3	4,789	6,677	6,171	5,922	10,482			0,753	0,004				up	
Solyc02g062620	Nuclear cap-binding protein (AHRD V3.3 *** B8YFW4_SOLTU)		F:GO:0000339: C:GC	F:RNA cap binding; C:nuclear cap binding complex; P:mRNA cis			IPR000504 (SMART): IPR000504 (PF.	95,618	94,761	108,623	105,935	102,346									
Solyc02g062630	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *-* A0A151SCY2_CAJCA)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,049	1,095	0,840	1,022	0,895									
Solyc02g062640	Phosphopantetheine adenylyltransferase (AHRD V3.3 *** COAD_ARATH)		F:GO:0003824: P:GC	F:catalytic activity; P:biosynthetic process			IPR004821 (PFAM): IPR014729 (G3D	21,404	20,556	27,480	28,813	27,228									
Solyc02g062650	Laccase (AHRD V3.3 *** I1J8U1_SOYBN)		F:GO:0005507: P:GC	F:copper ion bindin	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR008972 (G3DSA:2.60.40.GENE3D	0,000	0,117	0,000	0,000	0,000									
Solyc02g062670	Tubby-like F-box protein (AHRD V3.3 *** M1C232_SOLTU)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS): IPR001810 (PF	4,472	4,990	2,654	2,829	3,488									
Solyc02g062680	Anaphase-promoting complex subunit 10 (AHRD V3.3 *** K4B6F6_SOLLC)		C:GO:0005680: P:GC	C:anaphase-promoting complex; P:anaphase-promoting comple:			IPR004939 (SMART): IPR004939 (PF.	24,563	24,233	21,052	15,675	19,327					-0,421	0,048			down
Solyc02g062690	bHLH transcription factor 012		P:GO:0006355: F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	1,195	0,676	0,278	0,521	0,284									
Solyc02g062700	AAA-type ATPase family protein (AHRD V3.3 *** AT2G18330.1)		F:GO:0005524: C:GC	F:ATP binding; C:mitochondrion; P:mitochondrion organization			IPR003593 (SMART): IPR021911 (PF.	14,608	16,869	12,531	12,617	12,377									
Solyc02g062710	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	7,607	5,467	11,445	10,813	10,951									
Solyc02g062720	DNA glycosylase (AHRD V3.3 *** A0A103XKQ6_CYNCS)		F:GO:0003824: P:GC	F:catalytic activity; P:base-excision repair			IPR003265 (SMART): IPR003265 (PF.	14,702	11,531	22,133	22,610	19,919									
Solyc02g062740	cytosine-5 DNA methyltransferase5	drm5	P:GO:0006306: F:GC	P:DNA methylation; F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	34,514	35,618	46,191	45,152	45,657									
Solyc02g062770	late embryogenesis abundant protein (AHRD V3.3 *** AT5G66780.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,115	0,613	0,173	0,879	0,116									
Solyc02g062780	chromatin remodeling 1 (AHRD V3.3 *** AT5G66750.1)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR014001 (SM	11,748	11,433	3,849	3,918	4,940									
Solyc02g062790	Receptor-like kinase (AHRD V3.3 *** G7LEU4_MEDTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001245 (PF.	0,181	0,080	0,100	0,120	0,047									
Solyc02g062800	F-box protein (AHRD V3.3 *** W9SND6_9ROSA)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): PTHR44519 (	10,037	13,987	8,526	10,913	10,774									
Solyc02g062810	Signal recognition particle subunit SRP68 (AHRD V3.3 *** K4B6G9_SOLLC)		F:GO:0005047: C:GC	F:signal recognition particle binding; C:signal recognition particle			IPR038253 (G3DSA:1.10.3450.GENE:	28,250	31,070	28,298	26,763	28,478									
Solyc02g062840	LOW QUALITY:Signal recognition particle subunit SRP68 (AHRD V3.3 *-* K4B6G9_SOLLC)		F:GO:0005047: C:GC	F:signal recognition particle binding; C:signal recognition particle			IPR038253 (G3DSA:1.10.3450.GENE:	0,000	0,019	0,000	0,000	0,000									
Solyc02g062870	Polyol monosaccharide transporter 7	PMT7	C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TIC	0,019	0,000	0,000	0,000	0,000									
Solyc02g062890	polyol monosaccharide transporter 5	PMT5	C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	0,142	0,257	0,074	0,000	0,000									
Solyc02g062910	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MBF2_ARALL)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	22,954	27,579	22,188	20,181	20,997									
Solyc02g062920	Splicing factor u2af large subunit, putative (AHRD V3.3 *-* B9SGJ4_RICCO)		F:GO:0003723: C:GC	F:RNA binding; C:nucleus; P:mRNA processing			IPR000504 (SMART): IPR003954 (SM	100,799	98,018	86,129	81,365	84,943									
Solyc02g062930	vacuolar iron transporter (VIT) family protein (AHRD V3.3 --* AT4G27860.4)							9,166	12,907	10,615	12,401	9,391									
Solyc02g062940	Zinc finger protein (AHRD V3.3 *-* K9P0T0_9ROSI)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	25,131	29,195	15,314	14,833	16,552									
Solyc02g062950	G-box binding	gbf12	F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	43,750	42,784	45,745	43,545	44,324									
Solyc02g062960	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9HET5_POPTR)		F:GO:0003677	F:DNA binding			IPR000047 (PRINT HD-ZIP	3,202	3,923	0,605	0,700	0,772									
Solyc02g062970	Xaa-Pro aminopeptidase 2	app2	F:GO:0070006	F:metalloaminopept	EC:3.4.11	Acting on peptide bor	IPR000994 (PFAM): IPR032416 (PFAI	295,455	256,143	320,172	299,082	308,252									
Solyc02g062975	Glycosyltransferase (AHRD V3.3 *-* K4B6I8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): mob	0,077	0,099	0,000	0,000	0,000									
Solyc02g062990	Glycosyltransferase (AHRD V3.3 *** M0ZZL3_SOLTU)		C:GO:0043231: F:GC	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl			G3DSA:3.40.50.2000 (GENE3D): PTH	0,076	0,039	0,000	0,000	0,000									
Solyc02g063000	Glycosyltransferase (AHRD V3.3 *** K4B6I8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	13,900	6,399	0,512	0,434	0,535									
Solyc02g063010	BRASSINAZOLE-RESISTANT 1 protein, putative (AHRD V3.3 *** B9SGI1_RICCO)		F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:transcription, DNA			IPR008540 (PFAM BES1	139,454	146,044	76,907	74,086	80,685									
Solyc02g063020	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K9PQR0_ZOSMR)		C:GO:0016021: P:GC	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,040	0,158	0,025	0,268	0,446									
Solyc02g063030	LuxR family transcriptional regulator, putative (AHRD V3.3 *** A0A072U7J6_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,276	3,890	0,374	0,099	0,071									
Solyc02g063040	cytochrome P450 family protein (AHRD V3.3 --* AT3G06150.1)							14,345	13,591	13,536	15,151	14,025									
Solyc02g063050	Tripartite motif-containing 29 (AHRD V3.3 *** A0A0B0P7U5_GOSAR)						G3DSA:2.60.40.2700 (GENE3D): mob	43,480	47,104	51,236	52,528	51,079									
Solyc02g063060	Zinc-finger domain of monoamine-oxidase A repressor R1 protein (AHRD V3.3 *** AT5G38690.2)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018501 (SMART): IPR018866 (PF.	16,074	14,326	5,785	5,218	5,600									
Solyc02g063070	tft4	tft4	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR023410 (SM	317,081	332,067	493,374	441,601	444,344									
Solyc02g063075	Target SNARE coiled-coil domain-containing protein (AHRD V3.3 *** A0A103XBX5_CYNCS)		P:GO:0015031: C:GC	P:protein transport; C:integral component of Golgi membrane			G3DSA:1.20.5.110 (GENE3D): mobidb	14,689	13,400	18,304	20,544	17,003									
Solyc02g063080	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 *-* NDHK_CYCTA)		F:GO:0051536: P:GC	F:iron-sulfur cluster binding; P:oxidation-reduction process			IPR006137 (PFAM): G3DSA:3.40.50.1	0,019	0,154	0,100	0,047	0,095									
Solyc02g063090	T-complex protein 1 subunit zeta 1 (AHRD V3.3 *** TCPZA_ARATH)		F:GO:0005524: P:GC	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR027413 (G3	56,887	62,362	64,789	58,088	58,255									
Solyc02g063110	LOW QUALITY:Alba DNA/RNA-binding protein (AHRD V3.3 --* AT1G76010.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,036	0,000	0,000	0,000									
Solyc02g063120	LOW QUALITY:auxin transport protein (BIG) (AHRD V3.3 --* AT3G02260.4)							0,040	0,078	0,000	0,022	0,047									
Solyc02g063125	Tubulin alpha chain (AHRD V3.3 *-* TBA_PRUDU)		C:GO:0005874: P:GC	C:microtubule; P:microtubule-based process			IPR018316 (PFAM): IPR037103 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc02g063130	Rad23 UV excision repair protein family (AHRD V3.3 *** AT3G02540.3)		F:GO:0003684: F:GC	F:damaged DNA binding; F:protein binding; C:nucleus; P:nucleot			IPR004806 (PRINTS): IPR015940 (SM	124,630	140,538	133,173	129,089	131,009									
Solyc02g063140	3-ketoacyl-CoA synthase (AHRD V3.3 *** B7SSK0_SOLTU)		P:GO:0006633: C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR013747 (PFAI	3,438	1,881	0,050	0,092	0,117									
Solyc02g063150	RuBP carboxylase small subunit	TOMRBCSD	F:GO:0004497: F:GC	F:monooxygenase a	EC:4.1.1.39	Ribulose-bisphospha	IPR024681 (PRINTS): IPR000894 (SM	83,374	230,938	3,672	3,591	15,132	1,498	0,000	2,032	0,000			up	up	
Solyc02g063160	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G16120.4)						IPR000073 (PRINTS): IPR022742 (PF	3,782	2,212	5,702	6,776	7,817									
Solyc02g063170	Abscisic acid-deficient 4 (AHRD V3.3 *** A0A061EPF5_THECC)		C:GO:0016021	C:integral component of membrane			IPR025461 (PFAM): PTHR34543:SF1	2,997	2,941	1,309	0,744	1,495									
Solyc02g063180	UDP-N-acetylenolpyruvoylglucosamine reductase (AHRD V3.3 *** A0A0B0NNK7_GOSAR)		F:GO:0008762: P:GC	F:UDP-N-acetylmur	EC:1.1.1.158	Acting on the CH-OH	IPR011601 (PFAM): IPR016167 (G3D	0,727	1,130	0,240	0,293	0,328									
Solyc02g063185	Kinase-like protein (AHRD V3.3 *-* A8BM53_9ROSA)		F:GO:0004674: F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,021	0,000	0,000	0,000	0,000									
Solyc02g063200	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G16120.2)						IPR000073 (PRINTS): IPR022742 (PF	0,021	0,018	0,025	0,000	0,024									
Solyc02g063210	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G26540.1)		F:GO:0004672: P:GC	F:protein kinase activity; P:protein phosphorylation			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,025	0,024									
Solyc02g063220	Mannose-6-phosphate isomerase (AHRD V3.3 *** K4B6K7_SOLLC)		F:GO:0004476: P:GC	F:mannose-6-phosı	EC:5.3.1.8	Mannose-6-phosphat	IPR016305 (PRINTS): IPR001250 (TIC	22,067	18,110	10,520	7,921	8,639									
Solyc02g063230	LOW QUALITY:membrane-associated kinase regulator (AHRD V3.3 *** AT1G67050.1)		F:GO:0016301: P:GC	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,120	0,059	0,000	0,025	0,047									
Solyc02g063240	Delta(7)-sterol-C5(6)-desaturase (AHRD V3.3 *** SC5D_TOBAC)		F:GO:0005506: P:GC	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR11863 (PAN	42,737	40,039	37,031	39,159	34,471									
Solyc02g063250	Peptide methionine sulfoxide reductase MsrA (AHRD V3.3 *** W9S0U3_9ROSA)		F:GO:0008113: P:GC	F:peptide-methionin	EC:1.8.4.11	Peptide-methionine (:	IPR036509 (G3DSA:3.30.1060.GENE:	0,260	4,025	0,895	2,360	0,658	3,926	0,000			1,395	0,007	up		up
Solyc02g063255	Enolase (AHRD V3.3 *-* A0A103XBT6_CYNCS)		C:GO:0009507: P:GC	C:chloroplast; P:cellular process			IPR020810 (PFAM)	0,224	0,380	0,000	2,299	0,141					7,590	0,000			up
Solyc02g063260	Protein DETOXIFICATION (AHRD V3.3 *** K4B6L1_SOLLC)		P:GO:0006855: F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): PTHR11206:SF2	3,789	2,181	0,049	0,000	0,096									
Solyc02g063270	Protein DETOXIFICATION (AHRD V3.3 *** A0A0V0IBD5_SOLCH)		P:GO:0006855: F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	246,875	211,256	129,594	108,666	114,823									
Solyc02g063280	stress response protein (AHRD V3.3 *-* AT1G60640.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,870	17,654	16,043	14,412	13,304									
Solyc02g063290	Histone chaperone (AHRD V3.3 *** A9TVI5_PHYPA)		C:GO:0005634: P:GC	C:nucleus; P:chromatin assembly or disassembly			IPR006818 (PFAM): IPR036747 (G3D	5,217	4,140	6,356	5,861	5,340									
Solyc02g063300	carboxypeptidase (AHRD V3.3 *** AT5G38060.1)		F:GO:0004180: P:GC	F:carboxypeptidase activity; P:proteolysis			PTHR35106 (PANTHER): PTHR35106	4,017	3,935	3,064	2,728	3,408									
Solyc02g063310	LOW QUALITY:NOD26-like intrinsic protein 4.3	NIP4.3	F:GO:0015267: C:GC	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,000	0,000	0,022	0,000	0,000									
Solyc02g063320	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PMJ3_ZOSMR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	0,852	1,442	3,227	2,266	2,431									
Solyc02g063330	Kinase family protein (AHRD V3.3 *** B9H386_POPTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	5,351	12,716	3,094	2,244	3,907	1,274	0,000					up		
Solyc02g063350	Calcium binding protein (AHRD V3.3 *** Q93YA8_SESRO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	5,926	4,759	3,231	4,719	4,661									

Solyc02g063360	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** F4K8L6_ARATH)						IPR000008 (SMART): IPR035892 (G3	46,280	74,508	76,407	111,084	97,685					0,542	0,004			up
Solyc02g063380	LOW QUALITY:Fad-dependent oxidoreductase family protein (AHRD V3.3 --* A0A061RE27_9CHLO)						PTHR33168:SF10 (PANTHER): PTHR	0,173	0,177	0,022	0,102	0,047									
Solyc02g063390	3-oxo-5-alpha-steroid 4-dehydrogenase (AHRD V3.3 *** G7ZZ33_MEDTR)		P:GO:0006629; F:GC	P:lipid metabolic process; F:oxidoreductase activity, acting on t			G3DSA:1.20.120.1630 (GENE3D): IPF	3,208	2,538	0,922	0,583	1,032									
Solyc02g063400	Auxin induced-like protein (AHRD V3.3 *** A0A0K9NX81_ZOSMR)		C:GO:0016020	C:membrane			IPR006593 (SMART): IPR005018 (PF	0,239	0,218	0,163	0,144	0,070									
Solyc02g063410	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)		C:GO:0016021	C:integral component of membrane			IPR037699 (PANTHER)	0,378	0,153	0,000	0,000	0,000									
Solyc02g063420	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,460	2,661	3,649	4,850	1,348			-1,429	0,001				down	
Solyc02g063430	bHLH transcription factor 078	bHLH078	F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	2,911	6,511	0,908	0,340	0,399	1,182	0,002					up		
Solyc02g063440	cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 -** AT2G32210.1)		C:GO:0016021	C:integral component of membrane			IPR028144 (PFAM): PTHR31568:SF3	14,332	14,899	5,799	4,121	7,052									
Solyc02g063450	DNA-binding protein, putative (duplicated DUF1399) (AHRD V3.3 *** AT2G22660.2)						IPR009836 (PFAM): PTHR34365:SF5	301,683	232,798	354,463	303,189	352,809									
Solyc02g063460	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168; C:GC	F:methyltransferase activity; C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D): PTHR	6,559	6,321	10,590	9,559	8,503									
Solyc02g063470	LOW QUALITY:Auxin induced-like protein (AHRD V3.3 *** E0Z5T8_PICSI)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane; P:oxidation-re			IPR006593 (SMART): IPR017214 (PIF	0,061	0,076	0,025	0,000	0,000									
Solyc02g063480	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03230.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,059	0,327	0,025	0,000	0,000									
Solyc02g063490	Malate dehydrogenase (AHRD V3.3 *** K4B6N4_SOLLC)		P:GO:0005975; P:GC	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR001236 (PFAM): IPR022383 (PFA	62,059	59,692	288,551	272,440	245,898									
Solyc02g063510	LOW QUALITY:GTPase-activating protein pac-1 (AHRD V3.3 *** A0A1D1Y9Q3_9ARAE)						PTHR32011:SF3 (PANTHER): PTHR3	3,588	5,345	0,439	0,147	0,535									
Solyc02g063520	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001356 (SMAF HD-ZIP	17,059	26,983	4,072	3,197	4,370									
Solyc02g064540	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT4G26650.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	0,179	0,230	0,169	0,169	0,235									
Solyc02g064550	Thioredoxin superfamily protein (AHRD V3.3 *** AT5G65840.1)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.40.30.10 (GENE3D): IPR03	14,906	18,941	18,545	17,882	23,856									
Solyc02g064560	LOW QUALITY:Protein PHLOEM PROTEIN 2-LIKE A10 (AHRD V3.3 *** A0A0B2PZA4_GLYSO)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			PTHR21477:SF12 (PANTHER): PTHR	0,000	0,021	0,000	0,000	0,000									
Solyc02g064570	VQ motif-containing protein (AHRD V3.3 *-* AT4G37710.2)						IPR008889 (PFAM): mobidb-lite (MOB	0,019	0,000	0,000	0,000	0,023									
Solyc02g064580	Transmembrane protein (AHRD V3.3 *** A0A0B0MN28_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR019358 (PFAM): PTHR31587 (PAN	17,492	14,952	25,641	24,168	24,151									
Solyc02g064590	Integrator complex subunit 7 (AHRD V3.3 *** A0A0B2PHC6_GLYSO)		P:GO:0016180; C:GC	P:snRNA processing; C:integrator complex			IPR033060 (PANTHER): IPR016024 (	0,318	0,244	0,214	0,412	0,281									
Solyc02g064595	Myb transcription factor (AHRD V3.3 *-* A0A072VG04_MEDTR)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; P:nucleosome assembly; P:snRI			IPR005818 (SMART): G3DSA:1.10.24	0,040	0,000	0,000	0,000	0,046									
Solyc02g064630	Myb transcription factor (AHRD V3.3 *** A0A072VG04_MEDTR)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR005818 (SMAF MYB_related	0,499	0,525	0,685	0,589	0,448									
Solyc02g064640	Adenylyl-sulfate kinase (AHRD V3.3 *** K4B6Q1_SOLLC)		P:GO:0000103; F:GC	P:sulfate assimilatic	EC:2.7.1.25	Adenylyl-sulfate kina	IPR006689 (PRINTS): SM00178 (SMA	0,000	0,057	0,025	0,000	0,024									
Solyc02g064650	xyloglucan endo-transglycosylase B2	txetb2	P:GO:0000103; F:GC	P:sulfate assimilatic	EC:2.7.1.25	Adenylyl-sulfate kina	PF01583 (PFAM): G3DSA:3.40.50.30	0,143	0,457	0,366	0,295	0,284									
Solyc02g064660	Protein DETOXIFICATION (AHRD V3.3 --* A0A067KFI1_JATCU)							0,059	0,182	0,072	0,118	0,094									
Solyc02g064670	60S ribosomal protein L26-1 (AHRD V3.3 *** RL261_ARATH)		F:GO:0003735; P:GC	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005824 (SMART): IPR014722 (G3	113,919	125,643	99,139	90,749	94,915									
Solyc02g064680	Calcium-transporting ATPase (AHRD V3.3 *** M1BXI4_SOLTU)		F:GO:0005388; F:GC	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRIN	887,121	623,787	206,867	306,456	459,242			1,148	0,000				up	
Solyc02g064690	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT2G23060.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			G3DSA:3.40.630.30 (GENE3D): IPR0	18,310	14,152	54,839	37,171	40,285			-0,447	0,032	-0,557	0,000		down	down
Solyc02g064700	Protein kinase superfamily protein (AHRD V3.3 *** AT2G23070.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	77,674	95,515	96,854	101,097	100,368									
Solyc02g064710	transcriptional regulator of RNA polII, SAGA, subunit (AHRD V3.3 *** AT4G33890.2)		C:GO:0070461	C:SAGA-type complex			IPR024738 (PFAM): PTHR21277:SF1	0,897	0,909	0,215	0,349	0,688									
Solyc02g064720	phototropic-responsive NPH3 family protein		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR000210 (PF	23,703	16,336	5,929	4,103	4,085									
Solyc02g064730	cyclin-dependent kinase B1-2 (AHRD V3.3 --* AT2G38620.3)						IPR039438 (PFAM): IPR007513 (PFA	591,888	578,810	620,480	525,888	526,675									
Solyc02g064740	Chaperone protein DnaJ (AHRD V3.3 *** A0A0B2RP83_GLYSO)						IPR001623 (PRINTS): IPR001623 (SM	40,375	30,446	31,820	31,753	33,592									
Solyc02g064750	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9T4J5_RICCO)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR006620 (SMART): IPR005123 (PF	36,330	34,702	30,424	27,898	29,229									
Solyc02g064770	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9SG47_RICCO)		F:GO:0080030; P:GC	F:methyl indole-3-ac	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	4,803	3,765	21,241	15,907	20,233									
Solyc02g064795	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT3G01410.2)							4,978	5,298	2,357	1,960	1,959									
Solyc02g064800	Transducin/WD-like repeat-protein (AHRD V3.3 *** A0A072W178_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR003603 (SM	5,062	6,057	2,830	4,164	3,232									
Solyc02g064802	chloride channel D (AHRD V3.3 --* AT5G26240.2)							0,081	0,041	0,025	0,022	0,000									
Solyc02g064804	GH3 (AHRD V3.3 *-* E2FHL2_9ROSI)						IPR004993 (PFAM): IPR004993 (PAN	0,000	0,039	0,072	0,067	0,118									
Solyc02g064806	Cytochrome P450 (AHRD V3.3 *-* A0A103Y530_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PFAM): IPR036396 (G3D	0,040	0,140	0,075	0,099	0,072									
Solyc02g064808	Histone H3 K4-specific methyltransferase SET7/9 family protein (AHRD V3.3 --* AT1G21920.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,039	0,209	0,273	0,282									
Solyc02g064810	GH3 (AHRD V3.3 *-* E2FHL1_9ROSI)						IPR004993 (PFAM): IPR004993 (PAN	0,040	0,041	0,046	0,022	0,165									
Solyc02g064830	Indole-3-acetic acid-amido synthetas 3-3	GH3_3					IPR004993 (PFAM): PTHR31901:SF7	1,815	7,195	1,895	1,785	2,067	2,005	0,003					up		
Solyc02g064850	Cytochrome P450, putative (AHRD V3.3 *** B9R747_RICCO)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc02g064870	Fertilization-related kinase 1 (AHRD V3.3 *** T2B355_SOLCH)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	0,019	0,018	0,000	0,000	0,000									
Solyc02g064950	CBS domain-containing protein-like (AHRD V3.3 *** B8AP73_ORYSI)		C:GO:0009507; P:GC	C:chloroplast; P:cell redox homeostasis			IPR000644 (SMART): IPR000644 (PF	43,592	65,306	73,125	68,086	79,449									
Solyc02g064960	APETALA2b	AP2b	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN AP2	2,277	2,301	0,627	0,451	0,660									
Solyc02g064970	Peroxidase		F:GO:0004601; P:GC	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	1,183	1,675	0,147	0,464	0,612									
Solyc02g064980	LOW QUALITY:MAP kinase kinase kinase	MAPKKK14	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	4,546	11,283	2,609	2,543	1,652	1,336	0,046					up		
Solyc02g064990	Remorin family protein (AHRD V3.3 *** B9H6G4_POPTR)						IPR005516 (PFAM): mobidb-lite (MOB	9,869	10,239	9,794	8,325	8,387									
Solyc02g065000	Calcium-binding EF-hand (AHRD V3.3 *** A0A103YH91_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	0,769	1,528	1,768	1,340	1,766									
Solyc02g065010	LOW QUALITY:EF hand calcium-binding protein family, putative (AHRD V3.3 *** A0A061DG88_THECC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	0,499	0,791	0,821	1,018	0,544									
Solyc02g065020	BEST plant protein match is: (TAIR:plant.1) protein, putative (AHRD V3.3 *** G7K7Z5_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR317	0,000	0,018	0,022	0,000	0,000									
Solyc02g065050	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT2G39710.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032799 (PF	6,049	2,851	0,605	0,359	0,757	-1,058	0,029					down		
Solyc02g065055	Protein-S-isoprenylcysteine O-methyltransferase (AHRD V3.3 *-* A0A0V0HYM3_SOLCH)		F:GO:0004671; P:GC	F:protein C-termina	EC:2.1.1.1	Protein-S-isoprenylcy	IPR007269 (PFAM): G3DSA:1.20.120	0,000	0,037	0,000	0,000	0,000									
Solyc02g065060	3-ketodihydrosphingosine reductase (AHRD V3.3 *** A0A0B0PNI7_GOSAR)						IPR002347 (PRINTS): IPR002347 (PF	3,915	8,826	0,262	0,164	0,445	1,197	0,005					up		
Solyc02g065070	CDPK-related kinase (AHRD V3.3 *** AT3G50530.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): G3DSA:1.10.51	11,693	13,461	6,859	8,765	8,464									
Solyc02g065080	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT3G50520.1)		P:GO:0016311; F:GC	P:dephosphorylation; F:phosphatase activity			IPR013078 (SMART): PIRSF000709 (	13,966	12,344	19,774	18,338	18,915									
Solyc02g065090	Patatin (AHRD V3.3 *** K4B6U4_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM): G3DSA:3.40.109	0,000	0,021	0,025	0,000	0,000									
Solyc02g065110	MAP kinase kinase kinase 15	MAPKKK15	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	11,444	11,896	7,458	8,786	10,873			0,538	0,026				up	
Solyc02g065150	LOB domain-containing 36-like protein (AHRD V3.3 *** A0A0B0PS92_GOSAR)		P:GO:0006355; P:GC	P:regulation of transcription, DNA-templated; P:proximal/distal p			IPR004883 (PFAM LBD	0,040	0,021	0,050	0,115	0,141									
Solyc02g065160	Upstream activation factor subunit spp27 (AHRD V3.3 *** A0A151TI11_CAJCA)		F:GO:0005515	F:protein binding			IPR019835 (SMART): IPR036885 (G3	0,323	0,154	0,000	0,025	0,000									
Solyc02g065170	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2RUS1_GLYSO)		F:GO:0005507; F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	23,645	43,720	1,611	4,157	4,664	0,914	0,011	1,524	0,000	1,362	0,002	up	up	up
Solyc02g065180	meiotically up-regulated protein (AHRD V3.3 *** AT5G66930.2)		P:GO:0006914	P:autophagy			IPR012445 (PFAM): mobidb-lite (MOB	6,371	5,758	9,985	10,855	9,770									
Solyc02g065190	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,058	0,018	0,119	0,120	0,046									
Solyc02g065210	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,000	0,019	0,000	0,000	0,000									
Solyc02g065220	Cytochrome P450 (AHRD V3.3 *** A0A103Y530_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	2,045	1,946	3,069	4,990	2,462									
Solyc02g065230	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,257	0,360	0,487	1,464	0,546									
Solyc02g065240	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:GC	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	12,927	21,647	133,456	221,084	67,493			-0,986	0,000	0,732	0,020		down	up
Solyc02g065250	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:GC	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	0,037	0,000	0,169	0,890	0,024									
Solyc02g065260	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151T437_CAJCA)		F:GO:0003676; P:GC	F:nucleic acid binding; P:DNA integration			IPR005162 (PFAM): IPR029472 (PFA	0,040	0,019	30,411	85,990	15,842					1,505	0,001			up
Solyc02g065270	Salicylic acid-binding protein 2 (AHRD V3.3 *-* SABP2_TOBAC)		P:GO:0009694; P:GC	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,072	0,226	0,024									
Solyc02g065280	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:GC	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	2,496	3,022	15,768	21,892	14,147									
Solyc02g065290	Dof zinc finger protein2		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,653	0,592	0,341	0,483	0,352									
Solyc02g065300	Leucyl-tRNA synthetase, putative (AHRD V3.3 *** B9SZE7_RICCO)		F:GO:0002161; F:GC	F:aminoacyl-tRNA e	EC:6.1.1.4; EC:3.1.1	Leucine--tRNA ligase	G3DSA:1.10.730.10 (GENE3D): IPR0	191,944	208,643	177,900	161,156	165,136									
Solyc02g065315	High mobility group protein 2 HMG2 (AHRD V3.3 --* Q40094_IPONI)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,036	0,025	0,098	0,023									
Solyc02g065320	B3 domain-containing REM16-like protein (AHRD V3.3 --* A0A0B0NG64_GOSAR)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus				0,156	0,018	0,093	0,025	0,047									
Solyc02g065330	initiator tRNA phosphoribosyl transferase family protein (AHRD V3.3 --* AT2G40570.3)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,057	0,000	0,022	0,000									
Solyc02g065350	B3 domain-containing transcription factor VRN1 (AHRD V3.3 *** A0A0B2Q684_GLYSO)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	1,573	1,328	0,490	0,294	0,376									
Solyc02g065360	MRNA, clone: rafl24-09-C04, putative isoform 1 (AHRD V3.3 *** A0A061DG15_THECC)		F:GO:0003677	F:DNA binding			IPR003340 (SMART): IPR015300 (G3	6,194	6,354	9,359	11,073	10,666									
Solyc02g065370	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase (AHRD V3.3 *** A0A0B0MSS3_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	74,361	65,830	62,082	54,340	50,745									
Solyc02g065380	Cold acclimation protein (AHRD V3.3 *** A0A1B0Z5D1_MUSPR)		C:GO:0016021	C:integral component of membrane			IPR008892 (PFAM): PTHR33596:SF1	31,789	38,966	46,603	62,003	47,890					0,415	0,006			up
Solyc02g065390	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_TECST)							0,185	0,142	0,118	0,022	0,144									
Solyc02g065400	33kDa precursor protein of oxygen-evolving complex	psbo	C:GO:0009654; P:GC	C:photosystem II oxygen evolving complex; P:photosystem II as			G3DSA:2.40.160.30 (GENE3D): G3DS	221,298	564,269	213,343	292,822	537,597	1,379	0,000	1,330	0,000	0,461	0,042	up	up	up
Solyc02g065410	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YH70_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,918	4,398	3,333	3,680	3,147	-0,987	0,011					down		
Solyc02g065420	CASP-like protein (AHRD V3.3 *** K4B6X5_SOLLC)		C:GO:0005886; C:GC	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021:SF2	24,192	14,697	12,907	15,216	11,859	-0,688	0,011					down		
Solyc02g065430	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7K9H8_MEDTR)						IPR025322 (PFAM): PTHR33052 (PAN	0,784	0,772	0,100	0,777	0,331									
Solyc02g065440	F-box/RNI-like/FBD-like domains-containing protein (AHRD V3.3 --* AT2G26030.4)						IPR006566 (PFAM)	0,000	0,000	0,025	0,000	0,000									
Solyc02g065460	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,000	0,000	0,050	0,050	0,024									
Solyc02g065470	pathogenesis-related protein-1-like protein (AHRD V3.3 *** AT2G19990.1)		C:GO:0005615	C:extracellular space			IPR001283 (PRINTS): IPR014044 (SM	49,821	43,365	12,632	8,458	11,511					-0,575	0,022			down
Solyc02g065480	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G66600.9)						IPR025757 (PFAM): IPR006869 (PFA	0,199	0,259	0,072	0,125	0,000									
Solyc02g065490	BEL1-related homeotic protein 22 (AHRD V3.3 *** Q8LLE0_SOLTU)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR001356 (SMAF TALE	0,576	0,236	0,068	0,123	0,093									
Solyc02g065500	Nucleolar pre-ribosomal-associated protein 1 (AHRD V3.3 *** A0A0B2NVN9_GLYSO)						IPR021714 (PFAM): IPR032436 (PFA	39,124	37,045	22,626	28,413	28,285									
Solyc02g065510	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T4W2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,888	3,206	2,265	2,167	1,856									
Solyc02g065515	transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 --* AT1G63490.3)							0,598	0,574	0,398	0,386	0,350									
Solyc02g065520	Receptor-like protein kinase (AHRD V3.3 *** W0TR82_ACAMN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	2,407	2,958	2,780	1,949	2,259									
Solyc02g065530	Hexosyltransferase (AHRD V3.3 *** K4B6Y5_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR002495 (PFAM): IPR029044 (G3D	4,931	6,001	0,025	0,025	0,000									
Solyc02g065540	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DGI8_THECC)		P:GO:0006511; C:GC	P:ubiquitin-dependent protein catabolic process; C:integral com			IPR001841 (SMART): IPR013083 (G3	12,791	11,526	12,084	14,829	11,802									
Solyc02g065550	ACI19	aci19	P:GO:0051560	P:mitochondrial calcium ion homeostasis			IPR006769 (PFAM): IPR039055 (PAN	22,761	14,841	5,426	7,153	8,282									
Solyc02g065555	Calcium uniporter, mitochondrial (AHRD V3.3 *** A0A0B0PJN2_GOSAR)		P:GO:0051560	P:mitochondrial calcium ion homeostasis			mobidb-lite (MOBIDB_LITE): PTHR134	77,585	46,734	17,566	21,257	25,952	-0,705	0,004					down		
Solyc02g065560	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9R8H7_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	7,663	7,050	3,349	3,726	3,617									
Solyc02g065570	LOW QUALITY:Rotundifolia-like protein (AHRD V3.3 *** A0A072V006_MEDTR)						IPR012552 (PFAM): mobidb-lite (MOB	14,243	3,819	1,360	1,565	1,190	-1,865	0,000					down		
Solyc02g065580	Cytochrome b561 (AHRD V3.3 *** Q3LGX4_CITLA)		C:GO:0016021; F:GC	C:integral component of membrane; F:oxidoreductase activity; F			IPR006593 (SMART): G3DSA:1.20.12	22,851	24,756	24,181	23,311	21,723									
Solyc02g065590	Carboxylic ester hydrolase (AHRD V3.3 *** A0A087H6F2_ARAAL)		C:GO:0016021; F:GC	C:integral component of membrane; F:hydrolase activity			IPR002018 (PFAM): IPR029058 (G3D	1,221	1,118	0,520	0,417	0,615									
Solyc02g065600	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	0,158	0,136	0,118	0,170	0,212									
Solyc02g065610	TRICHOME BIREFRINGENCE-LIKE 19 (AHRD V3.3 *** AT5G15900.2)		C:GO:0016021	C:integral component of membrane			IPR025846 (PFAM): IPR026057 (PFA	5,606	5,714	0,957	0,906	0,823									
Solyc02g065620	RING/U-box superfamily protein (AHRD V3.3 --* AT1G74990.1)		F:GO:0046872	F:metal ion binding			IPR001357 (SMART): IPR001841 (SM	14,936	15,990	13,457	11,533	13,992									
Solyc02g065630	Sarcolemmal membrane-associated protein, putative isoform 1 (AHRD V3.3 *** A0A061EPT5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	29,404	29,708	29,485	29,386	28,120									
Solyc02g065650	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G02340.2)		C:GO:0005737; P:GC	C:cytoplasm; P:protein ubiquitination; F:ligase activity; F:ubiquit			IPR001841 (SMART): IPR001841 (PF	12,780	16,974	20,838	20,564	17,905									
Solyc02g065660	WPP domain-interacting tail-anchored 1-like protein (AHRD V3.3 *** A0A0B0NVK1_GOSAR)		C:GO:0005635; C:GC	C:nuclear envelope; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	30,619	26,233	39,145	40,786	37,714									
Solyc02g065670	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,037	0,119	0,000	0,092	0,000									
Solyc02g065680	Amino acid transporter, putative (AHRD V3.3 *** B9T738_RICCO)		P:GO:0003333; F:GC	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): mobidb-lite (MOB	131,106	103,296	40,125	32,264	43,652									
Solyc02g065685	Biogenesis of lysosome-related organelles complex 1 subunit 2 (AHRD V3.3 *** A0A0B2R8E9_GLYSO)						IPR019269 (PFAM)	0,681	1,384	1,041	1,447	1,227									
Solyc02g065690	Biogenesis of lysosome-related organelles complex 1 subunit 2 (AHRD V3.3 *** A0A0B2R8E9_GLYSO)						IPR019269 (PFAM)	0,000	0,019	0,000	0,048	0,000									
Solyc02g065710	GDSL esterase/lipase 7 (AHRD V3.3 *-* W9R9P0_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	1,852	0,577	0,025	0,049	0,000									
Solyc02g065715	GDSL esterase/lipase (AHRD V3.3 *** A0A1D1YFA0_9ARAE)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	1,009	0,482	0,000	0,000	0,000									
Solyc02g065720	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EHB8_THECC)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART): IPR024766 (PF	14,024	15,516	19,837	17,196	16,689									
Solyc02g065730	MADS box transcription factor (AHRD V3.3 *** Q689E7_GENTR)		F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	0,000	0,000	0,000	0,000	0,024									
Solyc02g065740	Alpha-1,4-glucan-protein synthase [UDP-forming] (AHRD V3.3 *** UPTG_PEA)		F:GO:0016866; P:GC	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR004901 (PIRSF): IPR037595 (PFA	0,000	0,039	0,000	0,000	0,000									
Solyc02g065750	cytochrome P450 AB190445		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,000	0,019	0,000	0,000	0,000									
Solyc02g065770	COBRA protein (AHRD V3.3 *** K4B708_SOLLC)		P:GO:0010215; P:GC	P:cellulose microfibril organization; P:cell growth; C:anchored cc			IPR006918 (PIRSF): IPR006918 (PFA	265,210	220,254	19,652	13,148	18,876									
Solyc02g065780	LOW QUALITY:RALF-LIKE 27 family protein (AHRD V3.3 *** A9PEG6_POPTR)						IPR039252 (PANTHER)	88,004	49,868	1,860	0,738	1,078									
Solyc02g065790	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *-* AT3G29760.5)		F:GO:0004721; P:GC	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threor	IPR004274 (SMART): IPR004274 (PF	10,258	8,260	9,027	9,011	8,192									
Solyc02g065800	TCP transcription factor 28	TCP28					IPR017887 (PFAM TCP	0,926	0,610	0,977	0,857	0,944									
Solyc02g065805	furry (AHRD V3.3 *** AT5G08060.1)						PTHR36391 (PANTHER)	0,000	0,021	0,118	0,025	0,094									
Solyc02g066800	furry (AHRD V3.3 *** AT5G08060.1)						PTHR36391 (PANTHER)	12,331	8,241	10,537	11,307	11,007									
Solyc02g066810	LOW QUALITY:Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily protein (AHRD V3.3 --* AT1G67280.1)							1,684	1,579	2,538	2,518	2,269									
Solyc02g066820	LOW QUALITY:Integrin-linked protein kinase family (AHRD V3.3 --* AT3G58760.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	2,805	2,093	2,781	3,396	2,763									
Solyc02g066830	Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *** A0A061EH36_T		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): G3DSA:3.10.45	15,890	11,348	13,469	12,640	11,994									
Solyc02g066860	Ninja-family protein (AHRD V3.3 *-* A0A199VX64_ANACO)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): mobidb-lite (MOB	0,058	0,039	0,000	0,000	0,000									
Solyc02g066870	Ninja-family protein (AHRD V3.3 *-* A0A199VX64_ANACO)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): PTHR31413:SF1	0,000	0,041	0,000	0,000	0,000									
Solyc02g066910	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT3G17430.2)		C:GO:0005768; C:GC	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM): mobidb-lite (MOB	18,177	14,809	21,894	27,877	23,359									
Solyc02g066920	chlororespiratory reduction 7 (AHRD V3.3 *** AT5G39210.1)		C:GO:0009570; P:GC	C:chloroplast stroma; P:NAD(P)H dehydrogenase complex asse			IPR038150 (G3DSA:3.90.940.GENE3	1,782	5,801	0,477	1,166	2,812	1,727	0,000	2,520	0,000			up	up	
Solyc02g066930	RNA-binding protein (AHRD V3.3 *** Q941H9_TOBAC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	0,000	0,060	0,022	0,025	0,118									
Solyc02g066940	Protein RIK-like protein (AHRD V3.3 *** A0A0B0MTZ1_GOSAR)		F:GO:0003723; C:GC	F:RNA binding; C:nucleus			IPR036612 (G3DSA:3.30.1370.GENE	88,926	74,190	80,874	92,841	89,766									
Solyc02g066950	Alpha-amylase, putative (AHRD V3.3 *** B9SJF1_RICCO)		F:GO:0004556; F:GC	F:alpha-amylase ac	EC:3.2.1.1	Alpha-amylase	PTHR43447:SF8 (PANTHER): PTHR4	16,345	19,709	6,701	8,167	10,372									
Solyc02g066955	Alpha-amylase (AHRD V3.3 *-* A0A0A0R208_MORAL)		F:GO:0004556; F:GC	F:alpha-amylase ac	EC:3.2.1.1	Alpha-amylase	IPR012850 (SMART): IPR006047 (SM	13,539	17,690	5,623	6,520	8,212									
Solyc02g066960	Glycosyltransferase (AHRD V3.3 *** K4B728_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,115	0,099	0,000	0,022	0,000									
Solyc02g066970	LOW QUALITY:Transcription factor bHLH151, putative (AHRD V3.3 *-* A0A061EF71_THECC)		C:GO:0005575; P:GC	C:cellular_component; P:biological_process; F:protein dimerizat			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,313	0,025	0,000	0,000									
Solyc02g066980	LOW QUALITY:TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT5G15510.1)		C:GO:0005819; C:GC	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027329 (PFAM): mobidb-lite (MOB	0,078	0,081	0,000	0,047	0,000									

Solyc02g067000	Latex abundant protein 1 (AHRD V3.3 --* B9N9R7_POPTR)		F:GO:0070300	F:phosphatidic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,120	0,179	0,100	0,195	0,140									
Solyc02g067010	Pattern formation EMB30-like protein (AHRD V3.3 *** A0A0B0NVB0_GOSAR)		F:GO:0005086; P:GO	F:ARF guanyl-nucleotide exchange factor activity; P:regulation c			IPR000904 (SMART): IPR032691 (PF	11,451	7,677	7,493	5,636	6,194									
Solyc02g067030	SNF1	snf1	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR015940 (SM	43,464	38,762	51,641	42,679	46,277									
Solyc02g067040	DUF1336 family protein (DUF1336) (AHRD V3.3 *** AT3G29180.3)						IPR009769 (PFAM): PTHR31558 (PAN	0,487	0,749	13,348	12,890	11,596									
Solyc02g067050	UPF0301 protein (AHRD V3.3 *** A0A0B2NUC1_GLYSO)						IPR003774 (PFAM): G3DSA:3.40.174	0,019	0,113	0,022	0,000	0,047									
Solyc02g067060	Hexosyltransferase (AHRD V3.3 *** K4B738_SOLLC)	GAUT13-1	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	13,879	12,830	2,959	2,796	4,127									
Solyc02g067070	Zinc finger protein (AHRD V3.3 *** A0A0B0MNI3_GOSAR)		F:GO:0003676; F:GO	F:nucleic acid binding; F:zinc ion binding			IPR003604 (SMART): IPR013087 (SM	14,272	12,978	27,927	26,862	27,614									
Solyc02g067080	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT5G15490.1)		F:GO:0003979; F:GO	F:UDP-glucose 6-de	EC:1.1.1.22	UDP-glucose 6-dehy	IPR014027 (SMART): G3DSA:3.40.50	152,646	177,881	96,883	79,838	93,912									
Solyc02g067085	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_EUCGG)							1,281	2,192	1,506	1,193	1,486									
Solyc02g067090	Coilin (AHRD V3.3 *-* A0A0B0P2W2_GOSAR)		P:GO:0006396; F:GO	P:RNA processing; F:U1 snRNA binding; F:U2 snRNA binding			IPR031722 (PFAM): mobidb-lite (MOB	25,090	17,473	17,492	16,720	15,869									
Solyc02g067095	Coilin-like protein (AHRD V3.3 *-* U6BQ51_NICBE)		P:GO:0006396; F:GO	P:RNA processing; F:U1 snRNA binding; F:U2 snRNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	29,802	24,160	23,607	20,648	20,790									
Solyc02g067100	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT5G15510.1)		C:GO:0005819; C:GO	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027329 (PFAM): mobidb-lite (MOB	0,593	0,248	0,248	0,192	0,024									
Solyc02g067105	Cysteine protease (AHRD V3.3 --* A0A0A7TYC9_CICAR)		P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:1.20.5.170 (GENE3D): IPR00	3,682	5,445	1,903	2,019	2,422									
Solyc02g067110	LOW QUALITY:Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 --* AT4G35730.1)							0,040	0,000	0,000	0,000	0,000									
Solyc02g067120	DUF1997 family protein (AHRD V3.3 *** G7KKZ0_MEDTR)						IPR018971 (PFAM): PTHR34133 (PAN	12,072	16,826	17,388	19,031	24,636			0,502	0,013				up	
Solyc02g067130	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,000	0,025	0,296	0,000									
Solyc02g067150	Latex abundant protein 1 (AHRD V3.3 *** B9N9R7_POPTR)		F:GO:0070300	F:phosphatidic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc02g067160	SPX domain-containing family protein (AHRD V3.3 *** B9IK08_POPTR)		P:GO:0016036	P:cellular response to phosphate starvation			IPR004331 (PFAM): mobidb-lite (MOB	15,773	13,184	19,313	20,499	17,059									
Solyc02g067180	cystathionine gamma synthase		F:GO:0003824; F:GO	F:catalytic activity; F:pyridoxal phosphate binding			IPR015422 (G3DSA:3.90.1150.GENE	209,082	217,702	667,155	762,633	683,376									
Solyc02g067190	CASP-like protein (AHRD V3.3 *** K4B751_SOLLC)		C:GO:0005886; P:GO	C:plasma membrane; P:cell-cell junction assembly; C:integral cc			IPR006702 (PFAM): IPR006459 (TIGF	0,019	0,018	0,000	0,000	0,000									
Solyc02g067200	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T4E7_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	11,171	9,536	17,452	17,113	16,107									
Solyc02g067210	RNA-binding KH domain-containing protein		F:GO:0003723	F:RNA binding			IPR004087 (SMART): G3DSA:3.30.31	106,302	98,045	130,183	121,471	122,161									
Solyc02g067220	EF hand calcium-binding family protein (AHRD V3.3 *-* G7L207_MEDTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	0,140	0,082	0,071	0,049	0,000									
Solyc02g067230	Dof zinc finger protein3	Dof3	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM) Dof	4,794	3,551	4,057	4,167	2,657									
Solyc02g067240	Cysteine proteinase inhibitor (AHRD V3.3 --* M1A5Q0_SOLTU)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			G3DSA:3.10.450.10 (GENE3D): IPR0	0,021	0,076	0,022	0,000	0,000									
Solyc02g067250	ribosomal protein L34e superfamily protein (AHRD V3.3 *** AT5G15260.2)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR008195 (PANTHER): PTHR10759:	7,466	8,654	13,218	17,187	12,586									
Solyc02g067260	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G26800.1)		F:GO:0016874	F:ligase activity			SM01197 (SMART): IPR001841 (SMA	0,854	1,030	0,625	0,636	0,730									
Solyc02g067275	Dehydration-responsive protein RD22 (AHRD V3.3 --* K7XKT0_SOLTU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,768	1,682	1,981	1,687	2,407									
Solyc02g067280	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G61180.1)		C:GO:0016020; F:GO	C:membrane; F:ligase activity			IPR001841 (SMART): IPR013083 (G3	1,058	0,666	1,172	0,774	1,013									
Solyc02g067285	Structural maintenance of chromosomes protein (AHRD V3.3 *-* A0A068U3R5_COFCA)		F:GO:0005524; C:GO	F:ATP binding; C:nucleus; C:chromosome; P:chromosome orga			PTHR43939:SF1 (PANTHER): PTHR4	3,503	2,362	2,750	2,905	2,806									
Solyc02g067290	Structural maintenance of chromosomes protein (AHRD V3.3 *-* A0A068U3R5_COFCA)		F:GO:0005524; C:GO	F:ATP binding; C:nucleus; C:chromosome; P:chromosome orga			PTHR43939:SF1 (PANTHER): PTHR4	0,164	0,124	0,109	0,117	0,142									
Solyc02g067300	Structural maintenance of chromosomes protein (AHRD V3.3 *-* A0A0K9Q8I9_SPIOL)		F:GO:0005524; C:GO	F:ATP binding; C:nucleus; C:chromosome; P:chromosome organization				0,019	0,000	0,000	0,000	0,000									
Solyc02g067310	ZF-HD homeobox protein (AHRD V3.3 *** Q9ARE3_FLABI)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 ZF-HD	1,182	1,108	0,074	0,125	0,000									
Solyc02g067320	ZF-HD homeobox protein (AHRD V3.3 *** Q9ARE3_FLABI)		F:GO:0003677	F:DNA binding			IPR006455 (TIGRI ZF-HD	5,606	6,283	0,536	0,371	0,444									
Solyc02g067340	R2R3MYB transcription factor 96	R2R3MYB96/THM6	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	9,934	7,700	0,429	0,305	0,325									
Solyc02g067350	DUF1666 family protein (AHRD V3.3 *** Q2HVS4_MEDTR)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM): mobidb-lite (MOB	2,823	1,753	1,198	0,853	0,892									
Solyc02g067360	Protease Do-like 8, chloroplastic (AHRD V3.3 *** DEGP8_ARATH)		F:GO:0004252; F:GO	F:serine-type endop	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): IPR001478 (SM	7,141	6,967	4,096	3,186	4,491									
Solyc02g067370	Nucleosome assembly protein family (AHRD V3.3 *** A9RDJ7_PHYPA)		C:GO:0005634; P:GO	C:nucleus; P:nucleosome assembly			IPR002164 (PFAM): G3DSA:3.30.112	45,891	52,446	66,338	63,309	62,427									
Solyc02g067380	Transcription factor protein (AHRD V3.3 *** A0A0B0MSC8_GOSAR)		P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (PFAM) bHLH	4,162	4,073	0,000	0,025	0,024									
Solyc02g067390	RNA recognition motif-containing family protein (AHRD V3.3 *** B9IJW1_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	15,249	15,972	21,056	21,771	20,137									
Solyc02g067400	Glutaredoxin family protein (AHRD V3.3 *** AT5G39865.1)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR002109 (PFAM): G3DSA:3.40.30.1	0,019	0,043	0,022	0,025	0,000									
Solyc02g067410	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072U5Q1_MEDTR)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRINT HD-ZIP	0,280	0,289	0,215	0,192	0,165									
Solyc02g067420	Ubiquitin-conjugating enzyme (AHRD V3.3 *** Q5ZFS2_PLAMJ)		P:GO:0000209; F:GO	P:protein polyubiquitination; F:ATP binding; P:DNA repair; P:prot			SM00212 (SMART): IPR000608 (PFAI	24,134	22,912	21,556	20,165	21,548									
Solyc02g067440	meloidogyne-induced giant cell protein DB114	TOMTRALTAD	F:GO:0016702; P:GO	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR012864 (PFAM): IPR014710 (G3D	9,705	11,377	11,117	8,423	10,506									
Solyc02g067460	Mitochondrial outer membrane protein porin (AHRD V3.3 *** A0A1D1XW30_9ARAE)		C:GO:0005741; F:GO	C:mitochondrial outer membrane; F:voltage-gated anion channe			IPR027246 (PFAM): IPR023614 (G3D	93,992	113,350	101,316	91,434	100,261									
Solyc02g067470	Hypersensitive-induced response protein (AHRD V3.3 *** A6YGE4_CARPA)						IPR001107 (SMART): G3DSA:3.30.47	20,014	17,716	10,352	9,607	10,752									
Solyc02g067480	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT5G39940.1),Pfam:PF03486						PR00368 (PRINTS): IPR004792 (TIGF	2,385	3,035	2,648	3,190	3,370									
Solyc02g067490	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)						IPR007679 (PFAM): G3DSA:2.80.10.5	0,433	0,823	4,329	10,525	4,391					1,279	0,000			up
Solyc02g067510	Actin cross-linking protein, putative (AHRD V3.3 *-* A0A061E7B5_THECC)		F:GO:0051015	F:actin filament binding			IPR007679 (PFAM): G3DSA:2.80.10.5	0,058	0,159	0,174	0,623	0,400									
Solyc02g067520	Unknown protein (AHRD V3.3)							10,028	9,974	6,101	6,413	6,842									
Solyc02g067530	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9RUJ2_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR006620 (SMART): IPR003582 (SM	31,655	48,566	10,810	8,612	12,431									
Solyc02g067540	methyltransferase (AHRD V3.3 *** AT3G28460.1),Pfam:PF03602		F:GO:0008168; P:GO	F:methyltransferase activity; P:methylation			G3DSA:3.40.50.150 (GENE3D): PF03	17,374	20,397	35,856	34,469	37,647									
Solyc02g067550	LOW QUALITY:CLE protein 3		P:GO:0045168	P:cell-cell signaling involved in cell fate commitment			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,077	0,200	0,496	0,194	0,355									
Solyc02g067560	Receptor-like kinase (AHRD V3.3 *** A0A0K9P790_ZOSMR)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR013210 (PFAM): G3DSA:3.30.200	9,389	11,198	9,757	8,716	9,772									
Solyc02g067570	Paired amphipathic helix SIN3-like protein (AHRD V3.3 *** G7KJX2_MEDTR)		F:GO:0003714; P:GO	F:transcription corepressor activity; P:regulation of transcription			IPR013194 (SMART): G3DSA:1.20.11	90,551	70,303	95,175	90,653	91,708									
Solyc02g067580	B12D (AHRD V3.3 *** D2XQY6_WOLAR)		C:GO:0005777; C:GO	C:peroxisome; C:integral component of membrane			IPR010530 (PFAM): PTHR33417 (PAN	95,111	96,369	194,701	174,323	197,228									
Solyc02g067590	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_NANDO)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	G3DSA:3.90.1100.10 (GENE3D): IPR	0,000	0,000	0,025	0,075	0,046									
Solyc02g067600	Dehydrin family protein (AHRD V3.3 --* AT1G20450.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,204	0,025	0,000	0,000									
Solyc02g067610	LOW QUALITY:DNA helicase INO80-like protein (AHRD V3.3 --* AT3G57300.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,598	5,385	0,268	0,294	0,187	1,769	0,005					up		
Solyc02g067620	Metal tolerance protein 8 (AHRD V3.3 *** MTP8_ORYSJ)		P:GO:0006812; F:GO	P:cation transport; F:cation transmembrane transporter activity;			IPR002524 (TIGRFAM): IPR002524 (F	21,447	16,538	38,472	36,882	35,143									
Solyc02g067650	polygalacturonase 1	PG24-5(TAPG3)	F:GO:0004650; P:GO	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,000	0,019	0,000	0,000	0,000									
Solyc02g067660	Phytoalexin-deficient 4-1 protein (AHRD V3.3 *** Q2TNK3_SOLTU)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	21,079	33,639	1,652	1,840	2,135									
Solyc02g067670	Flap endonuclease 1 (AHRD V3.3 *-* A0A0K9NZY8_ZOSMR)		F:GO:0003697; F:GO	F:single-stranded DNA binding; F:endonuclease activity; C:nucle			IPR006084 (PRINTS): IPR001044 (PF	95,721	85,571	79,950	79,031	78,342									
Solyc02g067680	RING/U-box superfamily protein (AHRD V3.3 *** AT5G40250.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	1,392	1,581	0,415	0,410	0,447									
Solyc02g067690	Glycosyltransferase (AHRD V3.3 *** M1A9P1_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	180,106	131,888	89,111	48,523	79,436					-0,873	0,000			down
Solyc02g067700	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FV20_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR001841 (PF	0,219	0,812	0,746	0,629	0,677									
Solyc02g067710	ARM repeat superfamily protein (AHRD V3.3 *** AT5G14790.1)						IPR034085 (SMART): IPR011989 (G3	2,049	1,528	0,817	0,671	0,755									
Solyc02g067720	RNA exonuclease-like protein (AHRD V3.3 *** A0A072VJ45_MEDTR)		F:GO:0003676; P:GO	F:nucleic acid binding; P:rRNA processing; F:3'-5' exonuclease			IPR013520 (SMART): IPR036397 (G3	0,000	0,079	0,000	0,000	0,000									
Solyc02g067740	beta-galactosidase (AHRD V3.3 *** AT3G27930.1)		F:GO:0008308; P:GO	F:voltage-gated anion channel activity; P:inorganic anion transp			PTHR35738 (PANTHER)	11,943	12,234	16,772	17,250	16,190									
Solyc02g067750	Carbonic anhydrase (AHRD V3.3 *** B1VK36_SOLLC)		F:GO:0004089; F:GO	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001765 (SMART): IPR036874 (G3	0,118	0,543	196,611	128,453	15,145			-3,698	0,000				down	
Solyc02g067770	Cysteine-rich receptor-like kinase (AHRD V3.3 *-* G7K057_MEDTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR002902 (PFAM): IPR038408 (G3D	0,038	0,101	0,051	0,072	0,047									
Solyc02g067780	Protein kinase family protein (AHRD V3.3 *** C6ZRU6_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR002902 (PF	0,604	0,536	2,387	1,777	1,774									
Solyc02g067790	High affinity nitrate transporter (AHRD V3.3 *** A0A0G2UMZ8_9ROSA)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM): G3DSA:1.20.125	0,876	1,763	3,422	3,184	3,042									
Solyc02g067800	LOB domain-containing protein, putative (AHRD V3.3 *** B9S640_RICCO)						IPR004883 (PFAM) LBD	1,749	3,182	0,747	0,713	0,512									
Solyc02g067810	cyclin-dependent kinase inhibitor (AHRD V3.3 *** AT1G10690.1)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,176	0,490	0,050	0,022	0,164									
Solyc02g067820	Glycosylphosphatidylinositol anchor attachment 1 (AHRD V3.3 *** A0A0B0NDV8_GOSAR)		C:GO:0042765	C:GPI-anchor transamidase complex			IPR007246 (PIRSF): IPR007246 (PFA	39,297	30,099	32,658	30,564	30,793									
Solyc02g067830	Protein kinase (AHRD V3.3 *** Q02494_MAIZE)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	4,974	4,775	1,410	1,760	1,530									
Solyc02g067840	Sucrase/ferredoxin-like family protein (AHRD V3.3 *** AT5G40510.1)		C:GO:0016021	C:integral component of membrane			IPR009737 (PFAM): G3DSA:3.40.30.1	20,602	25,876	85,540	90,603	71,489									
Solyc02g067850	LOW QUALITY:U-box domain-containing 3-like protein (AHRD V3.3 *** A0A0B0MLP6_GOSAR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	0,096	0,039	0,025	0,070	0,117									
Solyc02g067860	aldose 1-epimerase family protein (AHRD V3.3 *** AT5G14500.2)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:isomerase activity; F:carb			IPR008183 (PFAM): IPR025532 (PIRS	30,316	30,102	42,353	43,215	37,030									
Solyc02g067870	chalcone isomerase	CHI	F:GO:0016872	F:intramolecular lyase activity			IPR016087 (PFAM): IPR016088 (G3D	2,213	1,556	0,217	0,465	0,235									
Solyc02g067890	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G14430.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	57,971	50,761	23,084	18,302	21,232									
Solyc02g067900	Transcription factor GTE1 (AHRD V3.3 *** A0A0B2NX09_GLYSO)		C:GO:0005634; P:GO	C:nucleus; P:regulation of transcription, DNA-templated			IPR038336 (G3DSA:1.20.1270.GENE	12,977	13,189	16,477	17,349	15,635									
Solyc02g067925	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ED84_THECC)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	6,674	9,098	4,520	5,150	5,442									
Solyc02g067930	Glycerol-3-phosphate dehydrogenase [NAD(+)] (AHRD V3.3 *** K4B7C5_SOLLC)		F:GO:0004367; P:GO	F:glycerol-3-phosph	EC:1.1.1.8; EC:1.1.1	Glycerol-3-phosphate	IPR006168 (PRINTS): IPR013328 (G3	1,131	0,530	0,313	0,834	0,421									
Solyc02g067950	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *-* A0A072U7R9_MEDTR)						IPR027329 (PFAM): mobidb-lite (MOB	0,837	1,211	0,912	1,008	0,802									
Solyc02g067960	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** A0A061GHZ3_THECC)		F:GO:0003690; P:GO	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR038538 (G3	4,759	4,248	4,560	4,464	4,337									
Solyc02g067970	Zinc finger family protein, putative (AHRD V3.3 *** A0A061EDJ4_THECC)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): PF13923 (PFAM	0,316	0,209	0,343	0,123	0,167									
Solyc02g067975	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* A0A0M4B472_9ARAE)							5,689	5,287	4,784	4,284	5,112									
Solyc02g067980	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9HTC9_POPTR)		C:GO:0000159; P:GO	C:protein phosphatase type 2A complex; P:signal transduction;			IPR011989 (G3DSA:1.25.10.GENE3D	31,592	25,215	21,762	25,187	23,486									
Solyc02g067990	HAUS augmin-like complex subunit 6 (AHRD V3.3 *** A0A061ECN9_THECC)		P:GO:0051225; C:GO	P:spindle assembly; C:HAUS complex			IPR028163 (PFAM): mobidb-lite (MOB	13,430	11,618	11,601	17,357	15,769					0,582	0,008			up
Solyc02g068000	F-box family protein (AHRD V3.3 *** U5G645_POPTR)						IPR032675 (G3DSA:3.80.10.GENE3D	12,347	10,698	9,696	8,699	10,242									
Solyc02g068010	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 *** A0A0K9PUQ1_ZOSM		C:GO:0016021	C:integral component of membrane			IPR006634 (PFAM): IPR040327 (PAN	12,217	9,656	27,464	33,477	25,643									
Solyc02g068040	RNI-like superfamily protein (AHRD V3.3 --* AT4G02760.9)							65,421	69,424	134,288	159,471	139,048									
Solyc02g068050	Rubisco methyltransferase family protein (AHRD V3.3 *** AT5G14260.3)		C:GO:0009570; F:GO	C:chloroplast stroma; F:protein-lysine N-methyltransferase activ			IPR015353 (PFAM): IPR036464 (G3D	21,202	20,928	32,316	29,769	35,172									
Solyc02g068060	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT5G14210.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	2,273	2,834	0,667	0,605	0,938									
Solyc02g068070	Lipase (AHRD V3.3 *** K4B7D9_SOLLC)		P:GO:0006629; F:GO	P:lipid metabolic process; F:hydrolase activity, acting on ester b			IPR025483 (PIRSF): IPR006693 (PFA	8,776	9,593	0,510	0,333	0,470									
Solyc02g068075	DNA-binding family protein (AHRD V3.3 --* AT4G34430.4)							0,037	0,000	0,000	0,000	0,000									
Solyc02g068080	Chloride channel protein (AHRD V3.3 *** M1A9T9_SOLTU)		F:GO:0005247; P:GO	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR002251 (PRINTS): IPR001807 (PF	15,536	12,805	1,429	2,868	3,246					0,976	0,048			up
Solyc02g068090	30S ribosomal protein S21 (AHRD V3.3 *** W9SIU2_9ROSA)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001911 (PRINTS): IPR001911 (PF	30,144	50,409	44,403	52,283	62,853	0,769	0,002	0,498	0,001			up	up	
Solyc02g068100	SWIB complex BAF60b domain-containing family protein (AHRD V3.3 *** B9GJS7_POPTR)		F:GO:0005515	F:protein binding			IPR019835 (SMART): IPR003121 (PF	95,400	92,860	196,968	190,306	185,211									
Solyc02g068110	Transcription and mRNA export factor SUS1 (AHRD V3.3 *** M1A9K0_SOLTU),Pfam:PF10163		C:GO:0000124; F:GO	C:SAGA complex; F:transcription coactivator activity; C:nuclear			IPR038212 (G3DSA:1.10.246.GENE3	26,362	21,341	41,054	36,731	36,343									
Solyc02g068120	DCD (Development and Cell Death) domain protein (AHRD V3.3 *** AT3G27090.3)						IPR013989 (SMART): IPR013989 (PF	27,961	49,456	2,197	1,132	1,529	0,850	0,007					up		
Solyc02g068125	Photosystem II CP43 reaction center protein (AHRD V3.3 --* PSBC_ACUOB)							0,000	0,043	0,000	0,000	0,000									
Solyc02g068130	Mitochondrial import receptor subunit TOM20 (AHRD V3.3 *** TOM20_SOLTU)		F:GO:0005515; C:GO	F:protein binding; C:mitochondrial outer membrane translocase			PF06552 (PFAM): IPR011990 (G3DS/	37,766	37,893	51,092	44,921	49,289									
Solyc02g068140	Major facilitator superfamily protein (AHRD V3.3 *** AT3G01930.2)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM): PTHR21576 (PAN	3,789	4,712	0,567	0,613	0,799									
Solyc02g068150	Nuclear transport factor 2 (AHRD V3.3 *** NTF2_ARATH)		P:GO:0006913; C:GO	P:nucleocytoplasmic transport; C:nuclear pore central transport			IPR002075 (PFAM): PTHR12612:SF1	26,504	29,755	33,923	29,404	31,278									
Solyc02g068160	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT5G63500.1)		C:GO:0016021	C:integral component of membrane			IPR021775 (PFAM): PTHR33128:SF1	0,019	0,021	0,000	0,000	0,000									
Solyc02g068180	ABC transporter family protein (AHRD V3.3 *** A0A097P9S1_HEVBR)	ABCI3	F:GO:0005524; F:GO	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	14,799	14,810	28,668	28,030	31,031									
Solyc02g068190	RNA helicase DEAD6	DEAD6	F:GO:0003676; F:GO	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	1,292	1,180	1,428	1,123	1,437									
Solyc02g068200	TCP transcription factor 18	TCP18					IPR017887 (PFAM) TCP	73,275	56,550	64,555	66,991	65,644									
Solyc02g068210	UDP-glycosyltransferase (AHRD V3.3 *-* A0A067XVF0_CICAR)		C:GO:0043231; F:GO	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl			G3DSA:3.40.50.2000 (GENE3D): PTH	0,000	0,039	0,000	0,074	0,000									
Solyc02g068220	UDP-glycosyltransferase (AHRD V3.3 *-* A0A067XVF0_CICAR)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): PTH	0,019	0,036	0,022	0,150	0,047									
Solyc02g068230	Membrane-anchored ubiquitin-fold protein (AHRD V3.3 *** F4YBD3_SOLNI)		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D): IPR03	25,430	22,453	20,926	19,973	21,948									
Solyc02g068240	Diacylglycerol acyltransferase 2 (AHRD V3.3 *** M4GID1_HELAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR007130 (PFAM): mobidb-lite (MOB	15,327	12,432	15,455	13,304	13,871									
Solyc02g068250	microspore-specific promoter 2 (AHRD V3.3 *-* AT5G46795.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,085	0,025	0,000	0,000									
Solyc02g068260	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061DXK2_THECC)		C:GO:0016021	C:integral component of membrane			IPR008217 (PFAM): mobidb-lite (MOB	2,630	1,653	2,378	2,556	1,866									
Solyc02g068270	Dimethylaniline monooxygenase [N-oxide-forming] 1 (AHRD V3.3 *** A0A1D1Y4W4_9ARAE)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR360	7,014	7,656	5,964	5,046	6,760									
Solyc02g068280	subtilisin-like protein		F:GO:0004252; P:GO	F:serine-type endop	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	40,164	27,271	52,534	60,489	60,267									
Solyc02g068290	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (AHRD V3.3 *** A0A1D1ZH53_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,985	1,873	2,355	1,629	2,196									
Solyc02g068300	clade XVI lectin receptor kinase		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:2.60.12	6,264	4,656	1,824	3,506	2,846					0,935	0,032			up
Solyc02g068310	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G14130.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	2,613	4,417	50,839	73,264	47,275									
Solyc02g068320	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A061DTA0_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	19,713	21,250	17,708	17,263	15,221									
Solyc02g068330	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** G7K2M3_MEDTR)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,325	0,415	0,000	0,127	0,000									
Solyc02g068340	Kinesin-like protein (AHRD V3.3 *** O24147_TOBAC)		F:GO:0003777; F:GO	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR019749 (SM	45,832	41,548	14,588	13,289	16,665									
Solyc02g068360	Phospholipid/glycerol acyltransferase family protein (AHRD V3.3 *** G7L7V8_MEDTR)		P:GO:0006644; F:GO	P:phospholipid metabolic process; F:transferase activity, transfe			IPR000872 (PFAM): PTHR12497:SF	13,043	11,227	10,773	9,571	9,090									
Solyc02g068365	Phospholipid/glycerol acyltransferase (AHRD V3.3 *-* A0A103XK21_CYNCS)		P:GO:0006644; F:GO	P:phospholipid metabolic process; F:transferase activity, transfe			IPR000872 (PRINTS): IPR002123 (PF	4,636	3,837	5,550	4,913	5,515									
Solyc02g068370	Kinase, putative (AHRD V3.3 *** B9S040_RICCO)		F:GO:0004713; F:GO	F:protein tyrosine k	EC:2.7.1	Transferring phospho	IPR020635 (SMART): IPR001304 (SM	15,381	17,973	17,138	22,543	21,584					0,396	0,042			up
Solyc02g068380	allantoate amidohydrolase (AHRD V3.3 *** AT4G20070.1)		F:GO:0016813	F:hydrolase activity, acting on carbon-nitrogen (but not peptide)			IPR002933 (PFAM): G3DSA:3.40.630	85,757	68,302	136,341	129,956	126,451									
Solyc02g068390	Mitochondrial inner membrane protease subunit 1 (AHRD V3.3 *** A0A1D1XGU0_9ARAE)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity; C:membrane			IPR000223 (PRINTS): IPR000223 (TI	5,855	6,702	6,437	6,943	7,472									
Solyc02g068400	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G20050.5)	PG71	F:GO:0004650	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,457	0,647	0,218	0,297	0,451									
Solyc02g068410	Polygalacturonase QRT3-like protein (AHRD V3.3 *** A0A0B0NBR9_GOSAR)		F:GO:0004650	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	0,849	0,379	0,000	0,025	0,000									
Solyc02g068420	Nop53 (60S ribosomal biogenesis) protein (AHRD V3.3 *** G7K7B9_MEDTR)		P:GO:0009987; C:GO	P:cellular process; C:nuclear lumen; P:ribosome biogenesis			IPR011687 (PFAM): IPR011687 (PIRS	154,052	140,482	103,280	100,086	110,972									
Solyc02g068430	Choline-phosphate cytidylyltransferase (AHRD V3.3 *** G7INF3_MEDTR)		F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process			IPR014729 (G3DSA:3.40.50.GENE3D	143,301	163,674	103,274	96,997	102,746									
Solyc02g068440	RNA binding protein, putative (AHRD V3.3 *** B9T5A2_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	5,014	4,579	4,840	4,416	5,180									
Solyc02g068445	F-box family protein (AHRD V3.3 --* AT3G19890.1)							0,118	0,117	0,137	0,260	0,211									
Solyc02g068450	V-type proton ATPase subunit F (AHRD V3.3 *** A0A0V0HAU3_SOLCH)		P:GO:0015991; C:GO	P:ATP hydrolysis cc	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR008218 (PFAM): IPR005772 (PIRS	49,188	49,797	74,136	80,247	70,695									
Solyc02g068460	LOW QUALITY:VQ motif-containing protein, putative (AHRD V3.3 *** A0A061DVP3_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	0,021	0,073	0,000	0,051	0,000									
Solyc02g068470	LOW QUALITY:VQ motif-containing protein, putative (AHRD V3.3 *-* A0A061DVP3_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	0,021	0,061	0,051	0,075	0,023									
Solyc02g068480	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** G7JRQ3_MEDTR)		P:GO:0000245; F:GO	P:spliceosomal con	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001607 (SMART): G3DSA:3.90.70	29,100	26,410	44,839	40,909	41,752									
Solyc02g068490	Heavy metal ATPase (AHRD V3.3 *** E5GCL7_CUCME)	RAN1	F:GO:0000166; F:GO	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRIN	41,036	43,853	35,564	30,635	32,393									

Solyc02g068500	Thioredoxin (AHRD V3.3 *** A0A103XJM9_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored			PR00421 (PRINTS); IPR013766 (PFA	20,718	20,404	36,279	34,937	34,554									
Solyc02g068510	PLATZ transcription factor family protein (AHRD V3.3 *** A0A061DWT2_THECC)		C:GO:0005634; F:G(	C:nucleus; F:zinc ion binding; P:leaf senescence			IPR006734 (PFAM); IPR006734 (PAN	0,000	0,000	0,000	0,022	0,000									
Solyc02g068530	N-acetylglucosamine-1-phosphate uridylyltransferase 1 (AHRD V3.3 *** AT1G31070.2)		F:GO:0070569	F:uridylyltransferase activity			G3DSA:3.40.1630.20 (GENE3D); IPR(	91,309	75,217	35,803	36,796	34,951									
Solyc02g068550	FAR1-related sequence 1 (AHRD V3.3 *** AT4G19990.5)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	9,048	8,129	9,389	9,959	9,949									
Solyc02g068560	CHD3-type chromatin-remodeling factor PICKLE (AHRD V3.3 *** A0A142CD29_9LAMI)		F:GO:0003677; F:G(	F:DNA binding; F:ATP binding			IPR001965 (SMART); IPR009463 (SM	76,255	70,222	57,288	57,484	59,794									
Solyc02g068565	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHRD V3.3 --* AT5G19420.3)							0,120	0,059	0,096	0,101	0,071									
Solyc02g068590	Potassium transporter (AHRD V3.3 *** M1AP28_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membra			IPR003855 (PFAM); IPR003855 (TIGF	58,410	56,427	158,903	175,590	159,060									
Solyc02g068600	Ankyrin repeat-containing protein (AHRD V3.3 *-* A0A103XBI3_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR026961 (PFAM); PTHR24177 (PAN	0,586	0,737	0,047	0,186	0,093									
Solyc02g068610	Ankyrin repeat family protein (AHRD V3.3 *-* AT5G35830.1)		F:GO:0005515	F:protein binding			IPR002110 (SMART); IPR036770 (G3	0,301	0,318	0,046	0,025	0,000									
Solyc02g068620	LOW QUALITY:Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B (AHRD V3.3 --* U5FJY5_POPTR)							9,306	8,736	0,173	0,388	0,023									
Solyc02g068630	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HF38_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	1,210	1,490	1,915	1,251	1,293									
Solyc02g068640	Pyrroline-5-carboxylate reductase (AHRD V3.3 *** A0A0V0HW05_SOLCH)		F:GO:0004735; P:G(	F:pyrroline-5-carbo:	EC:1.5.1.2	Pyrroline-5-carboxyla	IPR000304 (PIRSF); IPR028939 (PFA	40,962	44,744	34,261	28,746	33,300									
Solyc02g068645	LRR receptor-like serine/threonine-protein kinase ERECTA (AHRD V3.3 --* A0A0B0NI53_GOSAR)							0,977	0,558	0,809	0,821	0,822									
Solyc02g068650	tRNA (guanine-N(7)-)-methyltransferase (AHRD V3.3 *** K4B7J7_SOLLC)		P:GO:0006400; F:G(	P:tRNA modificatior	EC:2.1.1.33	tRNA (guanine(46)-N	PF02390 (PFAM); IPR003358 (TIGRF	9,589	10,999	11,775	10,243	10,340									
Solyc02g068660	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR025287 (PF.	0,243	1,522	0,000	0,000	0,000									
Solyc02g068670	Ankyrin repeat family protein (AHRD V3.3 *** B9ICR0_POPTR)		F:GO:0005515	F:protein binding			IPR002110 (SMART); IPR036770 (G3	1,699	5,649	0,531	0,590	1,506	1,753	0,023					up		
Solyc02g068680	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** A0A061G339_THECC)		P:GO:0035556	P:intracellular signal transduction			IPR001965 (SMART); IPR004146 (PF.	5,481	9,809	3,320	2,324	3,287									
Solyc02g068690	Exostosin-like protein (AHRD V3.3 *** A0A118K1L5_CYNCS)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM); IPR004263 (PAN	22,553	21,677	20,949	20,374	21,958									
Solyc02g068700	Zinc-binding family protein (AHRD V3.3 *** B9ICQ8_POPTR)		F:GO:0003824	F:catalytic activity			IPR001310 (PRINTS); IPR001310 (PF	0,042	0,041	0,025	0,025	0,046									
Solyc02g068710	Sulfiredoxin (AHRD V3.3 *** K4B7K3_SOLLC)		F:GO:0032542; P:G(	F:sulfiredoxin activi	EC:1.8.98.2	Sulfiredoxin	IPR003115 (SMART); IPR016692 (PIF	5,019	5,428	7,008	8,268	9,311									
Solyc02g068720	Nck-associated protein 1 (AHRD V3.3 *** B7ZGK5_LOTJA)		C:GO:0005634; C:G(	C:nucleus; C:endoplasmic reticulum membrane; P:actin filament			IPR019137 (PFAM); mobidb-lite (MOB	30,032	27,069	28,319	28,374	28,059									
Solyc02g068730	Chaperonin 60 alpha subunit (AHRD V3.3 *** Q9ZTV1_CANLI)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS); IPR001844 (TI(	17,588	18,007	27,312	26,187	25,265									
Solyc02g068740	Glycine cleavage system H family protein (AHRD V3.3 *** B9ICP5_POPTR)		C:GO:0005960; P:G(	C:glycine cleavage complex; P:glycine decarboxylation via glyci			IPR033753 (PFAM); G3DSA:2.40.50.1	44,034	41,209	63,193	63,525	56,656									
Solyc02g068750	LOW QUALITY:Glycoprotease M22 family protein (AHRD V3.3 *** D7ME14_ARALL)		C:GO:0000408; P:G(	C:EKC/KEOPS complex; P:tRNA threonylcarbamoyladenosine r			IPR017861 (PRINTS); IPR000905 (PF	23,210	22,469	29,729	28,821	25,666									
Solyc02g068760	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SQ91_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	0,394	1,648	0,282	0,218	0,445	2,061	0,001					up		
Solyc02g068770	50S ribosomal L30 (AHRD V3.3 *** A0A0B0MCX0_GOSAR)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005996 (TIGRFAM); IPR036919 ((	37,008	37,002	46,145	43,267	44,886									
Solyc02g068780	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT2G35140.6)		C:GO:0016021	C:integral component of membrane			IPR013989 (SMART); IPR013989 (PF.	79,349	69,546	64,086	63,858	63,559									
Solyc02g068790	DCD (Development and Cell Death) domain protein (AHRD V3.3 --* AT2G35140.6)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,039	0,068	0,122	0,142									
Solyc02g068795	Rho GTPase activation protein (RhoGAP) with PH domain-containing protein (AHRD V3.3 --* AT5G12150.2)							0,810	0,489	0,365	0,391	0,233									
Solyc02g068820	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT5G46330.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART); IPR000719 (SM	19,603	22,156	14,794	14,567	15,610									
Solyc02g068825	nucleosome assembly protein1-1 (AHRD V3.3 --* AT4G26110.2)							2,169	1,467	1,679	1,692	2,190									
Solyc02g068830	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART); IPR000719 (SM	0,533	0,757	0,368	0,443	0,520									
Solyc02g068850	LOW QUALITY:receptor-like kinase (AHRD V3.3 --* AT1G36005.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,061	0,079	0,025	0,025	0,023									
Solyc02g068860	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT1G08125.3)							0,021	0,000	0,000	0,000	0,000									
Solyc02g068863	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT2G33170.2)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	5,215	4,659	5,050	5,385	5,137									
Solyc02g068867	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	0,061	0,000	0,075	0,074	0,000									
Solyc02g068870	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic (AHRD V3.3 --* NDHJ_STAPU)							0,800	0,780	0,903	0,582	0,753									
Solyc02g068877	Phosphate-responsive 1 family protein (AHRD V3.3 *** B9ICP1_POPTR)		C:GO:0016021	C:integral component of membrane			IPR006766 (PFAM); PTHR31279:SF1	0,000	0,018	0,022	0,000	0,000									
Solyc02g068880	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	0,303	0,757	0,251	0,150	0,213									
Solyc02g068890	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061GDR6_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	3,692	3,959	2,187	2,121	2,539									
Solyc02g068895	BRI1-associated receptor kinase (AHRD V3.3 --* AT4G33430.2)							1,109	1,299	0,657	0,529	0,778									
Solyc02g068900	Glutathione S-transferase family protein (AHRD V3.3 *** AT4G19880.1)	GHR1	F:GO:0004364; F:G(	F:glutathione transf	EC:2.5.1.18	Glutathione transfera	G3DSA:1.20.1050.10 (GENE3D); PF1	35,444	29,255	53,547	48,142	45,631									
Solyc02g068910	Trypsin family protein (AHRD V3.3 *** AT5G45030.2)						PTHR31521 (PANTHER); PTHR31521	55,474	42,872	33,851	30,687	35,211									
Solyc02g068920	lecithine cholesterol acyltransferase		P:GO:0006629; F:G(	P:lipid metabolic process; F:O-acyltransferase activity			IPR003386 (PFAM); mobidb-lite (MOB	66,169	36,911	105,805	101,968	97,271	-0,814	0,004					down		
Solyc02g068930	Cytochrome c6 (AHRD V3.3 *** D7MKY9_ARALL)		F:GO:0009055; F:G(	F:electron transfer activity; F:heme binding			IPR009056 (PFAM); IPR036909 (G3D	3,957	3,882	4,709	4,671	5,671									
Solyc02g068970	LOW QUALITY:Zinc finger family protein (AHRD V3.3 --* B9GEM8_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.60 (GENE3D); mobic	0,057	0,208	0,022	0,000	0,000									
Solyc02g068980	LOW QUALITY:Zinc finger family protein (AHRD V3.3 --* B9GEM8_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.60 (GENE3D); mobic	0,208	0,155	0,000	0,000	0,024									
Solyc02g068990	Zinc finger family protein (AHRD V3.3 --* D7MP51_ARALL)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	9,806	9,166	9,081	8,092	8,685									
Solyc02g068995	Protein kinase superfamily protein (AHRD V3.3 --* AT5G58540.1)		F:GO:0009055; P:G(	F:electron transfer activity; P:photosynthetic electron transport in photosystem I; F:heme binding; F:met				0,057	0,059	0,093	0,073	0,046									
Solyc02g069000	LOW QUALITY:Zinc finger family protein (AHRD V3.3 --* B9HQP7_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (PROSITE_PROFILES)	0,000	0,019	0,000	0,000	0,000									
Solyc02g069010	Inositol monophosphatase family protein (AHRD V3.3 *** U5FXE5_POPTR)		F:GO:0008934; P:G(	F:inositol monophos	EC:3.1.3.25	Inositol-phosphate ph	IPR000760 (PRINTS); G3DSA:3.30.54	22,311	25,679	60,474	57,905	58,493									
Solyc02g069020	Phloem protein 2-like protein (AHRD V3.3 *** A0A103Y5W1_CYNCS)						IPR025886 (PFAM); mobidb-lite (MOB	14,183	12,925	10,415	11,764	11,310									
Solyc02g069025	Phloem protein 2-like protein (AHRD V3.3 *** A0A103Y5W1_CYNCS)						IPR025886 (PFAM); mobidb-lite (MOB	0,658	0,606	0,337	0,361	0,468									
Solyc02g069030	PHLOEM protein 2-like protein (AHRD V3.3 *** M1JV45_GOSHI)						IPR025886 (PFAM); mobidb-lite (MOB	2,428	2,695	1,661	1,995	2,120									
Solyc02g069040	transmembrane protein, putative (DUF594) (AHRD V3.3 *-* AT5G45540.1)		C:GO:0016021	C:integral component of membrane			IPR025315 (PFAM); IPR007658 (PFA	1,134	0,696	1,534	1,118	1,393									
Solyc02g069045	Phloem protein 2 (AHRD V3.3 *** D0R6I7_MALDO)						IPR025886 (PFAM); PTHR32278 (PAN	0,098	0,062	0,000	0,124	0,024									
Solyc02g069060	Phloem protein 2 (AHRD V3.3 *** D0R6I7_MALDO)						IPR025886 (PFAM); PTHR32278:SF8	0,817	1,757	0,440	0,351	0,211									
Solyc02g069070	ribonuclease H2 subunit C-like protein (AHRD V3.3 *** AT2G39440.2)		P:GO:0006401; C:G(	P:RNA catabolic process; C:ribonuclease H2 complex			IPR013924 (PFAM); G3DSA:3.30.200	2,975	2,774	1,205	0,863	1,483									
Solyc02g069080	Exocyst complex component 8 (AHRD V3.3 *** A0A0B0NCJ4_GOSAR)		C:GO:0000145; F:G(	C:exocyst; F:cystei	EC:3.4.22	Acting on peptide bor	IPR000668 (PRINTS); IPR000668 (SM	42,141	32,638	37,298	34,280	37,599									
Solyc02g069090	Cathepsin B-like cysteine proteinase (AHRD V3.3 *** Q40413_NICRU)		F:GO:0004197; P:G(	F:cysteine-type enc	EC:3.4.22	Acting on peptide bor	IPR000668 (PRINTS); IPR000668 (SM	1,878	1,638	2,441	2,736	3,132									
Solyc02g069100	Cathepsin B-like cysteine protease (AHRD V3.3 *** B7FJ05_MEDTR)		F:GO:0004197; P:G(	F:cysteine-type enc	EC:3.4.22	Acting on peptide bor	IPR000668 (PRINTS); IPR000668 (SM	134,445	153,928	214,386	206,276	201,734									
Solyc02g069110	Cathepsin B-like cysteine protease (AHRD V3.3 *** B7FJ05_MEDTR)		F:GO:0004197; P:G(	F:cysteine-type enc	EC:3.4.22	Acting on peptide bor	IPR000668 (PRINTS); IPR000668 (SM	18,599	15,047	20,029	17,779	22,451									
Solyc02g069120	Zinc finger ZPR1 protein (AHRD V3.3 *** A0A191VKH4_SOLTU)		F:GO:0008270	F:zinc ion binding			IPR004457 (SMART); IPR004457 (PF.	22,918	18,778	63,599	60,012	59,700									
Solyc02g069130	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 *** AT4G19830.1)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer	IPR001179 (PFAM); G3DSA:3.10.50.4	1,368	1,111	0,572	0,660	0,921									
Solyc02g069140	Leucyl-tRNA synthetase, putative (AHRD V3.3 *** B9SZE7_RICCO)		F:GO:0002161; F:G(	F:aminoacyl-tRNA ε	EC:6.1.1.4; EC:3.1.1	Leucine--tRNA ligase	IPR002300 (PFAM); IPR001179 (PFA	0,787	0,977	0,361	0,605	0,446									
Solyc02g069150	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9SVX6_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			IPR001388 (PRINTS); IPR010908 (SM	176,001	161,010	186,286	174,200	168,723									
Solyc02g069160	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT1G60000.1)		F:GO:0003676; P:G(	F:nucleic acid binding; P:mRNA 3'-end processing			IPR000504 (SMART); IPR038192 (G3	61,196	64,750	62,537	54,358	60,135									
Solyc02g069170	Transcription initiation factor TFIID subunit-like protein (AHRD V3.3 *-* A0A072VQR3_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR006565 (SMART); IPR009072 (G3	1,649	1,822	2,314	2,340	1,453									
Solyc02g069180	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT3G12920.1)		F:GO:0016874	F:ligase activity			PF13920 (PFAM); IPR013083 (G3DS/	37,309	118,025	78,961	52,645	73,010	1,689	0,000			-0,581	0,008	up		down
Solyc02g069190	iron-regulated transporter 2	irt2	F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM); IPR003689 (F	0,000	0,021	0,000	0,000	0,000									
Solyc02g069200	iron-regulated transporter 1	irt1	F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM); IPR003689 (F	0,084	0,094	0,000	0,050	0,000									
Solyc02g069203	SET-domain containing protein lysine methyltransferase family protein (AHRD V3.3 --* AT5G43990.8)							1,243	0,958	2,444	2,865	2,052									
Solyc02g069207	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XQA9_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	6,627	4,660	7,684	9,810	8,183									
Solyc02g069210	Metal ion transporter-like protein (AHRD V1 **** B4YHA7_HORVU)%3B contains Interpro domain(s) IPR004(		F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR003689 (PFAM); IPR004698 (TIGF	0,021	0,116	0,047	0,000	0,000									
Solyc02g069220	Cytosolic Fe-S cluster assembly factor NBP35 (AHRD V3.3 --* NBP35_ARATH)							0,676	0,529	1,006	0,770	0,937									
Solyc02g069230	RING/U-box superfamily protein (AHRD V3.3 *** AT4G19670.7)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	IPR001841 (SMART); IPR002867 (SM	41,803	44,431	51,228	41,725	45,697									
Solyc02g069240	LOW QUALITY:O-fucosyltransferase family protein (AHRD V3.3 *** AT3G05320.3)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM); G3DSA:3.40.50.1	3,658	2,682	12,973	19,860	14,628					0,621	0,005			up
Solyc02g069250	Cinnamyl alcohol dehydrogenase (AHRD V3.3 *** A0A1B0YY99_DAUCA)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART); G3DSA:3.90.18	0,970	5,068	0,256	0,321	0,494	2,393	0,000					up		
Solyc02g069260	Argonaute2a	AGO2a	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR003100 (SMART); IPR014811 (SM	225,560	229,512	70,249	108,536	102,407			0,540	0,006	0,629	0,003		up	up
Solyc02g069270	Argonaute 2b	AGO2b	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR014811 (SMART); IPR003100 (SM	0,477	0,717	0,025	0,000	0,141									
Solyc02g069280	Argonaute3	AGO.3	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR014811 (SMART); IPR003165 (SM	0,019	0,000	0,025	0,000	0,000									
Solyc02g069290	Transducin/WD40 repeat-like superfamily protein, putative (AHRD V3.3 *** A0A061GC79_THECC)		F:GO:0016874	F:ligase activity			IPR011989 (G3DSA:1.25.10.GENE3D	45,828	27,198	13,897	11,537	15,713									
Solyc02g069310	NIM1-like protein 1	nml1	F:GO:0005515	F:protein binding			IPR002110 (SMART); IPR000210 (SM	48,469	63,935	33,808	43,338	43,770									
Solyc02g069320	LOW QUALITY:Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 *** A0A061		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART); IPR038538 (G3	3,747	2,828	3,725	4,434	3,114									
Solyc02g069330	LOW QUALITY:Invertase inhibitor (AHRD V3.3 *** A0A0B5KSF6_MANES)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM); IPR035513 (G3D	0,199	0,073	0,000	0,000	0,000									
Solyc02g069340	RNA 3'-terminal phosphate cyclase (AHRD V3.3 *** A0A103YE55_CYNCS)		F:GO:0003824; C:G(	F:catalytic activity; C:nucleolus; P:RNA processing; C:integral c			IPR006634 (SMART); IPR013791 (PF.	28,570	33,828	30,477	30,526	30,265									
Solyc02g069350	pectinesterase (Protein of unknown function, DUF538) (AHRD V3.3 -** AT4G02370.1)							2,060	1,812	0,956	0,893	0,988									
Solyc02g069370	Ras-related GTP-binding protein (AHRD V3.3 *** Q40570_TOBAC)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00173 (SMAR	14,676	17,066	18,726	20,096	16,635									
Solyc02g069380	Membrane fusion protein Use1 (AHRD V3.3 *** AT3G55600.2)		C:GO:0016021	C:integral component of membrane			IPR019150 (PFAM); mobidb-lite (MOB	16,879	15,997	17,880	16,121	16,628									
Solyc02g069390	Transcription factor, putative (AHRD V3.3 *** B9RPY7_RICCO)						PF13837 (PFAM); Trihelix	0,096	0,099	0,558	0,538	0,521									
Solyc02g069400	Enhanced disease susceptibility 1 (AHRD V3.3 *** G3F1Q7_VITVI)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	11,812	13,843	7,089	7,056	7,956									
Solyc02g069410	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** AT5G45170.1)		C:GO:0009507	C:chloroplast			IPR023198 (G3DSA:1.10.150.GENE3I	8,105	8,955	12,789	11,036	14,152									
Solyc02g069420	Phospholipid-transporting ATPase (AHRD V3.3 *** M1BWN2_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR023299 (G3DSA:3.40.1110.GENE	24,425	12,335	95,086	133,973	99,869	-0,957	0,039			0,497	0,042	down		up
Solyc02g069430	Phospholipid-transporting ATPase (AHRD V3.3 *** K4B7S5_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR001757 (TIGRFAM); IPR006539 (T	29,158	16,996	135,702	173,486	128,063	-0,751	0,043					down		
Solyc02g069440	LOB domain protein (AHRD V3.3 *** G7JIR8_MEDTR)						IPR004883 (PFAN LBD	0,061	0,062	0,000	0,000	0,000									
Solyc02g069450	Photosystem I reaction center subunit III (AHRD V3.3 *** I3SN70_MEDTR)		C:GO:0009538; P:G(	C:photosystem I reaction center; P:photosynthesis			IPR003666 (PFAM); IPR036577 (G3D	0,334	1,748	0,187	0,302	0,613	2,371	0,000					up		
Solyc02g069455	F-box protein 7 (AHRD V3.3 --* AT1G21760.2)							0,242	0,541	0,149	0,237	0,117									
Solyc02g069460	Photosystem I reaction center subunit III (AHRD V3.3 *** I3SN70_MEDTR)		C:GO:0009538; P:G(	C:photosystem I reaction center; P:photosynthesis			IPR036577 (G3DSA:1.10.8.GENE3D);	0,099	0,021	0,146	0,096	0,119									
Solyc02g069470	Zinc finger family protein, putative (AHRD V3.3 *** A0A061GK45_THECC)						IPR002035 (SMART); IPR001841 (SM	33,020	29,432	63,134	78,833	70,697									
Solyc02g069490	Sterol reductase (AHRD V3.3 *** E1VD17_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR016169 (G3DSA:3.30.465.GENE3I	9,323	7,881	1,333	1,516	1,293									
Solyc02g069500	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XQS1_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,430	2,121	0,877	1,084	0,773									
Solyc02g069510	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT1G07090.1)		C:GO:0005634; P:G(	C:nucleus; P:post-embryonic plant morphogenesis			IPR006936 (PFAM); IPR040222 (PAN	1,532	1,450	0,219	0,244	0,375									
Solyc02g069515	mediator of RNA polymerase II transcription subunit-like protein (AHRD V3.3 *-* AT1G55080.1)		C:GO:0016592	C:mediator complex			IPR038790 (PANTHER)	0,861	0,633	0,951	0,861	0,568									
Solyc02g069520	mediator of RNA polymerase II transcription subunit-like protein (AHRD V3.3 *-* AT1G55080.1)		C:GO:0016592	C:mediator complex			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,715	1,040	1,315	1,448	0,985									
Solyc02g069540	Protein POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND REDISTRIBUTION (AHRD V3.3 ***		P:GO:0008356	P:asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,075	0,076	0,000	0,067	0,000									
Solyc02g069560	Protein CHUP1, chloroplastic-like protein (AHRD V3.3 *** A0A0B0NZW9_GOSAR)		C:GO:0009707	C:chloroplast outer membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,204	0,402	0,000	0,022	0,000									
Solyc02g069570	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T6B9_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	4,612	6,514	17,464	18,093	19,130									
Solyc02g069580	UDP-glucose 4-epimerase, putative (AHRD V3.3 *** B9SV82_RICCO)		F:GO:0003978; P:G(	F:UDP-glucose 4-eı	EC:5.1.3.2	UDP-glucose 4-epim	IPR016040 (PFAM); G3DSA:3.40.50.7	37,934	50,998	84,141	97,876	80,719									
Solyc02g069590	Coatomer epsilon subunit (AHRD V3.3 *** AT1G30630.1)		F:GO:0005198; F:G(	F:structural molecule activity; F:protein binding; P:retrograde ve			IPR011990 (G3DSA:1.25.40.GENE3D	55,750	58,016	55,870	50,977	50,547									
Solyc02g069600	Cytochrome P450 (AHRD V3.3 *** W9R7N2_9ROSA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,218	0,198	0,050	0,141	0,214									
Solyc02g069610	Got1/Sft2-like vescicle transport protein family (AHRD V3.3 *** AT5G01430.2)		P:GO:0016192	P:vesicle-mediated transport			IPR007305 (PFAM); PTHR21493:SF9	23,186	22,385	32,092	36,966	32,179									
Solyc02g069620	Ribose 5-phosphate isomerase-related family protein (AHRD V3.3 *** B9I0V6_POPTR)		F:GO:0004751; P:G(	F:ribose-5-phospha	EC:5.3.1.6	Ribose-5-phosphate	IPR004788 (PFAM); PTHR43748 (PAN	9,116	13,950	3,281	2,884	5,973			0,852	0,011				up	
Solyc02g069630	Subtilisin-like protease (AHRD V3.3 *** A0A0B0N731_GOSAR)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); PF17766 (PFA	3,068	2,232	0,237	0,310	0,237									
Solyc02g069640	gamma-soluble NSF attachment protein (AHRD V3.3 *** AT4G20410.1)		F:GO:0005515; P:G(	F:protein binding; P:intracellular protein transport			IPR011990 (G3DSA:1.25.40.GENE3D	34,865	32,253	72,647	71,881	63,918									
Solyc02g069650	Vacuolar protein sorting-associated protein 54 (AHRD V3.3 *** W9SA63_9ROSA)		C:GO:0000938; P:G(	C:GARP complex; P:retrograde transport, endosome to Golgi			IPR012501 (PFAM); mobidb-lite (MOB	28,034	27,517	23,863	25,220	23,897									
Solyc02g069660	Vacuolar protein sorting-associated protein 54 (AHRD V3.3 *-* A0A118JS09_CYNCS)		C:GO:0000938; P:G(	C:GARP complex; P:retrograde transport, endosome to Golgi			mobidb-lite (MOBIDB_LITE); IPR0397	17,328	13,739	13,229	14,303	13,841									
Solyc02g069670	Alpha-glucosidase (AHRD V3.3 *** AGLU_SPIOL)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR031727 (PFAM); IPR025887 (PFA	109,584	82,668	19,451	12,186	19,102									
Solyc02g069680	Vacuolar protein sorting-associated protein 2 homolog 2 (AHRD V3.3 *** VPS2B_ARATH)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM); mobidb-lite (MOB	13,981	13,224	2,876	1,811	3,583									
Solyc02g069690	FAD-binding Berberine family protein (AHRD V3.3 *** AT5G44400.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR012951 (PFAM); IPR016167 (G3D	2,902	2,442	2,090	0,902	1,624									
Solyc02g069700	Glucan endo-1,3-beta-glucosidase, basic isoform (AHRD V3.3 --* E13B_PHAVU)							0,554	0,280	0,354	0,267	0,284									
Solyc02g069710	Cation calcium exchanger (AHRD V3.3 *** G7L7L8_MEDTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1420.30 (GENE3D); IPR(	24,759	18,842	16,697	17,520	19,439									
Solyc02g069720	Zinc finger protein LSD1 (AHRD V3.3 *** F8RP38_PEA)		P:GO:0000303; P:G(	P:response to superoxide; P:response to hypoxia; P:response t			IPR005735 (TIGRI LSD	29,492	40,622	32,286	31,359	34,843									
Solyc02g069730	CASP-like protein (AHRD V3.3 *** K4B7V5_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006459 (TIGRFAM); IPR006702 (F	0,019	0,018	0,047	0,095	0,117									
Solyc02g069740	Transcription factor jumonji family protein (AHRD V3.3 *** D7MFJ7_ARALL)		C:GO:0005634	C:nucleus			IPR003349 (SMART); IPR003889 (SM	1,683	1,897	0,746	0,608	0,893									
Solyc02g069750	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G28580.2)		F:GO:0005524; C:G(	F:ATP binding; C:integral component of membrane; F:kinase act			G3DSA:3.90.1200.10 (GENE3D); PF0	15,529	29,982	10,241	10,713	11,602	0,974	0,012					up		
Solyc02g069760	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G10650.2)		C:GO:0005634; F:G(	C:nucleus; F:ubiquitin protein ligase activity			IPR001841 (SMART); IPR013083 (G3	0,019	0,043	0,000	0,000	0,000									
Solyc02g069770	WD40-repeat domain-contaning protein		F:GO:0005515; P:G(	F:protein binding; P:rRNA processing; F:U3 snoRNA binding			IPR020472 (PRINTS); IPR001680 (SM	11,746	15,853	9,706	9,665	9,158									
Solyc02g069780	SIT4 phosphatase-associated family protein (AHRD V3.3 *** AT1G30470.1)		C:GO:0005774	C:vacuolar membrane			IPR007587 (PFAM); IPR011989 (G3D	64,003	62,494	64,585	67,963	64,742									
Solyc02g069790	DNA-damage-repair/toleration protein (AHRD V3.3 *** W9RFT6_9ROSA)		F:GO:0003676; P:G(	F:nucleic acid binding; P:DNA repair; P:regulation of RNA splicir			IPR003954 (SMART); IPR000467 (SM	30,373	27,830	33,498	30,879	30,492									
Solyc02g069800	LOW QUALITY:Abhydrolase superfamily protein		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	308,474	403,945	681,758	726,734	627,196									
Solyc02g069810	Bromo-adjacent-like (BAH) domain protein (AHRD V3.3 *-* A0A072VCT6_MEDTR)		F:GO:0003682	F:chromatin binding			IPR001025 (SMART); IPR001025 (PF.	6,111	8,049	4,935	5,132	3,946									
Solyc02g069820	kxDL motif protein (AHRD V3.3 *** AT3G29130.2)		C:GO:0031083; P:G(	C:BLOC-1 complex; P:lysosome localization; C:BORC complex			IPR019371 (PFAM); IPR039843 (PAN	22,660	19,020	30,246	30,273	26,326									
Solyc02g069830	Homeobox leucine-zipper protein (AHRD V3.3 *** Q8H963_ZINVI)		F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			IPR002913 (SMAF HD-ZIP	18,706	19,117	10,794	8,572	11,030									
Solyc02g069840	50S ribosomal protein L20 (AHRD V3.3 *** A0A0V0GV30_SOLCH)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR005813 (PRINTS); IPR005813 (TI(	14,391	15,709	22,679	20,911	18,663									
Solyc02g069850	ribosomal protein S25		C:GO:0005840	C:ribosome			IPR004977 (PFAM); G3DSA:1.10.10.2	146,290	175,471	138,513	133,304	138,103									
Solyc02g069860	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR001289 (SMAF NF-YA	11,715	15,248	11,087	11,886	12,704									
Solyc02g069880	E3 ubiquitin-protein ligase (AHRD V3.3 *** M1BWA5_SOLTU)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal			IPR008974 (G3DSA:2.60.210.GENE3I	9,390	9,685	11,614	10,276	10,542									
Solyc02g069910	LOW QUALITY:BnaC07g36860D protein (AHRD V3.3 -** A0A078DYT9_BRANA)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR371	25,286	22,873	9,621	12,154	14,915									
Solyc02g069920	2-succinylbenzoate--CoA ligase, chloroplastic/peroxisomal (AHRD V3.3 *-* A0A0B2Q2Z1_GLYSO)		C:GO:0005777; C:G(	C:peroxisome; C:chloroplast; F:ligase activity; P:phylloquinone I			PTHR43201:SF7 (PANTHER); PTHR4:	0,932	1,125	0,884	0,883	1,221									
Solyc02g069925	4-coumarate--CoA ligase-like 4 (AHRD V3.3 *** 4CLL4_ORYSJ)	4CL-like	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM); G3DSA:3.30.300	1,729	2,857	3,980	4,261	4,933									
Solyc02g069930	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A0K9PC40_ZOSMR)		C:GO:0016020	C:membrane			IPR000073 (PRINTS); IPR022742 (PF	0,021	0,021	0,277	0,600	0,376									

Solyc02g069935	RING/U-box superfamily protein (AHRD V3.3 --* AT2G25360.1)					0,392	0,412	1,223	0,714	0,616									
Solyc02g069940	WPP domain associated protein				PTHR33883:SF2 (PANTHER): IPR037	18,912	13,068	41,429	41,816	36,175									
Solyc02g069950	KRR1 small subunit processome component (AHRD V3.3 *** K4B7X7_SOLLC)		F:GO:0003723	F:RNA binding	PF17903 (PFAM): IPR024166 (PIRSF	121,473	117,680	80,325	82,743	76,602									
Solyc02g069960	NAC domain-containing protein, putative (AHRD V3.3 *** B9RI29_RICCO)	NAC016	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM): NAC	0,000	0,000	0,050	0,050	0,000									
Solyc02g069965	Kinase, putative (AHRD V3.3 *** B9SB26_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR021720 (PF	1,537	1,022	0,461	0,372	0,537									
Solyc02g069970	Beta-conglycinin, alpha' chain (AHRD V3.3 --* GLCAP_SOYBN)					0,586	0,407	0,415	0,199	0,445									
Solyc02g069980	RING/FYVE/PHD zinc finger-containing protein (AHRD V3.3 *-* F4ISG1_ARATH)		F:GO:0008270	F:zinc ion binding	IPR001965 (SMART): IPR019787 (PF	14,788	10,231	12,180	10,972	10,361									
Solyc02g069983	alpha-1,2-Mannosidase (AHRD V3.3 --* A0A199UY19_ANACO)					1,509	0,844	1,074	1,204	0,751									
Solyc02g069987	Obg-like ATPase 1 (AHRD V3.3 --* B7FK99_MEDTR)					1,313	1,977	1,746	1,852	1,245									
Solyc02g069990	Rubber elongation factor protein (REF) (AHRD V3.3 --* AT2G47780.1)					0,000	0,000	0,025	0,000	0,047									
Solyc02g070000	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT4G20940.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	26,791	16,889	22,307	25,544	21,732									
Solyc02g070020	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	11,604	23,477	317,275	457,630	340,540					0,532	0,002			up
Solyc02g070030	Small RNA 2'-O-methyltransferase (AHRD V3.3 *** A0A0E4B3V6_NICBE)		P:GO:0001510; F:GO	P:RNA methylation; F:O-methyltransferase activity; F:RNA meth	G3DSA:3.40.50.150 (GENE3D): PTHR	6,949	7,118	5,368	6,785	6,119									
Solyc02g070035	Small RNA 2'-O-methyltransferase (AHRD V3.3 *** W9R7I9_9ROSA)		P:GO:0001510; F:GO	P:RNA methylation; F:O-methyltransferase activity; F:RNA meth	PF18441 (PFAM): G3DSA:3.40.50.15	17,650	17,227	12,890	15,256	15,002									
Solyc02g070040	LOW QUALITY:Ethylene-responsive nuclear protein (AHRD V3.3 *** Q38MV1_SOLLC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	17,693	6,424	3,087	8,772	4,463	-1,438	0,000			1,500	0,000	down		up
Solyc02g070050	fatty acid hydroxylase 2 (AHRD V3.3 *** AT4G20870.2)		F:GO:0005506; P:GO	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas	IPR006694 (PFAM): PTHR12863 (PAN	22,078	19,508	27,787	29,622	28,014									
Solyc02g070060	FAD-binding Berberine family protein, putative (AHRD V3.3 *** A0A061G791_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	IPR016167 (G3DSA:3.30.43.GENE3D	0,134	0,305	0,000	0,025	0,000									
Solyc02g070070	FAD-binding Berberine family protein (AHRD V3.3 *** AT2G34790.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	G3DSA:3.40.462.20 (GENE3D): IPR0	0,401	0,473	0,025	0,025	0,048									
Solyc02g070090	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061G7Z5_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	IPR016167 (G3DSA:3.30.43.GENE3D	0,000	0,000	0,000	0,092	0,023									
Solyc02g070100	RNA helicase DEAD7	DEAD7	F:GO:0003676; F:GO	F:nucleic acid binding; F:ATP binding	IPR014001 (SMART): IPR001650 (SM	35,737	34,718	41,191	42,985	37,251									
Solyc02g070110	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061GF79_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	IPR016167 (G3DSA:3.30.43.GENE3D	0,081	0,531	0,121	0,164	0,187									
Solyc02g070170	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061GF79_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	IPR012951 (PFAM): G3DSA:3.30.465.	0,188	0,139	0,000	0,000	0,000									
Solyc02g070180	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061G763_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	G3DSA:3.30.465.50 (GENE3D): IPR0	0,042	0,043	4,898	7,729	3,388									
Solyc02g070190	FAD-binding Berberine family protein (AHRD V3.3 *-* AT5G44360.2)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	G3DSA:3.40.462.20 (GENE3D): PTHR	0,000	0,000	0,000	0,025	0,000									
Solyc02g070200	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061GF79_THECC)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	IPR016167 (G3DSA:3.30.43.GENE3D	0,000	0,000	0,000	0,000	0,071									
Solyc02g070210	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** A0A061G966_THECC)				PR00180 (PRINTS): IPR001251 (SMA	1,440	2,012	0,200	0,172	0,255									
Solyc02g070215	Phosphatidic acid phosphatase (PAP2) family protein (AHRD V3.3 --* AT3G58490.2)					0,021	0,019	0,000	0,000	0,000									
Solyc02g070220	nucleic acid binding protein (AHRD V3.3 *** AT1G30660.3)				IPR006171 (SMART): G3DSA:3.40.13	6,404	6,487	6,437	6,945	6,955									
Solyc02g070230	Nucleic acid binding protein, putative (AHRD V3.3 *-* B9SAY5_RICCO)					4,001	4,054	3,314	3,599	3,916									
Solyc02g070240	Zinc finger transcription factor 17	C3H17	F:GO:0003723; F:GO	F:RNA binding; F:metal ion binding	IPR000571 (SMART): IPR007275 (PF	22,377	21,855	35,427	36,212	34,327									
Solyc02g070250	Accelerated cell death 11 (AHRD V3.3 *** A0A097PRE2_SOLLC)		C:GO:0005737; P:GO	C:cytoplasm; P:intermembrane lipid transfer; F:intermembrane li	IPR014830 (PFAM): IPR036497 (G3D	18,442	16,565	32,711	31,780	31,896									
Solyc02g070260	Leucine-rich repeat-containing protein (AHRD V3.3 *** A0A103XCI4_CYNCS)		F:GO:0005515	F:protein binding	IPR025875 (PFAM): G3DSA:2.60.40.2	228,266	188,215	43,279	40,352	46,519									
Solyc02g070270	Cationic amino acid transporter, putative (AHRD V3.3 *** B9SAY1_RICCO)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmem	G3DSA:1.20.1740.10 (GENE3D): IPR0	0,000	0,132	0,049	0,119	0,117									
Solyc02g070280	Cationic amino acid transporter, putative (AHRD V3.3 *** B9SKU5_RICCO)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmem	IPR002293 (PFAM): IPR002293 (PIRS	1,674	3,641	6,983	10,995	10,926			0,643	0,037	0,659	0,005		up	up
Solyc02g070290	Cation-chloride cotransporter 1 (AHRD V3.3 *** CCC1_ARATH)		P:GO:0006811; F:GO	P:ion transport; F:cation:chloride symporter activity; C:integral c	IPR004842 (TIGRFAM): G3DSA:1.20.	23,241	24,946	20,955	23,047	20,869									
Solyc02g070300	Protection of telomeres 1 protein (AHRD V3.3 *** B7T1K5_SOLTU)		P:GO:0000723; C:GO	P:telomere maintenance; C:nuclear chromosome, telomeric regi	IPR011564 (SMART): IPR032042 (PF	4,907	4,479	3,805	3,976	3,601									
Solyc02g070310	60S ribosomal protein L32 (AHRD V3.3 *** D7MRE7_ARALL)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001515 (SMART): IPR001515 (PF	576,871	638,684	370,082	354,200	349,609									
Solyc02g070330	40S ribosomal protein S4 (AHRD V3.3 *-* RS4_SOLTU)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR005824 (SMART): IPR002942 (SM	242,206	262,762	290,596	248,488	259,104									
Solyc02g070340	40S ribosomal protein S4 (AHRD V3.3 *** RS4_SOLTU)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR002942 (SMART): IPR005824 (SM	2,154	2,752	2,701	2,247	2,370									
Solyc02g070390	plastid transcriptionally active 12 (AHRD V3.3 *** AT2G34640.1)	HEMERA/pTAC12	C:GO:0005634; P:GO	C:nucleus; P:regulation of transcription, DNA-templated; C:chlor	mobidb-lite (MOBIDB_LITE): mobidb-lit	20,665	26,118	89,735	93,621	88,247									
Solyc02g070397	GDP-mannose 3,5-epimerase (AHRD V3.3 --* GME_ARATH)					0,061	0,203	0,022	0,025	0,024									
Solyc02g070400	Hexosyltransferase (AHRD V3.3 *** A0A0V0IVQ1_SOLCH)		P:GO:0006486; F:GO	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR001079 (SMART): G3DSA:2.60.12	27,166	21,854	24,166	25,100	23,039									
Solyc02g070410	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	0,098	0,039	0,000	0,050	0,000									
Solyc02g070420	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT2G34530.4)		C:GO:0016020	C:membrane	mobidb-lite (MOBIDB_LITE): PTHR363	0,336	0,355	0,025	0,025	0,024									
Solyc02g070430	Gibberellin 2 oxidase (AHRD V3.3 *** Q53C60_NEROL)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS): IPR026992 (PFA	0,754	1,297	2,080	1,330	2,161									
Solyc02g070440	Katanin p60 ATPase-containing subunit, putative (AHRD V3.3 *** B9S114_RICCO)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): G3DSA:1.10.8.6	21,218	20,649	29,290	31,310	31,668									
Solyc02g070450	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9S109_RICCO)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR000490 (PFAM): G3DSA:3.20.20.8	0,021	0,062	0,025	0,000	0,000									
Solyc02g070460	Cullin, putative (AHRD V3.3 *** B9S106_RICCO)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR016158 (SMART): IPR019559 (SM	56,105	51,864	54,540	54,567	51,033									
Solyc02g070480	F-box family protein (AHRD V3.3 *-* AT5G46170.1)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): G3DSA:1.20.128	23,325	18,754	21,519	19,959	18,534									
Solyc02g070483	F-box family protein (AHRD V3.3 *-* AT4G18380.2)				PTHR31215 (PANTHER): PTHR31215	12,514	11,679	11,671	10,692	12,126									
Solyc02g070487	methylthioalkylmalate synthase 1 (AHRD V3.3 --* AT5G23010.3)					0,021	0,037	0,047	0,098	0,046									
Solyc02g070490	Alpha/beta hydrolase, putative (AHRD V3.3 *** B9RYL3_RICCO)	PPHL3			IPR000073 (PRINTS): IPR029058 (G3	0,749	0,929	0,650	0,487	0,708									
Solyc02g070500	LOW QUALITY:DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)				IPR007493 (PFAM): IPR036758 (G3D	43,592	51,246	43,157	59,662	32,783					0,471	0,002			up
Solyc02g070510	Proteasome subunit alpha type (AHRD V3.3 *** M1BWH6_SOLTU)		F:GO:0004298; C:GO	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR000426 (SMART): IPR029055 (G3	41,827	43,462	63,680	62,956	61,247									
Solyc02g070520	alpha-1,2-Mannosidase (AHRD V3.3 *** K4B833_SOLLC)		F:GO:0004571; F:GO	F:mannosyl-oligosa EC:3.2.1.113; EC:3.2 Mannosyl-oligosacch	IPR001382 (PRINTS): IPR001382 (PF	23,192	26,324	56,399	57,808	52,265									
Solyc02g070530	Potassium channel NKT6 (AHRD V3.3 *** T2ASV3_NICSY)		F:GO:0005249; P:GO	F:voltage-gated potassium channel activity; P:potassium ion tra	IPR003938 (PRINTS): IPR000595 (SM	2,206	2,135	0,288	0,555	0,447									
Solyc02g070540	carbohydrate binding domain-containing protein		C:GO:0005886; C:GO	C:plasma membrane; C:integral component of membrane	IPR008979 (G3DSA:2.60.120.GENE3	34,658	41,286	5,781	4,708	6,226									
Solyc02g070550	RNA-binding protein (AHRD V3.3 *** AT5G46250.1)		F:GO:0003723; C:GO	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprote	IPR002344 (PRINTS): IPR006630 (SM	348,310	276,930	326,894	252,151	283,054									
Solyc02g070560	ribosomal protein S11 family protein		F:GO:0008963; C:GO	F:phospho-N-acetyl EC:2.7.8.13 Phospho-N-acetylmu	IPR000715 (PFAM): IPR003524 (TIGF	24,122	22,685	20,781	19,704	22,419									
Solyc02g070570	30S ribosomal protein S11 (AHRD V3.3 *** A0A0K9PCU6_ZOSMR)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001971 (PIRSF): IPR036967 (G3D	296,858	299,175	198,179	180,841	190,342									
Solyc02g070580	sterol 22-desaturase	sd1	F:GO:0004497; F:GO	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR002403 (PRINTS): IPR001128 (PF	3,923	2,524	14,579	29,908	15,113					1,040	0,000			up
Solyc02g070600	F-box protein (AHRD V3.3 *** W9RLE9_9ROSA)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR001810 (PF	0,075	0,107	0,025	0,025	0,000									
Solyc02g070610	Protein glycosylationmyb-like TTH transcriptional regulator (AHRD V3.3 *** A0A077SKU6_9MAGN)				IPR029058 (G3DSA:3.40.50.GENE3D	0,816	0,759	0,649	0,469	0,474									
Solyc02g070620	F-box family protein (AHRD V3.3 *** B9HMA7_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR017451 (TIC	1,296	0,909	0,050	0,050	0,094									
Solyc02g070630	60S ribosomal protein L18a, putative (AHRD V3.3 *-* B9S129_RICCO)		C:GO:0005840; C:GO	C:ribosome; C:integral component of membrane	IPR028877 (PANTHER): PTHR10052:	85,115	76,191	74,049	65,335	67,289									
Solyc02g070640	60S ribosomal protein L18a (AHRD V3.3 *** Q3HRW8_SOLTU)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:3.10.20.10 (GENE3D): IPR02	66,497	79,717	67,378	57,801	60,236									
Solyc02g070650	60S ribosomal protein L18a (AHRD V3.3 *** Q3HRW8_SOLTU)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:3.10.20.10 (GENE3D): IPR02	94,395	103,418	62,274	56,345	56,728									
Solyc02g070660	Cytochrome B561-related protein, putative (AHRD V3.3 *** A0A061GEA2_THECC)		F:GO:0003924; P:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR006593 (SMART): G3DSA:1.20.12	0,399	0,179	0,022	0,050	0,047									
Solyc02g070670	urease accessory protein G (AHRD V3.3 *** AT2G34470.2)		F:GO:0003924; P:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	42,698	44,272	51,928	44,074	50,905									
Solyc02g070680	Cytochrome b561-related family protein (AHRD V3.3 *** A9PIJ8_POPTR)		F:GO:0003924; P:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	35,901	44,267	43,242	43,686	37,665									
Solyc02g070700	Growth-regulating factor (AHRD V3.3 --* A0A072TW62_MEDTR)		C:GO:0016020	C:membrane	IPR014977 (PFAM): mobidb-lite (MOB	0,216	0,159	0,022	0,000	0,000									
Solyc02g070705	Non-specific serine/threonine protein kinase (AHRD V3.3 --* M1CRR5_SOLTU)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane		0,987	0,564	0,849	0,629	0,543									
Solyc02g070710	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HGU1_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	2,677	2,270	2,217	2,981	2,366									
Solyc02g070720	S-norcoclaurine synthase 1 (AHRD V3.3 --* NCS1_COPJA)					0,059	0,000	0,090	0,192	0,118									
Solyc02g070730	LOW QUALITY:NBS-LRR resistance protein (AHRD V3.3 *** A0A060AEY4_9SOLN)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): G3DSA:3.40.50.3	0,120	0,160	0,330	0,605	0,447									
Solyc02g070760	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061GF24_THECC)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.50.720 (GENE3D): IPR0	2,545	4,002	2,152	2,187	3,106									
Solyc02g070770	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G34460.1)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.50.720 (GENE3D): IPR0	44,365	50,962	59,066	54,416	63,533									
Solyc02g070780	DNA helicase (AHRD V3.3 *** K4B859_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:ATP binding; P:DNA replication initiation; C:MC	IPR001208 (PRINTS): IPR008046 (PF	25,701	22,573	14,406	11,183	14,025									
Solyc02g070790	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** A0A0V0IG10_SOLCH)		P:GO:0006633; F:GO	P:fatty acid biosynthetic process; F:transferase activity, transfe	IPR020841 (SMART): IPR016039 (G3	20,578	22,298	9,858	9,669	13,158									
Solyc02g070800	Thiamine monophosphate synthase (AHRD V3.3 *** I3SV46_MEDTR)		F:GO:0003824	F:catalytic activity	IPR007570 (PFAM): IPR013785 (G3D	0,176	0,626	0,255	0,239	0,304									
Solyc02g070810	Nuclear pore complex protein gp210b (AHRD V3.3 *** W6JLZ0_NICBE)		F:GO:0003824	F:catalytic activity	IPR003343 (SMART): IPR003343 (PF	30,444	25,554	16,721	16,497	19,012									
Solyc02g070820	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 180 (AHRD V3.3 *** Q9FQZ1_TOBAC)		C:GO:0016021	C:integral component of membrane	PTHR33726 (PANTHER): PTHR33726	0,293	0,221	0,342	0,166	0,286									
Solyc02g070840	secretory carrier 3 (AHRD V3.3 --* AT1G61250.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,938	1,301	1,268	0,898	1,369									
Solyc02g070845	F-box family protein (AHRD V3.3 *-* B9IAP0_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): PTHR44355 (PAN	3,263	3,214	2,173	2,020	2,098									
Solyc02g070850	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT1G80440.1)					2,483	2,396	1,346	1,284	1,506									
Solyc02g070855	Plant/F17J16-140 protein (AHRD V3.3 *-* A0A072UQU0_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR31142:SF4 (PANTHER): IPR040	7,607	7,156	4,274	3,683	4,695									
Solyc02g070860	Tobamovirus multiplication protein 1 (AHRD V3.3 *-* A0A199W7B2_ANACO)		C:GO:0016021	C:integral component of membrane	IPR009457 (PFAM): PTHR31142:SF4	11,990	12,613	11,594	12,326	11,679									
Solyc02g070870	Mitochondrial inner membrane protease subunit 1 (AHRD V3.3 *** A0A103XCT3_CYNCS)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity; C:membrane	IPR000223 (PRINTS): IPR000223 (TIC	3,758	3,308	5,533	5,106	4,595									
Solyc02g070877	Conserved peptide upstream open reading frame 35 (AHRD V3.3 *** B3H687_ARATH)				PTHR35281 (PANTHER): PTHR35281	16,963	19,641	19,004	23,734	21,000									
Solyc02g070880	Helix-loop-helix DNA-binding	BHLH1	P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF: bHLH	46,047	53,893	53,181	60,061	57,027									
Solyc02g070890	Ontology_term=GO:0004675	fls2	F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): IPR003591 (SM	4,735	32,152	31,277	67,037	38,645	2,786	0,000			1,104	0,000	up		up
Solyc02g070910	Ontology_term=GO:0004675		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): SM00365 (SMA	2,521	2,374	2,951	2,431	2,651									
Solyc02g070915	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G22490.2)					0,000	0,000	0,000	0,025	0,000									
Solyc02g070920	Serine/threonine-protein kinase SAPK7 (AHRD V3.3 --* SAPK7_ORYSJ)					0,141	0,296	0,124	0,403	0,330									
Solyc02g070935	Pectate lyase (AHRD V3.3 *-* A0A199VAW8_ANACO)					0,000	0,041	0,000	0,000	0,000									
Solyc02g070940	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	203,697	577,853	93,529	114,725	216,970	1,532	0,000	1,210	0,000			up	up	
Solyc02g070950	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	12,303	96,555	2,633	6,087	11,101	3,000	0,000	2,065	0,000	1,209	0,005	up	up	up
Solyc02g070970	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	15,297	161,294	2,458	6,647	8,534	3,425	0,000	1,783	0,000	1,429	0,000	up	up	up
Solyc02g070980	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4B876_SOLLC)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	10,483	70,183	1,596	4,599	7,758	2,767	0,000	2,256	0,000	1,511	0,003	up	up	up
Solyc02g070990	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4B877_SOLLC)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	18,392	203,318	1,294	2,014	5,544	3,493	0,000	2,075	0,000			up	up	
Solyc02g071000	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4B878_SOLLC)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	7,318	58,510	0,618	2,548	2,980	3,024	0,000	2,234	0,000	2,016	0,000	up	up	up
Solyc02g071010	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	1,521	7,608	0,233	0,287	1,155	2,342	0,000					up		
Solyc02g071020	centrosomal protein (AHRD V3.3 --* AT1G79390.1)					0,181	0,260	0,094	0,095	0,116									
Solyc02g071040	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *** A0A0V0IXC3_SOLCH)	STS3	F:GO:0004373	F:glycogen (starch) EC:2.4.1.11 Glycogen(starch) syr	G3DSA:3.40.50.2000 (GENE3D): IPR0	36,743	36,472	50,436	55,063	52,549									
Solyc02g071050	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): PTHR31376:SF17 (	18,344	19,687	24,807	22,378	24,942									
Solyc02g071060	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): IPR030182 (PANTH	1,029	1,022	0,448	0,338	0,422									
Solyc02g071070	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:GO	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR006153 (PFAM): IPR038770 (G3D	0,000	0,021	0,147	0,249	0,284									
Solyc02g071080	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): PTHR31376:SF17 (	2,866	2,732	135,491	132,169	113,737									
Solyc02g071090	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): PTHR31376:SF17 (	5,751	2,566	70,067	57,367	50,846	-1,139	0,017					down		
Solyc02g071100	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): PTHR31376:SF17 (	7,617	6,412	43,754	31,660	32,538					-0,463	0,012			down
Solyc02g071110	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane	PF16913 (PFAM): PTHR31376:SF17 (	6,441	5,258	19,941	18,079	19,088									
Solyc02g071120	protein REDUCED WALL ACETYLATION-like		C:GO:0005794; P:GO	C:Golgi apparatus; P:plant-type secondary cell wall biogenesis;	IPR012419 (PFAM): PTHR13533 (PAN	67,079	72,827	43,503	48,415	42,932									
Solyc02g071130	WRKY transcription factor 71	WRKY71	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF: WRKY	0,224	2,369	0,692	0,770	0,655									
Solyc02g071140	Outward rectifying potassium channel protein (AHRD V3.3 *** A0A072UNK3_MEDTR)		F:GO:0005267; C:GO	F:potassium channel activity; C:membrane; P:potassium ion tra	IPR003280 (PRINTS): IPR013099 (PF	6,151	4,709	5,357	4,269	4,304									
Solyc02g071160	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G29790.2)		F:GO:0008168	F:methyltransferase activity	G3DSA:3.40.50.150 (GENE3D): IPR0	29,716	27,523	19,401	16,530	15,546									
Solyc02g071165	1-deoxy-D-xylulose 5-phosphate reductoisomerase (AHRD V3.3 --* AT5G62790.2)					1,183	1,490	0,720	0,853	1,036									
Solyc02g071170	Coatomer subunit zeta-2 (AHRD V3.3 *** A0A151T692_CAJCA)		P:GO:0006890; C:GO	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r	IPR022775 (PFAM): G3DSA:3.30.450	35,433	33,409	41,751	36,506	34,403									
Solyc02g071180	RNA polymerase II degradation factor-like protein (DUF1296) (AHRD V3.3 *** AT1G29370.1)		F:GO:0005515	F:protein binding	IPR009719 (PFAM): mobidb-lite (MOB	74,336	94,612	76,775	84,495	83,842									
Solyc02g071190	Carboxyl-terminal-processing protease (AHRD V3.3 *-* W9RE51_9ROSA)		F:GO:0004175; P:GO	F:endopeptidase activity; P:proteolysis; F:serine-type peptidase	G3DSA:3.30.750.44 (GENE3D): PTHR	1,705	2,067	4,017	4,625	4,254									
Solyc02g071200	Carboxyl-terminal-processing protease (AHRD V3.3 *** A0A0B2PB29_GLYSO)		F:GO:0005515; P:GO	F:protein binding; P:proteolysis; F:serine-type peptidase activity	IPR012946 (SMART): IPR005151 (SM	6,146	7,105	10,991	15,355	12,855									
Solyc02g071210	Cold acclimation protein WCOR413 (AHRD V3.3 *** A0A103STZ1_CYNCS)		C:GO:0016021	C:integral component of membrane	IPR008892 (PFAM): IPR008892 (PAN	3,834	4,282	2,096	1,435	1,975									
Solyc02g071220	type-A response regulator2	TRR8B	P:GO:0000160	P:phosphorelay signal transduction system	IPR001789 (SMART): G3DSA:3.40.50	23,770	15,142	3,860	4,834	2,887									
Solyc02g071240	Pre-mRNA-processing factor 39, putative (AHRD V3.3 *-* A0A072TV09_MEDTR)		F:GO:0005515; P:GO	F:protein binding; P:RNA processing	IPR003107 (SMART): IPR011990 (G3	16,008	12,227	11,021	11,892	12,119									
Solyc02g071250	CTD small phosphatase-like protein 2 (AHRD V3.3 *** A0A061GEH1_THECC)		F:GO:0016791	F:phosphatase activity	IPR004274 (SMART): IPR023214 (G3	44,838	37,228	51,630	59,837	51,295									
Solyc02g071260	Phytochrome (AHRD V3.3 *** A0A067JEN0_JATCU)	PHYE	F:GO:0000155; P:GO	F:phosphorelay ser EC:2.7.13.3 Histidine kinase	IPR001294 (PRINTS): IPR003661 (SM	21,902	20,694	6,075	4,204	6,492									
Solyc02g071265	Ankyrin repeat family protein (AHRD V3.3 --* AT2G44090.5)					4,620	4,044	7,131	6,390	6,240									
Solyc02g071270	Protein MEI2-like 2 (AHRD V3.3 *** A0A0B2RZ29_GLYSO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR007201 (PF	44,987	35,081	66,501	67,337	60,003									
Solyc02g071280	16S rRNA processing protein RimM family (AHRD V3.3 *** AT5G46420.1)		C:GO:0005840; P:GO	C:ribosome; P:rRNA processing; F:ribosome binding	IPR011961 (TIGRFAM): IPR029044 ((	20,183	25,388	70,625	64,774	72,641									
Solyc02g071285	60S ribosomal protein L32, putative (AHRD V3.3 *-* B9T5H6_RICCO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		10,950	16,614	8,451	7,576	6,893									
Solyc02g071290	LOW QUALITY:51 kDa subunit of complex I (AHRD V3.3 --* AT5G08530.1)					0,000	0,018	0,000	0,025	0,000									
Solyc02g071300	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** A0A061GEI5_THECC)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding	IPR032867 (PFAM): IPR002885 (PFA	0,689	0,801	0,950	0,973	0,894									
Solyc02g071310	AWPM-19-like membrane family protein (AHRD V3.3 *** B9N9D5_POPTR)		C:GO:0016021	C:integral component of membrane	IPR008390 (PFAM): PTHR33294:SF1	0,619	0,349	0,541	0,692	0,563									
Solyc02g071320	AGAMOUS-like 31 (AHRD V3.3 --* AT5G65050.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	84,198	78,245	88,932	92,485	93,807									
Solyc02g071330	SH3 domain-containing protein (AHRD V3.3 *** AT4G18060.1)		F:GO:0005515	F:protein binding	PR00499 (PRINTS): IPR001452 (SMA	24,820	23,052	39,407	41,264	37,629									
Solyc02g071350	ABC transporter B family protein (AHRD V3.3 *** G7ILW7_MEDTR)	ABCB2	F:GO:0005524; C:GO	F:ATP binding; C:inl EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	2,565	4,109	2,044	1,953	2,104									
Solyc02g071360	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G17010.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR027443 (G3D	7,742	10,214	21,041	20,185	18,700									
Solyc02g071380	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G17010.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR027443 (G3D	0,084	0,206	0,123	0,127	0,095									
Solyc02g071410	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G25300.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR026992 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc02g071420	Ypt/Rab-GAP domain of gyp1p superfamily protein isoform 1 (AHRD V3.3 *** A0A061GNG6_THECC)				IPR000195 (SMART): G3DSA:1.10.8.2	0,123	0,224	0,049	0,164	0,095									
Solyc02g071430	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G17010.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR027443 (G3D	0,021	0,039	0,000	0,047	0,023									
Solyc02g071440	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G25300.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR027443 (G3D	0,040	0,000	0,025	0,025	0,094									

Solyc02g071450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G25300.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR027443 (G3D	21,636	20,649	27,387	26,959	29,066									
Solyc02g071475	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G25300.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3	0,104	1,117	0,366	0,365	0,635									
Solyc02g071490	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT4G25300.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR027443 (G3D	5,739	4,593	12,746	14,209	16,891									
Solyc02g071510	Transcription factor GTE12-like protein (AHRD V3.3 *** A0A0B0PNT5_GOSAR)		F:GO:0005515	F:protein binding	IPR001487 (PRINTS): IPR001487 (SM	38,195	34,569	43,039	43,546	40,268									
Solyc02g071520	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4B8C8_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D): IPI	0,057	0,077	0,000	0,025	0,000									
Solyc02g071530	Flap endonuclease 1 (AHRD V3.3 *-* A0A0K9PF59_ZOSMR)		F:GO:0003677: P:G(	F:DNA binding; P:D(EC:3.1.11; EC:3.1.1! Acting on ester bond:	IPR006084 (PRINTS): IPR008918 (SM	0,992	0,873	0,140	0,072	0,069									
Solyc02g071540	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *** AT1G29640.1)				IPR007608 (PFAM): PTHR33083 (PAI	0,059	0,137	0,000	0,025	0,000									
Solyc02g071550	LOW QUALITY:Senescence regulator (AHRD V3.3 *** A0A103Y1D7_CYNCS)				IPR007608 (PFAM): mobidb-lite (MOB	0,019	0,019	0,000	0,022	0,000									
Solyc02g071560	Subtilisin-like protease (AHRD V3.3 *** A0A0B0Q303_GOSAR)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR010259 (PF	0,491	0,928	0,122	0,050	0,140									
Solyc02g071570	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061GEM0_THECC)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	2,005	1,982	2,570	1,841	2,595									
Solyc02g071580	Subtilisin-like protease (AHRD V3.3 *** W9RLB7_9ROSA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	4,254	5,945	6,873	7,768	9,298									
Solyc02g071587	RNA-dependent RNA polymerase 2 (AHRD V3.3 --* AT4G11130.1)					0,178	0,120	0,072	0,025	0,073									
Solyc02g071590	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *-* B9S8H7_RICCO)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	IPR003337 (TIGRFAM): IPR003337 (F	1,615	1,377	0,881	0,839	0,870									
Solyc02g071593	trehalose-6-phosphate synthase (AHRD V3.3 *-* AT1G78580.4)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	G3DSA:3.40.50.2000 (GENE3D): IPR(	0,487	0,271	0,143	0,173	0,189									
Solyc02g071595	Trehalose-6-phosphate synthase 1 (AHRD V3.3 *-* B3VL84_9POAL)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	IPR001830 (PFAM)	0,172	0,098	0,049	0,025	0,070									
Solyc02g071597	trehalose-6-phosphate synthase (AHRD V3.3 *-* AT1G78580.4)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	G3DSA:3.40.50.2000 (GENE3D): IPR(	1,099	1,073	0,651	0,537	0,496									
Solyc02g071600	ATP synthase subunit b, chloroplastic (AHRD V3.3 --* ATPF_CHLSC)				PTHR36806 (PANTHER)	6,667	6,195	7,694	6,746	6,171									
Solyc02g071610	GDSL-lipase protein (AHRD V3.3 *** Q08ET5_CAPAN)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	11,454	14,438	0,000	0,047	0,000									
Solyc02g071620	GDSL-motif lipase/hydrolase family protein 1	GDSL1	F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	12,063	27,159	1,723	2,478	2,540	1,194	0,022					up		
Solyc02g071630	LOW QUALITY:VQ motif-containing family protein (AHRD V3.3 --* B9GUZ2_POPTR)					0,000	0,000	0,000	0,025	0,000									
Solyc02g071640	Lipase, GDSL (AHRD V3.3 *-* A0A103XTV4_CYNCS)		C:GO:0016021: F:G(	C:integral component of membrane; F:hydrolase activity, acting	PTHR22835:SF177 (PANTHER): PTHI	1,045	1,647	1,006	1,039	1,244									
Solyc02g071645	Lipase, GDSL (AHRD V3.3 *-* A0A103XTV4_CYNCS)		C:GO:0004806: C:G(	F:triglyceride lipase EC:3.1.1.1; EC:3.1.1 Carboxylesterase; Tr	PTHR22835:SF478 (PANTHER): PTHI	0,019	0,000	0,000	0,025	0,000									
Solyc02g071660	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT3G27473.1)					0,829	0,702	0,411	0,448	0,633									
Solyc02g071670	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 --* AT2G18370.1)					1,321	1,153	0,550	0,941	0,803									
Solyc02g071675	GDSL esterase/lipase (AHRD V3.3 *-* A0A172Q426_CITMA)		C:GO:0016021: F:G(	C:integral component of membrane; F:hydrolase activity, acting	PTHR22835:SF177 (PANTHER): PTHI	0,363	0,395	0,240	0,169	0,188									
Solyc02g071680	GDSL esterase/lipase (AHRD V3.3 *-* A0A172Q426_CITMA)		C:GO:0016021: F:G(	C:integral component of membrane; F:hydrolase activity, acting	PTHR22835:SF177 (PANTHER): PTHI	0,342	0,406	0,146	0,213	0,139									
Solyc02g071685	Lipase, GDSL (AHRD V3.3 --* A0A103Y1R3_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds		0,260	0,529	0,344	0,390	0,211									
Solyc02g071690	Lipase, GDSL (AHRD V3.3 *** A0A124S9Z4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,025	0,000									
Solyc02g071700	Lipase, GDSL (AHRD V3.3 *** A0A103XTV4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,593	0,738	0,025	0,126	0,024									
Solyc02g071710	Lipase, GDSL (AHRD V3.3 *** A0A124S9Z4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,000	0,021	0,022	0,000	0,000									
Solyc02g071720	Lipase, GDSL (AHRD V3.3 *** A0A103XTV4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,042	0,000	0,000	0,022	0,000									
Solyc02g071730	Tomato AGAMOUS 1	tag1	F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRIN' MIKC_MADS	52,405	70,067	50,388	56,034	68,067			0,430	0,005				up	
Solyc02g071740	MAP kinase kinase kinase 16	MAPKKK16	F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR001245 (PRINTS): IPR002110 (SM	24,583	39,478	11,950	13,794	16,815									
Solyc02g071750	RNA ligase/cyclic nucleotide phosphodiesterase family protein (AHRD V3.3 *** A0A097PLR7_SOLLC)		F:GO:0004112	F:cyclic-nucleotide phosphodiesterase activity	G3DSA:3.90.1140.10 (GENE3D): IPR(	12,144	12,468	22,536	18,566	19,453									
Solyc02g071760	histone acetyltransferase (DUF1264) (AHRD V3.3 *** AT1G29680.1)				IPR010686 (PFAM): PTHR31360:SF1	2,288	4,527	1,311	3,437	0,308									
Solyc02g071770	histone acetyltransferase (DUF1264) (AHRD V3.3 *** AT5G45690.1)				IPR010686 (PFAM): mobidb-lite (MOB	20,565	16,357	45,697	43,496	41,453									
Solyc02g071780	MACPF domain protein (AHRD V3.3 *** G7ILM1_MEDTR)		C:GO:0005886: P:G(	C:plasma membrane; P:plant-type hypersensitive response; P:n	IPR020864 (SMART): IPR020864 (PF	49,774	77,886	18,466	24,265	31,067			0,747	0,010				up	
Solyc02g071790	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGM8_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR032675 (G3DSA:3.80.10.GENE3D	0,061	0,134	0,101	0,094	0,189									
Solyc02g071800	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART): IPR021720 (PF	33,206	40,697	120,771	110,010	108,311									
Solyc02g071810	Receptor-like protein kinase (AHRD V3.3 *** C6FF64_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	7,349	7,680	0,918	0,642	0,797									
Solyc02g071815	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGF2_ARATH)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	1,378	1,489	0,306	0,212	0,210									
Solyc02g071820	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART): G3DSA:3.30.20	57,932	215,471	23,453	25,886	38,617	1,915	0,005					up		
Solyc02g071830	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *-* A0A118JRY8_CYNCS)		C:GO:0005737: C:G(	C:cytoplasm; C:plasma membrane; C:plasmodesma; P:stomatal	PF05664 (PFAM): IPR008528 (PANTI	2,799	4,304	3,334	4,046	3,795									
Solyc02g071850	LOW QUALITY:Unknown protein (AHRD V3.3)					0,000	0,000	0,000	0,045	0,000									
Solyc02g071860	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART): IPR021720 (PF	64,473	69,158	64,237	84,440	85,443			0,408	0,032	0,397	0,029		up	up
Solyc02g071870	Receptor protein kinase, putative (AHRD V3.3 *** Q9C6G5_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:2.60.12	6,122	5,635	1,834	1,735	1,836									
Solyc02g071875	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGF2_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR032675 (G3DSA:3.80.10.GENE3D	2,734	2,089	0,695	0,684	0,868									
Solyc02g071880	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR001245 (PF	44,223	27,318	8,519	5,136	8,671	-0,668	0,008			-0,728	0,041	down		down
Solyc02g071890	Histidinol dehydrogenase, chloroplastic (AHRD V3.3 *** K4B8G4_SOLLC)		P:GO:0000105: F:G(	P:histidine biosynth EC:1.1.1.23 Histidinol dehydroger	IPR012131 (PRINTS): IPR012131 (PF	43,414	49,964	65,258	65,891	69,902									
Solyc02g071900	Seipin (AHRD V3.3 *** A0A151RDH9_CAJCA)		P:GO:0019915	P:lipid storage	IPR009617 (PFAM): mobidb-lite (MOB	6,648	5,886	10,971	10,350	8,123									
Solyc02g071910	NOD26-like intrinsic protein 2.2	NIP2.2	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR000425 (PF	0,021	0,043	0,051	0,025	0,024									
Solyc02g071920	NOD26-like intrinsic protein 1.2	NIP1.2	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR023271 (G3	10,979	9,197	0,996	1,273	1,720									
Solyc02g071930	LOW QUALITY:CTD small phosphatase-like protein (AHRD V3.3 *** W9SMG6_9ROSA)		F:GO:0016791	F:phosphatase activity	IPR004274 (SMART): IPR011948 (TIC	0,175	0,136	0,025	0,000	0,000									
Solyc02g071940	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT4G19510.10)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	PTHR36896 (PANTHER)	3,961	3,485	2,572	1,791	1,529									
Solyc02g071970	LOW QUALITY:F-box and Leucine Rich Repeat domains containing protein (AHRD V3.3 --* AT1G80960.6)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	4,894	10,094	0,115	0,167	0,235									
Solyc02g071980	RING/FYVE/PHD zinc finger-containing protein (AHRD V3.3 *** F4I346_ARATH)		F:GO:0046872	F:metal ion binding	IPR000306 (SMART): IPR013083 (G3	35,346	29,941	49,843	51,391	46,463									
Solyc02g071990	Brassinazole-resistant 1 protein (AHRD V3.3 *** A0A059CDQ1_EUCGR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:transcription, DNA	IPR008540 (PFAM) BES1	48,725	53,644	29,709	35,182	36,863									
Solyc02g072000	SolycHsfA4c	HSF-17	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN' HSF	17,609	19,121	12,567	15,825	14,069									
Solyc02g072010	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JSM9_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM): IPR011990 ((	1,070	1,187	1,300	0,781	1,077									
Solyc02g072020	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JSM9_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,442	1,250	1,347	0,823	1,367									
Solyc02g072030	LOW QUALITY:ovate family protein 5	OFP5	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (TIGRFAM): IPR006458 (I	0,471	0,234	0,050	0,022	0,093									
Solyc02g072040	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)		C:GO:0016021	C:integral component of membrane	PTHR33916:SF1 (PANTHER): PTHR3:	0,890	3,020	0,221	0,520	0,118									
Solyc02g072050	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)		C:GO:0016021	C:integral component of membrane	PTHR33916:SF1 (PANTHER): PTHR3:	1,816	6,179	0,000	0,025	0,000									
Solyc02g072070	Serine/threonine-protein kinase (AHRD V3.3 *** M1CRP0_SOLTU)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,079	0,039	0,050	0,176	0,164									
Solyc02g072080	U-box domain-containing protein 17 (AHRD V3.3 *** A0A0B2ST26_GLYSO)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR003613 (SMART): IPR000225 (SM	83,090	30,992	31,985	104,462	57,245	-1,399	0,000	0,837	0,011	1,710	0,000	down	up	up
Solyc02g072090	DNA polymerase III subunit gamma/tau (AHRD V3.3 *** A0A0B2ST31_GLYSO)		F:GO:0003677: F:G(	F:DNA binding; F:D(EC:2.7.7.7 DNA-directed DNA pc	IPR003593 (SMART): PF13177 (PFAM	10,822	12,956	11,443	15,187	13,941									
Solyc02g072100	Ubiquitin domain-containing protein (AHRD V3.3 *** AT1G53400.1)				IPR032752 (PFAM): IPR038169 (G3D	5,449	3,273	1,657	1,330	1,786									
Solyc02g072105	Dihydroorotase, mitochondrial, putative (AHRD V3.3 *** B9RVX9_RICCO)		F:GO:0004151: P:G(	F:dihydroorotase ac EC:3.5.2.3 Dihydroorotase	IPR006680 (PFAM): G3DSA:3.20.20.1	5,206	6,740	4,126	4,791	4,775									
Solyc02g072120	ER lumen protein-retaining receptor (AHRD V3.3 *** K4B8I6_SOLLC)		P:GO:0006621: C:G(	P:protein retention in ER lumen; C:integral component of membr	IPR000133 (PRINTS): IPR000133 (PF	7,838	5,879	8,817	10,449	8,257									
Solyc02g072130	Protein transport protein Sec61 subunit alpha (AHRD V3.3 *** A0A0B2SPC7_GLYSO)		P:GO:0015031: C:G(	P:protein transport; C:membrane	IPR002208 (TIGRFAM): IPR019561 (I	335,920	405,774	345,535	372,417	355,417									
Solyc02g072140	LOW QUALITY:UNE1-like protein (AHRD V3.3 *** G7L787_MEDTR)		P:GO:0009639: P:G(	P:response to red or far red light; P:negative gravitropism	IPR006943 (PFAM): PTHR31161:SF7	1,384	1,398	0,170	0,296	0,165									
Solyc02g072150	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S8D6_RICCO)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	IPR003337 (TIGRFAM): IPR006379 (1	95,228	66,644	29,049	60,744	69,608			1,257	0,000	1,063	0,001		up	up
Solyc02g072160	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G18810.1)		P:GO:0032981	P:mitochondrial respiratory chain complex I assembly	IPR016040 (PFAM): G3DSA:3.40.50.7	55,022	68,961	117,968	111,566	141,850									
Solyc02g072170	Transcription factor TGA2 (AHRD V3.3 --* TGA2_ARATH)				PTHR34287:SF2 (PANTHER): PTHR3-	1,431	1,174	2,173	2,034	1,554									
Solyc02g072180	Rab family GTPase (AHRD V3.3 *** D8SVZ0_SELML)		F:GO:0003924: F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	15,526	14,817	4,211	3,527	4,376									
Solyc02g072190	WRKY transcription factor 79	WRKY79	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of transc	IPR003657 (SMAF WRKY	0,000	0,019	0,168	0,398	0,234									
Solyc02g072210	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072V475_MEDTR)				IPR012881 (PFAM): mobidb-lite (MOB	1,443	0,591	1,210	1,071	0,967									
Solyc02g072220	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072V475_MEDTR)				IPR012881 (PFAM): PTHR31865 (PAI	0,445	0,131	0,065	0,073	0,188									
Solyc02g072230	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G45760.1)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR001680 (PF	13,020	12,747	20,198	19,835	19,354									
Solyc02g072240	cellulose synthase family protein (AHRD V3.3 *** AT4G18780.1)		C:GO:0016020: F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (I	IPR027934 (PFAM): IPR005150 (PFA	4,693	3,000	0,278	0,075	0,191									
Solyc02g072250	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9NVS3_ZOSMR)		F:GO:0005515	F:protein binding	IPR001611 (PFAM): IPR032675 (G3D	0,019	0,081	0,047	0,072	0,000									
Solyc02g072260	SAP-like protein BP-73 (AHRD V3.3 *-* M8BMZ0_AEGTA)		P:GO:0006353	P:DNA-templated transcription, termination	G3DSA:1.10.720.10 (GENE3D): IPR0	2,877	4,709	18,913	19,809	21,509									
Solyc02g072270	RING/FYVE/PHD zinc finger superfamily protein, putative (AHRD V3.3 *** A0A061GDI8_THECC)		F:GO:0008270	F:zinc ion binding	IPR011016 (SMART): IPR011016 (PF	3,782	4,290	6,861	6,575	7,119									
Solyc02g072280	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.3(	0,000	0,018	0,000	0,000	0,000									
Solyc02g072290	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): PF17766 (PFAI	0,925	1,864	0,022	0,000	0,000									
Solyc02g072300	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	113,042	122,685	74,827	61,200	67,298									
Solyc02g072305	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 --* AT3G07170.1)				mobidb-lite (MOBIDB_LITE)	21,179	24,550	13,030	12,111	12,438									
Solyc02g072310	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT5G45780.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	2,112	1,649	0,870	1,604	1,132									
Solyc02g072320	LRR-RLK (AHRD V3.3 *-* A0A140G4J1_9ROSI)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,555	0,423	0,367	0,295	0,374									
Solyc02g072330	Subtilisin-like protease (AHRD V3.3 *-* A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR000209 (PFAM): PF17766 (PFAM)	0,000	0,039	0,074	0,049	0,095									
Solyc02g072335	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	G3DSA:3.50.30.30 (GENE3D): IPR00:	0,078	0,093	0,346	0,394	0,260									
Solyc02g072340	Subtilisin-like protease (AHRD V3.3 *-* Q9LWA3_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	PF17766 (PFAM): G3DSA:2.60.40.23	0,000	0,000	0,025	0,025	0,000									
Solyc02g072350	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,000	0,021	0,000	0,051	0,000									
Solyc02g072370	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,000	0,019	0,427	1,692	0,378									
Solyc02g072393	Receptor-kinase, putative (AHRD V3.3 *** B9RVA8_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART): IPR003591 (SM	0,360	0,473	0,140	0,243	0,118									
Solyc02g072397	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT3G44480.5)					1,947	0,951	1,049	0,987	0,821									
Solyc02g072410	26S proteasome regulatory subunit RPN13 (AHRD V3.3 --* RPN13_ARATH)					0,000	0,000	0,022	0,094	0,071									
Solyc02g072420	F-box family protein, putative (AHRD V3.3 *** A0A061G2V2_THECC)		F:GO:0005515	F:protein binding	IPR013187 (PFAM): IPR017451 (TIGF	0,019	0,057	0,074	0,000	0,000									
Solyc02g072430	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding	IPR013210 (PFAM): IPR001810 (PFA	0,180	0,101	0,022	0,025	0,071									
Solyc02g072440	Leucine-rich repeat protein kinase family protein, putative (AHRD V3.3 *** A0A061F9W0_THECC)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	PR00019 (PRINTS): SM00365 (SMAR	15,806	9,610	3,368	2,797	2,215									
Solyc02g072443	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein (AHRD V3.3 --* AT4G21750.4)					0,000	0,018	0,025	0,000	0,000									
Solyc02g072447	Receptor-kinase, putative (AHRD V3.3 *-* B9RVA8_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR003591 (SMART): IPR000719 (SM	1,121	1,665	2,953	4,037	3,240									
Solyc02g072450	LOW QUALITY:Receptor-like kinase (AHRD V3.3 *-* A0A072TRW0_MEDTR)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,200	0,136	0,443	0,533	0,494									
Solyc02g072470	LRR receptor-like kinase (AHRD V3.3 *** A0A072V4N4_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	PR00019 (PRINTS): IPR003591 (SMA	2,729	14,313	7,833	15,570	17,200	2,408	0,003	1,135	0,000	0,995	0,000	up	up	up
Solyc02g072480	LRR receptor-like kinase (AHRD V3.3 *** A0A072V4N4_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	SM00365 (SMART): IPR003591 (SMA	0,143	0,583	0,097	0,314	0,235									
Solyc02g072500	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LJF6_MEDTR)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR006043 (PFAM): PTHR11119 (PAI	0,531	0,782	0,213	0,289	0,257									
Solyc02g072510	Transcriptional regulator family protein, putative (AHRD V3.3 *** G7IEI1_MEDTR)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR012479 (PFAM): mobidb-lite (MOB	20,606	20,457	24,490	25,425	23,724									
Solyc02g072520	Receptor kinase, putative (AHRD V3.3 *** A0A061GFM9_THECC)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR003591 (SMART): IPR032675 (G3	11,735	17,311	23,272	22,764	23,514									
Solyc02g072530	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IL28_SOLCH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR004041 (PF	32,733	29,694	31,554	37,775	36,471									
Solyc02g072540	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IFU0_SOLCH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	0,077	0,165	0,000	0,000	0,000									
Solyc02g072550	Delay of germination 1, putative (AHRD V3.3 *-* A0A061GFN4_THECC)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	PTHR22952:SF210 (PANTHER): PTHI	0,019	0,000	0,000	0,025	0,023									
Solyc02g072560	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	IPR025422 (PFAM): PTHR22952:SF2	0,061	0,019	0,000	0,025	0,000									
Solyc02g072570	transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	IPR025422 (PFAM): PTHR22952 (PAI	0,078	0,164	0,050	0,126	0,023									
Solyc02g073570	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	IPR025422 (PFAM): mobidb-lite (MOB	0,037	0,060	0,000	0,000	0,000									
Solyc02g073571	UPF0183 protein family (AHRD V3.3 *-* A0A151TIL6_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR005373 (PFAM): IPR039156 (PAN	0,019	0,019	0,025	0,074	0,070									
Solyc02g073572	ATP-dependent DNA helicase Q-like 4B (AHRD V3.3 --* RQL4B_ARATH)					0,000	0,000	0,000	0,025	0,047									
Solyc02g073574	Disease resistance protein (AHRD V3.3 *** A0A124SFK9_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:ADP binding	PR00364 (PRINTS): IPR003591 (SMA	4,832	3,672	3,963	5,800	3,275									
Solyc02g073576	LOW QUALITY:Polynucleotidyl transferase, Ribonuclease H fold (AHRD V3.3 --* A2Q2M9_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bond:	IPR036397 (G3DSA:3.30.420.GENE3	0,000	0,000	0,000	0,022	0,000									
Solyc02g074600	Unknown protein (AHRD V3.3)					0,539	0,318	0,486	0,427	0,378									
Solyc02g075610	Golgin candidate 6 (AHRD V3.3 *-* A0A0B0P8X2_GOSAR)		C:GO:0000139: P:G(	C:Golgi membrane; P:intracellular protein transport; P:vesicle fu	IPR006953 (PFAM): IPR011989 (G3D	68,985	70,453	77,091	77,947	77,869									
Solyc02g075615	LOW QUALITY:Golgin candidate 6 (AHRD V3.3 *-* W9SQ07_9ROSA)		C:GO:0005737: P:G(	C:cytoplasm; P:intracellular protein transport; F:protein transpor	IPR006955 (PFAM)	17,063	18,530	20,055	16,392	19,183									
Solyc02g075625	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	IPR025422 (PFAM): PTHR22952 (PAI	0,040	0,021	0,049	0,225	0,000									
Solyc02g075630	UPF0183 protein (AHRD V3.3 *-* A0A0B2RUE4_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR005373 (PFAM): IPR039156 (PAN	22,527	18,540	29,210	26,764	25,213									
Solyc02g076640	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *-* AT4G18650.1)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindi	IPR025422 (PFAM): PTHR22952 (PAI	0,195	0,222	0,115	0,202	0,164									
Solyc02g076660	Receptor protein kinase, putative (AHRD V3.3 *** B9T7R3_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR001611 (PFAM): IPR001245 (PFA	3,876	4,076	3,444	5,149	4,232									
Solyc02g076670	MYB-like transcription factor family protein (AHRD V3.3 *** A0A072TT31_MEDTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(G2-like	0,683	0,552	0,193	0,364	0,285									
Solyc02g076680	DUF688 family protein (AHRD V3.3 *** G7ZXK0_MEDTR)				IPR007789 (PFAM): mobidb-lite (MOB	9,942	17,685	86,996	79,585	80,022	0,861	0,027					up		
Solyc02g076690	Cysteine protease (AHRD V3.3 *** Q7XYU8_ANTAD)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (SM	21,544	36,103	5,538	4,743	11,615	0,774	0,033	1,065	0,000			up	up	
Solyc02g076695	Endo-1,4-beta-xylanase A (AHRD V3.3 *-* A0A0B0NIZ4_GOSAR)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:xylan	catabolic process	0,340	0,568	0,778	0,373	0,402									
Solyc02g076700	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y3C8_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFA	1,090	1,355	1,778	1,187	1,694									
Solyc02g076710	Cysteine protease (AHRD V3.3 *** Q7XYU8_ANTAD)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000118 (SM	446,762	270,203	2406,757	1723,258	1717,023			-0,490	0,035	-0,478	0,017		down	down
Solyc02g076720	Phosphoribosylformylglycinamidine synthase family protein (AHRD V3.3 *** B9HT78_POPTR)		F:GO:0004642: F:G(	F:phosphoribosylfor EC:6.3.5.3 Phosphoribosylformy	SM01211 (SMART): IPR029062 (G3D	93,417	78,452	81,069	79,494	81,093									
Solyc02g076730	Cysteine protease, putative (AHRD V3.3 *-* B9T6U3_RICCO)		F:GO:0008234	F:cysteine-type peptidase activity	IPR000118 (SMART): IPR037277 (G3	5,465	3,639	1,701	1,368	1,250									
Solyc02g076740	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 --* AT5G44310.2)				mobidb-lite (MOBIDB_LITE)	4,494	3,810	1,567	1,245	1,099									
Solyc02g076750	Cysteine protease, putative (AHRD V3.3 *** B9T6U3_RICCO)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (SMART): IPR013201 (SM	11,962	9,196	3,385	3,717	2,896									
Solyc02g076760	Phosphoribosylanthranilate isomerase (AHRD V3.3 *** F1BPW4_SOLPN)		F:GO:0004640: P:G(	F:phosphoribosylan EC:5.3.1.24 Phosphoribosylanthr	IPR001240 (PFAM): IPR013785 (G3D	17,321	23,131	26,124	27,161	28,138									
Solyc02g076780	MAP kinase kinase kinase 17	MAPKKK17	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	12,608	19,318	17,454	14,537	15,687	0,642	0,025					up		
Solyc02g076790	U-box domain containing protein (AHRD V3.3 --* H6W648_ARALL)		C:GO:0016021	C:integral component of membrane	IPR011989 (G3DSA:1.25.10.GENE3D	18,302	16,403	20,427	20,552	18,981									
Solyc02g076800	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IWW8_MEDTR)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation	IPR025322 (PFAM): mobidb-lite (MOB	13,636	7,915	2,183	2,782	1,298									
Solyc02g076810	Transcription factor (AHRD V3.3 *** A0A072VEJ2_MEDTR)		C:GO:0005634: F:G(	C:nucleus; F:sequence-specific DNA binding; F:transcription reg	PF13837 (PFAM): Trihelix	47,620	48,425	37,719	42,630	43,607									
Solyc02g076820	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)		C:GO:0005634: P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus	IPR006936 (PFAM): mobidb-lite (MOB	132,130	103,492	150,036	128,070	137,066									

Solyc02g076830	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A199VI10_ANACO)		P:GO:0048544	P:recognition of pollen	IPR001480 (SMART): IPR003609 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc02g076840	SCAR family protein (AHRD V3.3 *-* AT2G34150.2)		C:GO:0005856; P:G(	C:cytoskeleton; P:actin cytoskeleton organization	G3DSA:1.20.58.1570 (GENE3D): G3D	45,520	35,147	27,019	30,122	28,229									
Solyc02g076850	Dof zinc finger protein4		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM) Dof	0,081	0,165	0,000	0,022	0,023									
Solyc02g076860	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** AT4G18596.1)		C:GO:0005615	C:extracellular space	PF01190 (PFAM): IPR006041 (PTHR	0,000	0,000	0,365	0,483	0,378									
Solyc02g076870	Alpha/beta-hydrolase superfamily protein (AHRD V3.3 *** G7LIR3_MEDTR)		P:GO:0044255	P:cellular lipid metabolic process	IPR007751 (PFAM): IPR029058 (G3D	21,849	22,530	90,214	92,950	94,966									
Solyc02g076890	LOW QUALITY:DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)				IPR007493 (PFAM): IPR036758 (G3D	0,037	0,000	0,000	0,000	0,000									
Solyc02g076900	dual specificity protein phosphatase-like protein (AHRD V3.3 *** AT4G18593.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,580	1,938	3,123	2,703	2,401									
Solyc02g076910	Cysteine protease (AHRD V3.3 *** E7D4U5_TOBAC)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR013201 (SM	0,000	0,000	0,394	1,001	0,327									
Solyc02g076920	bHLH transcription factor 013		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	3,639	2,297	0,999	0,413	1,271									
Solyc02g076930	U-box domain-containing 7-like protein (AHRD V3.3 *** A0A0B0P2C2_GOSAR)				IPR011989 (G3DSA:1.25.10.GENE3D	1,038	1,627	0,363	0,766	0,285									
Solyc02g076940	DnaJ P58IPK-like protein (AHRD V3.3 --* AT5G03160.1)				PTHR34659:SF1 (PANTHER): PTHR3	0,993	1,001	1,222	0,781	1,082									
Solyc02g076945	maternal effect embryo arrest 18 (AHRD V3.3 *** AT2G34090.1)				IPR002882 (PFAM): PTHR31240 (PAN	3,852	5,597	5,909	6,282	6,080									
Solyc02g076970	Cathepsin B-like cysteine proteinase (AHRD V1 **-* CYSP_SCHMA)%3B contains Interpro domain(s) IPR01		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (SM	0,330	0,277	0,405	0,523	0,330									
Solyc02g076980	cysteine protease		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR013201 (SM	0,037	0,329	0,068	0,075	0,234									
Solyc02g077030	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	0,202	0,136	0,000	0,025	0,047									
Solyc02g077040	phytophthora-inhibited protease 1	pip1	P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR013201 (SM	11,631	50,601	47,184	151,868	70,552	2,141	0,000	0,578	0,004	1,690	0,000	up	up	up
Solyc02g077050	Cathepsin B-like cysteine proteinase (AHRD V1 **-* CYSP_SCHMA)%3B contains Interpro domain(s) IPR01		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (SM	4,982	10,686	0,548	1,319	0,956	1,122	0,020					up		
Solyc02g077060	LOW QUALITY:RPW8.2-like protein (AHRD V3.3 *-* A0A059UJ39_VITPS)		P:GO:0050832	P:defense response to fungus	IPR008808 (PFAM): IPR039203 (PAN	1,720	1,986	0,263	0,741	0,444									
Solyc02g077070	Photosystem II reaction center protein K (AHRD V3.3 --* PSBK_LIRTU)					0,666	0,763	0,490	0,606	0,825									
Solyc02g077080	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)				IPR026057 (PFAM): IPR025846 (PFA	230,641	127,776	250,658	218,648	263,402	-0,825	0,003					down		
Solyc02g077090	Protein CHUP1, chloroplastic-like protein (AHRD V3.3 *-* A0A0B0P0R5_GOSAR)		C:GO:0009707	C:chloroplast outer membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	14,549	10,926	2,889	2,274	4,200									
Solyc02g077100	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GF41_THECC)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	35,157	37,820	45,904	43,908	41,650									
Solyc02g077110	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G18550.2)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	G3DSA:3.40.50.12520 (GENE3D): IPF	1,786	5,372	1,530	1,902	1,409	1,604	0,005					up		
Solyc02g077120	GDSL esterase/lipase (AHRD V3.3 *** A0A199UWQ2_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,747	0,596	0,000	0,224	0,142									
Solyc02g077130	GDSL esterase/lipase (AHRD V3.3 *-* A0A199W258_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,313	0,399	0,099	0,025	0,072									
Solyc02g077140	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GF41_THECC)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	G3DSA:3.40.50.12520 (GENE3D): IPF	0,042	0,000	0,000	0,000	0,000									
Solyc02g077160	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GF41_THECC)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	16,066	14,742	6,996	4,598	5,302									
Solyc02g077170	XH/XS domain-containing protein (AHRD V3.3 *-* AT1G15910.1)		P:GO:0031047	P:gene silencing by RNA	IPR005379 (PFAM): G3DSA:2.40.50.1	0,040	0,136	0,025	0,025	0,024									
Solyc02g077190	chromatin remodeling factor18 (AHRD V3.3 --* AT1G48310.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	4,060	3,080	1,799	1,356	1,371									
Solyc02g077220	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2PL48_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	3,461	3,670	2,253	1,892	1,678									
Solyc02g077225	Outer arm dynein light chain 1 protein (AHRD V3.3 --* AT2G34680.2)				mobidb-lite (MOBIDB_LITE)	0,019	0,000	0,025	0,025	0,000									
Solyc02g077230	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G03140.9)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,021	0,025	0,050	0,072									
Solyc02g077240	Pyruvate decarboxylase (AHRD V3.3 *** Q1I1D9_CITSI)		F:GO:0000287; F:G(	F:magnesium ion binding; F:carboxy-lyase activity; F:thiamine p	G3DSA:3.40.50.970 (GENE3D): IPR0	150,480	141,933	362,038	302,583	340,046									
Solyc02g077250	LOW QUALITY:TCP transcription factor 1	TCP1			IPR017887 (PFAM) TCP	0,350	0,529	0,022	0,025	0,046									
Solyc02g077260	SUN-like protein5	SUN5	F:GO:0005515	F:protein binding	IPR000048 (SMART): IPR000048 (PF	0,783	1,716	0,165	0,538	0,447									
Solyc02g077270	Calcium-binding EF-hand (AHRD V3.3 *-* A0A103XMB0_CYNCS)		F:GO:0005509; C:G(	F:calcium ion binding; C:integral component of membrane; P:tra	IPR002048 (SMART): G3DSA:1.10.23	3,789	3,843	3,433	3,610	4,584									
Solyc02g077280	GTP-binding protein Era-like protein (AHRD V3.3 *** AT5G66470.2)		F:GO:0003723; F:G(	F:RNA binding; F:GTP binding	G3DSA:3.40.50.300 (GENE3D): IPR0	21,493	22,199	27,894	26,971	35,241									
Solyc02g077290	glutamate receptor 1.2		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART): IPR001638 (PF	0,063	0,171	0,462	0,904	1,082									
Solyc02g077300	Peroxidase (AHRD V3.3 *** K4B8V7_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,102	0,092	0,000	0,000	0,000									
Solyc02g077310	D-tyrosyl-tRNA(Tyr) deacylase (AHRD V3.3 *** M1AQ86_SOLTU)		C:GO:0005737; F:G(	C:cytoplasm; F:D-a EC:3.1.1.96; EC:3.1. D-aminoacyl-tRNA de	IPR023509 (G3DSA:3.50.80.GENE3D	3,323	2,586	1,566	1,045	1,556									
Solyc02g077315	Unknown protein (AHRD V3.3)					1,586	1,796	0,774	0,362	0,918									
Solyc02g077320	SNI1 (AHRD V3.3 *** Q0ZFU7_SOLTU)		C:GO:0005634; P:G(	C:nucleus; P:cellular response to DNA damage stimulus; C:Smc	IPR034561 (PANTHER)	16,875	23,078	12,874	11,213	11,683									
Solyc02g077330	GDSL esterase/lipase family (AHRD V3.3 *** A0A151SAY8_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	20,690	28,173	0,025	0,025	0,117									
Solyc02g077340	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2QGN0_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,177	0,211	0,000	0,000	0,000									
Solyc02g077350	LOW QUALITY:26S proteasome non-ATPase regulatory subunit 3 homolog B (AHRD V3.3 --* PSD3B_ARATH)					0,019	0,000	0,000	0,047	0,046									
Solyc02g077360	Ethylene Response Factor B.2	ERF_B_2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,000	0,021	0,000	0,000	0,000									
Solyc02g077370	Ethylene Response Factor C.5	ERF_C_5	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	2,016	7,264	0,547	1,059	1,082	1,869	0,009					up		
Solyc02g077390	compound inflorescence	s	F:GO:0003677	F:DNA binding	IPR001356 (SMAF WOX	0,761	0,936	0,000	0,022	0,000									
Solyc02g077400	Rac-like GTP binding protein (AHRD V3.3 *** Q9S821_PHYPA)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	0,233	0,291	0,240	0,265	0,165									
Solyc02g077410	28 kDa heat-and acid-stable phosphoprotein (AHRD V3.3 *** A0A151SAQ2_CAJCA)				IPR019380 (PFAM): mobidb-lite (MOB	150,000	147,208	141,693	139,448	134,147									
Solyc02g077420	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	0,000	0,021	0,000	0,000	0,000									
Solyc02g077430	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:3.1.1.32; EC:3.1. Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	0,059	2,117	0,000	0,000	0,000	4,952	0,000					up		
Solyc02g077440	Transcription elongation factor 1 homolog (AHRD V3.3 *** ELOF1_ORYSJ)		F:GO:0000993; F:G(	F:RNA polymerase II complex binding; F:translation elongation f	IPR038567 (G3DSA:2.20.25.GENE3D	10,794	10,390	8,468	7,509	8,460									
Solyc02g077450	Vascular plant one zinc finger transcription factor protein (AHRD V3.3 *** V6BQR5_9BRYO)		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:positive regulati	mobidb-lite (MOBI[VOZ	53,727	46,519	76,970	62,170	66,739									
Solyc02g077460	Lipoate-protein ligase B, putative (AHRD V3.3 *** B9SJ07_RICCO)		P:GO:0009249; F:G(	P:protein lipoylation EC:2.3.1.181 Lipoyl(octanoyl) trans	IPR000544 (TIGRFAM): G3DSA:3.30.9	10,225	8,191	9,560	7,559	9,902									
Solyc02g077470	Optic atrophy 3 protein (OPA3) (AHRD V3.3 *** AT1G28510.1)		C:GO:0005739; P:G(	C:mitochondrion; P:regulation of lipid metabolic process	IPR010754 (PFAM): IPR010754 (PAN	43,867	90,714	12,064	14,006	16,472									
Solyc02g077480	Histone H3 (AHRD V3.3 *** A0A068VC55_COFCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS): IPR000164 (SM	37,060	46,827	30,670	25,372	30,911									
Solyc02g077490	Werner Syndrome-like exonuclease (AHRD V3.3 *-* A0A199W7Y7_ANACO)		P:GO:0003676	F:nucleic acid binding	IPR036397 (G3DSA:3.30.420.GENE3	0,000	0,000	0,044	0,092	0,000									
Solyc02g077500	Ethylene insensitive 3 family protein (AHRD V3.3 --* AT5G10120.1)					0,000	0,000	0,000	0,025	0,000									
Solyc02g077510	O-methyltransferase (AHRD V3.3 *** A5HK00_VITVI)	ASMT02	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR001077 (PFAM): G3DSA:3.40.50.1	0,038	0,018	0,000	0,000	0,000									
Solyc02g077520	O-methyltransferase, putative (AHRD V3.3 *** B9S932_RICCO)	ASMT03	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR001077 (PFAM): IPR012967 (PFA	0,000	0,039	0,022	0,000	0,000									
Solyc02g077530	O-methyltransferase, putative (AHRD V3.3 *** B9S932_RICCO)	ASMT04	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR036388 (G3DSA:1.10.10.GENE3D	0,019	0,043	0,099	0,398	0,000									
Solyc02g077540	transmembrane protein%2C putative (Protein of unknown function%2C DUF599) (AHRD V3.3 *** AT3G1821		C:GO:0016021	C:integral component of membrane	IPR006747 (PFAM): PTHR31168 (PAN	0,019	0,018	0,087	0,141	0,023									
Solyc02g077550	transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT3G18215.1)		C:GO:0016021	C:integral component of membrane	IPR006747 (PFAM): PTHR31168 (PAN	0,042	0,021	0,068	0,253	0,166									
Solyc02g077560	auxin response factor 3	ARF3	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ten	IPR003340 (SMAF ARF	104,032	86,740	99,452	87,942	89,544									
Solyc02g077570	MLO-like protein (AHRD V3.3 *-* U5FZ43_POPTR)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane	IPR004326 (PFAM): PTHR31942 (PAN	0,082	0,039	0,000	0,022	0,000									
Solyc02g077575	MLO-like protein (AHRD V3.3 *** G9BBX3_CAPAN)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane	IPR004326 (PFAM): PTHR31942 (PAN	0,141	0,060	0,000	0,047	0,000									
Solyc02g077580	Glutaredoxin-like family protein (AHRD V3.3 *** B9H2P7_POPTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	G3DSA:3.40.30.10 (GENE3D): mobidb	0,140	0,185	0,000	0,025	0,000									
Solyc02g077590	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)		F:GO:0003677	F:DNA binding	IPR000047 (PRIN HD-ZIP	11,219	5,044	1,885	0,905	0,588	-1,122	0,000	-1,673	0,004			down	down	
Solyc02g077600	Guanylate-binding family protein (AHRD V3.3 *** AT5G46070.1)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR015894 (PFAM): G3DSA:1.20.100	6,729	6,229	3,739	4,466	4,171									
Solyc02g077610	NAC domain-containing protein (AHRD V3.3 *** A0A060A5P2_BOENI)	NAC018	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	1,550	2,122	0,405	1,034	1,257									
Solyc02g077615	Resistance protein PLTR (AHRD V3.3 --* Q2KQ06_ARAHY)					0,198	0,156	0,121	0,415	0,118									
Solyc02g077620	Sulfotransferase (AHRD V3.3 *** K4B8Y7_SOLLC)		F:GO:0008146	F:sulfotransferase activity	IPR000863 (PFAM): G3DSA:3.40.50.3	1,724	1,260	2,105	1,600	1,767									
Solyc02g077630	Receptor-like protein kinase HSL1 (AHRD V3.3 *** HSL1_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR003591 (SMART): IPR000719 (SM	61,775	54,334	58,993	42,063	56,579					-0,485	0,001			down
Solyc02g077645	dicarboxylate transporter 2.2 (AHRD V3.3 --* AT5G64280.1)					0,335	0,434	0,175	0,271	0,235									
Solyc02g077650	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9N3J7_POPTR)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	1,557	2,442	1,600	1,274	1,627									
Solyc02g077660	Homeobox protein, putative (AHRD V3.3 *** B9RB95_RICCO)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR018501 (SMAF HB-other	133,160	159,924	158,680	159,859	166,124									
Solyc02g077670	DnaJ-like protein (AHRD V3.3 *** Q9SP09_TOBAC)		P:GO:0006457; F:G(	P:protein folding; F:unfolded protein binding	IPR001623 (PRINTS): IPR001623 (SM	60,234	37,781	151,596	162,509	155,095	-0,648	0,030					down		
Solyc02g077680	Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** K4B8Z3_SOLLC)		P:GO:0005975; F:G(	P:carbohydrate met EC:2.4.1.1 Glycogen phosphoryl	G3DSA:3.40.50.2000 (GENE3D): IPR	43,079	45,447	62,957	65,848	66,409									
Solyc02g077690	Myosin heavy chain-like protein, putative (AHRD V3.3 *** G7ISF7_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR34360 (PANTHER): PTHR34360	5,089	6,099	5,419	6,748	5,275									
Solyc02g077710	LOW QUALITY:ROX1 homologue (AHRD V3.3 *** I7GSE9_TOBAC)		F:GO:0003677; F:G(	F:DNA binding; F:kinase activity; P:phosphorylation	mobidb-lite (MOBIDB_LITE): mobidb-lit	322,190	246,903	2097,598	3424,648	2158,694					0,711	0,008			up
Solyc02g077720	Transmembrane protein, putative (AHRD V3.3 *** G7ISF1_MEDTR)				PTHR33544:SF2 (PANTHER): IPR040	4,498	3,727	12,891	14,465	11,594									
Solyc02g077730	nuclear fusion defective 6 (AHRD V3.3 *** AT2G20585.5)		P:GO:0000741	P:karyogamy	IPR033251 (PTHR33156:PANTHER):	9,793	11,291	12,447	10,862	10,446									
Solyc02g077740	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103XEX3_CYNCS)				G3DSA:2.40.50.140 (GENE3D): mobic	28,496	33,996	35,267	34,328	32,664									
Solyc02g077750	Dehydration-induced 19 (AHRD V3.3 *** A0A0B0N551_GOSAR)		F:GO:0005515	F:protein binding	IPR027935 (PFAM): IPR008598 (PFA	159,951	120,864	82,051	88,537	79,350									
Solyc02g077760	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 --* AT2G35970.1)					4,098	3,413	1,951	2,260	2,311									
Solyc02g077770	bidirectional amino acid transporter 1 (AHRD V3.3 --* AT2G01170.2)					2,846	1,717	1,935	2,056	1,645									
Solyc02g077780	MACPF domain-containing protein (AHRD V3.3 *** A0A0B2S5Z8_GLYSO)		C:GO:0005886; P:G(	C:plasma membrane; P:plant-type hypersensitive response	IPR020864 (SMART): IPR020864 (PF	19,108	27,175	34,214	30,250	30,883									
Solyc02g077790	LOW QUALITY:Ethylene-responsive transcription factor (AHRD V3.3 --* A0A087HKS2_ARAAL)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR036955 (G3DSA:3.30.730.GENE3	0,467	0,214	17,019	11,330	4,875			-1,802	0,001				down	
Solyc02g077800	LOW QUALITY:Serine/arginine-rich splicing factor RSZ23 (AHRD V3.3 --* RZP23_ORYSJ)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding	IPR001878 (SMART): IPR001878 (PF	0,265	0,041	0,000	0,000	0,000									
Solyc02g077810	LOW QUALITY:Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A087HKS2_ARAAL)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,303	0,361	0,000	0,000	0,000									
Solyc02g077820	LOW QUALITY:Ethylene-responsive transcription factor (AHRD V3.3 --* V5QP37_MOMCH)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; C:nu	mobidb-lite (MOBIDB_LITE)	1,068	1,449	0,049	0,050	0,000									
Solyc02g077830	LOW QUALITY:Anthocyanidin 3-O-glucoside 6''-O-acyltransferase (AHRD V3.3 --* 3AT_PERFR)					0,000	0,021	0,000	0,000	0,000									
Solyc02g077840	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RBB0_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,569	1,412	0,094	0,218	0,187									
Solyc02g077850	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A0K9NYE0_ZOSMR)		F:GO:0005515	F:protein binding	G3DSA:2.60.120.430 (GENE3D): IPR	30,264	25,530	32,658	32,511	31,080									
Solyc02g077860	LOW QUALITY:Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_PERAE)		F:GO:0000287; F:G(	F:magnesium ion binding; F:structural constituent of ribosome; (	IPR022669 (PFAM): IPR000685 (PFA	0,172	0,750	0,468	1,294	0,776									
Solyc02g077880	auxin repressed/dormancy associated protein				IPR008406 (PFAM): mobidb-lite (MOB	625,769	376,621	422,405	379,842	411,760	-0,704	0,014					down		
Solyc02g077890	Ring finger protein, putative (AHRD V3.3 *** B9RBB3_RICCO)		F:GO:0016874	F:ligase activity	mobidb-lite (MOBIDB_LITE): mobidb-lit	16,975	16,595	11,428	9,735	10,774									
Solyc02g077900	peroxisomal leader peptide-processing protease		F:GO:0004252; C:G(	F:serine-type endo(EC:3.4.21 Acting on peptide bor	PF13365 (PFAM): G3DSA:2.40.10.12(	56,558	51,131	105,234	109,701	100,752									
Solyc02g077910	Mitochondrial carrier protein, expressed (AHRD V3.3 *** A0A0K9PZC5_ZOSMR)		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	3,645	3,952	3,289	2,926	2,684									
Solyc02g077920	Colorless non-ripening	CNR	F:GO:0003677; C:G(	F:DNA binding; C:nucleus	IPR004333 (PFAM) SBP	102,120	82,962	178,180	262,606	199,610					0,563	0,000			up
Solyc02g077930	LOW QUALITY:Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 --* AT3G07960.4)				mobidb-lite (MOBIDB_LITE)	3,858	3,700	7,698	8,757	7,227									
Solyc02g077940	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G45060.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	5,771	4,612	9,972	13,936	11,690									
Solyc02g077950	Dof zinc finger protein5		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM) Dof	3,362	3,352	1,998	3,044	2,592									
Solyc02g077960	Dof zinc finger protein (AHRD V3.3 *** W9S9I5_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM) Dof	0,437	0,678	0,189	0,341	0,304									
Solyc02g077970	Late embryogenesis abundant, putative (AHRD V3.3 *** B9RBC1_RICCO)				G3DSA:1.10.287.700 (GENE3D): mob	5,758	7,956	2,168	5,674	0,844									
Solyc02g077980	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 --* AT4G13230.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,326	2,450	0,691	1,933	0,070									
Solyc02g077990	Ribosomal protein S5 family protein (AHRD V3.3 *** AT2G33800.1)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio	IPR014721 (G3DSA:3.30.230.GENE3	57,529	97,038	138,944	142,568	189,302	0,782	0,002	0,444	0,007			up	up	
Solyc02g078010	transcriptional corepressor LEUNIG (AHRD V3.3 *-* AT4G32551.2)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR015943 (G3	19,844	18,306	18,250	18,997	18,732									
Solyc02g078020	Telomerase activating protein Est1, putative (AHRD V3.3 *** A0A061GFN7_THECC)		F:GO:0005515	F:protein binding	IPR019458 (PFAM): IPR018834 (PFA	29,035	19,653	92,982	99,874	92,956	-0,536	0,044					down		
Solyc02g078030	VQ motif-containing protein (AHRD V3.3 *** AT1G28280.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	59,319	97,109	126,427	137,481	123,624									
Solyc02g078040	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** AT2G34700.1)		F:GO:0005199	F:structural constituent of cell wall	IPR003882 (PRINTS): PF01190 (PFAI	77,163	88,696	7,495	17,844	14,400									
Solyc02g078050	120 kDa pistil extensin-like protein (AHRD V3.3 *-* Q49I27_9SOLA)		F:GO:0005199	F:structural constituent of cell wall	PR01217 (PRINTS): PF01190 (PFAM	0,183	0,165	0,074	0,047	0,187									
Solyc02g078080	Repetitive proline-rich cell wall protein (AHRD V3.3 *** PRP_MEDSA)		C:GO:0016020	C:membrane	PR01217 (PRINTS): mobidb-lite (MOB	0,327	3,880	0,025	0,000	0,000									
Solyc02g078100	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *-* A0A124SHL8_CYNCS)		F:GO:0005199	F:structural constituent of cell wall	IPR003882 (PRINTS): PF01190 (PFAI	0,063	0,041	0,000	0,022	0,023									
Solyc02g078120	Eukaryotic translation initiation factor 3 subunit D (AHRD V3.3 *** K4B937_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in	IPR007783 (PIRSF): IPR007783 (PFA	124,027	151,994	153,171	154,489	138,496									
Solyc02g078130	bHLH transcription factor 079		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase	IPR036638 (G3DS bHLH	0,019	0,162	0,000	0,025	0,023									
Solyc02g078140	MAP kinase kinase kinase 18	MAPKKK18	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PRINTS): IPR000719 (SM	32,540	32,940	84,333	97,127	82,919									
Solyc02g078150	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)				IPR006502 (TIGRFAM): IPR006502 (F	20,270	13,060	5,652	11,098	9,068					0,972	0,004			up
Solyc02g078160	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)				IPR006502 (PFAM): IPR006502 (TIGF	106,897	33,205	25,448	42,714	29,450	-1,660	0,000			0,746	0,014	down		up
Solyc02g078170	Clade VII lectin receptor kinase (AHRD V3.3 *** A0A0K1U1X8_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	0,630	0,771	0,025	0,047	0,142									
Solyc02g078180	DUF616 family protein (AHRD V3.3 *** G7IPT3_MEDTR)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra	IPR006852 (PFAM): mobidb-lite (MOB	7,866	6,389	4,048	6,751	5,975					0,735	0,017			up
Solyc02g078200	50S ribosomal protein L21, related protein (AHRD V3.3 *** G7KWH0_MEDTR)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR028909 (PFAM): IPR001787 (TIGF	26,595	28,666	41,183	36,244	39,519									
Solyc02g078210	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** U5FV88_POPTR)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin conjugating enzyme activity	SM00212 (SMART): IPR016135 (G3D	74,298	64,421	40,570	33,173	62,439			0,617	0,001				up	
Solyc02g078230	Callose synthase-like protein (AHRD V3.3 *** A0A072V5B8_MEDTR)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar EC:2.4.1.34 1,3-beta-glucan syntl	IPR026899 (SMART): IPR026899 (PF	26,467	23,378	20,345	23,768	30,124			0,563	0,000				up	
Solyc02g078240	Phosphoglycerate mutase, putative (AHRD V3.3 *-* B9RZ93_RICCO)		C:GO:0005737	C:cytoplasm	IPR013078 (PFAM): IPR029033 (G3D	3,287	3,613	1,077	0,793	1,441									
Solyc02g078250	CASP-like protein (AHRD V3.3 *** K4B950_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 in	IPR006459 (TIGRFAM): IPR006702 (F	0,101	0,041	0,075	0,096	0,141									
Solyc02g078260	RNA polymerase II subunit 2	rpb2	F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA pc	IPR007641 (PFAM): IPR007120 (PFA	207,283	169,446	200,699	193,188	177,004									
Solyc02g078270	LSD1 zinc finger family protein (AHRD V3.3 *-* AT4G20380.7)				IPR005735 (PFAM) LSD	7,031	6,179	8,022	7,233	6,319									
Solyc02g078280	DNA ligase-like protein (AHRD V3.3 *** AT2G33793.2)		P:GO:0007131; F:G(	P:reciprocal meiotic recombination; F:ligase activity	G3DSA:1.20.5.1230 (GENE3D): PTHR	0,584	0,574	0,650	0,592	0,494									
Solyc02g078285	Transcription initiation factor TFIID subunit 13 (AHRD V3.3 *** A0A0B0MGR7_GOSAR)		P:GO:0006366; F:G(	P:transcription by RNA polymerase II; F:protein heterodimerizati	IPR003195 (PFAM): IPR009072 (G3D	1,643	1,034	0,831	0,489	0,564									
Solyc02g078290	DNA ligase-like protein (AHRD V3.3 *** AT2G33793.2)		P:GO:0007131; F:G(	P:reciprocal meiotic recombination; F:ligase activity	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,139	1,179	0,000	0,000	0,000									
Solyc02g078300	Transcription initiation factor TFIID subunit 13 (AHRD V3.3 *** A0A0B0MGR7_GOSAR)		P:GO:0006366; F:G(	P:transcription by RNA polymerase II; F:protein heterodimerizati	IPR003195 (PFAM): IPR009072 (G3D	6,404	6,796	6,016	4,979	5,789									
Solyc02g078320	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G19310.1)		F:GO:0046872	F:metal ion binding	IPR001841 (SMART): IPR018957 (PF	10,026	10,858	14,083	10,490	11,836									
Solyc02g078330	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RW07_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM): IPR011990 ((	5,545	5,117	4,569	4,409	3,880									
Solyc02g078340	SolycHsfB5	HSF-23	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (SMAF HSF	0,117	0,140	0,099	0,269	0,351									
Solyc02g078350	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H2W0_POPTR)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFA	4,130	3,686	3,522	3,659	4,001									
Solyc02g078360	Glutaredoxin (AHRD V3.3 *** A0A124SB49_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR004480 (TIGRFAM): G3DSA:3.40.:	58,442	60,199	81,918	83,209	74,953									
Solyc02g078370	Anther-specific protein TA-29 (AHRD V3.3 *** TA29_TOBAC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,127	0,538	20,237	26,996	12,278									
Solyc02g078380	Stem-specific protein TSJT1 (AHRD V3.3 *** A0A151T7D1_CAJCA)				IPR024286 (PFAM): IPR024286 (PF	104,102	111,041	28,040	30,161	40,285									
Solyc02g078390	DNA mismatch repair protein MutS2 (AHRD V3.3 *** G7ZZ93_MEDTR)		F:GO:0004519; F:G(	F:endonuclease act EC:3.6.1.3; EC:3.6.1. Adenosinetriphospha	IPR000432 (SMART): IPR007696 (SM	5,405	7,913	5,469	7,941	7,130									

Solyc02g078400	allantoinase (AHRD V3.3 *** AT4G04955.1)		P:GO:0000256; F:G(	P:allantoin catabolic EC:3.5.2.5	Allantoinase	IPR006680 (PFAM): G3DSA:3.20.20.1	13,840	21,198	813,169	880,823	639,179									
Solyc02g078410	Thioesterase family protein (AHRD V3.3 *** D7KCZ7_ARALL)		C:GO:0005777; C:G(	C:peroxisome; C:cytosol; P:phylloquinone biosynthetic process;		IPR003736 (TIGRFAM): IPR006683 (F	7,879	6,900	28,529	27,780	21,711									
Solyc02g078420	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast		IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,025	0,050	0,000									
Solyc02g078440	transcription factor-like protein (AHRD V3.3 *** AT4G17020.3)		C:GO:0000439; F:G(	C:transcription factor TFIIH core complex; F:ATPase activator a		PF18307 (PFAM): IPR004598 (PFAM)	19,254	19,547	17,667	15,300	16,294									
Solyc02g078450	Tetraspanin family protein (AHRD V3.3 *** AT2G20740.1)		C:GO:0016021	C:integral component of membrane		IPR000301 (PRINTS): IPR018499 (PF	0,719	0,931	0,146	0,459	0,474									
Solyc02g078460	abscisic acid-insensitive RING protein 4-like		F:GO:0016874	F:ligase activity		IPR001841 (SMART): IPR013083 (G3	24,275	18,696	66,317	51,072	48,203			-0,463	0,011				down	
Solyc02g078470	Tetratricopeptide repeat-like superfamily protein, putative isoform 1 (AHRD V3.3 *** A0A061GFU9_THECC)		F:GO:0005515	F:protein binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	19,537	18,307	65,199	65,918	59,523									
Solyc02g078480	CBS domain-containing protein (AHRD V3.3 *** A0A061GEK1_THECC)					IPR000644 (PFAM): PTHR13780:SF5	26,412	105,692	16,277	16,378	17,865	2,026	0,000					up		
Solyc02g078490	TSA: Wollemia nobilis Ref_Wollemi_Transcript_5456_2539 transcribed RNA sequence (AHRD V3.3 --* A0A(		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:mRNA processing; P:RNA splicing		mobidb-lite (MOBIDB_LITE): mobidb-lit	5,987	5,217	8,228	6,708	7,184									
Solyc02g078500	Stem-specific protein TSJT1, putative (AHRD V3.3 *** B9RZ68_RICCO)					IPR024286 (SMART): IPR024286 (PF.	1,945	1,896	0,672	0,768	1,036									
Solyc02g078510	Acylsugar acyltransferase 3 (AHRD V3.3 *-* A0A0B5JC18_SOLHA)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR003480 (PFAM): IPR023213 (G3D	0,797	0,516	0,090	0,195	0,234									
Solyc02g078515	Mediator of RNA polymerase II transcription subunit 16-like protein (AHRD V3.3 *-* A0A0U3CDG5_REHGL)		P:GO:0006355; C:G(	P:regulation of transcription, DNA-templated; C:mediator comple		IPR038836 (PANTHER)	25,130	23,222	35,024	30,725	31,561									
Solyc02g078520	Mediator of RNA polymerase II transcription subunit 16-like protein (AHRD V3.3 *** A0A0U3CDG5_REHGL)		P:GO:0006355; C:G(	P:regulation of transcription, DNA-templated; C:mediator comple		mobidb-lite (MOBIDB_LITE): mobidb-lit	54,634	43,407	75,573	72,124	71,114									
Solyc02g078530	Kinase family protein (AHRD V3.3 *** B9IG83_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): PIRSF000654 (	5,245	10,707	1,709	1,786	2,584									
Solyc02g078540	Clathrin light chain (AHRD V3.3 *** A0A103XF03_CYNCS)		F:GO:0005198; P:G(	F:structural molecule activity; P:intracellular protein transport; P		IPR000996 (PFAM): mobidb-lite (MOB	170,363	197,953	192,335	181,934	179,014									
Solyc02g078550	RNA polymerase II C-terminal domain phosphatase-like protein (AHRD V3.3 *** A0A0K9PYY1_ZOSMR)		F:GO:0008420; P:G(	F:RNA polymerase EC:3.1.3.16	Protein-serine/threor	IPR014720 (SMART): IPR004274 (SM	38,395	31,312	50,202	56,420	52,460									
Solyc02g078560	Wings apart-like protein like (AHRD V3.3 *** A0A0B2PLL7_GLYSO)		P:GO:0045132; P:G(	P:meiotic chromosome segregation; P:regulation of chromosom		IPR022771 (PFAM): IPR011989 (G3D	52,857	40,313	58,853	55,179	50,694									
Solyc02g078570	Epoxide hydrolase (AHRD V3.3 *** I3SWK6_MEDTR)		F:GO:0003824	F:catalytic activity		IPR000639 (PRINTS): IPR000073 (PF	253,647	236,248	33,920	32,186	29,464									
Solyc02g078580	RNA polymerase-associated protein RTF1 like (AHRD V3.3 *** A0A0B2PDF2_GLYSO)		F:GO:0003677; P:G(	F:DNA binding; P:transcription elongation from RNA polymerase		IPR004343 (SMART): IPR004343 (PF.	29,369	30,057	25,808	20,477	23,450									
Solyc02g078590	Alpha 1,4-glycosyltransferase family protein, putative (AHRD V3.3 *** A0A061GEM3_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans		IPR007652 (PFAM): IPR007577 (PFA	26,880	16,817	7,616	6,982	7,766	-0,647	0,014					down		
Solyc02g078600	polyol monosaccharide transporter 1	PMT1	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport		IPR003663 (PRINTS): IPR005828 (PF	5,792	11,386	0,292	0,174	0,165	0,999	0,018					up		
Solyc02g078610	Splicing factor 3B subunit 2 (AHRD V3.3 *** A0A151SEI3_CAJCA)		C:GO:0005634	C:nucleus		IPR006568 (SMART): IPR007180 (PF.	87,149	83,542	93,663	77,293	82,049									
Solyc02g078620	Dof zinc finger protein (AHRD V3.3 *** W9RD26_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated		IPR003851 (PFAM: Dof	5,817	2,240	0,119	0,025	0,000									
Solyc02g078630	LOW QUALITY:Fiber protein Fb34 (AHRD V3.3 *** A0A0A0L071_CUCSA)		C:GO:0016021	C:integral component of membrane		IPR009606 (PFAM): PTHR31769:SF1(	12,312	9,119	9,327	8,891	8,048									
Solyc02g078640	Protein MOR1 (AHRD V3.3 *** A0A0B2P031_GLYSO)		C:GO:0000776; C:G(	C:kinetochore; C:spindle pole; C:centrosome; P:spindle organiz		IPR034085 (SMART): IPR011989 (G3	184,930	145,068	105,511	107,382	107,716									
Solyc02g078650	Polyphenol oxidase (AHRD V3.3 *** A0A118JXA6_CYNCS)		F:GO:0004097; P:G(	F:catechol oxidase EC:1.1.3; EC:1.1.3.1	Acting on diphenols a	IPR002227 (PRINTS): IPR008922 (G3	0,021	0,080	0,000	0,196	0,046									
Solyc02g078660	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *-* AT1G61080.6)		C:GO:0009707; C:G(	C:chloroplast outer membrane; C:integral component of membra		mobidb-lite (MOBIDB_LITE): mobidb-lit	6,188	8,548	1,501	2,658	2,166									
Solyc02g078665	Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 --* A0A072UP10_MEDTR)		C:GO:0009707; C:G(	C:chloroplast outer membrane; C:integral component of membra		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,588	0,706	0,000	0,146	0,163									
Solyc02g078670	COP1-interacting protein, putative (AHRD V3.3 *** A0A072VAF6_MEDTR)					mobidb-lite (MOBIDB_LITE): mobidb-lit	178,360	90,846	44,569	34,562	53,198	-0,945	0,001					down		
Solyc02g078690	Carboxypeptidase (AHRD V3.3 *** K4B993_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): G3DSA:3.40.5(	0,223	1,113	0,072	0,022	0,000									
Solyc02g078700	LisH and RanBPM domains containing protein (AHRD V3.3 *** AT1G61150.9)					IPR013144 (SMART): IPR006595 (SM	1,666	0,907	0,398	0,298	0,351									
Solyc02g078720	Multidrug resistance 3 (AHRD V3.3 *** A0A0B0MAA3_GOSAR)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,992	0,710	0,291	0,240	0,328									
Solyc02g078740	Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein (AHRD V3.3 --* AT1G63010.7)						0,281	0,139	0,171	0,097	0,072									
Solyc02g078750	G-type lectin S-receptor-like Serine/Threonine-kinase (AHRD V3.3 *** AT4G03230.4)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR001480 (SMART): IPR000719 (SM	4,708	6,818	2,283	2,656	3,265									
Solyc02g078760	LOW QUALITY:BEST plant protein match is: (TAIR:plant.1) protein, putative (AHRD V3.3 *** G7INX9_MEDTR)					mobidb-lite (MOBIDB_LITE): mobidb-lit	8,195	14,455	0,287	0,148	0,189	0,848	0,022					up		
Solyc02g078780	Kinase (AHRD V3.3 *** A0A0K9P5P6_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		IPR003591 (SMART): IPR032675 (G3	19,687	18,149	8,077	9,734	8,606									
Solyc02g078790	Transcription factor jumonji domain protein (AHRD V3.3 *** G7I8M9_MEDTR)		C:GO:0000785; F:G(	C:chromatin; F:transcription regulatory region sequence-specifi		IPR003347 (SMART): IPR003347 (PF	49,058	45,312	63,427	65,503	60,290									
Solyc02g078800	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *-* K4B9A4_SOLLC)		F:GO:0005515	F:protein binding		IPR020472 (PRINTS): IPR001680 (SM	14,756	9,384	11,542	12,207	13,523									
Solyc02g078805	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *** K4B9A4_SOLLC)		C:GO:0005874; F:G(	C:microtubule; F:microtubule binding; C:katanin complex; P:micr		IPR028021 (PFAM): mobidb-lite (MOB	26,070	21,354	25,051	25,081	23,804									
Solyc02g078810	Bromodomain 4, putative (AHRD V3.3 *** A0A061GG17_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding		IPR001005 (SMAF MYB_related	3,716	9,176	6,630	6,178	6,657	1,327	0,000					up		
Solyc02g078820	lysine ketoglutarate reductase trans-splicing-like protein (DUF707) (AHRD V3.3 *** AT1G61240.6)		C:GO:0016021	C:integral component of membrane		IPR007877 (PFAM): mobidb-lite (MOB	25,811	35,262	86,058	89,742	81,382									
Solyc02g078830	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G65030.1)		F:GO:0005515	F:protein binding		IPR020472 (PRINTS): IPR001680 (SM	36,273	33,587	28,333	24,382	25,516									
Solyc02g078840	Secretory carrier membrane protein (AHRD V3.3 *** B3TLU6_ELAGV)		P:GO:0015031; C:G(	P:protein transport; C:integral component of membrane		IPR007273 (PFAM): mobidb-lite (MOB	21,772	24,929	50,638	56,089	46,791									
Solyc02g078850	glycine-rich protein (AHRD V3.3 *** AT4G21620.1)					PTHR34789 (PANTHER): PTHR34789	0,769	1,130	0,100	0,050	0,046									
Solyc02g078860	3(2),5-bisphosphate nucleotidase HAL2 (AHRD V3.3 *** A0A118JXE0_CYNCS)		P:GO:0006790; F:G(	P:sulfur compound r EC:3.1.3.7; EC:3.1.3	3'(2'),5'-bisphosphate	IPR006239 (TIGRFAM): G3DSA:3.30.(	11,427	12,647	11,440	9,905	14,968									
Solyc02g078880	RNA helicase DEAD8	DEAD8	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding		IPR014001 (SMART): IPR011545 (PF	43,035	43,656	41,594	37,851	39,640									
Solyc02g078890	LOW QUALITY:F-box associated ubiquitination effector family protein (AHRD V3.3 --* AT3G23685.1)					mobidb-lite (MOBIDB_LITE): PTHR36(	3,938	13,485	1,883	1,259	1,547	1,800	0,000					up		
Solyc02g078900	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial (AHRD V3.3 *** A0A199VZH3_AN		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PR00368 (PRINTS): G3DSA:3.50.50.1	46,261	73,122	81,849	91,345	81,222									
Solyc02g078910	endonuclease AM238701	tbn1	F:GO:0003676; F:G(	F:nucleic acid binding; F:endonuclease activity; P:DNA cataboli		IPR003154 (PFAM): IPR008947 (G3D	0,825	1,124	2,159	3,702	1,995									
Solyc02g078920	Nuclease S1 (AHRD V3.3 *** A0A0B0P7M2_GOSAR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:endonuclease activity; P:DNA cataboli		IPR008947 (G3DSA:1.10.575.GENE3	19,543	17,256	15,160	16,852	17,324									
Solyc02g078930	Late embryogenesis abundant-related protein (AHRD V3.3 *** Q9FZ41_ARATH)					IPR009646 (PFAM): PTHR31656:SF5	0,120	0,018	0,109	0,123	0,047									
Solyc02g078940	Oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 *** A8MRW5_ARATH)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR020843 (SMART): IPR013154 (PF.	151,363	122,314	611,999	511,131	562,809									
Solyc02g078950	Beta-galactosidase (AHRD V3.3 *** M1C1C4_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR001944 (PRINTS): IPR008979 (G3	24,793	24,807	3,555	2,995	4,362									
Solyc02g078960	Organic solute transporter ostalpha protein (AHRD V3.3 *** G7ILE3_MEDTR)		C:GO:0016021	C:integral component of membrane		IPR005178 (PFAM): PTHR23423:SF1	16,245	16,711	16,438	18,233	17,621									
Solyc02g078970	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G10580.1)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:protein binding; C:catalytic		IPR020472 (PRINTS): IPR001680 (SM	49,608	51,126	56,132	52,241	53,269									
Solyc02g078980	TatD related DNase (AHRD V3.3 *** AT5G17570.2)		F:GO:0016788	F:hydrolase activity, acting on ester bonds		IPR001130 (PFAM): IPR001130 (PIRS	10,840	10,674	16,723	21,561	16,720									
Solyc02g078990	thiosulfate sulfurtransferase	tst	F:GO:0016740	F:transferase activity		IPR001763 (SMART): IPR001763 (PF	44,422	41,398	61,947	58,131	59,756									
Solyc02g079000	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** G7LB10_MEDTR)		F:GO:0004222; F:G(	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): IPR000642 (PF	25,504	25,109	36,907	38,286	37,515									
Solyc02g079010	Cotton fiber expressed protein (AHRD V3.3 *** A0A109Y892_GOSBA)		C:GO:0016021	C:integral component of membrane		IPR025520 (PFAM): IPR008480 (PFA	12,126	15,068	21,971	38,146	22,021					0,800	0,000			up
Solyc02g079020	B3 domain-containing protein (AHRD V3.3 *-* W9QZ54_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding		IPR003340 (SMAF B3	26,425	26,227	16,922	13,927	18,822									
Solyc02g079025	B3 domain-containing protein (AHRD V3.3 *-* A0A0B2PLR3_GLYSO)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; F:zinc ion binding		mobidb-lite (MOBIDB_LITE): PTHR233	10,010	9,213	6,023	4,930	6,789									
Solyc02g079030	Sphingosine kinase, putative (AHRD V3.3 *** B9SFA5_RICCO)		F:GO:0003951	F:NAD+ kinase acti EC:2.7.1.23	NAD(+) kinase	IPR001206 (SMART): IPR001206 (PF	6,817	10,829	8,115	14,125	11,211					0,799	0,000			up
Solyc02g079040	Calmodulin-binding protein (AHRD V3.3 *** A0A072V4D6_MEDTR)		F:GO:0005516	F:calmodulin binding		IPR012416 (PFAM): mobidb-lite (MOB	224,053	274,983	54,087	85,752	108,734			1,004	0,001	0,665	0,037		up	up
Solyc02g079050	Anaphase-promoting complex subunit 4 (AHRD V3.3 *** A0A151T237_CAJCA)		F:GO:0005515; C:G(	F:protein binding; C:anaphase-promoting complex; P:regulation		IPR001680 (SMART): IPR024977 (PF	13,229	10,861	11,732	10,773	10,697									
Solyc02g079060	Eukaryotic translation initiation factor 3 subunit J (AHRD V3.3 *** K4B9D0_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in		IPR013906 (PFAM): IPR023194 (G3D	129,400	141,335	178,431	174,320	156,856									
Solyc02g079070	Myosin-related family protein (AHRD V3.3 *-* B9H5P2_POPTR)		F:GO:0005515	F:protein binding		IPR000048 (SMART): IPR000048 (PF	0,042	0,021	0,000	0,022	0,024									
Solyc02g079080	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,510	0,472	0,168	0,322	0,234									
Solyc02g079090	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding		IPR001810 (SMART): IPR032675 (G3	1,820	1,557	3,458	4,238	2,475									
Solyc02g079095	Alcohol dehydrogenase 1 (AHRD V3.3 --* ADH1_MAIZE)						0,217	0,439	0,462	0,792	0,524									
Solyc02g079100	riboflavin kinase/FMN hydrolase (AHRD V3.3 *** AT4G21470.1)		F:GO:0008531; P:G(	F:riboflavin kinase a EC:2.7.1.26	Riboflavin kinase	IPR015865 (SMART): PF13419 (PFAM	48,146	44,012	93,955	93,466	88,422									
Solyc02g079110	WD40 repeat-containing protein (AHRD V3.3 *** A0A118JSZ2_CYNCS)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR015943 (G3	7,775	12,288	6,089	5,131	6,586									
Solyc02g079130	Protein translocase subunit SecA 1 (AHRD V3.3 *** A0A199UM53_ANACO)					IPR004027 (PFAM): PTHR36750 (PAN	11,203	13,327	14,855	14,615	14,375									
Solyc02g079140	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (AHRD V3.3 *-* A0A1D1ZDK4_9ARAE)		F:GO:0005515	F:protein binding		IPR003877 (SMART): IPR003877 (PF	3,823	2,786	3,483	5,512	4,619					0,669	0,038			up
Solyc02g079150	F-box family protein (AHRD V3.3 *** B9H220_POPTR)		F:GO:0005515	F:protein binding		PTHR34049 (PANTHER): PTHR34049	0,121	0,139	0,044	0,048	0,072									
Solyc02g079160	Transmembrane protein, putative (AHRD V3.3 *** A0A072V590_MEDTR)		C:GO:0016021	C:integral component of membrane		PTHR37746 (PANTHER)	0,774	0,415	0,973	1,312	0,375									
Solyc02g079170	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial (AHRD V3.3 *** NDB2_ARATH)		F:GO:0005509; F:G(	F:calcium ion binding; F:oxidoreductase activity; P:oxidation-rec		PR00368 (PRINTS): IPR002048 (SMA	6,518	22,455	44,141	63,902	43,575	1,807	0,000			0,536	0,000	up		up
Solyc02g079180	LOW QUALITY:SolycHsf2	HSF-25	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR000232 (PRIN' HSF	0,040	0,197	0,050	0,072	0,047									
Solyc02g079190	TRANSPORT INHIBITOR RESPONSE 1 protein, putative (AHRD V3.3 *** B9SFB7_RICCO)		F:GO:0005515	F:protein binding		IPR001810 (SMART): IPR006553 (SM	64,251	42,465	13,899	19,412	17,709									
Solyc02g079210	DAG protein (AHRD V3.3 *** B6SJX7_MAIZE)		P:GO:0016554	P:cytidine to uridine editing		mobidb-lite (MOBIDB_LITE): mobidb-lit	42,778	39,608	61,393	51,315	49,832									
Solyc02g079220	Sugar transporter protein 1	STP1	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport		IPR003663 (PRINTS): IPR005828 (PF	2,385	10,082	0,527	0,448	0,927	2,103	0,000					up		
Solyc02g079230	Vesicle-associated 4-2-like protein (AHRD V3.3 *** A0A0B0MUH3_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane		IPR000535 (PFAM): IPR013783 (G3D	13,607	18,826	18,341	19,495	18,788									
Solyc02g079240	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 --* AT4G10265.1)					IPR022251 (PFAM): mobidb-lite (MOB	0,019	0,311	0,049	0,072	0,046									
Solyc02g079250	3'(2'),5'-bisphosphate nucleotidase-like protein (AHRD V3.3 *** Q682R6_ARATH)		P:GO:0046854	P:phosphatidylinositol phosphorylation		G3DSA:3.40.190.80 (GENE3D): IPR0(	7,125	9,528	8,925	8,818	9,701									
Solyc02g079255	Metallothionein-like protein 2 (AHRD V3.3 --* MT2_TRIRP)						0,000	0,037	0,000	0,000	0,000									
Solyc02g079260	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YG02_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding		IPR002885 (TIGRFAM): IPR002885 (F	3,475	2,710	1,948	1,956	2,022									
Solyc02g079270	3'(2'),5'-bisphosphate nucleotidase-like protein (AHRD V3.3 *-* Q682R6_ARATH)		C:GO:0005737; F:G(	C:cytoplasm; F:3'(2 EC:3.1.3.7; EC:3.1.3	3'(2'),5'-bisphosphate	G3DSA:3.30.540.10 (GENE3D): PTHF	0,574	0,839	0,437	0,456	0,751									
Solyc02g079273	3'(2'),5'-bisphosphate nucleotidase-like protein (AHRD V3.3 *** Q682R6_ARATH)		P:GO:0046854	P:phosphatidylinositol phosphorylation		G3DSA:3.40.190.80 (GENE3D): IPR0(	1,619	1,701	1,711	1,756	2,045									
Solyc02g079277	Inositol monophosphatase family protein (AHRD V3.3 --* AT4G05090.2)		C:GO:0005737; F:G(	C:cytoplasm; F:3'(2 EC:3.1.3.7; EC:3.1.3	3'(2'),5'-bisphosphate	nucleotidase; Nucleotidase	0,136	0,179	0,025	0,174	0,141									
Solyc02g079280	MYB transcription factor (AHRD V3.3 *** A0A0U3IU11_MESCR)	R2R3MYB102	F:GO:0003677	F:DNA binding		IPR001005 (SMAF MYB	0,100	1,176	0,197	0,125	0,188									
Solyc02g079290	protein SELF PRUNING 2G					IPR036610 (G3DSA:3.90.280.GENE3	6,661	8,670	4,034	4,204	3,153									
Solyc02g079300	Transcription factor jumonji (JmjC) domain protein (AHRD V3.3 *** A0A072V3U7_MEDTR)		C:GO:0000785; F:G(	C:chromatin; F:transcription regulatory region sequence-specifi		IPR003347 (SMART): IPR003347 (PF	21,505	21,494	21,541	20,716	21,815									
Solyc02g079310	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con		IPR002259 (PFAM): PTHR10332:SF3	0,019	0,039	0,000	0,000	0,000									
Solyc02g079320	Anthocyanidin reductase ((2S)-flavan-3-ol-forming) (AHRD V3.3 --* ANRCS_VITVI)		C:GO:0016021	C:integral component of membrane			2,049	1,967	0,472	0,271	0,469									
Solyc02g079330	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con		IPR002259 (PIRSF): IPR002259 (PFA	0,102	0,158	0,047	0,050	0,000									
Solyc02g079340	OBP3-responsive protein 1 (AHRD V3.3 --* AT5G53450.3)		C:GO:0016021	C:integral component of membrane			1,862	1,743	0,392	0,291	0,329									
Solyc02g079350	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con		IPR002259 (PFAM): IPR002259 (PIRS	0,156	0,098	0,050	0,022	0,116									
Solyc02g079360	Octicosapeptide/Phox/Bem1p family protein (AHRD V3.3 *** AT4G05150.1)		F:GO:0005515	F:protein binding		IPR000270 (SMART): G3DSA:3.10.20	3,846	3,969	0,579	0,460	0,538									
Solyc02g079380	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2R2D6_GLYSO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding		IPR011990 (G3DSA:1.25.40.GENE3D	3,930	4,762	5,124	4,821	5,032									
Solyc02g079390	Plant cadmium resistance 8-like protein (AHRD V3.3 *** A0A0B0NN69_GOSAR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		IPR006461 (PANTHER): IPR006461 (I	2,729	3,137	0,894	1,238	1,126									
Solyc02g079400	Nitric oxide synthase-interacting protein homolog (AHRD V3.3 *** K4B9G4_SOLLC)		F:GO:0061630	F:ubiquitin protein ligase activity		IPR001841 (SMART): IPR027799 (PF	39,299	42,350	47,782	41,833	43,470									
Solyc02g079410	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)		C:GO:0005829; C:G(	C:cytosol; C:plasma membrane		IPR006015 (PRINTS): IPR006016 (PF	20,505	21,734	28,624	27,855	27,311									
Solyc02g079415	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G26600.1)		F:GO:0003723; F:G(	F:RNA binding; P:rRNA processing; F:S-adenosylmethionine-de		IPR023267 (PRINTS): IPR023273 (PF	15,086	19,054	5,726	4,932	5,933									
Solyc02g079430	Zinc finger, B-box (AHRD V3.3 *-* A0A103Y479_CYNCS)	BBX29	F:GO:0008270	F:zinc ion binding		IPR000315 (SMART): IPR000315 (PF	1,866	1,271	0,520	0,286	0,283									
Solyc02g079440	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20860.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI		G3DSA:3.40.462.20 (GENE3D): IPR0	0,232	0,525	0,091	0,123	0,070									
Solyc02g079450	FAD-binding Berberine family protein (AHRD V3.3 *** AT5G44360.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI		G3DSA:3.30.465.50 (GENE3D): IPR0	0,730	0,310	0,000	0,000	0,000									
Solyc02g079460	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20860.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI		IPR006094 (PFAM): IPR016167 (G3D	0,019	0,111	0,000	0,098	0,023									
Solyc02g079480	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20860.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI		IPR016167 (G3DSA:3.30.43.GENE3D	0,000	0,081	0,000	0,000	0,000									
Solyc02g079490	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061G8N7_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3	0,042	0,039	2,933	5,302	3,264					0,856	0,025			up
Solyc02g079500	Peroxidase (AHRD V1 **** Q50LG4_TOBAC)%3B contains Interpro domain(s) IPR019793 Peroxidases hea		F:GO:0004601; P:G(	F:peroxidase activi EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	650,490	552,472	17,812	9,676	18,482					-0,878	0,000			down
Solyc02g079510	Peroxidase (AHRD V1 **** Q50LG4_TOBAC)%3B contains Interpro domain(s) IPR019793 Peroxidases hea		F:GO:0004601; P:G(	F:peroxidase activi EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	56,157	97,261	3,359	2,639	4,398	0,822	0,010					up		
Solyc02g079520	Calcium-binding EF-hand protein (AHRD V3.3 *** G7ILC0_MEDTR)		F:GO:0005509	F:calcium ion binding		IPR002048 (PFAM): G3DSA:1.10.238	2,699	4,697	0,191	0,098	0,164									
Solyc02g079530	GTPase Der (DUF707) (AHRD V3.3 --* AT4G12840.3)						0,081	0,307	0,025	0,050	0,024									
Solyc02g079533	Serine/threonine-protein kinase (AHRD V3.3 *** E5D7E5_TOBAC)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,660	2,993	0,440	0,405	0,636	2,199	0,007					up		
Solyc02g079540	Serine/threonine-protein kinase (AHRD V3.3 *** E5D7E5_TOBAC)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	16,668	33,032	2,196	2,759	5,658			1,360	0,004				up	
Solyc02g079550	Serine/threonine-protein kinase (AHRD V3.3 *** B9H1U5_POPTR)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR003609 (SMART): IPR001480 (SM	0,472	2,549	0,953	1,374	2,309	2,448	0,006	1,277	0,005			up	up	
Solyc02g079570	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IWF8_SOLCH)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	11,722	11,084	1,585	1,564	2,930									
Solyc02g079580	Serine/threonine-protein kinase (AHRD V3.3 *** M5WPV3_PRUPE)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	2,738	3,801	1,897	2,885	3,094									
Solyc02g079590	Serine/threonine-protein kinase (AHRD V3.3 *** M1A226_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	84,574	134,901	33,322	58,729	52,735			0,660	0,003	0,819	0,000		up	up
Solyc02g079600	Receptor-like protein kinase (AHRD V3.3 *** A0A061EYK6_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): G3DSA:1.10.51	0,733	3,711	0,866	1,033	1,826	2,351	0,000					up		
Solyc02g079630	Serine/threonine-protein kinase (AHRD V3.3 *** A0A124SDG2_CYNCS)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR001480 (SM	0,078	0,140	0,000	0,074	0,070									
Solyc02g079640	Serine/threonine-protein kinase (AHRD V3.3 *** M1B363_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR003609 (SMART): IPR001480 (SM	18,660	15,008	17,904	18,811	20,583									
Solyc02g079700	Serine/threonine-protein kinase (AHRD V3.3 *-* M1B352_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): mobic	0,582	1,284	1,039	1,101	1,361									
Solyc02g079710	Serine/threonine-protein kinase (AHRD V3.3 *** K4B9J2_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR003609 (SMART): IPR000719 (SM	1,921	3,474	2,629	3,063	5,754			1,125	0,003				up	
Solyc02g079720	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding		IPR002048 (SMART): IPR002048 (PF	0,037	0,000	0,051	0,073	0,095									
Solyc02g079730	Thioredoxin family protein, putative (AHRD V3.3 *** G7LIP5_MEDTR)		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:chloroplast orga		G3DSA:3.40.30.10 (GENE3D): mobidb	6,591	9,712	14,743	14,552	14,548									
Solyc02g079740	U-box domain-containing family protein (AHRD V3.3 *** B9HYS7_POPTR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot(		IPR003613 (SMART): IPR013083 (G3	10,631	10,797	15,065	13,013	12,429									
Solyc02g079750	Quinone reductase family protein (AHRD V3.3 *** AT4G27270.1)		F:GO:0003955; F:G(	F:NAD(P)H dehydrc EC:1.6.5.2	NAD(P)H dehydroger	IPR005025 (PFAM): IPR029039 (G3D	38,214	37,808	184,545	251,218	154,327									
Solyc02g079760	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G61660.7)		F:GO:0046983	F:protein dimerization activity		IPR036638 (G3DS bHLH	5,854	8,719	7,166	6,652	6,500									
Solyc02g079770	DAG protein (AHRD V3.3 *** B6TYI4_MAIZE)		P:GO:0016554	P:cytidine to uridine editing		mobidb-lite (MOBIDB_LITE): IPR0392(	33,836	47,840	79,369	81,989	87,403	0,527	0,030					up		
Solyc02g079780	LOW QUALITY:DNA-binding bromodomain-containing protein (AHRD V3.3 --* AT1G58025.2)		F:GO:0070300	F:phosphatidic acid binding		mobidb-lite (MOBIDB_LITE): IPR0389(	35,418	23,661	17,838	30,278	28,786			0,685	0,004	0,762	0,000		up	up
Solyc02g079790	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT3G07470.3)		C:GO:0016021	C:integral component of membrane		IPR036758 (G3DSA:2.30.240.GENE3	10,502	7,316	0,360	0,289	0,679									
Solyc02g079810	bHLH transcription factor 080		F:GO:0046983	F:protein dimerization activity		PTHR31945:SF20_bHLH	0,159	0,153	0,000	0,000	0,000									
Solyc02g079815	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT5G57150.5)		F:GO:0046983	F:protein dimerization activity		IPR036638 (G3DSA:4.10.280.GENE3	0,383	0,309	0,261	0,338	0,352									
Solyc02g079830	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061GG29_THECC)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (PFA	7,317	8,409	10,327	9,485	9,391									
Solyc02g079840	terpene synthase		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity		IPR001906 (PFAM): IPR036965 (G3D	0,165	0,060	0,022	0,047	0,000									
Solyc02g079860	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** U5FHY7_POPTR)		F:GO:0005515	F:protein binding		IPR000210 (SMART): G3DSA:3.30.71	0,391	0,257	0,754	1,046	0,566									
Solyc02g079870	multimeric translocon complex in the outer envelope membrane 132 (AHRD V3.3 --* AT2G16640.3)						1,114	1,256	0,769	0,627	0,467									
Solyc02g079880	Eukaryotic translation initiation factor-related family protein (AHRD V3.3 *** B9HYT9_POPTR)		F:GO:0003743	F:translation initiation factor activity		mobidb-lite (MOBIDB_LITE): mobidb-lit	126,442	97,316	151,644	153,359	146,611									
Solyc02g079890	Terpene synthase (AHRD V3.3 *** G5CV49_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity		IPR001906 (PFAM): IPR008949 (G3D	0,000	0,000	0,025	0,067	0,000									
Solyc02g079920	C2H2-like zinc finger protein (AHRD V3.3 *** G7JF39_MEDTR)		F:GO:0003676	F:nucleic acid binding		G3DSA:3.90.228.10 (GENE3D): PTHF	0,499	0,879	5,942	8,371	5,585									
Solyc02g079930	phosphosulfolactate synthase	psr	F:GO:0003824	F:catalytic activity		IPR003830 (PFAM): IPR013785 (G3D	182,778	112,765	211,496	187,203	195,725	-0,668	0,049					down		

Solyc02g079940	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)		C:GO:0016021	C:integral component of membrane	IPR009606 (PFAM): PTHR31769:SF1	0,058	0,508	0,025	0,022	0,188									
Solyc02g079950	photosystem II oxygen-evolving complex protein 3	psbq	F:GO:0005509: C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple	IPR008797 (PFAM): G3DSA:1.20.120	108,709	236,419	81,907	94,357	171,304	1,149	0,000	1,061	0,000			up	up	
Solyc02g079960	Thioredoxin (AHRD V3.3 *** A0A061F6X0_THECC)		P:GO:0006662: F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu	G3DSA:3.40.30.10 (GENE3D): IPR01:	66,988	76,354	57,908	61,276	74,767									
Solyc02g079970	bHLH transcription factor 014		F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DS bHLH	192,642	205,468	130,520	114,686	143,845									
Solyc02g079980	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT1G61740.1)		C:GO:0016021	C:integral component of membrane	IPR002781 (PFAM): PTHR14255:SF3	0,787	0,962	0,349	0,356	0,234									
Solyc02g079990	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *** G7KDB1_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR002902 (PF	12,530	25,204	2,941	2,503	4,999	1,035	0,001					up		
Solyc02g080010	Receptor-like protein kinase (AHRD V3.3 *** C6ZRS0_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR038408 (G3	2,552	7,548	1,956	1,321	2,529	1,589	0,000					up		
Solyc02g080020	Receptor-like kinase (AHRD V3.3 *-* G8A106_MEDTR)		F:GO:0004672: P:G(	F:protein kinase activity; P:protein phosphorylation	G3DSA:1.10.510.10 (GENE3D): IPR0(	0,000	0,021	0,000	0,000	0,000									
Solyc02g080030	Receptor-like protein kinase (AHRD V3.3 *** C6F1T6_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	0,000	0,247	0,000	0,075	0,000									
Solyc02g080040	Receptor-like kinase (AHRD V3.3 *** G8A106_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	10,471	32,636	8,622	23,233	24,762	1,661	0,007	1,521	0,000	1,434	0,000	up	up	up
Solyc02g080050	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *-* A0A072VRC1_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR002902 (PFAM): IPR038408 (G3D	3,463	9,148	3,019	7,038	8,588			1,503	0,000	1,222	0,000		up	up
Solyc02g080060	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *** A0A072VRC1_MEDTR)		F:GO:0004674: C:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	IPR002902 (PFAM): IPR038408 (G3D	0,000	0,061	0,197	1,565	0,686					2,940	0,000			up
Solyc02g080070	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *** G7KDB1_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR038408 (G3	13,601	25,567	36,061	42,334	45,343									
Solyc02g080080	Receptor-like protein kinase (AHRD V3.3 *** C6ZRS0_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR002902 (PF	12,421	24,207	3,825	4,008	7,342			0,940	0,041				up	
Solyc02g080090	Receptor-like kinase (AHRD V3.3 *** G8A106_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	0,000	0,043	0,050	0,000	0,000									
Solyc02g080100	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0009506: C:G(	C:plasmodesma; C:integral component of membrane; C:anchore	IPR004864 (PFAM): PTHR31415 (PAI	0,080	0,060	0,025	0,049	0,023									
Solyc02g080110	Transmembrane protein, putative (AHRD V3.3 *** A0A072VQK9_MEDTR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	8,012	7,026	20,389	28,745	20,457					0,497	0,003			up
Solyc02g080120	Gibberellin 2-beta- dioxygenase 7		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR027443 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc02g080130	DnaJ (AHRD V3.3 *** B6TJ19_MAIZE)		C:GO:0005789: P:G(	C:endoplasmic reticulum membrane; P:protein folding	IPR001623 (PRINTS): IPR001623 (SM	81,551	73,978	131,271	121,945	106,385									
Solyc02g080140	Cysteine-rich PDZ-binding (AHRD V3.3 *** A0A0B0MIJ3_GOSAR)				IPR019367 (PFAM): IPR019367 (PAN	19,880	19,228	26,793	31,230	29,559									
Solyc02g080150	CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 1 (AHRD V3.3 *-* A0A061DL35_THECC)				mobidb-lite (MOBIDB_LITE): PTHR343	3,766	4,881	4,903	4,914	4,642									
Solyc02g080160	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4B9N7_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR008264 (PRINTS): IPR010713 (PF	21,766	30,720	1,712	2,005	2,936									
Solyc02g080165	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *-* B9H1G1_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,279	0,317	0,477	0,687	0,425									
Solyc02g080170	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H1G1_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,677	1,356	2,246	2,446	1,652									
Solyc02g080180	Magnesium transporter protein 1 (AHRD V3.3 *** A0A118JXD0_CYNCS)		F:GO:0004579: C:G(	F:dolichyl-diphospho EC:2.4.1.119 Glycosyltransferases	IPR021149 (PFAM): G3DSA:3.40.30.1	1,494	1,307	4,347	4,514	3,648									
Solyc02g080190	Nuclear transport factor 2-like protein (AHRD V3.3 *** A0A0B0NHI4_GOSAR)		P:GO:0006913: C:G(	P:nucleocytoplasmic transport; C:nuclear pore central transport	G3DSA:3.10.450.50 (GENE3D): IPR0(	0,576	0,391	0,726	0,617	0,730									
Solyc02g080220	Pectinesterase (AHRD V3.3 *** K4B9P3_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR006501 (SMART): IPR000070 (PF	0,097	0,043	0,022	0,000	0,047									
Solyc02g080230	ROP-interactive CRIB motif-containing protein 10 (AHRD V3.3 *-* A0A061GGE1_THECC)		C:GO:0016021	C:integral component of membrane	IPR000095 (SMART): IPR036936 (G3	0,080	0,079	0,022	0,051	0,116									
Solyc02g080260	Woolly	wo	F:GO:0003677: F:G(	F:DNA binding; F:lipid binding	IPR001356 (SMAF HD-ZIP	2,213	2,138	0,489	0,585	0,398									
Solyc02g080265	Vacuolar iron transporter homolog 2 (AHRD V3.3 --* VITH2_ORYSJ)					0,197	0,092	0,025	0,000	0,000									
Solyc02g080270	Vacuolar protein sorting-associated protein VPS28 family protein (AHRD V3.3 *** AT4G05000.3)		C:GO:0000813: P:G(	C:ESCRT I complex; P:endosome transport via multivesicular b	IPR007143 (PFAM): IPR037206 (G3D	34,476	31,247	57,246	68,205	52,055									
Solyc02g080280	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 *-* NU1C_SOLLC)		C:GO:0016020: P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM): PTHR11432:SF1	0,113	0,265	0,025	0,200	0,211									
Solyc02g080290	Beta-glucosidase, putative (AHRD V3.3 *** B9RXP7_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001360 (PRINTS): IPR001360 (PF	3,667	4,207	5,195	5,751	5,281									
Solyc02g080300	Beta-glucosidase, putative (AHRD V3.3 *** B9RXP7_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001360 (PRINTS): IPR001360 (PF	2,594	2,288	3,244	3,903	4,469									
Solyc02g080310	Beta-glucosidase, putative (AHRD V3.3 *** B9RXP7_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001360 (PRINTS): IPR001360 (PF	0,330	0,419	0,000	0,050	0,024									
Solyc02g080320	Pseudouridine synthase family protein (AHRD V3.3 *** AT4G21770.1)		P:GO:0001522: F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn	IPR006145 (PFAM): G3DSA:3.30.23	10,385	11,368	12,975	10,773	13,498									
Solyc02g080330	Cytochrome P450 family protein (AHRD V3.3 *** B9H1E5_POPTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	0,538	0,639	0,000	0,025	0,000									
Solyc02g080340	Patatin (AHRD V3.3 *** A0A067JMP9_JATCU)		F:GO:0005515: P:G(	F:protein binding; P:lipid metabolic process	IPR000225 (SMART): IPR003591 (SM	19,582	23,925	16,635	18,363	17,988									
Solyc02g080350	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K719_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,596	2,259	1,197	1,322	1,224									
Solyc02g080355	Patatin (AHRD V3.3 *-* A0A067JMP9_JATCU)		F:GO:0004620: C:G(	F:phospholipase ac EC:3.1.1.23; EC:3.1. Acylglycerol lipase; C	mobidb-lite (MOBIDB_LITE)	0,339	0,661	0,286	0,361	0,635									
Solyc02g080360	BnaA01g11610D protein (AHRD V3.3 *** A0A078CSV3_BRANA)				PTHR35131 (PANTHER)	0,194	0,132	0,000	0,025	0,000									
Solyc02g080370	obamovirus multiplication 1	th3	C:GO:0009705: C:G(	C:plant-type vacuole membrane; C:integral component of memb	IPR009457 (PFAM): PTHR31142:SF2	116,914	113,079	71,573	68,877	67,233									
Solyc02g080380	Derlin (AHRD V3.3 *** K4B9Q9_SOLLC),Pfam:PF04511		C:GO:0005789: C:G(	C:endoplasmic reticulum membrane; C:integral component of me	IPR007599 (PFAM): PTHR11009:SF2	49,543	40,869	57,733	53,294	51,809									
Solyc02g080400	Abnormal spindle-like microcephaly-associated-like protein, putative (AHRD V3.3 *** G7JI24_MEDTR)		F:GO:0005515: P:G(	F:protein binding; P:spindle organization	IPR000225 (SMART): IPR000048 (SM	0,806	0,847	0,046	0,073	0,071									
Solyc02g080420	RNA-binding family protein (AHRD V3.3 *** A0A061FD24_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	128,979	138,061	138,413	122,105	123,019									
Solyc02g080430	Mediator of RNA polymerase II transcription subunit 21 (AHRD V3.3 *** A0A0S2LKQ9_REHGL)		C:GO:0016592	C:mediator complex	IPR021384 (PFAM): G3DSA:1.20.58.4	21,702	21,521	35,259	31,030	30,173									
Solyc02g080440	ATP-binding-cassette transporter family protein (AHRD V3.3 *** B9H1C6_POPTR)		P:GO:0016226	P:iron-sulfur cluster assembly	IPR000825 (PFAM): IPR010231 (TIGF	24,186	20,931	58,095	54,286	56,593									
Solyc02g080450	LOW QUALITY:CELLULOSE SYNTHASE INTERACTIVE 3 (AHRD V3.3 --* AT1G77460.4)				PTHR35687 (PANTHER)	0,197	0,179	0,000	0,025	0,000									
Solyc02g080460	Kinesin-like protein (AHRD V3.3 *-* A0A0R0FW85_SOYBN)		F:GO:0003777: F:G(	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	PTHR24115:SF515 (PANTHER): IPR0	0,257	0,158	0,071	0,072	0,070									
Solyc02g080465	Protein kinase family protein (AHRD V3.3 --* Q9LQ29_ARATH)		P:GO:0006629: F:G(	P:lipid metabolic process; F:O-acyltransferase activity; C:membrane; C:integral component of membran		0,098	0,142	0,068	0,025	0,000									
Solyc02g080470	Heat shock protein 70 family protein (AHRD V3.3 *** A0A061F4U1_THECC)		F:GO:0005524: C:G(	F:ATP binding; C:nucleus; C:cytosol	IPR013126 (PRINTS): G3DSA:3.30.42	31,840	36,994	45,271	45,750	42,527									
Solyc02g080480	Protein DETOXIFICATION (AHRD V3.3 *** K4B9R9_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (PFAM): IPR002528 (TIGF	10,437	10,732	1,545	1,375	1,951									
Solyc02g080490	Protein DETOXIFICATION (AHRD V3.3 *** K4B9S0_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (TIGRFAM): IPR002528 (I	27,433	25,386	7,078	5,345	5,813									
Solyc02g080500	GPI-anchored protein (AHRD V3.3 *** AT2G30700.2)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane	PTHR33831:SF2 (PANTHER): IPR040	32,231	24,210	18,812	16,519	18,803									
Solyc02g080510	Senescence regulator (AHRD V3.3 *** A0A103XFA1_CYNCS)				IPR007608 (PFAM): mobidb-lite (MOB	79,112	49,438	164,051	102,814	124,329			-0,402	0,039	-0,670	0,000		down	down
Solyc02g080520	F11F12.2 protein (AHRD V3.3 *** Q9LPT5_ARATH)				mobidb-lite (MOBIDB_LITE): PTHR310	5,623	3,918	23,332	23,306	21,853									
Solyc02g080530	Peroxidase (AHRD V3.3 *** K4B9S4_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	281,134	252,050	23,023	8,492	14,017					-1,437	0,001			down
Solyc02g080540	ATP synthase gamma-subunit (AHRD V3.3 *** I0ZA63_COCSC)		P:GO:0015986: C:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR000131 (PRINTS): IPR000131 (PF	80,050	196,620	43,711	63,596	143,227	1,324	0,000	1,708	0,000			up	up	
Solyc02g080550	SH3 domain-binding protein 1, putative (AHRD V3.3 *** A0A061F5K7_THECC)				PTHR35495 (PANTHER): PTHR35495	4,283	3,308	0,875	0,554	0,732									
Solyc02g080560	LOW QUALITY:F-box family protein (AHRD V3.3 --* AT4G35930.4)				PTHR35495 (PANTHER): PTHR35495	3,826	5,887	2,819	1,847	2,234									
Solyc02g080570	Soluble starch synthase 3, chloroplastic/amyloplastic (AHRD V3.3 *** SSY3_SOLTU)		F:GO:0004373: F:G(	F:glycogen (starch) EC:2.4.1.11 Glycogen(starch) syr	IPR005085 (SMART): IPR001296 (PF	71,320	83,786	119,746	115,161	122,909									
Solyc02g080580	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *** AT4G04630.1)				IPR007608 (PFAM): mobidb-lite (MOB	0,101	0,139	0,126	0,089	0,047									
Solyc02g080590	Autophagy-related protein (AHRD V3.3 *** A0A0V0GZQ3_SOLCH)		C:GO:0005737: P:G(	C:cytoplasm; P:autophagy; P:cellular response to nitrogen starv	G3DSA:3.10.20.90 (GENE3D): IPR00	14,957	15,064	42,542	46,279	39,417									
Solyc02g080615	Ankyrin repeat family protein (AHRD V3.3 *** AT1G62050.1)		F:GO:0005515	F:protein binding	IPR002110 (SMART): IPR021832 (PF	3,771	4,224	0,075	0,072	0,093									
Solyc02g080620	Arogenate dehydratase (AHRD V3.3 *** K4B9T3_SOLLC)		F:GO:0004664: P:G(	F:prephenate dehyc EC:4.2.1.51 Prephenate dehydrat	G3DSA:3.40.190.10 (GENE3D): G3DS	2,943	6,522	0,823	0,713	0,654	1,177	0,007					up		
Solyc02g080630	Lactoylglutathione lyase (AHRD V3.3 *** K4B9T4_SOLLC)		F:GO:0004462: F:G(	F:lactoylglutathione EC:4.4.1.5 Lactoylglutathione ly	IPR029068 (G3DSA:3.10.180.GENE3	604,140	508,876	1059,934	853,704	1023,462									
Solyc02g080635	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_JASNU)		C:GO:0009521: P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl	IPR000932 (PFAM): G3DSA:1.10.10.6	1,650	1,999	1,525	2,522	1,763									
Solyc02g080640	adenylyl-sulfate reductase	asr	F:GO:0016671: P:G(	F:oxidoreductase activity, acting on a sulfur group of donors, di	G3DSA:3.40.30.10 (GENE3D): IPR01	66,695	74,136	106,610	97,087	106,471									
Solyc02g080650	ARM repeat superfamily protein, putative isoform 2 (AHRD V3.3 *** A0A061FBW8_THECC)		P:GO:0009793	P:embryo development ending in seed dormancy	IPR011989 (G3DSA:1.25.10.GENE3D	11,226	11,554	11,874	12,568	11,673									
Solyc02g080660	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RXJ9_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012946 (SMART): IPR012946 (PF	8,506	7,008	6,023	5,292	5,580									
Solyc02g080670	L-ascorbate oxidase (AHRD V3.3 *** A0A0B0MPT8_GOSAR)		F:GO:0005507: F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red	IPR011706 (PFAM): IPR008972 (G3D	0,588	0,918	0,025	0,025	0,000									
Solyc02g080710	Myb family transcription factor (AHRD V3.3 *-* D7LIV0_ARALL)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(G2-like	0,098	0,227	0,025	0,000	0,000									
Solyc02g080720	MYB-like transcription factor family protein (AHRD V3.3 *-* G7KSC8_MEDTR)		F:GO:0003677	F:DNA binding	IPR006447 (TIGRI G2-like	0,019	0,000	0,000	0,000	0,000									
Solyc02g080730	MYB-like transcription factor family protein (AHRD V3.3 *-* G7KSC8_MEDTR)		F:GO:0003677	F:DNA binding	IPR006447 (TIGRI G2-like	0,040	0,018	0,000	0,000	0,000									
Solyc02g080740	Homeodomain-like superfamily protein (AHRD V3.3 *-* A0A061GH60_THECC)		F:GO:0003677	F:DNA binding	IPR001005 (PFAM G2-like	0,000	0,043	0,000	0,000	0,000									
Solyc02g080755	Homeodomain-like superfamily protein (AHRD V3.3 --* A0A061GH60_THECC)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter	PTHR31496 (PANTHER): PTHR31496	0,000	0,019	0,000	0,000	0,000									
Solyc02g080780	Orotidine 5'-phosphate decarboxylase (AHRD V3.3 *** A0A0B0MNV8_GOSAR)				PTHR37197 (PANTHER)	10,800	13,482	8,313	9,282	10,466									
Solyc02g080790	Deoxyhypusine synthase	DHS	P:GO:0008612	P:peptidyl-lysine modification to peptidyl-hypusine	IPR002773 (PFAM): IPR036982 (G3D	0,496	0,543	0,075	0,047	0,093									
Solyc02g080800	deoxyhypusine synthase	DHS	P:GO:0008612	P:peptidyl-lysine modification to peptidyl-hypusine	IPR002773 (PFAM): IPR036982 (G3D	22,002	19,702	29,436	26,330	25,529									
Solyc02g080810	Aminomethyltransferase (AHRD V3.3 *** K4B9V1_SOLLC)		F:GO:0004047: F:G(	F:aminomethyltrans EC:2.1.2.1 Aminomethyltransfera	G3DSA:2.40.30.110 (GENE3D): IPR0:	87,835	145,137	56,135	49,425	74,010	0,753	0,023	0,396	0,019			up	up	
Solyc02g080820	Peroxisomal membrane protein PMP22 (AHRD V3.3 *** A0A151T6U9_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR007248 (PFAM): IPR007248 (PAN	13,970	15,001	20,512	21,799	20,533									
Solyc02g080830	F-box plant-like protein, putative (AHRD V3.3 *** A0A072V4I2_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR027949 (PFAM): PTHR33358:SF1	0,019	0,299	0,075	0,051	0,024									
Solyc02g080860	MYB transcription factor-like (AHRD V3.3 *-* A0A0K9PMY6_ZOSMR)		F:GO:0003677	F:DNA binding	IPR001005 (PFAM G2-like	0,140	0,143	0,000	0,000	0,000									
Solyc02g080870	B-cell receptor-associated 31-like (AHRD V3.3 *** A0A061GGS0_THECC)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,081	0,000	0,072	0,025	0,070									
Solyc02g080880	Aspartic proteinase (AHRD V3.3 *** ASPR_CUCPE)		F:GO:0004190: P:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR001461 (PRINTS): IPR008139 (SM	75,060	76,135	96,211	114,868	98,548									
Solyc02g080890	WRKY transcription factor 6	WRKY6	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	1,954	6,409	11,355	17,959	14,528	1,732	0,001					up		
Solyc02g080900	Wall-associated receptor kinase 3-like protein (AHRD V3.3 *** A0A0B0PL73_GOSAR)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR33355:SF5	2,208	1,882	0,411	0,580	0,703									
Solyc02g080940	Proline synthase co-transcribed bacterial (AHRD V3.3 *** A0A1D1ZCG0_9ARAE)		F:GO:0030170	F:pyridoxal phosphate binding	IPR011078 (TIGRFAM): IPR001608 (I	4,887	5,109	4,520	3,392	4,520									
Solyc02g080950	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XCX1_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:pyridoxal phosphate binding	IPR029066 (G3DSA:3.20.20.GENE3D	4,225	4,803	3,740	3,922	3,621									
Solyc02g080960	transmembrane protein, putative (DUF1068) (AHRD V3.3 *** AT1G05070.1)		C:GO:0016021	C:integral component of membrane	IPR010471 (PFAM): PTHR32254:SF1	1,525	2,491	1,360	1,085	1,154									
Solyc02g080970	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT1G62305.1)		F:GO:0008375: C:G(	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM): PTHR31042 (PAI	20,787	25,108	26,540	27,647	24,380									
Solyc02g080990	Leucyl-tRNA synthetase (AHRD V3.3 *** G7JJA8_MEDTR)		F:GO:0002161: F:G(	F:aminoacyl-tRNA e EC:6.1.1.4; EC:3.1.1 Leucine--tRNA ligase	IPR002302 (PRINTS): IPR013155 (PF	18,474	27,147	21,844	22,119	26,956	0,582	0,030					up		
Solyc02g080995	Major pollen allergen Aln g 1 (AHRD V3.3 --* MPAG1_ALNGL)					2,419	2,590	2,407	3,434	2,164									
Solyc02g081000	Leucyl-tRNA synthetase, putative (AHRD V3.3 *-* B9RXG5_RICCO)		F:GO:0004823: F:G(	F:leucine-tRNA liga: EC:6.1.1.4 Leucine--tRNA ligase	IPR014729 (G3DSA:3.40.50.GENE3D	0,244	0,260	0,200	0,095	0,234									
Solyc02g081010	Transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 *-* AT1G11950.3)		F:GO:0008168: P:G(	F:methyltransferase activity; P:methylation	IPR003347 (SMART): G3DSA:2.60.12	36,532	35,108	36,047	38,780	36,948									
Solyc02g081030	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G22120.6)		C:GO:0016020	C:membrane	IPR032880 (PFAM): IPR027815 (PFA	67,960	129,098	82,522	80,620	85,365	0,951	0,001					up		
Solyc02g081040	Receptor protein kinase, putative (AHRD V3.3 *** B9SH40_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	0,123	0,283	0,116	0,050	0,023									
Solyc02g081050	Receptor protein kinase, putative (AHRD V3.3 *** B9RXG1_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR001245 (PF	0,235	0,156	0,210	0,363	0,259									
Solyc02g081060	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *** A0A151T5P9_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid	IPR003435 (PFAM): IPR013103 (PFA	0,000	0,289	0,025	0,022	0,093									
Solyc02g081070	Kinase (AHRD V3.3 *** D7ME76_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR001611 (PFAM): IPR001245 (PFA	72,791	54,885	117,956	120,150	134,031									
Solyc02g081080	O-fucosyltransferase family protein		P:GO:0006004: C:G(	P:fucose metabolic process; C:integral component of membrane	IPR024709 (PIRSF): IPR019378 (PFA	21,641	20,401	35,032	33,026	32,076									
Solyc02g081081	AP2-like ethylene-responsive transcription factor BBM2 (AHRD V3.3 --* BBM2_BRANA)				PTHR33144 (PANTHER): PTHR33144	0,019	0,000	0,000	0,000	0,000									
Solyc02g081120	class 1 knotted-like homeodomain protein	TKN2	F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter	IPR005540 (SMAF TALE	6,717	9,829	2,648	1,759	2,292									
Solyc02g081130	BAH-PHD domain-containing protein (AHRD V3.3 *** A0A0K9P0E3_ZOSMR)		F:GO:0003682	F:chromatin binding	IPR001965 (SMART): IPR001025 (SM	0,672	0,651	0,022	0,000	0,000									
Solyc02g081140	UBX domain-containing protein, putative (AHRD V3.3 *** B9SH50_RICCO)		F:GO:0005515	F:protein binding	IPR012989 (SMART): IPR001012 (SM	40,808	55,243	53,085	51,898	48,087									
Solyc02g081150	LOW QUALITY:serine/arginine repetitive matrix-like protein (AHRD V3.3 *** AT4G22190.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	7,823	8,096	0,977	0,765	0,867									
Solyc02g081160	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 *** PFPB_SOLTU)		F:GO:0003872: F:G(	F:6-phosphofructok EC:2.7.1.9; EC:2.7.1 Diphosphate--fructos	IPR022953 (PRINTS): G3DSA:1.10.1(	396,197	344,646	327,349	268,409	284,693									
Solyc02g081170	plastid lipid associated protein CHRC	chrc	P:GO:0009414: C:G(	P:response to water deprivation; C:chloroplast thylakoid membr	IPR006843 (PFAM): IPR039633 (PAN	106,416	122,219	448,523	418,422	485,967									
Solyc02g081180	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03965.1)				IPR001841 (SMART): IPR013083 (G3	0,000	0,000	0,047	0,022	0,000									
Solyc02g081190	1-aminocyclopropane-1-carboxylate oxidase 4	ACO4	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3	61,165	65,019	36,670	40,967	40,071									
Solyc02g081200	LOW QUALITY:Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repeat-containing		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR000270 (SM	18,725	24,665	34,009	33,133	34,868									
Solyc02g081210	Expansin (AHRD V3.3 *** Q9ZP33_SOLLC)	EXPA24	C:GO:0005576: P:G(	C:extracellular region; P:plant-type cell wall organization	IPR007118 (PRINTS): IPR002963 (PF	6,006	4,864	0,895	0,742	0,989									
Solyc02g081220	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20840.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAD	G3DSA:3.40.462.20 (GENE3D): G3DS	0,419	0,385	0,661	0,507	0,450									
Solyc02g081230	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein (AHRD V3.3 *** AT3G03210.1)		C:GO:0016021	C:integral component of membrane	PTHR13533 (PANTHER): PTHR13533	1,554	1,208	1,976	2,023	1,438									
Solyc02g081240	Glutathione s-transferase, putative (AHRD V3.3 *** B9SKR6_RICCO)	GSTU7	F:GO:0005515	F:protein binding	PF13410 (PFAM): IPR004045 (PFAM)	0,000	0,000	0,025	0,048	0,000									
Solyc02g081250	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103Y0J8_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:metal ion binding	IPR000408 (PRINTS): IPR000306 (SM	7,223	5,480	3,914	4,108	4,118									
Solyc02g081260	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHI		C:GO:0005773: C:G(	C:vacuole; C:plasma membrane; F:metal ion binding	PTHR22870 (PANTHER): PTHR22870	0,698	0,850	0,781	0,823	0,447									
Solyc02g081270	NAC domain protein, (AHRD V3.3 *** A0A061EDT4_THECC)	NAC019	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,198	0,222	0,025	0,025	0,000									
Solyc02g081280	LOW QUALITY:Unknown protein (AHRD V3.3)					0,000	0,000	0,000	0,022	0,000									
Solyc02g081290	RNA helicase DEAD9	DEAD9	F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding	IPR014001 (SMART): IPR001650 (SM	7,589	5,873	7,190	5,944	6,812									
Solyc02g081300	Sucrose synthase (AHRD V3.3 *** A0A0C5DIW2_CAMSI)	SUS7	P:GO:0005985: F:G(	P:sucrose metaboli EC:2.4.1.13 Sucrose synthase	G3DSA:3.10.450.330 (GENE3D): G3D	4,584	4,706	4,642	3,820	3,819									
Solyc02g081310	50S ribosomal L15 (AHRD V3.3 *** A0A0B0P1T4_GOSAR)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:large ribos	IPR005749 (TIGRFAM): G3DSA:3.100	19,395	23,103	29,320	23,798	27,088									
Solyc02g081320	Protein SET DOMAIN GROUP, putative (AHRD V3.3 *** B9T3H1_RICCO)		F:GO:0005515	F:protein binding	IPR001214 (PFAM): PTHR13271 (PAI	11,301	11,074	14,512	13,813	13,655									
Solyc02g081330	phytoene synthase 2	PSY2	F:GO:0004310: P:G(	F:farnesyl-diphosph EC:2.5.1.29; EC:2.5. Geranylgeranyl diphc	IPR008949 (G3DSA:1.10.600.GENE3	28,906	43,159	39,322	35,707	42,847									
Solyc02g081340	Glutathione S-transferase (AHRD V3.3 *** E1AWJ7_CAPAN)	GSTT1	F:GO:0005515	F:protein binding	G3DSA:3.40.30.10 (GENE3D): G3DS/	0,080	0,849	0,090	0,050	0,095									
Solyc02g081350	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)		F:GO:0003824	F:catalytic activity	G3DSA:3.40.50.12780 (GENE3D): IPF	0,061	0,268	0,000	0,000	0,046									
Solyc02g081360	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)		F:GO:0003824	F:catalytic activity	IPR025110 (PFAM): IPR000873 (PFA	0,737	5,779	0,290	0,870	1,252	2,980	0,000					up		
Solyc02g081380	Ras-related GTP-binding protein (AHRD V3.3 *** Q40570_TOBAC)		F:GO:0003924: F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	26,484	26,444	30,829	31,622	27,107									
Solyc02g081390	Amine oxidase family protein (AHRD V3.3 *** B9H3J5_POPTR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR001613 (PRINTS): G3DSA:3.90.66	291,166	366,814	834,058	959,196	811,907									
Solyc02g081400	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT3G02720.1)		F:GO:0019172: P:G(	F:glyoxalase III activity; P:lactate biosynthetic process; P:meth	IPR002818 (PFAM): IPR029062 (G3D	184,261	178,408	548,480	487,841	515,053									
Solyc02g081410	Beta-catenin-like protein 1 (AHRD V3.3 *** A0A1D1YKG0_9ARAE)		C:GO:0005681	C:spliceosomal complex	IPR013180 (SMART): IPR011989 (G3	39,346	39,000	40,313	41,651	41,328									
Solyc02g081420	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061E		F:GO:0004386: C:G(	F:helicase activity; EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): G3DS	8,852	7,903	16,709	21,098	15,593									
Solyc02g081430	microsomal glutathione s-transferase (AHRD V3.3 *** AT1G65820.1)	MGST1	F:GO:0004364: F:G(	F:glutathione transfi EC:2.5.1.18; EC:1.1 Glutathione transfera	IPR001129 (PFAM): IPR023352 (G3D	0,239	0,653	0,291	0,262	0,095									
Solyc02g081440	microsomal glutathione s-transferase (AHRD V3.3 *-* AT1G65820.3)				IPR001129 (PFAM): IPR023352 (G3D	0,449	0,504	0,050	0,196	0,094									
Solyc02g081445	Cellulose synthase (AHRD V3.3 --* A0A151RTU1_CAJCA)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE)	3,147	1,622	0,853	1,088	1,060									
Solyc02g081460	Gamma-tubulin complex component (AHRD V3.3 *** K4BA16_SOLLC)		C:GO:0000922: C:G(	C:spindle pole; C:microtubule organizing center; P:microtubule n	IPR040457 (PFAM): G3DSA:1.20.120	22,378	20,731	18,136	18,921	18,580									
Solyc02g081470	Receptor-like kinase (AHRD V3.3 *-* G7I978_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	0,037	0,281	0,000	0,069	0,070									
Solyc02g081480	Kinase superfamily protein, putative (AHRD V3.3 *-* A0A061FW08_THECC)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR27009 (PAI	0,851	1,298	1,782	2,401	2,123									
Solyc02g081485	Receptor-like kinase (AHRD V3.3 *** A0A072VF58_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	3,002	6,517	6,578	7,728	6,697									
Solyc02g081500	Receptor kinase LRK10		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	30,670	52,433	2,398	2,766	6,481	0,798	0,034	1,432	0,000			up	up	
Solyc02g081510	Receptor-like kinase (AHRD V3.3 *** G7I978_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	0,096	0,640	0,121	0,173	0,237									

Solyc02g081520	Nijmegen breakage syndrome 1, putative isoform 1 (AHRD V3.3 *** A0A061EEL2_THECC)		F:GO:0005515: P:G(	F:protein binding: P:double-strand break repair: P:mitotic G2 DN			G3DSA:2.60.200.20 (GENE3D): IPR0:	18,244	14,424	21,285	23,446	20,619									
Solyc02g081530	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT1G06440.1)						IPR021099 (PFAM): mobidb-lite (MOB	3,303	3,404	2,404	2,260	2,195									
Solyc02g081535	lipoic acid synthase 1 (AHRD V3.3 --* AT2G20860.3)							0,663	0,527	0,433	0,442	0,352									
Solyc02g081540	LOW QUALITY:GDA1/CD39 nucleoside phosphatase family protein (AHRD V3.3 --* AT1G14240.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,219	0,195	0,197	0,119	0,046									
Solyc02g081550	LeftsH6FtsH protease	ftsh6	F:GO:0004222: F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): G3DSA:1.20.58	9,239	10,937	38,588	33,162	38,980									
Solyc02g081570	Oligopeptide transporter, putative (AHRD V3.3 *** B9SIR4_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM): IPR004813 (TIGF	0,097	0,018	0,025	0,047	0,024									
Solyc02g081580	NC domain-containing family protein (AHRD V3.3 *** A9P901_POPTR)						IPR007053 (PFAM): G3DSA:3.90.172(	109,576	87,486	77,656	65,231	67,330									
Solyc02g081590	FACT complex subunit SPT16 (AHRD V3.3 *-* W9RSN6_9ROSA)		C:GO:0035101	C:FACT complex			IPR029148 (SMART): IPR029149 (G3	73,566	80,782	143,194	155,525	135,769									
Solyc02g081600	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)		F:GO:0005385: C:G(	F:zinc ion transmembrane transporter activity: C:integral compo			IPR003689 (PFAM): IPR004698 (TIGF	5,795	3,628	0,682	0,559	0,679									
Solyc02g081610	Phosphatidylinositol N-acetylglucosaminyltransferase (AHRD V3.3 *** A0A103YG15_CYNCS)		P:GO:0006506: C:G(	P:GPI anchor biosy	EC:2.4.1.198	Phosphatidylinositol I	IPR009450 (PIRSF): IPR009450 (PFA	5,474	5,770	8,165	9,113	8,085									
Solyc02g081620	Zinc finger family protein (AHRD V3.3 *** B9GY13_POPTR)		F:GO:0003677	F:DNA binding			IPR013087 (SMART): G3DSA:3.30.16	51,380	47,139	59,627	55,862	56,709									
Solyc02g081640	Transcription factor TFIIIB component B (AHRD V3.3 *** A0A0B0N2G5_GOSAR)		C:GO:0000126: F:G(	C:transcription factor TFIIIB complex: F:RNA polymerase III ger			IPR001005 (SMAF MYB_related	46,781	43,397	58,296	62,241	59,998									
Solyc02g081650	Enhancer of polycomb-like protein (AHRD V3.3 *** K4BA35_SOLLC)		P:GO:0006357: C:G(	P:regulation of transcription by RNA polymerase II: C:Piccolo N(			IPR019542 (PFAM): mobidb-lite (MOB	21,613	18,164	17,221	17,313	16,341									
Solyc02g081660	GTP-binding family protein (AHRD V3.3 *** AT1G30960.1)		F:GO:0003723: F:G(	F:RNA binding; F:GTP binding			G3DSA:3.40.50.300 (GENE3D): IPR0'	10,363	11,652	10,438	9,639	9,783									
Solyc02g081670	anantha	an	F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF.	0,080	0,185	0,162	0,167	0,187									
Solyc02g081680	Nucleolar complex protein 2 like (AHRD V3.3 *** A0A0B2RJJ2_GLYSO)		C:GO:0005654: C:G(	C:nucleoplasm: C:nucleolus: C:integral component of membrane			IPR005343 (PFAM): mobidb-lite (MOB	25,430	27,045	28,326	23,889	23,723									
Solyc02g081690	Glycosyltransferase (AHRD V3.3 *** V4UHR4_9ROSI)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,698	1,456	1,215	1,170	1,808									
Solyc02g081700	Proteasome subunit alpha type (AHRD V3.3 *** K4BA40_SOLLC)		F:GO:0004298: P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000426 (SMART): IPR001353 (PF.	86,994	91,443	166,616	156,785	146,953									
Solyc02g081710	Polyol monosaccharide transporter 8	PMT8	C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,000	0,000	0,050	0,000	0,023									
Solyc02g081730	Reticulon-like protein (AHRD V3.3 *** A0A0V0IQH2_SOLCH)		F:GO:0003854: P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D): IPR0(	13,422	12,489	6,915	5,305	6,586									
Solyc02g081740	Acyl-transferase (AHRD V3.3 *** Q4W6D5_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	1,296	0,563	0,000	0,000	0,000									
Solyc02g081745	Acyl-transferase (AHRD V3.3 *** Q4W6D5_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	1,048	0,948	0,000	0,000	0,000									
Solyc02g081760	Acyl-transferase (AHRD V3.3 *** Q4W6D5_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	2,854	2,353	0,000	0,000	0,000									
Solyc02g081770	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,021	0,021	0,000	0,000	0,000									
Solyc02g081780	B3 domain-containing protein (AHRD V3.3 *** A0A0B2PYF9_GLYSO)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,192	0,282	0,000	0,000	0,000									
Solyc02g081800	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,019	0,120	0,479	0,702	0,613									
Solyc02g081810	H/ACA ribonucleoprotein complex subunit 4 (AHRD V3.3 *** CBF5_ARATH)		P:GO:0001522: F:G(	P:pseudouridine synthesis: F:RNA binding: P:RNA processing: F			IPR002478 (SMART): IPR012960 (SM	70,543	88,137	55,894	46,582	44,747									
Solyc02g081830	Haloacid dehalogenase-like hydrolase domain-containing protein 3 (AHRD V3.3 *** W9RRW5_9ROSA).Pfar		F:GO:0016787	F:hydrolase activity			IPR006439 (PRINTS): PF00702 (PFAI	16,039	18,899	192,524	180,058	145,914									
Solyc02g081840	Translocator assembly and maintenance-like protein (AHRD V3.3 *** G8A1V5_MEDTR)		F:GO:0004605: P:G(	F:phosphatidate cyt	EC:2.7.7.41	Phosphatidate cytidy	IPR015222 (PIRSF): IPR015222 (PFA	6,227	6,262	6,960	7,875	6,772									
Solyc02g081845	non-specific phospholipase C5 (AHRD V3.3 --* AT3G03540.1)							0,158	0,163	0,268	0,367	0,212									
Solyc02g081850	Cationic amino acid transporter (AHRD V3.3 *** G7INC3_MEDTR)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmem			IPR002293 (PFAM): IPR029485 (PFA	0,239	0,243	0,200	0,215	0,188									
Solyc02g081860	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT4G20090.2)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,796	1,969	3,443	3,445	2,497									
Solyc02g081870	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG34	F:GO:0005524: C:G(	F:ATP binding: C:m	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	0,431	0,740	0,068	0,000	0,000									
Solyc02g081880	Molybdenum cofactor sulfurase family protein (AHRD V3.3 *** AT1G30910.1)		F:GO:0003824: F:G(	F:catalytic activity: F:molybdenum ion binding: F:pyridoxal phos			IPR005302 (PFAM): IPR005303 (PFA	324,196	247,399	364,822	293,288	322,829									
Solyc02g081890	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein, putative (AHRD V3.3 *** A0A06		F:GO:0008375: C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297 (PAI	9,255	5,701	1,893	3,217	4,081									
Solyc02g081900	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YLQ2_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR032867 (PFA	0,858	1,278	0,546	0,996	1,063									
Solyc02g081910	DNA topoisomerase (AHRD V3.3 *** K4BA61_SOLLC)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:5.99.1.2	DNA topoisomerase	IPR013497 (PRINTS): IPR003602 (SN	19,966	19,597	27,554	26,599	28,148									
Solyc02g081920	plastid transcriptionally active 14 (AHRD V3.3 *** AT4G20130.1)		F:GO:0005515	F:protein binding			IPR036464 (G3DSA:3.90.1420.GENE	25,342	29,961	30,161	28,958	35,565									
Solyc02g081930	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* A0A061DVU2_THECC)							1,504	1,295	1,968	1,332	1,647									
Solyc02g081940	RNA binding protein (AHRD V3.3 *** A0A0K9P1B7_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR003954 (SMART): IPR000504 (SM	31,530	27,405	39,786	38,091	39,054									
Solyc02g081950	RNA ligase/cyclic nucleotide phosphodiesterase (AHRD V3.3 *** A0A103Y4Y2_CYNCS),Pfam:PF13563						G3DSA:3.90.1140.10 (GENE3D): PF1	12,646	12,913	13,959	13,914	12,586									
Solyc02g081960	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein (AHRD V3.3 *'		F:GO:0003723: F:G(	F:RNA binding; F:protein binding; P:RNA processing			IPR000626 (SMART): IPR000061 (SM	56,780	46,877	54,213	52,044	54,063									
Solyc02g081970	Vacuolar sorting receptor family protein (AHRD V3.3 *** B9GYG5_POPTR)		F:GO:0005509	F:calcium ion binding			IPR001881 (SMART): IPR003137 (PF.	10,627	24,912	66,685	92,183	89,793	1,250	0,049					up		
Solyc02g081980	Apyrase (AHRD V3.3 *** APY_SOLTU)		F:GO:0016787	F:hydrolase activity			G3DSA:3.30.420.150 (GENE3D): IPR(	7,943	29,430	1,107	1,498	2,375	1,916	0,001	1,091	0,018			up	up	
Solyc02g081990	Pectinesterase (AHRD V3.3 *** K4BA69_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Carl	IPR006501 (SMART): IPR035513 (G3	0,000	0,000	0,022	0,000	0,024									
Solyc02g082000	Ribosomal protein S19 family protein (AHRD V3.3 *** AT5G09500.1)		F:GO:0003735: P:G(	F:structural constituent of ribosome: P:translation: C:small ribos			IPR002222 (PRINTS): IPR002222 (PI	568,022	638,687	386,824	344,672	370,820									
Solyc02g082010	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G07900.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding: P:regulation of transcription. DN			IPR003690 (SMART): IPR038538 (G3	4,428	4,119	7,091	7,545	7,779									
Solyc02g082020	BnaC08g09400D protein (AHRD V3.3 *** A0A078FGX7_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	19,243	24,185	19,689	18,247	17,193									
Solyc02g082030	Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic (AHRD V3.3 *** TGD2_ARATH)		F:GO:0005319: F:G(	F:lipid transporter activity: F:phospholipid binding: P:lipid transpo			IPR003399 (PFAM): mobidb-lite (MOB	26,597	32,039	48,893	46,471	48,517									
Solyc02g082035	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 -** A0A072TYZ0_MEDTR)							0,021	0,019	0,000	0,000	0,000									
Solyc02g082040	R2R3MYB transcription factor 56	R2R3MYB56	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,042	0,174	0,050	0,000	0,000									
Solyc02g082050	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.2)		F:GO:0005515: P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR003591 (SMA	1,120	1,174	0,237	0,293	0,353									
Solyc02g082060	LOW QUALITY:PPPDE putative thiol peptidase family protein (AHRD V3.3 *** AT4G25680.1)						IPR008580 (SMART): G3DSA:3.90.17	22,214	24,466	15,167	15,505	15,437									
Solyc02g082070	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,985	2,083	0,660	0,654	0,472									
Solyc02g082080	Copper transporter (AHRD V3.3 *** E9LK45_VITVI)		F:GO:0005375: C:G(	F:copper ion transmembrane transporter activity: C:integral com			IPR007274 (PFAM): PTHR12483:SF5:	35,105	43,571	35,978	39,079	39,894									
Solyc02g082100	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G34920.2)						IPR013083 (G3DSA:3.30.40.GENE3D	28,577	14,600	5,835	8,036	13,533	-0,944	0,008	1,203	0,000			down	up	
Solyc02g082110	Zinc finger transcription factor 18	C3H18	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	16,309	14,818	10,438	10,280	11,793									
Solyc02g082120	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9SVU2_RICCO)		P:GO:0006284: F:G(	P:base-excision rep	EC:3.2.2.21: EC:3.2.	DNA-3-methyladenine	IPR005019 (PFAM): G3DSA:1.10.340	2,717	3,091	1,968	2,772	3,111									
Solyc02g082130	LOW QUALITY:Surfeit locus protein 6 (AHRD V3.3 *** AT5G05210.2)		F:GO:0003677: F:G(	F:DNA binding: F:RNA binding: C:nucleolus: C:cytosolic large rit			IPR029188 (PFAM): IPR029190 (PFA	50,517	67,401	55,566	53,903	52,636									
Solyc02g082140	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT4G20170.1)		C:GO:0016021: F:G(	C:integral component of membrane: F:transferase activity, trans			IPR008166 (PFAM): mobidb-lite (MOB	121,741	95,371	36,466	36,871	45,175									
Solyc02g082150	LOW QUALITY:root hair specific 4 (AHRD V3.3 *-* AT1G30850.1)		C:GO:0009535: P:G(	C:chloroplast thylakoid membrane: P:photosystem I assembly: F			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,941	1,356	0,237	0,273	0,307									
Solyc02g082155	Ycf3-interacting protein 1, chloroplastic (AHRD V3.3 *-* A0A199VDY5_ANACO)		C:GO:0016020	C:membrane				0,500	0,855	0,508	0,539	0,518									
Solyc02g082160	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061F2D9_THECC)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (TIGF	2,027	1,839	1,002	1,296	1,253									
Solyc02g082170	Purine permease-related family protein (AHRD V3.3 *** B9GYR4_POPTR)		F:GO:0005215: C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	9,552	4,448	2,575	0,819	1,439					-1,632	0,001			down
Solyc02g082180	DNA helicase (AHRD V3.3 *** K4BA88_SOLLC)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:3.6.1.15	Nucleoside-triphosph	IPR008049 (PRINTS): IPR001208 (PF	20,520	20,313	27,893	23,039	25,150									
Solyc02g082190	CTP synthase (AHRD V3.3 *** M1B2B1_SOLTU)		F:GO:0003883: P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR004468 (TIGRFAM): IPR029062 ((	20,448	22,975	20,745	23,225	22,695									
Solyc02g082200	Glutaredoxin (AHRD V3.3 *** F5C0G4_SOLCH)		F:GO:0009055: F:G(	F:electron transfer activity: F:protein disulfide oxidoreductase a			IPR004480 (TIGRFAM): G3DSA:3.40.:	59,952	73,136	145,657	151,015	155,522									
Solyc02g082210	transmembrane protein (AHRD V3.3 *** AT3G26950.1)		C:GO:0016021	C:integral component of membrane			PTHR35736 (PANTHER)	10,230	10,239	8,191	6,931	7,405									
Solyc02g082215	transmembrane protein (AHRD V3.3 *-* AT3G26950.1)		C:GO:0016021	C:integral component of membrane			PTHR35736 (PANTHER)	8,336	6,878	7,611	6,369	6,585									
Solyc02g082220	Transport protein Sec24 (AHRD V3.3 *** B9HM39_POPTR)		P:GO:0006886: P:G(	P:intracellular protein transport: P:endoplasmic reticulum to Gol(			IPR007123 (PFAM): IPR036465 (G3D	108,577	93,497	129,449	141,865	131,568									
Solyc02g082230	Serine/threonine-protein phosphatase (AHRD V3.3 *** K4BA93_SOLLC)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SN	28,600	28,052	37,955	36,834	35,162									
Solyc02g082240	LOW QUALITY:UDP-N-acetylenolpyruvoylglucosamine reductase (AHRD V3.3 -** A0A1D1XWN5_9ARAE)						PTHR34996 (PANTHER): PTHR34996	0,302	0,412	0,170	0,098	0,187									
Solyc02g082250	Thioredoxin reductase (AHRD V3.3 *** K4BA95_SOLLC)		F:GO:0004791: C:G(	F:thioredoxin-disulfi	EC:1.8.1.9	Thioredoxin-disulfide	IPR000103 (PRINTS): PR00368 (PRIN	1,285	1,099	1,400	1,863	2,004									
Solyc02g082260	3-hydroxy-3-methylglutaryl CoA reductase		F:GO:0004420: P:G(	F:hydroxymethylglut	EC:1.1.1.34	Hydroxymethylglutary	IPR002202 (PRINTS): IPR009023 (G3	48,911	72,490	16,281	21,681	21,533	0,595	0,027					up		
Solyc02g082270	RNA binding protein, putative (AHRD V3.3 *** B9R8T5_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	141,465	113,663	136,103	182,204	173,329					0,424	0,029			up
Solyc02g082280	Trafficking particle complex subunit 11 (AHRD V3.3 *** A0A0B0N1N2_GOSAR)						IPR021773 (PFAM): IPR025876 (PFA	36,528	33,095	31,146	31,542	29,293									
Solyc02g082290	MORC family CW-type zinc finger protein 3 (AHRD V3.3 *** A0A1D1ZIG9_9ARAE)		F:GO:0008270	F:zinc ion binding			PF17942 (PFAM): G3DSA:3.30.40.10(	22,668	27,078	4,592	4,945	5,411									
Solyc02g082300	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A0K9NSQ5_ZOSMR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	2,005	1,889	2,259	2,580	2,563									
Solyc02g082310	Kinase-like protein (AHRD V3.3 *-* A0A0K9NZY4_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	2,593	2,107	2,111	1,805	1,999									
Solyc02g082315	F-box family protein (AHRD V3.3 --* AT2G41473.1)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128(	0,000	0,061	0,000	0,076	0,023									
Solyc02g082320	LOW QUALITY:F-box family protein (AHRD V3.3 *-* B9IAP0_POPTR)						PTHR31790:SF28 (PANTHER): PTHR:	0,019	0,000	0,025	0,022	0,024									
Solyc02g082330	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G12770.2)						mobidb-lite (MOBIDB_LITE)	0,461	0,379	1,115	0,904	1,149									
Solyc02g082340	RNA polymerase I specific transcription initiation factor RRN3 protein (AHRD V3.3 *** AT2G34750.1)		F:GO:0001042: F:G(	F:RNA polymerase I core binding: F:RNA polymerase I general t			IPR007991 (PFAM): mobidb-lite (MOB	424,900	301,668	163,555	161,669	154,978									
Solyc02g082350	Leucine-rich repeat-containing protein, putative (AHRD V3.3 *** B9T2K7_RICCO)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR003591 (SMA	35,901	24,078	24,572	31,022	31,700									
Solyc02g082360	Eukaryotic translation initiation factor 6 (AHRD V3.3 *** K4BAA6_SOLLC)		P:GO:0042256: F:G(	P:mature ribosome assembly; F:ribosome binding			IPR002769 (SMART): IPR002769 (PF.	2,180	2,064	2,153	2,303	2,640									
Solyc02g082370	LOW QUALITY:myb-like transcription factor family protein (AHRD V3.3 --* AT5G47390.1)							0,000	0,000	0,000	0,000	0,023									
Solyc02g082390	LOW QUALITY:MYB-like transcription factor family protein (AHRD V3.3 *** A0A072USM0_MEDTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,166	0,232	0,121	0,170	0,261									
Solyc02g082400	Transcription factor jumonji domain-containing protein (AHRD V3.3 *** D7KN75_ARALL)		C:GO:0000785: F:G(	C:chromatin: F:transcription regulatory region sequence-specifi(			IPR003347 (SMART): IPR003347 (PF.	53,871	43,827	56,199	53,170	51,182									
Solyc02g082410	Tonoplast monosaccharide transporter 3	TMT3	C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	1,330	0,980	0,992	0,800	0,850									
Solyc02g082420	RING/U-box superfamily protein (AHRD V3.3 *** AT1G20823.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	17,271	18,080	8,941	7,450	9,278									
Solyc02g082430	MLO-like protein (AHRD V3.3 *** K4BAB3_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	51,599	64,842	62,242	62,527	61,449									
Solyc02g082435	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A0B2SBZ1_GLYSO)		F:GO:0005524: P:G(	F:ATP binding: P:mismatch repair: P:reciprocal meiotic recombination: F:ATPase activity: C:mismatch r				2,526	6,498	0,977	1,647	1,670	1,389	0,002					up		
Solyc02g082440	NSP-interacting kinase 2 (AHRD V3.3 --* AT3G25560.3)							16,113	26,068	6,803	9,205	8,967									
Solyc02g082450	Auxin efflux carrier family protein (AHRD V3.3 *** AT2G17500.4)		C:GO:0016021: P:G(	C:integral component of membrane: P:transmembrane transport			IPR004776 (PFAM): PTHR31651:SF3	0,823	1,967	1,800	3,159	3,145									
Solyc02g082460	DIS3-like exonuclease 2 (AHRD V3.3 *-* A0A1D1YDW5_9ARAE)		F:GO:0003723: F:G(	F:RNA binding; F:ribonuclease activity			IPR002716 (SMART): IPR001900 (SM	70,501	68,152	65,415	65,855	66,439									
Solyc02g082470	Kinase, putative (AHRD V3.3 *** B9S6W8_RICCO)		F:GO:0004540: F:G(	F:ribonuclease activity: F:protein kinase activity: F:protein bindi			IPR018997 (PFAM): IPR000719 (SM	69,324	58,716	134,725	141,512	132,554									
Solyc02g082480	glutamate receptor-like 3.5	GLR3_5	F:GO:0004970: C:G(	F:ionotropic glutamate receptor activity; C:membrane			PR01176 (PRINTS): IPR001320 (SMA	36,128	28,630	22,572	23,057	23,224									
Solyc02g082490	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G51470.1)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF.	5,313	6,545	3,041	3,518	4,122									
Solyc02g082500	Ribosomal protein L11 (AHRD V3.3 *** A9P9X1_POPTR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR036796 (G3	24,607	28,235	24,392	19,433	21,505									
Solyc02g082510	Amino acid transporter, putative (AHRD V3.3 *** B9S6V9_RICCO)		P:GO:0003333: F:G(	P:amino acid transmembrane transport: F:amino acid transmem			IPR013057 (PFAM): PTHR22950:SF4(	43,454	80,921	43,885	52,356	46,858									
Solyc02g082520	Amino acid transporter, putative (AHRD V3.3 *** B9S6V9_RICCO)		P:GO:0003333: F:G(	P:amino acid transmembrane transport: F:amino acid transmem			IPR013057 (PFAM): PTHR22950 (PAI	0,124	0,057	2,247	5,107	3,327					1,187	0,000			up
Solyc02g082540	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XCL1_CYNCS)		F:GO:0005509: F:G(	F:calcium ion binding; F:protein binding			IPR000261 (SMART): IPR002048 (SM	138,929	120,983	135,169	132,377	134,535									
Solyc02g082550	Kinase family protein (AHRD V3.3 *** B9H679_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	72,499	72,999	18,211	30,564	29,477			0,692	0,003	0,748	0,000		up	up
Solyc02g082557	CTP synthase family protein (AHRD V3.3 --* AT4G20320.6)		F:GO:0005524: P:G(	F:ATP binding: P:mi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR029062 (G3DSA:3.40.50.GENE3D	8,224	9,385	5,635	8,883	8,122					0,656	0,023			up
Solyc02g082560	CTP synthase family protein (AHRD V3.3 *-* AT4G02120.5)		F:GO:0000166: F:G(	F:nucleotide binding	EC:6.3.4.2	CTP synthase (glutar	IPR017926 (PFAM): IPR029062 (G3D	0,021	0,098	0,025	0,025	0,000									
Solyc02g082570	Fact complex subunit spt16 (AHRD V3.3 *** A0A0B0N975_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	40,817	40,386	52,043	51,827	50,525									
Solyc02g082590	Trypsin-like peptidase domain protein (AHRD V3.3 *** G7KBB1_MEDTR)		P:GO:0006508: F:G(	P:proteolysis; F:peptidase activity			G3DSA:2.40.10.10 (GENE3D): PTHR2	1,856	1,443	3,314	3,557	3,297									
Solyc02g082600	Trypsin-like peptidase domain protein (AHRD V3.3 *-* G7KBB1_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:2.30.42.10 (GENE3D): PF178	2,748	2,797	4,789	4,488	4,102									
Solyc02g082610	Proliferating cell nuclear antigen (AHRD V3.3 --* PCNA_TOBAC)							1,103	0,710	0,393	1,090	0,614									
Solyc02g082613	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT1G03010.3)		P:GO:0006259: F:G(	P:DNA metabolic process; F:organic cyclic compound binding; F:heterocyclic compound binding				15,879	13,539	8,303	13,799	11,992					0,732	0,042			up
Solyc02g082615	DNA mismatch repair protein mutL (AHRD V3.3 --* W9RKQ1_9ROSA)		F:GO:0005524: P:G(	F:ATP binding: P:mismatch repair: P:reciprocal meiotic recombination: F:ATPase activity: F:mismatchec				1,670	1,670	0,925	1,153	0,754									
Solyc02g082617	Catalase (AHRD V3.3 --* D0VUY2_CITMA)							1,100	2,553	1,422	2,723	1,932									
Solyc02g082620	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT4G20940.1)							0,379	0,405	0,169	0,214	0,097									
Solyc02g082630	Phosphoinositide phosphatase SAC1 (AHRD V3.3 *-* G7K029_MEDTR)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			PTHR11200 (PANTHER): IPR030069	2,448	3,829	1,772	2,184	1,695									
Solyc02g082650	Mitochondrial transcription termination factor family protein (AHRD V3.3 --* AT2G21710.1)							2,775	4,205	2,300	5,105	3,483					1,142	0,001			up
Solyc02g082660	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)		F:GO:0005524: P:G(	F:ATP binding: P:mi	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR014790 (SMART): IPR013507 (SM	40,763	45,604	44,484	55,385	51,012									
Solyc02g082670	WUSCHEL-related homeobox 8 (AHRD V3.3 *** A0A151U858_CAJCA)		F:GO:0003677	F:DNA binding			IPR001356 (SMAF WOX	28,323	47,428	116,723	105,515	108,464	0,770	0,025					up		
Solyc02g082680	RB1-inducible coiled-coil protein 1, putative isoform 2 (AHRD V3.3 *** A0A061DL48_THECC)						IPR032795 (PFAM): mobidb-lite (MOB	38,273	27,512	24,364	23,323	22,091									
Solyc02g082690	Transducin/WD40 repeat protein (AHRD V3.3 *** A0A072TSJ0_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	60,730	53,406	122,206	122,964	118,515									
Solyc02g082700	High mobility group protein (AHRD V3.3 *** O49948_SOLTU)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			IPR009071 (SMART): IPR009071 (PF.	6,830	7,643	3,518	3,949	4,555									
Solyc02g082710	tail-anchored protein insertion receptor WRB-like protein (AHRD V3.3 *** AT4G16444.1)		P:GO:0071816	P:tail-anchored membrane protein insertion into ER membrane			IPR028945 (PFAM): PTHR11760 (PAI	8,869	8,020	12,029	11,728	10,784									
Solyc02g082720	Trypsin-like peptidase domain protein (AHRD V3.3 *** G7KBB1_MEDTR)		F:GO:0004252: F:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): IPR001478 (SN	2,787	5,596	7,349	7,983	8,411	1,030	0,025					up		
Solyc02g082730	GDP dissociation inhibitor family protein (AHRD V3.3 *** B9H5A6_POPTR)		F:GO:0005092: C:G(	F:GDP-dissociation inhibitor activity: C:Rab-protein geranylgera			IPR018203 (PRINTS): IPR036188 (G3	31,624	32,996	34,572	31,429	31,020									
Solyc02g082740	Dirigent protein (AHRD V3.3 *** K4BAE4_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495:SF6	55,309	59,937	2,941	1,226	2,606					-1,263	0,005			down
Solyc02g082750	Phosphoinositide phosphatase family protein (AHRD V3.3 *** AT5G66020.1)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			IPR002013 (PFAM): IPR030069 (PTH	0,996	1,128	0,501	0,452	0,637									
Solyc02g082760	ethylene-responsive catalase	er60	F:GO:0004096: P:G(	F:catalase activity:	EC:1.11.1.7: EC:1.1'	Peroxidase: Catalase	IPR018028 (PRINTS): IPR011614 (SN	48,067	96,654	48,738	50,666	74,945	1,034	0,000	0,618	0,000			up	up	
Solyc02g082763	Phosphoinositide phosphatase family protein (AHRD V3.3 *-* AT5G66020.1)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			IPR002013 (PFAM): IPR030069 (PTH	3,181	2,720	4,139	4,320	4,060									
Solyc02g082767	ARM repeat superfamily protein (AHRD V3.3 --* AT3G60740.3)		F:GO:0005524: P:G(	F:ATP binding: P:mismatch repair: P:reciprocal meiotic recombination: F:ATPase activity: F:mismatchec				14,721	15,822	20,512	19,635	21,097									
Solyc02g082770	Phosphoinositide phosphatase family protein (AHRD V3.3 *-* AT3G51460.1)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			PTHR11200 (PANTHER): IPR030069	18,925	18,655	27,113	27,718	28,557									
Solyc02g082800	Ubiquitin 1, related protein (AHRD V3.3 *** G7K017_MEDTR)		F:GO:0005515	F:protein binding			IPR000626 (SMART): IPR015940 (SM	139,549	130,180	163,629	164,182	159,335									
Solyc02g082810	Poly(A) polymerase, putative (AHRD V3.3 *** B9S6T6_RICCO)		F:GO:0003723: P:G(	F:RNA binding: P:RNA processing: F:nucleotidyltransferase acti			IPR032828 (PFAM): G3DSA:3.30.460	11,970	10,719	9,657	10,101	9,607									
Solyc02g082820	cyclin B2	cycb2	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	0,213	0,168	0,000	0,000	0,000									
Solyc02g082830	Phosphoserine aminotransferase (AHRD V3.3 *** K4BAF3_SOLLC)		F:GO:0004648: P:G(	F:O-phospho-L-seri	EC:2.6.1.52	Phosphoserine trans	IPR015421 (G3DSA:3.40.640.GENE3I	52,717	68,952	28,025	20,163	23,927									
Solyc02g082840	Protein GRIP (AHRD V3.3 *** A0A0B2S9J7_GLYSO)		C:GO:0005802: P:G(	C:trans-Golgi network; P:reciprocal meiotic recombination			IPR000237 (SMART): IPR000237 (PF.	77,499	64,418	53,382	47,900	53,219									
Solyc02g082850	Serine acetyltransferase (AHRD V3.3 *** G7K010_MEDTR)		C:GO:0005737: P:G(	C:cytoplasm: P:cys	EC:2.3.1.3	Serine O-acetyltrans	IPR010493 (SMART): G3DSA:2.160.1	7,065	6,635	11,850	10,108	13,399									
Solyc02g082860	Isocitrate dehydrogenase, putative (AHRD V3.3 *** B9SRZ2_RICCO)		F:GO:0004449: P:G(	F:isocitrate dehydro	EC:1.1.1.41	Isocitrate dehydroge	IPR024084 (SMART): IPR004434 (TIC	11,673	12,177	16,661	17,496	16,085									
Solyc02g082870	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity			IPR025110 (PFAM): G3DSA:3.30.300	0,100	0,174	0,000	0,000	0,000									
Solyc02g082880	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity			G3DSA:3.30.300.310 (GENE3D): IPR(	0,000	0,101	0,000	0,022	0,094									
Solyc02g082890	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT2G29840.1)		F:GO:0008270: P:G(	F:zinc ion binding: P:protein ubiquitination: F:metal ion binding: F			IPR001841 (SMART): IPR013083 (G3	0,105	0,121	0,000	0,022	0,000									
Solyc02g082900	Adipocyte plasma membrane-associated protein (AHRD V3.3 *** W9T0J8_9ROSA)		P:GO:0009058: F:G(	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR018119 (PFAM): IPR011042 (G3D	40,128	34,758	8,247	11,892	13,136									
Solyc02g082910	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): IPR025110 (PFA	0,337	0,798	1,690	2,045	2,377									

Solyc02g082920	acidic extracellular 26 kD chitinase		F:GO:0004568; P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR000726 (PFAM); G3DSA:1.10.530	3,307	33,971	19,057	53,146	69,780	3,383	0,000	1,868	0,000	1,483	0,003	up	up	up
Solyc02g082930	acidic extracellular 27 kD chitinase		F:GO:0004568; P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR000726 (PFAM); G3DSA:1.10.530	8,133	17,961	107,766	180,167	165,409					0,745	0,012			up
Solyc02g082940	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM); IPR026057 (PFA	0,474	0,394	0,097	0,307	0,143									
Solyc02g082950	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	1,244	2,143	2,247	3,252	2,076									
Solyc02g082960	Chitinase (AHRD V3.3 *** Q9FS45_VITVI)		F:GO:0004568; P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR000726 (PFAM); G3DSA:1.10.530	0,040	0,138	0,072	0,025	0,048									
Solyc02g082970	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SH83_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	7,009	7,749	10,216	8,197	8,337									
Solyc02g082980	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7JYV4_MEDTR)						IPR004320 (PFAM); PTHR33070:SF3	0,000	0,060	0,000	0,025	0,024									
Solyc02g082985	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *-* G7K002_MEDTR)						IPR004320 (PFAM); PTHR33070 (PAN	0,038	0,073	0,122	0,022	0,047									
Solyc02g083000	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); mobidb-lite (MOB	0,061	0,039	0,046	0,120	0,070									
Solyc02g083010	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); PTHR31509:SF1	0,253	0,021	0,025	0,073	0,000									
Solyc02g083020	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); PTHR31509:SF1	0,118	0,059	0,000	0,000	0,119									
Solyc02g083030	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); mobidb-lite (MOB	0,000	0,043	0,025	0,025	0,000									
Solyc02g083040	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA86_MEDTR)						IPR004320 (PFAM); PTHR33070:SF1	0,115	0,021	0,022	0,048	0,024									
Solyc02g083050	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); PTHR33070:SF1	0,158	0,122	0,025	0,022	0,023									
Solyc02g083060	LOW QUALITY:Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 --* AT5G07300.1)							0,443	0,307	0,168	0,218	0,283									
Solyc02g083070	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA86_MEDTR)						IPR004320 (PFAM); mobidb-lite (MOB	0,278	0,211	0,075	0,069	0,071									
Solyc02g083080	LOW QUALITY:cysteine-rich RECEPTOR-like kinase (AHRD V3.3 --* AT4G23160.3)							0,080	0,037	0,025	0,025	0,023									
Solyc02g083090	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA83_MEDTR)						IPR004320 (PFAM); PTHR31509:SF1	0,322	0,156	0,050	0,072	0,023									
Solyc02g083100	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *-* G7LA83_MEDTR)						IPR004320 (PFAM); mobidb-lite (MOB	0,221	0,220	0,022	0,050	0,024									
Solyc02g083110	LOW QUALITY:DUF641 family protein (AHRD V3.3 *** A0A072UXH5_MEDTR)		P:GO:0009639; P:G(	P:response to red or far red light; P:negative gravitropism			IPR006943 (PFAM); mobidb-lite (MOB	83,648	72,701	24,374	20,841	26,687									
Solyc02g083120	DUF241 domain protein (AHRD V3.3 *** G7LA88_MEDTR)						IPR004320 (PFAM); PTHR31509 (PAN	9,780	12,451	5,786	5,641	5,269									
Solyc02g083130	Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *** AT4G35730.1)		P:GO:0015031	P:protein transport			IPR005061 (PFAM); G3DSA:1.20.126	12,849	21,125	7,879	9,054	8,593	0,742	0,049					up		
Solyc02g083140	ribonuclease E		F:GO:0003723; F:G(	F:RNA binding; F:ribonuclease activity; P:RNA processing			G3DSA:2.40.50.140 (GENE3D); IPR0(	18,746	20,735	19,600	21,454	23,654									
Solyc02g083150	S-acyltransferase (AHRD V3.3 *** K4BAI3_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM); PTHR22883 (PAN	12,500	11,718	24,113	23,719	23,087									
Solyc02g083170	F-box protein (AHRD V3.3 *** G7LA96_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR001810 (PF.	0,319	0,179	0,170	0,145	0,093									
Solyc02g083180	UPF0548 protein (AHRD V3.3 *** A0A061DGD7_THECC)						IPR018960 (PFAM); PTHR34202 (PAN	0,040	0,021	0,071	0,048	0,023									
Solyc02g083190	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9MX84_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR001810 (PF.	6,355	5,094	1,520	1,667	1,790									
Solyc02g083200	LOW QUALITY:F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT1G11270.2)		C:GO:0005739	C:mitochondrion			PTHR34890 (PANTHER)	0,481	0,680	0,638	0,636	0,779									
Solyc02g083220	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* K4BAK3_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	IPR007080 (PFAM); mobidb-lite (MOB	28,176	31,432	25,598	25,913	24,722									
Solyc02g083250	Ganglioside-induced differentiation-associated protein 2 (AHRD V3.3 *** A0A199VGA4_ANACO)						IPR001251 (SMART); IPR036865 (G3	48,905	48,125	57,990	46,750	51,030									
Solyc02g083260	GPI mannosyltransferase 1 (AHRD V3.3 *** PIGM_ARATH)		P:GO:0006506; C:G(	P:GPI anchor biosynthetic process; C:integral component of me			IPR007704 (PFAM); IPR007704 (PAN	11,555	11,051	13,170	14,905	12,430									
Solyc02g083270	anti-PCD protein 2	JJH2	C:GO:0016021	C:integral component of membrane			IPR012932 (SMART); G3DSA:3.40.30	24,542	26,678	18,251	16,811	22,487									
Solyc02g083280	Rhodanese-related sulfurtransferase (AHRD V3.3 *** B7FGV4_MEDTR)		F:GO:0016740	F:transferase activity			IPR001763 (SMART); IPR001763 (PF.	192,826	161,121	401,530	441,458	446,501									
Solyc02g083290	Kinase family protein (AHRD V3.3 *** B9N912_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS); IPR000719 (SM	25,522	27,728	37,166	44,685	39,860									
Solyc02g083310	Wound-responsive family protein, putative (AHRD V3.3 *** A0A061DF47_THECC)		F:GO:0004518	F:nuclease activity			IPR003729 (PFAM); IPR036104 (G3D	30,828	26,618	12,351	10,401	11,987									
Solyc02g083320	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT4G35785.2)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR000504 (PF.	91,745	90,681	119,684	111,304	109,031									
Solyc02g083330	LOW QUALITY:Terpenoid cyclases/Protein prenyltransferases superfamily protein (AHRD V3.3 --* AT3G29410.2)							0,019	0,021	0,000	0,025	0,023									
Solyc02g083340	Phospholipase D (AHRD V3.3 *-* K4BAK2_SOLLC)		F:GO:0003824	F:catalytic activity			IPR001736 (SMART); G3DSA:3.30.87	6,285	6,254	1,157	1,365	1,218									
Solyc02g083345	Phospholipase D (AHRD V3.3 *** K4BAK2_SOLLC)		F:GO:0003824	F:catalytic activity			IPR000008 (SMART); IPR001736 (PF.	14,302	12,793	2,174	2,491	2,864									
Solyc02g083350	RNA polymerase 2 largest subunit 1	RPB1	F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	PR01217 (PRINTS); IPR006592 (SMA	186,274	160,331	187,491	191,798	200,432									
Solyc02g083360	methionine-S-oxide reductase (AHRD V3.3 *** AT2G17705.1)						G3DSA:2.170.150.20 (GENE3D); PTH	7,966	7,703	7,368	7,882	7,038									
Solyc02g083370	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 --* AT1G58400.3)							0,436	0,498	0,359	0,665	0,494									
Solyc02g083375	Big1 (AHRD V3.3 *-* AT2G17710.1)						mobidb-lite (MOBIDB_LITE); PTHR338	2,588	2,339	24,219	30,326	26,171									
Solyc02g083380	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* A0A1D1ZDU6_9ARAE)						PTHR33872 (PANTHER); PTHR33872	3,083	3,154	25,421	29,536	25,714									
Solyc02g083390	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9SXB7_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR006620 (SMART); IPR005123 (PF.	49,553	49,206	49,780	42,949	47,282									
Solyc02g083400	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DF87_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART); IPR013083 (G3	30,178	27,172	17,902	20,317	20,793									
Solyc02g083410	Receptor-like protein kinase THESEUS 1 (AHRD V3.3 *** A0A061DGF7_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF.	10,338	10,682	19,093	22,024	22,354									
Solyc02g083420	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G38520.2)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART); IPR001932 (PF.	42,251	56,343	40,626	39,133	42,546									
Solyc02g083430	ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *** G7LB48_MEDTR)		C:GO:0016020	C:membrane			IPR027815 (PFAM); IPR003864 (PFA	12,358	11,183	10,980	11,161	11,426									
Solyc02g083440	F-box (AHRD V3.3 *** A0A0B0N0V1_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc02g083450	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT4G35880.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS); IPR032861 (PF	4,744	4,695	2,842	3,474	2,620									
Solyc02g083460	aspartyl protease family protein		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS); IPR032861 (PF	10,612	28,976	12,050	17,893	19,653	1,472	0,010	0,704	0,005	0,573	0,042	up	up	up
Solyc02g083470	Pre-rRNA-processing protein ESF1, putative (AHRD V3.3 *** B9T718_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:rRNA processing			IPR012580 (PFAM); mobidb-lite (MOB	34,622	47,760	31,327	30,302	27,313									
Solyc02g083480	Peroxidase (AHRD V3.3 *** K4BAL6_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,552	0,060	0,075	0,022	0,192									
Solyc02g083490	Peroxidase (AHRD V3.3 *** K4BAL7_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,852	1,324	0,143	0,050	0,024									
Solyc02g083500	cell wall integrity/stress response component (AHRD V3.3 *** AT5G66090.1)						IPR014729 (G3DSA:3.40.50.GENE3D	7,566	9,812	12,900	12,240	15,977									
Solyc02g083510	plasma membrane intrinsic protein 2.11	PIP2.11	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR000425 (PF	0,970	1,548	0,523	0,561	0,542									
Solyc02g083520	LOW QUALITY:BZIP transcription factor (AHRD V3.3 *** G7LB63_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (SMAF bZIP	0,000	0,021	0,000	0,022	0,000									
Solyc02g083540	MID1-complementing activity-like protein (AHRD V3.3 *** G7JXK8_MEDTR)						IPR006461 (PFAM); IPR006461 (TIGF	18,898	17,544	13,765	13,102	13,126									
Solyc02g083550	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** G7JXK3_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); IPR0(	0,019	0,064	0,198	0,152	0,023									
Solyc02g083560	Vacuolar protein sorting-associated protein 35 (AHRD V3.3 *** K4BAM4_SOLLC)		P:GO:0015031; C:G(	P:protein transport; C:retromer, cargo-selective complex; P:retr			IPR005378 (PFAM); IPR005378 (PIRS	32,224	26,615	31,279	32,353	32,724									
Solyc02g083570	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** G7JMD8_MEDTR)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART); IPR016135 (G3D	11,345	12,261	10,082	14,407	12,192									
Solyc02g083580	ROP GTPases family protein		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); SM00173 (SMAR	8,974	13,783	6,856	6,239	6,261									
Solyc02g083590	Dehydroquinate synthase (AHRD V1 ***- Q8RU74_SOLLC)%3B contains Interpro d	DHQS	F:GO:0003856; C:G(	F:3-dehydroquinate	EC:4.2.3.4	3-dehydroquinate syn	G3DSA:1.20.1090.10 (GENE3D); G3D	62,674	68,656	145,501	129,688	133,501									
Solyc02g083600	Cell cycle checkpoint protein RAD17 (AHRD V3.3 *** W9SMX8_9ROSA)		C:GO:0005634; P:G(	C:nucleus; P:DNA repair			IPR003593 (SMART); PF03215 (PFAM	3,960	4,101	3,399	3,422	3,742									
Solyc02g083610	bZIP transcription factor (DUF630 and DUF632) (AHRD V3.3 *-* AT2G27090.2)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM); IPR006868 (PFA	1,870	1,051	1,088	1,260	0,635									
Solyc02g083620	L-ascorbate peroxidase 5		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS); IPR002016 (PF	2,084	2,708	1,118	1,380	1,387									
Solyc02g083630	Ascorbate peroxidase (AHRD V3.3 *** Q9XGS8_ZANAE)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS); IPR002016 (PF	1,255	1,631	0,198	0,575	0,446									
Solyc02g083640	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G51280.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	0,116	0,157	0,000	0,000	0,000									
Solyc02g083650	Receptor-like protein 12 (AHRD V3.3 *-* A0A199UKR0_ANACO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	21,899	19,690	43,915	38,570	35,635									
Solyc02g083670	histidine kinase 1 (AHRD V3.3 *** AT2G17820.1)		F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS); IPR003594 (SM	34,871	20,224	3,620	3,256	3,770	-0,757	0,029					down		
Solyc02g083690	LOW QUALITY:Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)		C:GO:0005886	C:plasma membrane			IPR009686 (PFAM); mobidb-lite (MOB	0,282	0,413	0,146	0,246	0,142									
Solyc02g083700	Alpha-mannosidase (AHRD V3.3 *** K4BAN8_SOLLC)		F:GO:0004559; P:G(	F:alpha-mannosidas	EC:3.2.1.24	Alpha-mannosidase	IPR015341 (SMART); G3DSA:2.70.98	77,648	72,775	108,996	74,335	101,718					-0,550	0,001			down
Solyc02g083710	26S proteasome non-ATPase regulatory subunit 4 (AHRD V3.3 *** A0A0B2PG91_GLYSO)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; C:proteasome regulatory particle, base su			IPR003903 (SMART); IPR002035 (SM	112,404	114,228	197,806	191,925	184,252									
Solyc02g083720	MLO-like protein (AHRD V3.3 *** K4BAP0_SOLLC)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM); PTHR31942:SF9	0,059	0,061	0,025	0,125	0,000									
Solyc02g083725	MLO-like protein (AHRD V3.3 *-* K4BAP0_SOLLC)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM); PTHR31942 (PAN	0,059	0,019	0,000	0,025	0,024									
Solyc02g083730	Rhodanese-related sulfurtransferase (AHRD V3.3 *** G7JXI1_MEDTR)		F:GO:0016740	F:transferase activity			IPR001763 (SMART); IPR036873 (G3	0,575	1,038	0,343	0,739	0,566									
Solyc02g083740	Oligopeptide transporter, putative (AHRD V3.3 *** B9SUI4_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM); IPR004813 (TIGF	6,053	6,575	2,411	2,266	1,812									
Solyc02g083760	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7JWA0_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS); IPR001938 (SM	46,743	28,181	19,660	12,551	16,505	-0,704	0,019			-0,643	0,002	down		down
Solyc02g083765	Transformation/transcription domain-associated protein (AHRD V3.3 *-* A0A0B2SCB0_GLYSO)		C:GO:0000124; F:G(	C:SAGA complex; F	EC:2.7.11	Transferring phosphorus-containing groups		0,507	0,643	0,632	0,538	0,426									
Solyc02g083770	LOW QUALITY:L-lactate dehydrogenase (AHRD V3.3 --* LDH_MAIZE)							0,019	0,000	0,000	0,025	0,023									
Solyc02g083775	Transformation/transcription domain-associated protein (AHRD V3.3 *-* A0A0B0NIX5_GOSAR)		C:GO:0000123; P:G(	C:histone acetyltransferase complex; P:histone acetylation			PTHR11139 (PANTHER); IPR033317	1,896	2,623	1,565	1,864	1,766									
Solyc02g083780	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SU41_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	13,465	12,800	9,332	9,881	10,672									
Solyc02g083785	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G03240.1)							2,871	2,820	2,178	1,726	1,998									
Solyc02g083790	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7JW96_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS); IPR001938 (SM	2,753	1,773	3,006	3,230	2,921									
Solyc02g083800	Cold-shock DNA-binding family protein (AHRD V3.3 *** B9MXF4_POPTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR002059 (PRINTS); IPR011129 (SM	16,455	17,445	27,061	24,040	22,520									
Solyc02g083810	Ferredoxin--NADP reductase (AHRD V3.3 *** A0A0V0I3W8_SOLCH)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001709 (PRINTS); IPR001433 (PF	137,257	273,237	119,601	123,250	244,737	1,021	0,001	1,030	0,000			up	up	
Solyc02g083815	Lysine-specific histone demethylase 1 homolog 3 (AHRD V3.3 --* LDL3_ORYSI)							0,000	0,000	0,000	0,000	0,024									
Solyc02g083820	Armadillo repeat only (AHRD V3.3 *** W0TQK6_ACAMN)		F:GO:0005515; P:G(	F:protein binding; P:cell surface receptor signaling pathway			IPR000225 (SMART); IPR011989 (G3	47,116	24,175	24,732	50,258	38,682	-0,937	0,000	0,641	0,005	1,023	0,000	down	up	up
Solyc02g083830	Pectinesterase (AHRD V3.3 *** K4BAQ1_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM); IPR012334 (G3D	0,000	0,079	0,000	0,000	0,000									
Solyc02g083835	Chaperone DnaJ-like protein (AHRD V3.3 *** A0A1C6ZYA6_MEDSA)						IPR001623 (PRINTS); IPR001623 (SM	60,918	97,302	93,882	55,421	87,647					-0,757	0,000			down
Solyc02g083840	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G71420.1)							0,021	0,021	0,025	0,076	0,000									
Solyc02g083850	Calcium-dependent protein kinase (AHRD V3.3 *** C6KGT3_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART); IPR002048 (SM	13,050	25,802	10,128	6,940	9,785	1,007	0,006					up		
Solyc02g083860	flavanone 3-dioxygenase	F3H	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM); IPR005123 (PFA	191,444	187,526	1024,865	878,212	995,286									
Solyc02g083870	Gibberellin-regulated protein 2, putative (AHRD V3.3 *** B9SLF4_RICCO)						IPR003854 (PFAM); PTHR23201 (PAN	0,094	0,037	0,044	0,025	0,048									
Solyc02g083880	Gibberellin-regulated protein 2, putative (AHRD V3.3 *** B9SLF4_RICCO)						IPR003854 (PFAM); PTHR23201:SF2	33,417	39,711	3,047	2,037	3,079									
Solyc02g083890	Chalcone-flavanone isomerase family protein (AHRD V3.3 *** AT5G66230.1)	CHI					mobidb-lite (MOBIDB_LITE); PTHR280	0,748	0,928	0,192	0,076	0,071									
Solyc02g083900	Transformation/transcription domain-associated protein (AHRD V3.3 *** A0A0B0NPB1_GOSAR)		C:GO:0000123; F:G(	C:histone acetyltransferase complex; F:protein binding; F:kinase			IPR000403 (SMART); IPR003152 (SM	267,215	193,933	225,651	239,317	248,971									
Solyc02g083910	WEB family protein (AHRD V3.3 *-* A0A0B2RND5_GLYSO)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			PTHR32054:SF9 (PANTHER); PTHR3	0,000	0,021	0,000	0,000	0,000									
Solyc02g083920	WEB family protein (AHRD V3.3 *** A0A0B2SGS1_GLYSO)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			PTHR32054 (PANTHER); PTHR32054	0,000	0,039	0,000	0,000	0,000									
Solyc02g083930	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* A0A061DFB2_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	7,690	11,022	0,495	0,504	0,776									
Solyc02g083940	ubiquitin ligase complex subunit 1-like		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	12,891	21,684	13,538	12,241	13,421	0,776	0,027					up		
Solyc02g083950	wuschel	wus	F:GO:0003677	F:DNA binding			IPR001356 (SMAF WOX	0,021	0,018	0,000	0,000	0,000									
Solyc02g083960	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein (AHRD V3.3 *** Q9SL49_ARATH)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR037151 (G3DSA:2.60.120.GENE3	13,943	16,030	12,437	18,947	16,092					0,611	0,007			up
Solyc02g083980	Endoglucanase (AHRD V3.3 *** K4BAR6_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001701 (PFAM); IPR012341 (G3D	6,947	5,434	10,523	9,950	11,166									
Solyc02g083990	polyamine-modulated factor 1-binding protein (AHRD V3.3 *** AT2G17990.3)		P:GO:0009639; P:G(	P:response to red or far red light; P:negative gravitropism			PTHR31161:SF6 (PANTHER); IPR040	25,345	24,748	17,239	16,257	19,380									
Solyc02g084000	Protein AF-9 like (AHRD V3.3 *** A0A0B2RW51_GLYSO)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR005033 (PFAM); IPR038704 (G3D	7,297	6,274	16,274	19,102	17,697									
Solyc02g084005	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G34760.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM); PTHR31374:SF3	0,040	0,000	0,000	0,000	0,000									
Solyc02g084020	Small nuclear ribonucleoprotein (AHRD V3.3 *** G7LBD3_MEDTR)		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:spliceosomal complex			IPR001163 (SMART); IPR001163 (PF.	22,489	22,945	22,134	18,669	18,922									
Solyc02g084030	Peptide methionine sulfoxide reductase family protein (AHRD V3.3 *** AT2G18030.1)		F:GO:0008113; P:G(	F:peptide-methionin	EC:1.8.4.11	Peptide-methionine (	IPR002569 (PFAM); IPR002569 (TIGF	17,439	17,735	18,935	19,729	19,748									
Solyc02g084037	stress response NST1-like protein (AHRD V3.3 --* AT4G25690.2)							0,144	0,181	0,047	0,025	0,046									
Solyc02g084060	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT1G49450.1)							0,021	0,021	0,000	0,000	0,023									
Solyc02g084070	LOW QUALITY:Fatty acid desaturase 3 (AHRD V3.3 --* W9RE23_9ROSA)							0,000	0,037	0,000	0,025	0,000									
Solyc02g084090	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* A0A0B2QD15_GLYSO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR003959 (PFAM); G3DSA:3.40.50.3	0,197	0,136	0,119	0,222	0,047									
Solyc02g084100	LOW QUALITY:Regulator of G-protein signaling 5 (AHRD V3.3 -** A0A1D1YHJ0_9ARAE)							0,000	0,000	0,050	0,097	0,046									
Solyc02g084110	LOW QUALITY:Zinc finger CCCH domain-containing protein 30 (AHRD V3.3 --* W9SCT2_9ROSA)		F:GO:0046872	F:metal ion binding			PTHR33400 (PANTHER); PTHR33400	0,059	0,140	0,025	0,166	0,024									
Solyc02g084117	Cytochrome b561/ferric reductase transmembrane protein family (AHRD V3.3 --* AT2G30890.1)							0,203	0,473	0,093	0,100	0,165									
Solyc02g084120	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* W9RJ61_9ROSA)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR003959 (PFAM); G3DSA:3.40.50.3	0,416	0,295	0,369	0,574	0,282									
Solyc02g084130	uridine kinase-like 5 (AHRD V3.3 --* AT3G27440.3)							0,203	0,626	0,145	0,101	0,331									
Solyc02g084140	LOW QUALITY:Receptor-like protein kinase FERONIA (AHRD V3.3 --* M7YNS4_TRIUA)							0,000	0,021	0,022	0,000	0,000									
Solyc02g084150	LOW QUALITY:ATP-dependent Clp protease ATP-binding subunit clpX (AHRD V3.3 *-* M8CXA9_AEGTA)		F:GO:0004176; F:G(	F:ATP-dependent p	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,120	0,082	0,096	0,047	0,000									
Solyc02g084160	ATP-dependent clp protease ATP-binding subunit clpx, putative (AHRD V3.3 --* B9SPA4_RICCO)		F:GO:0046872	F:metal ion binding			PTHR33400 (PANTHER); PTHR33400	0,414	0,749	0,352	0,757	0,239									
Solyc02g084163	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* A0A0B2R7F7_GLYSO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			G3DSA:1.10.8.60 (GENE3D); PTHR11	0,217	0,156	0,223	0,345	0,190									
Solyc02g084167	DNA mismatch repair protein mutL (AHRD V3.3 --* A0A151THR9_CAJCA)							0,427	0,949	0,563	0,819	0,754									
Solyc02g084170	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* A0A0B2R7F7_GLYSO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			G3DSA:1.10.8.60 (GENE3D); IPR019	0,084	0,100	0,071	0,169	0,071									
Solyc02g084180	MUTL protein homolog 3 (AHRD V3.3 --* AT4G35520.8)							0,042	0,021	0,022	0,025	0,024									
Solyc02g084190	FORMS APLOID AND BINUCLEATE CELLS 1A (AHRD V3.3 --* AT1G34260.4)							0,098	0,099	0,097	0,170	0,024									
Solyc02g084200	Zinc finger transcription factor 19	C3H19	F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIL C3H	0,977	0,850	0,550	0,642	0,776									
Solyc02g084210	GDP-mannose 4,6 dehydratase 1 (AHRD V3.3 *** GMD1_ARATH)		F:GO:0008446; P:G(	F:GDP-mannose 4,	EC:4.2.1.47	GDP-mannose 4,6-de	IPR006368 (TIGRFAM); IPR016040 (F	5,566	5,778	0,212	0,263	0,187									
Solyc02g084220	Sodium-dependent phosphate transporter 1 (AHRD V3.3 *** A0A0B0PU91_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,736	3,622	4,326	5,003	3,888									
Solyc02g084230	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN87_SOLLC)						IPR010409 (SMAF BBR-BPC	103,059	67,140	118,083	101,297	97,042									
Solyc02g084240	H1 histone-like protein		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR005819 (PRINTS); IPR005818 (SM	81,377	79,087	262,266	200,100	195,307									
Solyc02g084250	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A0B2SBZ1_GLYSO)						IPR036890 (G3DSA:3.30.565.GENE3	0,019	0,019	0,000	0,000	0,000									
Solyc02g084270	Kinase family protein (AHRD V3.3 *-* D7M6L5_ARALL)		F:GO:0000166; F:G(	F:nucleotide binding; F:protein kinase activity; F:protein serine/t			G3DSA:3.30.200.20 (GENE3D)	0,021	0,059	0,000	0,000	0,000									
Solyc02g084280	Nuclear pore complex protein Nup98b (AHRD V3.3 *-* W6JLG1_NICBE)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural constituent of nuclear pore				5,882	8,362	1,820	3,208	3,229									
Solyc02g084285	Nuclear pore complex protein (AHRD V3.3 --* W9SV07_9ROSA)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural constituent of nuclear pore				1,501	2,920	0,865	1,037	1,178									
Solyc02g084290	Protein kinase superfamily protein (AHRD V3.3 --* AT1G18150.3)							0,176	0,062	0,074	0,121	0,118									
Solyc02g084300	CTP synthase (AHRD V3.3 *-* M1B2B1_SOLTU)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR017926 (PFAM); IPR029062 (G3D	0,276	0,343	0,122	0,219	0,167									
Solyc02g084310	CTP synthase (AHRD V3.3 *-* M1BXT3_SOLTU)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	PTHR11550:SF23 (PANTHER); IPR00	0,061	0,115	0,000	0,073	0,071									
Solyc02g084315	embryo defective 2410 (AHRD V3.3 --* AT2G25660.4)							0,473	0,896	0,352	0,852	0,730									
Solyc02g084330	decapping 5-like protein (AHRD V3.3 --* AT5G45330.3)							0,572	1,484	1,099	0,718	0,709									

Solyc02g084340	Pre-mRNA-splicing factor cwc25 (AHRD V3.3 *-* A0A151T6B0_CAJCA)				IPR019339 (SMART): IPR019339 (PF	28,306	28,876	38,166	35,445	36,173									
Solyc02g084350	NAC domain-containing protein, putative (AHRD V3.3 *** B9SZU8_RICCO)	NAC020	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,000	0,019	0,000	0,000	0,000									
Solyc02g084360	V-type proton ATPase proteolipid subunit (AHRD V3.3 *-* A0A0D3DHQ4_BRAOL)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis c	IPR000245 (PRINTS): IPR011555 (TI(	323,301	310,554	419,231	372,162	409,812									
Solyc02g084370	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BAV3_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR003591 (SMART): IPR000719 (SM	0,670	0,742	0,072	0,000	0,071									
Solyc02g084380	Ribosomal protein S6 (AHRD V3.3 *** A0A103XMX6_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR014717 (G3DSA:3.30.70.GENE3D	12,296	12,366	20,102	19,599	18,600									
Solyc02g084390	Kinesin-like protein (AHRD V3.3 *** A0A0V0IYV5_SOLCH)		F:GO:0003777; F:G(	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	51,852	48,683	3,014	2,584	2,815									
Solyc02g084400	Protein kinase-like (AHRD V3.3 *** Q2HTV1_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph	IPR004147 (PFAM): PTHR10566 (PAI	19,447	14,430	1,590	0,611	2,203									
Solyc02g084410	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DGQ7_THECC)		F:GO:0004462; F:G(	F:lactoylglutathione EC:4.4.1.5 Lactoylglutathione ly	IPR004360 (PFAM): IPR029068 (G3D	3,191	4,114	1,634	1,784	2,213									
Solyc02g084420	B-box zinc finger family protein (AHRD V3.3 *** AT2G21320.1)	BBX18	F:GO:0008270	F:zinc ion binding	IPR000315 (SMAF DBB	12,696	6,318	13,534	12,473	15,047	-0,980	0,004					down		
Solyc02g084430	B-box type zinc finger family protein (AHRD V3.3 *-* A0A061E6F9_THECC)		F:GO:0008270	F:zinc ion binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	15,440	8,221	16,230	15,505	18,864	-0,882	0,004					down		
Solyc02g084440	Fructose-bisphosphate aldolase		F:GO:0004332; P:G(	F:fructose-bisphosp EC:4.1.2.13 Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	2541,028	3017,401	1171,251	1149,129	2056,980			0,810	0,000				up	
Solyc02g084450	Disease resistance protein (AHRD V3.3 *** A0A124SFK9_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:ADP binding	PR00364 (PRINTS): IPR003591 (SMA	5,142	4,631	4,123	3,742	4,242									
Solyc02g084455	LOW QUALITY:Ribonuclease H (AHRD V3.3 *** A2Q596_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bonds	IPR002156 (PFAM): IPR036397 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc02g084480	Golgin candidate 6 (AHRD V3.3 *-* A0A0B0P8X2_GOSAR)		C:GO:0000139; P:G(	C:Golgi membrane; P:intracellular protein transport; F:protein tra	IPR011989 (G3DSA:1.25.10.GENE3D	138,505	126,242	137,164	141,043	140,547									
Solyc02g084500	UPF0183 protein (AHRD V3.3 *** A0A0B2RUE4_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR005373 (PFAM): IPR005373 (PTH	17,163	12,103	22,760	20,110	19,722									
Solyc02g084510	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *-* W9SN42_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding	IPR019835 (SMART): IPR001965 (SM	15,219	14,978	16,292	17,300	16,906									
Solyc02g084520	Zinc finger transcription factor 20	C3H20	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding	IPR003169 (SMAF C3H	44,733	48,938	52,385	45,469	51,390									
Solyc02g084530	Transmembrane and coiled-coil domain-containing protein 4 (AHRD V3.3 *-* A0A0B2RW71_GLYSO)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,002	0,126	0,495	0,022	0,093									
Solyc02g084540	Transmembrane and coiled-coil domain-containing protein 4 (AHRD V3.3 *** A0A151R318_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR029058 (G3DSA:3.40.50.GENE3D	3,365	3,309	2,405	1,738	1,384									
Solyc02g084550	altered inheritance of mitochondria protein (AHRD V3.3 *** AT3G51100.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	27,915	33,765	36,410	35,641	34,470									
Solyc02g084560	Coiled-coil domain-containing 90B, mitochondrial (AHRD V3.3 *** A0A0B0NYS6_GOSAR)		C:GO:0005739; C:G(	C:mitochondrion; C:vacuolar membrane; C:integral component c	IPR024461 (PFAM): PTHR14360:SF1	3,956	4,468	3,502	3,491	3,858									
Solyc02g084570	Cytochrome P450 family protein (AHRD V3.3 *** B9MXJ3_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	5,650	6,157	0,968	1,483	1,793									
Solyc02g084580	LOW QUALITY:(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1 (AHRD V3.3 --* C80B1_ESCCA)				mobidb-lite (MOBIDB_LITE)	0,021	0,096	0,000	0,000	0,000									
Solyc02g084590	GATA transcription factor (AHRD V3.3 *** K4BAX4_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ion	IPR000679 (SMAF GATA	4,310	3,822	2,059	3,024	3,840			0,888	0,037				up	
Solyc02g084600	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** A0A061DFG6_THECC)		F:GO:0005515	F:protein binding	PR00019 (PRINTS): IPR003591 (SMA	32,859	30,574	6,852	7,693	7,555									
Solyc02g084610	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A0K9PNT4_ZOSMR)		F:GO:0005515	F:protein binding	IPR001611 (PFAM): IPR032675 (G3D	10,861	7,788	2,471	1,948	2,629									
Solyc02g084620	Forkhead-associated (FHA) domain-containing protein (AHRD V3.3 *-* AT3G54350.5)		F:GO:0002151; F:G(	F:G-quadruplex RNA binding; F:protein binding; C:Ino80 complex	IPR000253 (SMART): G3DSA:2.60.20	28,109	21,929	18,109	17,421	17,713									
Solyc02g084630	TDR6 transcription factor	tdr6	F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRINT MIKC_MADS	97,248	84,876	21,484	16,941	21,395									
Solyc02g084640	Aldehyde dehydrogenase (AHRD V3.3 *** K4BAX9_SOLLC)		P:GO:0006081; F:G(	P:cellular aldehyde metabolic process; F:oxidoreductase activit	IPR016162 (G3DSA:3.40.605.GENE3I	56,755	47,861	10,913	7,922	9,946									
Solyc02g084650	oxidoreductase-like protein, amino-terminal protein (AHRD V3.3 *-* AT5G17280.1)				IPR019180 (PFAM): mobidb-lite (MOB	19,196	20,977	17,537	19,261	17,083									
Solyc02g084660	Glutaredoxin (AHRD V3.3 *-* A0A124SH95_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): IPR011899 (TI(	10,475	11,042	11,131	14,321	13,487									
Solyc02g084670	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT3G51070.1)		F:GO:0008168	F:methyltransferase activity	G3DSA:3.40.50.150 (GENE3D): IPR0(	0,401	0,533	0,433	0,528	0,189									
Solyc02g084680	Lateral root primordium protein-related, putative (AHRD V3.3 *** A0A061DFV6_THECC)				IPR006510 (TIGRI SRS	4,589	4,746	3,480	3,655	3,336									
Solyc02g084690	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** A0A0B0NWT2_GOSAR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR342	155,269	132,645	209,030	195,165	185,450									
Solyc02g084700	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0P1Q2_GOSAR)				PF17942 (PFAM): PF13589 (PFAM): I	58,712	51,955	66,770	66,063	64,690									
Solyc02g084710	Thioredoxin (AHRD V3.3 *** E2GMW1_VITVI)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu	PR00421 (PRINTS): G3DSA:3.40.30.1	0,040	0,019	0,000	0,022	0,000									
Solyc02g084720	beta-galactosidase 6	tbg6	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS): G3DSA:3.20.20	315,795	243,399	86,984	73,917	85,827									
Solyc02g084730	rRNA adenine N(6)-methyltransferase (AHRD V3.3 *** K4BAY8_SOLLC)		P:GO:0000154; F:G(	P:rRNA modification; F:rRNA (adenine-N6,N6-)-dimethyltransfer	IPR020598 (SMART): G3DSA:3.40.50	0,900	0,972	1,014	0,818	1,188									
Solyc02g084740	Cytochrome P450 (AHRD V3.3 *** D7MBI4_ARALL)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR002403 (PRINTS): IPR001128 (PF	8,983	13,945	7,537	12,175	6,269	0,659	0,042			0,699	0,018	up		up
Solyc02g084750	Radical sam protein, putative (AHRD V3.3 *** B9S686_RICCO)		P:GO:0006400; F:G(	P:tRNA modification; F:transferase activity; F:4 iron, 4 sulfur clu	IPR006638 (SMART): IPR005839 (TI(	13,241	13,976	19,767	19,535	20,069									
Solyc02g084760	Ubiquitin conjugating enzyme (AHRD V3.3 *** A6MUS6_GOSHI)		F:GO:0005524; F:G(	F:ATP binding; F:transferase activity; P:seed trichome elongatio	SM00212 (SMART): IPR000608 (PFAI	32,170	31,520	50,769	51,757	45,443									
Solyc02g084770	Mitochondrial carrier protein, expressed (AHRD V3.3 *** Q6AVS9_ORYSJ)		F:GO:0022857	F:transmembrane transporter activity	IPR018108 (PFAM): IPR023395 (G3D	6,450	6,490	2,261	2,422	2,491									
Solyc02g084800	Peroxidase (AHRD V3.3 *** A0A0D9X2X2_9ORYZ)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,174	0,165	0,194	0,495	0,516									
Solyc02g084810	AT4G36440-like protein (AHRD V3.3 *** A0A097PKG1_SOLLC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR357	21,021	19,153	18,483	17,605	17,289									
Solyc02g084820	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 *** AT1G75420.1)		C:GO:0016021	C:integral component of membrane	PF16994 (PFAM): G3DSA:3.40.50.20(	44,932	39,504	48,931	47,713	45,189									
Solyc02g084830	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YGR3_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (TIGRFAM): IPR002885 (F	6,717	7,423	6,582	6,025	5,922									
Solyc02g084840	Dhn1 protein (AHRD V3.3 *** O48621_SOLCO)		P:GO:0009415	P:response to water	IPR000167 (PFAM): mobidb-lite (MOB	4,836	13,588	9,339	24,292	2,292									
Solyc02g084850	Abscisic acid and environmental stress-inducible protein TAS14 (AHRD V3.3 *** TAS14_SOLLC)		P:GO:0009415	P:response to water	IPR000167 (PFAM): mobidb-lite (MOB	12,798	22,447	13,194	4,601	5,040									
Solyc02g084860	BZIP transcription factor family protein (AHRD V3.3 *** B9H4F3_POPTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	1,775	2,666	0,025	0,000	0,047									
Solyc02g084870	mitogen-activated protein kinase 8	mapk8	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	16,211	17,152	60,213	84,784	53,367					0,497	0,008			up
Solyc02g084880	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G27660.1)		F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DS bHLH	0,356	0,459	0,359	0,573	0,378									
Solyc02g084890	NBS-LRR disease resistance protein NBS50 (AHRD V3.3 *** A0A0F6RAM2_9ROSI)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): PF18052 (PFAM)	97,572	31,875	12,304	57,258	32,882	-1,590	0,000	1,412	0,000	2,215	0,000	down	up	up
Solyc02g084900	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G18193.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): G3DSA:3.40.50	51,738	39,881	19,988	28,470	29,808			0,572	0,016	0,509	0,039		up	up
Solyc02g084910	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G17760.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): G3DSA:3.40.50	0,634	0,470	0,420	0,681	0,562									
Solyc02g084920	fruit-specific protein TOM2A11		F:GO:0004298; C:G(	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR001353 (PFAM): IPR029055 (G3D	248,449	264,590	278,482	270,078	260,992									
Solyc02g084930	Cytochrome P450 family protein (AHRD V3.3 *** G7LDW2_MEDTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,952	1,624	0,234	0,381	0,658									
Solyc02g084950	Carboxyl methyltransferase (AHRD V3.3 *** A0A1B4Z3V4_9ROSA)		F:GO:0008168	F:methyltransferase activity	IPR005299 (PFAM): G3DSA:3.40.50.1	5,552	2,434	19,160	19,555	19,331	-1,156	0,035					down		
Solyc02g084960	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072TTD0_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR33640:SF1 (PANTHER): PTHR3	2,643	4,617	0,827	1,286	0,870									
Solyc02g084970	Phosphatidic acid phosphatase family protein, putative (AHRD V3.3 *** A0A061DFN2_THECC)		P:GO:0006487; P:G(	P:protein N-linked g EC:3.6.1.43 Dolichyldiphosphatas	G3DSA:1.20.144.10 (GENE3D): IPR0(	0,622	1,101	0,896	1,095	0,939									
Solyc02g084980	Hexosyltransferase (AHRD V3.3 *** K4BB12_SOLLC)		P:GO:0006012; F:G(	P:galactose metabo EC:2.4.1.123 Inositol 3-alpha-galac	IPR029044 (G3DSA:3.90.550.GENE3I	3,472	8,272	17,615	20,496	24,278									
Solyc02g084990	Mannan endo-1,4-beta-mannosidase-like protein (AHRD V3.3 *** G7KF03_MEDTR)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001547 (PFAM): G3DSA:3.20.20.8	318,142	264,279	137,703	102,947	103,322									
Solyc02g085000	Bacteriophage N4 adsorption B (AHRD V3.3 *** A0A0B0PFT8_GOSAR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	53,157	54,628	125,619	131,177	115,878									
Solyc02g085005	BnaC08g22290D protein (AHRD V3.3 *** A0A078CC33_BRANA)				PTHR35291 (PANTHER)	0,808	0,909	0,769	0,718	0,798									
Solyc02g085010	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3-like protein (AHRD V3.3 --* AT1G17770.1)				PTHR35291 (PANTHER)	21,337	11,414	1,869	5,127	3,941	-0,879	0,046	1,076	0,012	1,456	0,000	down	up	up
Solyc02g085020	dihydroflavonol 4-reductase	DFR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding	G3DSA:3.40.50.720 (GENE3D): IPR0(	1,952	1,909	0,096	0,195	0,351									
Solyc02g085025	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 --* AT5G37740.2)					0,019	0,043	0,025	0,025	0,000									
Solyc02g085030	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103XYN8_CYNCS)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR036869 (G3DSA:1.10.287.GENE3I	8,787	5,685	5,517	4,226	5,717									
Solyc02g085035	Chaperone DnaJ-domain containing protein (AHRD V3.3 *** F4JPR4_ARATH)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	mobidb-lite (MOBIDB_LITE): mobidb-lit	23,118	13,002	13,735	10,981	12,942									
Solyc02g085040	GAMMA carbonic anhydrase (AHRD V3.3 *** G5DWW7_SILLA)				G3DSA:2.160.10.10 (GENE3D): IPR0(	76,228	71,801	79,404	63,670	69,930									
Solyc02g085050	Soluble inorganic pyrophosphatase (AHRD V3.3 *** S4SPV0_HEVBR)		F:GO:0000287; F:G(	F:magnesium ion bi EC:3.6.1.1 Inorganic diphosphat	IPR008162 (PFAM): IPR036649 (G3D	46,133	49,331	47,856	44,689	44,262									
Solyc02g085060	Replication factor C subunit 3 (AHRD V3.3 *** A0A151TIB1_CAJCA)		F:GO:0003677; P:G(	F:DNA binding; P:DNA replication	G3DSA:3.40.50.300 (GENE3D): mobi(	0,019	0,000	0,000	0,022	0,023									
Solyc02g085070	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G36530.2)		F:GO:0003824	F:catalytic activity	IPR000639 (PRINTS): IPR000073 (PF	0,040	0,064	0,049	0,050	0,046									
Solyc02g085080	Transmembrane protein 53 (AHRD V3.3 *** A0A151TIA0_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR008547 (PFAM): PTHR12265:SF1	13,030	13,495	22,045	20,035	22,553									
Solyc02g085090	Syntaxin, putative (AHRD V3.3 *** A0A061DM52_THECC)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport	IPR006011 (SMART): IPR000727 (SM	0,259	0,431	0,071	0,144	0,093									
Solyc02g085100	Galactose mutarotase-like superfamily protein (AHRD V3.3 *** AT5G66530.3)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:isomerase activity; F:cart	IPR008183 (PFAM): IPR014718 (G3D	27,161	34,216	18,076	16,303	21,349									
Solyc02g085110	Laccase (AHRD V3.3 *** I1J8U1_SOYBN)		F:GO:0005507; P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR017761 (TIGRFAM): IPR008972 ((	0,181	0,176	0,090	0,048	0,093									
Solyc02g085120	Laccase (AHRD V3.3 *** I1LHT8_SOYBN)		F:GO:0005507; P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR011706 (PFAM): IPR008972 (G3D	1,142	3,243	0,022	0,072	0,257	1,530	0,002					up		
Solyc02g085130	Tubby-like F-box protein (AHRD V3.3 *** K4BB27_SOLLC)		F:GO:0005515	F:protein binding	IPR000007 (PRINTS): G3DSA:1.20.12	9,849	9,884	6,385	4,892	6,523									
Solyc02g085140	U-box domain-containing family protein (AHRD V3.3 *** U5GHQ7_POPTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR003613 (SMART): IPR003613 (PF	34,527	46,393	10,673	13,469	15,040									
Solyc02g085150	Late embryogenesis abundant (LEA) protein (AHRD V3.3 *** AT4G36600.2)		F:GO:0003677	F:DNA binding	IPR001005 (SMART): IPR004238 (PF	1,852	4,303	0,811	0,656	0,186									
Solyc02g085160	ZF-HD homeobox protein (AHRD V3.3 *** A0A0B2NTS1_GLYSO)		F:GO:0003677	F:DNA binding	IPR006455 (TIGRI ZF-HD	5,267	4,185	2,892	2,727	3,535									
Solyc02g085170	Sugar facilitator protein 10	SFP10	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): G3DSA:1.20.12	1,893	2,482	8,890	12,114	9,432									
Solyc02g085180	alpha/beta fold family protein		F:GO:0003824	F:catalytic activity	IPR000073 (PRINTS): IPR000639 (PF	25,722	24,998	13,174	9,280	11,542									
Solyc02g085190	GATA transcription factor, putative (AHRD V3.3 *** B9S6H2_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR000679 (SMAF GATA	0,019	0,019	0,022	0,000	0,000									
Solyc02g085220	Vacuolar sorting protein 39 (AHRD V3.3 *** AT4G36630.1)		P:GO:0016192	P:vesicle-mediated transport	IPR001180 (PFAM): IPR019452 (PFAI	6,839	5,192	4,568	4,786	4,769									
Solyc02g085230	Nucleolar 6 (AHRD V3.3 *** A0A0B0N3X3_GOSAR)		F:GO:0003723; C:G(	F:RNA binding; C:cytosol; P:rRNA processing; P:tRNA export fro	IPR035371 (PFAM): IPR035368 (PFAI	11,781	13,228	6,887	6,775	6,965									
Solyc02g085240	AP-1 complex subunit sigma-like protein (AHRD V3.3 *** G7LES2_MEDTR)		F:GO:0008565; P:G(	F:protein transporter activity; P:protein transport; C:AP-3 adapto	IPR022775 (PFAM): IPR016635 (PIRS	2,183	1,883	2,059	1,563	2,168									
Solyc02g085245	Histone deacetylase (AHRD V3.3 --* A0A090M7H3_OSTTA)					0,167	0,103	0,172	0,165	0,094									
Solyc02g085250	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT5G49555.1)		F:GO:0005507; C:G(	F:copper ion binding; C:mitochondrion; F:oxidoreductase activit	IPR036188 (G3DSA:3.50.50.GENE3D	25,646	29,227	20,182	16,186	21,569									
Solyc02g085260	LOW QUALITY:Peptidase M20/M25/M40 family protein (AHRD V3.3 --* AT1G44180.3)				PTHR33622 (PANTHER): PTHR33622	0,000	0,080	0,000	0,000	0,047									
Solyc02g085280	ribosomal protein L6 family protein (AHRD V3.3 *** AT2G18400.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR019906 (PRINTS): IPR020040 (PF	31,300	30,322	28,274	27,244	29,194									
Solyc02g085285	Protein with RING/U-box and TRAF-like domain (AHRD V3.3 --* AT1G66660.1)					20,338	28,493	16,660	21,912	19,913					0,397	0,035			up
Solyc02g085290	Maf protein, putative (AHRD V3.3 *** B9SNZ2_RICCO)		F:GO:0047429	F:nucleoside-tripho EC:3.6.1.19 Acting on acid anhyd	IPR029001 (G3DSA:3.90.950.GENE3I	5,636	9,512	2,014	2,064	3,339	0,782	0,028					up		
Solyc02g085300	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G75170.2)		F:GO:0008526; P:G(	F:phosphatidylinositol transporter activity; P:phospholipid transp	IPR011074 (SMART): IPR001251 (SM	1,671	1,584	2,330	2,101	2,734									
Solyc02g085310	plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 --* AT3G17227.1)					32,205	38,847	27,249	28,266	28,987									
Solyc02g085315	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 --* A0A061DH70_THECC)					3,877	6,994	14,715	13,711	13,182									
Solyc02g085320	Maturase K (AHRD V3.3 --* MATK_PAESU)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,620	2,350	7,390	7,545	6,463									
Solyc02g085330	LOW QUALITY:late embryogenesis abundant protein (AHRD V3.3 *** AT5G66780.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,117	0,080	0,050	0,025	0,000									
Solyc02g085340	GRAS family transcription factor (AHRD V3.3 *** AT5G66770.1)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM GRAS	18,842	20,525	4,304	5,100	5,242									
Solyc02g085350	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (AHRD V3.3 *** K4BB47_SOLLC)		P:GO:0006099; F:G(	P:tricarboxylic acid cycle; F:oxidoreductase activity, acting on t	IPR027477 (G3DSA:3.90.700.GENE3I	374,119	322,524	1317,713	1272,321	1189,550									
Solyc02g085360	CYP90B3 mRNA for cytochrome P450	CYP90B3	F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR001128 (PRINTS): IPR002403 (PF	8,418	4,476	4,086	5,505	5,541	-0,882	0,034					down		
Solyc02g085370	plant U-box 23 (AHRD V3.3 --* AT2G35930.1)					3,503	3,288	4,660	4,372	3,911									
Solyc02g085380	Like-COV protein (AHRD V3.3 *** G7L895_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane	IPR007462 (PFAM): mobidb-lite (MOB	5,650	3,443	0,208	0,050	0,023									
Solyc02g085390	chromatin remodeling 1 (AHRD V3.3 *** AT5G66750.1)		F:GO:0005524	F:ATP binding	IPR014001 (SMART): IPR001650 (SM	9,004	10,322	4,044	1,792	3,053					-1,171	0,004			down
Solyc02g085400	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)		C:GO:0016021	C:integral component of membrane	IPR002781 (PFAM): PTHR14255 (PAI	1,942	4,073	1,233	1,238	1,544									
Solyc02g085420	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G43370.1)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U1 snRNP; F:U1 snRNA b	IPR000504 (SMART): IPR000504 (PF	323,718	315,738	320,358	293,517	313,307									
Solyc02g085430	Protein kinase superfamily protein (AHRD V3.3 *** AT4G34440.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	3,069	3,147	0,793	0,806	1,032									
Solyc02g085440	F-box protein (AHRD V3.3 *-* W9SND6_9ROSA)		F:GO:0005515	F:protein binding	PTHR44519 (PANTHER): IPR036047 (	0,402	0,843	0,137	0,100	0,257									
Solyc02g085450	BAC19.2 (AHRD V3.3 *** Q9FYX4_SOLLC)					1,352	0,962	2,773	2,247	2,359									
Solyc02g085460	sec23/sec24 transport family protein (AHRD V3.3 --* AT2G27460.1)					1,453	1,006	2,270	2,559	2,360									
Solyc02g085470	Transcription initiation factor IIB (AHRD V3.3 *** A0A0B0NFI7_GOSAR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:TBP-class prote	IPR000812 (PRINTS): IPR013763 (SM	8,770	8,462	8,747	7,902	7,660									
Solyc02g085480	Sugar transporter, putative (AHRD V3.3 *** A0A061DGB7_THECC)		C:GO:0016021	C:integral component of membrane	IPR010608 (PFAM): PTHR34358:SF2	5,066	6,053	3,880	4,065	4,091									
Solyc02g085490	DUF620 family protein (AHRD V3.3 *** G7ZW25_MEDTR)				IPR006873 (PFAM): PTHR31300:SF9	0,972	2,283	0,209	0,123	0,142									
Solyc02g085495	LOW QUALITY:30S ribosomal protein S7, chloroplastic (AHRD V3.3 *-* RR7_TOBAC)		P:GO:0006412	P:translation	IPR036823 (G3DSA:1.10.455.GENE3I	0,057	0,037	0,022	0,148	0,072									
Solyc02g085500	ovate	OVATE	P:GO:0045892	P:negative regulation of transcription, DNA-templated	mobidb-lite (MOBIDB_LITE): mobidb-lit	6,452	2,106	6,254	13,383	8,054	-1,594	0,001			1,096	0,000	down		up
Solyc02g085510	ovate family protein 1	OVATE	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (PFAM): IPR006458 (TIGF	0,879	0,321	0,801	1,711	1,063									
Solyc02g085520	Adenylosuccinate synthetase, chloroplastic (AHRD V3.3 *** PURA_SOLBU)		F:GO:0004019; F:G(	F:adenylosuccinate EC:6.3.4.4 Adenylosuccinate sy	IPR001114 (SMART): G3DSA:3.40.44	31,982	37,881	59,968	54,912	56,430									
Solyc02g085530	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* D7MBF2_ARALL)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,193	0,183	0,201	0,200	0,187									
Solyc02g085535	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* D7MBF2_ARALL)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	0,037	0,041	0,025	0,025	0,046									
Solyc02g085540	LOW QUALITY:NADH:ubiquinone oxidoreductase, ESSS subunit (AHRD V3.3 *** A0A118JWW1_CYNCS)				mobidb-lite (MOBIDB_LITE): PTHR313	177,820	180,501	309,435	285,134	294,219									
Solyc02g085550	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MBF2_ARALL)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,019	0,000	0,000	0,025	0,000									
Solyc02g085560	DNA-directed RNA polymerase III subunit RPC5 (AHRD V3.3 *** A0A0B2RSA7_GLYSO)		F:GO:0003899; C:G(	F:DNA-directed 5'-3 EC:2.7.7.6 DNA-directed RNA po	IPR006886 (PFAM): mobidb-lite (MOB	18,214	15,970	16,056	17,870	16,562									
Solyc02g085570	Splicing factor u2af large subunit, putative (AHRD V3.3 *-* B9SGJ4_RICCO)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:mRNA processing	IPR000504 (SMART): IPR000504 (PF	64,418	68,695	80,585	78,809	77,136									
Solyc02g085580	Zinc finger protein (AHRD V3.3 *** K9P0T0_9ROSI)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	3,570	8,104	1,817	2,497	2,657	1,205	0,006					up		
Solyc02g085590	BAC19.13 (AHRD V3.3 *** Q9FYW3_SOLLC)		F:GO:0045735	F:nutrient reservoir activity	IPR006045 (SMART): IPR014710 (G3	36,279	43,484	3,097	10,869	0,998									
Solyc02g085600	Transcription factor GRAS (AHRD V3.3 *** A0A103YGV0_CYNCS)	GRAS	P:GO:0030154; P:G(	P:cell differentiation; P:regulation of shoot system development	IPR005202 (PFAM GRAS	24,687	31,795	127,000	135,067	131,964									
Solyc02g085610	LEGBF4G L.esculentum GBF4G-box binding protein	gbf4	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	10,886	11,091	12,418	13,569	12,162									
Solyc02g085620	Protein kinase (AHRD V3.3 *** A0A087GEP9_ARAAL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PRINTS): IPR000719 (SM	0,575	0,597	0,025	0,000	0,000									
Solyc02g085630	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MXR7_POPTR)		F:GO:0003677	F:DNA binding	IPR000047 (PRINT HD-ZIP	1,997	3,917	1,534	5,793	4,484			1,532	0,019	1,901	0,000		up	up
Solyc02g085640	Xaa-Pro aminopeptidase 1	app1	F:GO:0070006	F:metalloaminopept EC:3.4.11 Acting on peptide bor	IPR000994 (PFAM): IPR029149 (G3D	58,482	56,920	82,465	76,034	80,470									
Solyc02g085650	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MBF2_ARALL)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	8,170	8,992	8,500	7,420	6,453									
Solyc02g085655	Aminopeptidase-like protein (AHRD V3.3 *** O23206_ARATH)		P:GO:0006508; F:G(	P:proteolysis; F:me EC:3.4.11 Acting on peptide bor	G3DSA:3.90.230.10 (GENE3D): IPR0(	0,240	0,245	0,219	0,148	0,284									
Solyc02g085660	Glycosyltransferase (AHRD V3.3 *** K4BB77_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	2,462	3,093	103,763	128,225	109,943									
Solyc02g085670	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K9PQR0_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM): G3DSA:1.20.125(	8,463	8,796	15,499	18,637	16,258									
Solyc02g085672	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* AT2G18600.2)		F:GO:0000166; F:G(	F:nucleotide binding; F:ATP binding; F:transferase activity	PTHR43953 (PANTHER): PTHR43953	0,222	0,241	0,158	0,049	0,094									
Solyc02g085676	alkaline/neutral invertase (AHRD V3.3 --* AT5G22510.2)					0,344	0,417	0,242	0,268	0,166									
Solyc02g085678	DNA mismatch repair Mlh3 (AHRD V3.3 *-* A0A0B0N7I8_GOSAR)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched		2,228	1,729	1,102	0,817	0,892									
Solyc02g085690	ubiquitin-conjugating enzyme family protein		F:GO:0005524; F:G(	F:ATP binding; F:transferase activity; F:ligase activity	SM00212 (SMART): IPR016135 (G3D	1,439	1,025	0,563	0,439	0,519									
Solyc02g085700	geranylgeranyl pyrophosphate synthetase	GGPS1	P:GO:0008299	P:isoprenoid biosynthetic process	IPR000092 (PFAM): IPR008949 (G3D	29,393	35,225	77,508	88,944	88,509									
Solyc02g085705	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 --* AT2G22190.2)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of		0,301	0,548	0,334	0,325	0,351									
Solyc02g085710	Geranylgeranyl pyrophosphate synthase 4 (AHRD V3.3 *** K7P523_TOBAC)	GGPS4	P:GO:0008299	P:isoprenoid biosynthetic process	IPR000092 (PFAM): IPR008949 (G3D	4,573	3,210	5,529	7,639	6,673									

Solyc02g085720	Geranylgeranyl pyrophosphate synthase 4 (AHRD V3.3 *** K7P523_TOBAC)		P:GO:0008299	P:isoprenoid biosynthetic process			IPR000092 (PFAM): IPR008949 (G3D	1,221	1,206	0,769	0,720	0,775									
Solyc02g085730	allene oxide cyclase	aoc	P:GO:0009695; F:G(	P:jasmonic acid bio	EC:5.3.99.6	Allene-oxide cyclase	IPR034871 (G3DSA:2.40.480.GENE3I	102,458	191,397	52,145	36,664	46,574	0,929	0,000			-0,505	0,005	up		down
Solyc02g085740	Ribosome biogenesis ERB1 (AHRD V3.3 *** A0A0B0NU98_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR37383 (PANTHER)	11,275	10,702	14,066	14,478	12,985									
Solyc02g085745	Rhomboid-like protein (AHRD V3.3 *** K4BB87_SOLLC)		F:GO:0004252; C:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR035952 (G3DSA:1.20.1540.GENE	29,416	76,609	25,049	44,990	72,012	1,409	0,000	1,521	0,000	0,849	0,000	up	up	up
Solyc02g085750	LuxR family transcriptional regulator, putative (AHRD V3.3 *** A0A072U7J6_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc02g085780	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G16040.1)						IPR000408 (PRINTS): IPR009091 (G3	56,177	54,472	55,589	42,531	48,720					-0,383	0,013			down
Solyc02g085790	T-complex protein 1 subunit zeta 1 (AHRD V3.3 *** TCPZA_ARATH)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR002423 (PF	58,404	58,439	89,298	81,420	84,481									
Solyc02g085810	HEAT repeat-containing protein (AHRD V3.3 *** AT1G67140.3)		C:GO:0005829; P:G(	C:cytosol; P:starch metabolic process; P:trehalose metabolic pr			IPR011989 (G3DSA:1.25.10.GENE3D	104,578	88,702	66,794	80,451	76,775									
Solyc02g085820	NADPH--cytochrome P450 reductase (AHRD V3.3 *** A0A0D9X5R3_9ORYZ)		F:GO:0003958; F:G(	F:NADPH-hemoprot	EC:1.6.2.4	NADPH--hemoproteir	IPR001709 (PRINTS): IPR001094 (PF	4,324	3,621	3,679	3,668	3,769									
Solyc02g085833	Rad23 UV excision repair protein family (AHRD V3.3 *** AT3G02540.3)		F:GO:0003684; F:G(	F:damaged DNA binding; F:protein binding; C:nucleus; P:nucleot			IPR004806 (PRINTS): IPR015940 (SM	57,842	54,785	67,431	66,842	65,091									
Solyc02g085850	ALG6, ALG8 glycosyltransferase family (AHRD V3.3 *-* A0A061EPH1_THECC)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:dolichol-linked oligosaccl			IPR004856 (PFAM): IPR004856 (PAN	3,712	2,885	2,947	3,239	3,859									
Solyc02g085860	ALG6, ALG8 glycosyltransferase family protein (AHRD V3.3 *** A0A072U6Q6_MEDTR)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:dolichol-linked oligosaccl			IPR004856 (PFAM): IPR039488 (PTH	5,302	4,413	4,741	4,795	4,541									
Solyc02g085870	beta-ketoacyl-coenzyme A synthase	CER6	P:GO:0006633; C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR016039 (G3D	55,229	42,173	26,209	39,847	24,697					0,604	0,012			up
Solyc02g085880	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	1,057	1,709	0,000	0,050	0,000									
Solyc02g085910	LOB domain-containing protein (AHRD V3.3 *** A0A0K9PUI8_ZOSMR)						IPR004883 (PFAM_LBD	3,117	5,975	13,406	14,598	8,675			-0,627	0,048				down	
Solyc02g085920	antigenic heat-stable protein (AHRD V3.3 *** AT1G56420.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	63,512	49,586	41,753	42,423	40,840									
Solyc02g085930	Peroxidase (AHRD V3.3 *** K4BBA2_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,592	0,523	0,309	0,218	0,259									
Solyc02g085935	Complex 1 LYR protein (AHRD V3.3 *** A0A103XDK3_CYNCS)						IPR008011 (PFAM): PTHR13166:SF4	4,046	3,601	3,695	4,260	3,608									
Solyc02g085950	cell wall protein X77373		F:GO:0004497; F:G(	F:monooxygenase a	EC:4.1.1.39	Ribulose-bisphospha	IPR024681 (PRINTS): IPR000894 (SM	16,479	92,082	0,643	0,563	1,621	2,508	0,000					up		
Solyc02g085960	LOW QUALITY:Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 --* C4J164_MAIZE)							1,214	1,519	0,000	0,126	0,000									
Solyc02g085980	no pollen germination related 1 (AHRD V3.3 --* AT1G27460.3)							0,019	0,041	0,097	0,139	0,094									
Solyc02g085990	60S ribosomal protein L17-1 (AHRD V3.3 --* RL171_HORVU)							0,098	0,092	0,075	0,147	0,024									
Solyc02g086000	indeterminate(ID)-domain 4 (AHRD V3.3 --* AT2G02080.5)		P:GO:0008150	P:biological_process			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,233	0,165	0,000	0,025	0,000									
Solyc02g086010	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT5G16120.4)						IPR029058 (G3DSA:3.40.50.GENE3D	0,180	0,392	0,025	0,073	0,163									
Solyc02g086020	LOW QUALITY:neurofilament protein-like protein (AHRD V3.3 --* AT3G05900.2)							0,019	0,000	0,000	0,000	0,000									
Solyc02g086030	LOW QUALITY:WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)							0,665	0,303	0,000	0,000	0,000									
Solyc02g086040	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G16120.4)						IPR000073 (PRINTS): IPR029058 (G3	0,019	0,104	0,046	0,025	0,023									
Solyc02g086050	Abscisic acid-deficient 4 (AHRD V3.3 *** A0A061EPF5_THECC)		C:GO:0016021	C:integral component of membrane			IPR025461 (PFAM): PTHR34543:SF1	2,572	2,965	4,929	5,238	4,707									
Solyc02g086060	zinc transporter (AHRD V3.3 *** AT5G38380.1)		C:GO:0016021	C:integral component of membrane			PTHR11562:SF58 (PANTHER): PTHR	8,411	7,284	11,048	10,229	9,381									
Solyc02g086080	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G38360.1)						IPR000073 (PFAM): IPR029058 (G3D	4,944	6,537	5,764	6,442	5,386									
Solyc02g086095	Mannose-6-phosphate isomerase (AHRD V3.3 *** K4BBB7_SOLLC)		F:GO:0004476; P:G(	F:mannose-6-phosp	EC:5.3.1.8	Mannose-6-phosphat	IPR016305 (PRINTS): IPR014710 (G3	11,119	12,558	8,046	8,378	7,742									
Solyc02g086100	AT2G18410-like protein (AHRD V3.3 *** A0A097PMT0_SOLLC)		P:GO:0002098; C:G(	P:tRNA wobble uridine modification; C:Elongator holoenzyme co			IPR019519 (PFAM): mobidb-lite (MOB	8,975	8,123	8,630	7,923	7,813									
Solyc02g086110	peptidase M50B-like protein (AHRD V3.3 *** AT1G67060.1),Pfam:PF13398		C:GO:0016021	C:integral component of membrane			PF13398 (PFAM): PTHR33979:SF3 (P	0,992	1,020	1,995	1,987	1,436									
Solyc02g086130	DnaA initiator-associating diaA (AHRD V3.3 *** A0A0B0PTA6_GOSAR)						IPR025486 (PFAM): IPR032795 (PFA	55,689	43,610	29,788	31,701	33,772									
Solyc02g086140	LOW QUALITY:homeobox Hox-B3-like protein (AHRD V3.3 *** AT5G38300.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,397	0,287	0,511	0,633	0,610									
Solyc02g086145	Major facilitator superfamily protein (AHRD V3.3 *** AT1G05030.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	44,371	49,244	73,239	72,583	84,791									
Solyc02g086150	Peptidyl-tRNA hydrolase (AHRD V3.3 *** A0A103Y0A6_CYNCS)		F:GO:0004045	F:aminoacyl-tRNA h	EC:3.1.1.29; EC:3.1.	Aminoacyl-tRNA hydr	IPR001328 (PFAM): IPR001328 (TIGF	7,413	7,776	11,454	13,651	15,087									
Solyc02g086170	Wall-associated receptor kinase-like 14 (AHRD V3.3 --* A0A0B2QLM0_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,151	4,564	5,889	5,871	7,015									
Solyc02g086180	Delta(7)-sterol-C5(6)-desaturase (AHRD V3.3 *** SC5D_TOBAC)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR11863 (PAN	4,096	6,982	1,262	1,206	1,365									
Solyc02g086200	Chloroplastic group IIA intron splicing facilitator CRS1 (AHRD V3.3 *** W9S0T5_9ROSA)		F:GO:0003723	F:RNA binding			IPR001890 (SMART): IPR001890 (PF.	0,040	0,000	0,000	0,000	0,000									
Solyc02g086210	Receptor-like kinase (AHRD V3.3 *** G7KUD4_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR025287 (PF.	6,492	15,919	2,065	4,533	7,015	1,315	0,046	1,753	0,000	1,129	0,006	up	up	up
Solyc02g086220	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G38220.3)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	40,118	36,967	25,852	24,631	26,728									
Solyc02g086225	B-block-binding subunit of TFIIIC protein (AHRD V3.3 --* AT1G59453.1)		P:GO:0003006; P:G(	P:developmental process involved in reproduction; P:embryo development ending in seed dormancy; P:				2,089	2,148	1,177	1,429	1,317									
Solyc02g086230	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T3G5_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	2,214	1,836	1,359	1,100	1,131									
Solyc02g086240	Ribosomal L5P family protein (AHRD V3.3 *** AT5G45775.2)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002132 (PIRSF): IPR031309 (PFA	132,155	130,700	119,501	100,333	110,376									
Solyc02g086250	titan9 (AHRD V3.3 *** AT3G20070.4)		P:GO:0009793; P:G(	P:embryo development ending in seed dormancy; P:endosperm			mobidb-lite (MOBIDB_LITE): PTHR354	2,781	3,026	0,505	0,334	0,468									
Solyc02g086260	LOW QUALITY:50S ribosomal protein-related, putative (AHRD V3.3 *** A0A061EGK7_THECC)						mobidb-lite (MOBIDB_LITE): PTHR345	18,364	14,040	10,990	12,455	11,850									
Solyc02g086270	Protein kinase family protein (AHRD V3.3 *** AT5G38210.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	18,350	29,812	11,053	10,729	16,502									
Solyc02g086280	Kinase family protein (AHRD V3.3 *-* U5GCQ9_POPTR)		F:GO:0030247	F:polysaccharide binding			IPR032872 (PFAM): IPR025287 (PFA	1,135	2,362	1,068	0,734	1,683									
Solyc02g086290	Kinase family protein (AHRD V3.3 *-* U5GCQ9_POPTR)		F:GO:0005488; C:G(	F:binding; C:membrane; F:kinase activity; P:phosphorylation			IPR032872 (PFAM): PTHR33138 (PAN	0,469	0,431	0,096	0,176	0,023									
Solyc02g086300	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)		F:GO:0016787	F:hydrolase activity			IPR029062 (G3DSA:3.40.50.GENE3D	186,259	147,277	18,776	22,337	24,580									
Solyc02g086310	lipid-transfer protein 7k-LTP		P:GO:0006869	P:lipid transport			IPR016140 (SMART): G3DSA:1.10.11	72,008	101,837	11,220	38,923	8,943					1,803	0,017			up
Solyc02g086315	E2F/DP family winged-helix DNA-binding domain-containing protein (AHRD V3.3 --* AT4G19003.6)							0,258	0,188	0,146	0,174	0,141									
Solyc02g086320	LisH domain and HEAT repeat-containing protein (AHRD V3.3 *-* A0A0B0ML79_GOSAR)		C:GO:0005802; P:G(	C:trans-Golgi network; P:intracellular cholesterol transport				7,992	7,541	8,356	7,833	7,923									
Solyc02g086330	LisH domain and HEAT repeat-containing protein KIAA1468-like protein (AHRD V3.3 *** A0A0B2SQV2_GLY		F:GO:0005515; C:G(	F:protein binding; C:trans-Golgi network; P:intracellular choleste			IPR006594 (SMART): IPR011989 (G3	42,648	35,652	41,201	43,726	41,806									
Solyc02g086350	Protein PLASTID MOVEMENT IMPAIRED 2 (AHRD V3.3 *** W9S0V7_9ROSA)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			IPR008545 (PFAM): mobidb-lite (MOB	0,363	0,437	0,116	0,287	0,163									
Solyc02g086360	Phox/Bem1p (AHRD V3.3 *** A0A124SEH3_CYNCS)		F:GO:0005515	F:protein binding			IPR000270 (SMART): IPR000270 (PF.	7,598	7,902	7,511	8,559	8,033									
Solyc02g086370	Lipid phosphate phosphatase-like protein (AHRD V3.3 *** I3SWU2_MEDTR)		F:GO:0008195; C:G(	F:phosphatidate phc	EC:3.1.3.4	Phosphatidate phosp	IPR000326 (SMART): G3DSA:1.20.14	12,906	13,245	6,689	7,107	8,289									
Solyc02g086385	DNA mismatch repair protein mutL (AHRD V3.3 --* A0A0B2SBZ1_GLYSO)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,082	0,021	0,000	0,025	0,024									
Solyc02g086390	LOW QUALITY:ABC transporter D family member 1 (AHRD V3.3 --* A0A0B2R4B6_GLYSO)							0,019	0,018	0,025	0,000	0,023									
Solyc02g086400	RING/U-box superfamily protein (AHRD V3.3 --* AT5G01160.2)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,510	0,462	0,122	0,220	0,259									
Solyc02g086402	CTP synthase (AHRD V3.3 *-* A0A059CB45_EUCGR)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR004468 (PANTHER): PTHR11550:	0,119	0,080	0,121	0,099	0,047									
Solyc02g086404	DNA mismatch repair protein mutL (AHRD V3.3 --* A0A0B2SBZ1_GLYSO)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	PTHR11550:SF23 (PANTHER): IPR00	0,038	0,021	0,025	0,072	0,095									
Solyc02g086406	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	PTHR11550:SF23 (PANTHER): IPR00	0,000	0,000	0,025	0,025	0,000									
Solyc02g086408	DNA mismatch repair protein mutL (AHRD V3.3 --* W9RKQ1_9ROSA)							0,059	0,118	0,075	0,098	0,117									
Solyc02g086410	YlmG homolog protein 1-2, chloroplastic (AHRD V3.3 --* YMG12_ARATH)							0,040	0,000	0,000	0,048	0,000									
Solyc02g086430	Zinc finger transcription factor 21	C3H21	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF_C3H	0,209	0,057	0,000	0,000	0,000									
Solyc02g086440	F-box/LRR protein (AHRD V3.3 *** A0A072TZ55_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR032675 (G3	16,116	10,204	11,060	13,056	12,728									
Solyc02g086450	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 *** AT1G10690.1)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,818	0,368	0,046	0,097	0,000									
Solyc02g086460	A-kinase anchor-like protein (AHRD V3.3 --* AT5G40450.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	58,994	73,183	74,323	87,512	83,225									
Solyc02g086463	ARM repeat superfamily protein (AHRD V3.3 --* AT3G54790.3)						mobidb-lite (MOBIDB_LITE)	0,080	0,021	0,047	0,095	0,047									
Solyc02g086467	Histone H4 (AHRD V3.3 --* A0A0D3DSU9_BRAOL)						mobidb-lite (MOBIDB_LITE)	0,163	0,210	0,096	0,193	0,212									
Solyc02g086470	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061EDJ2_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	1,529	1,750	0,417	0,239	0,258									
Solyc02g086480	LOB domain-containing protein, putative (AHRD V3.3 *** B9S640_RICCO)						IPR004883 (PFAM_LBD	0,469	0,363	0,428	0,146	0,141									
Solyc02g086490	Oleosin (AHRD V3.3 *** K4BBF7_SOLLC)		C:GO:0012511; C:G(	C:monolayer-surrounded lipid storage body; C:integral compone			IPR000136 (PFAM): mobidb-lite (MOB	73,692	76,797	4,219	12,720	0,720									
Solyc02g086500	ARM repeat superfamily protein, putative (AHRD V3.3 *** A0A061EBW7_THECC)		P:GO:0006723; P:G(	P:cuticle hydrocarbon biosynthetic process; P:embryo developn			IPR022542 (PFAM): PTHR16212 (PAN	58,268	49,595	48,101	47,331	48,682									
Solyc02g086513	Zinc finger family protein / RNA recognition motif-containing protein, putative (AHRD V3.3 *-* A0A061ECV5		F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (SMART): IPR000504 (PF.	5,107	4,676	5,959	6,666	6,172									
Solyc02g086517	DNA/RNA-binding protein KIN17 (AHRD V3.3 --* A0A0B2S1P2_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,939	2,065	2,428	3,017	2,446									
Solyc02g086520	DNA binding protein, putative (AHRD V3.3 *** B9SF87_RICCO)						IPR010820 (PFAM): mobidb-lite (MOB	44,945	51,788	56,264	50,318	47,858									
Solyc02g086530	Raffinose synthase family protein (AHRD V3.3 *** AT5G40390.1)		P:GO:0010325; F:G(	P:raffinose family o	EC:2.4.1.82	Galactinol--sucrose (	IPR008811 (PFAM): PTHR31268:SF2	0,816	2,704	0,140	0,321	0,140	1,735	0,015					up		
Solyc02g086540	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT5G14550.1)		F:GO:0005515; F:G(	F:protein binding; F:acetylglucosaminyltransferase activity; C:m			IPR006910 (PFAM): IPR006909 (PFA	0,000	0,076	0,000	0,025	0,000									
Solyc02g086550	Core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT5G14550		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR31042:SF6	0,242	0,359	0,165	0,337	0,283									
Solyc02g086560	Sirohydrochlorin ferrochelatase, putative (AHRD V3.3 *** B9SF92_RICCO)		P:GO:0009236; F:G(	P:cobalamin biosyn	EC:4.99.1.3	Sirohydrochlorin coba	IPR002762 (PFAM): G3DSA:3.40.50.1	12,284	12,988	29,260	26,330	28,596									
Solyc02g086570	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061EJI9_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	4,193	3,905	4,716	4,874	4,905									
Solyc02g086580	DNA helicase ROCK-N-ROLLERS (AHRD V3.3 *-* AT3G27730.5)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): G3DSA:3.40.50	0,124	0,018	0,050	0,022	0,000									
Solyc02g086585	DNA helicase ROCK-N-ROLLERS (AHRD V3.3 *** AT3G27730.7)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR004179 (SMART): IPR001650 (SM	0,866	0,704	0,402	0,428	0,236									
Solyc02g086590	Kinase, putative (AHRD V3.3 *** B9SF98_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR038408 (G3	13,308	19,944	7,274	7,036	6,910									
Solyc02g086600	polyribonucleotide nucleotidyltransferase (AHRD V3.3 *** AT5G14580.1)		F:GO:0003723; F:G(	F:RNA binding; F:pc	EC:2.7.7.8	Polyribonucleotide nu	IPR022967 (SMART): IPR027408 (G3	25,884	26,368	21,953	21,099	19,803									
Solyc02g086610	Isocitrate dehydrogenase [NADP] (AHRD V3.3 *** K4BBG9_SOLLC)		F:GO:0004450; P:G(	F:isocitrate dehydro	EC:1.1.1.42	Isocitrate dehydroge	IPR024084 (SMART): IPR024084 (PF.	30,371	35,897	46,830	44,665	45,060									
Solyc02g086620	RING/U-box superfamily protein (AHRD V3.3 --* AT2G15260.1)		P:GO:0007064	P:mitotic sister chromatid cohesion				0,392	0,429	0,484	0,681	0,428									
Solyc02g086625	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 --* A0A0B2P9B8_GLYSO)						mobidb-lite (MOBIDB_LITE)	0,911	0,766	1,290	3,145	1,384					1,275	0,000			up
Solyc02g086630	Sister chromatid cohesion PDS5 B-B (AHRD V3.3 *-* A0A0B0PPN5_GOSAR)		P:GO:0007064	P:mitotic sister chromatid cohesion			IPR039776 (PANTHER): PTHR12663:	1,771	1,236	3,268	3,937	3,109									
Solyc02g086640	WUSCHEL related homeobox 11 (AHRD V3.3 --* AT3G03660.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,388	0,816	1,249	0,558	1,129									
Solyc02g086650	Phosphoenolpyruvate/phosphate translocator (AHRD V3.3 *** A0A0D3QJC6_CAMSI)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR004696 (TIGRFAM): IPR004853 (F	2,467	5,582	0,944	1,114	1,244									
Solyc02g086660	RNA helicase DEAD10	DEAD10	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; F:ATP binding			IPR001650 (SMART): IPR001202 (SM	47,937	58,095	39,313	32,970	40,512									
Solyc02g086670	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	48,793	44,605	108,113	119,315	107,518									
Solyc02g086680	peptide deformylase AF250958		C:GO:0005739; P:G(	C:mitochondrion; P:	EC:3.5.1.88	Peptide deformylase	IPR023635 (PRINTS): IPR036821 (G3	15,794	18,781	36,107	39,030	39,868									
Solyc02g086700	Beta-1,3-glucanase (AHRD V3.3 *** Q9SYX6_TOBAC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00(	0,161	0,193	0,087	0,242	0,260									
Solyc02g086710	Monodehydroascorbate reductase (NADH)-like protein		F:GO:0016491; F:G(	F:oxidoreductase activity; F:flavin adenine dinucleotide binding;			PR00368 (PRINTS): PR00411 (PRINT	51,638	58,297	154,251	148,231	145,948									
Solyc02g086730	50S ribosomal protein L12, chloroplastic (AHRD V3.3 *** RK12_NICSY)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000206 (TIGRFAM): IPR014719 ((	36,965	69,190	41,323	46,656	71,243	0,932	0,000	0,783	0,000			up	up	
Solyc02g086740	50S ribosomal protein L12, chloroplastic (AHRD V3.3 *** RK12_NICSY)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR008932 (PFAM): IPR013823 (PFA	1,049	3,620	0,510	0,756	1,530	1,803	0,001	1,570	0,002			up	up	
Solyc02g086750	Serine/threonine-protein kinase ATM (AHRD V3.3 *** A0A151R6X6_CAJCA)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR000313 (SMART): IPR000313 (PF.	80,518	69,862	97,898	98,622	95,155									
Solyc02g086760	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G01516.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,142	3,065	0,047	0,025	0,024									
Solyc02g086770	Cinnamoyl-CoA reductase (AHRD V3.3 *** A0A172WBP6_DAUCA)	CCR	F:GO:0003854; P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	IPR002225 (PFAM): G3DSA:3.40.50.7	1,650	2,658	0,280	0,192	0,423									
Solyc02g086780	Proteasome assembly chaperone 3 (AHRD V3.3 *** A0A1D1YK33_9ARAE)		C:GO:0000502	C:proteasome complex			IPR018788 (PFAM): G3DSA:3.30.230	9,358	9,589	10,065	8,699	8,369									
Solyc02g086790	Protein kinase (AHRD V3.3 *** A7L4B0_CARPA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	68,054	62,327	74,197	74,791	70,605									
Solyc02g086795	Protein kinase superfamily protein (AHRD V3.3 --* AT1G33770.1)							9,635	8,252	9,888	12,406	9,798									
Solyc02g086800	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0J0X6_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR023299 (G3D	24,851	25,581	12,768	14,158	13,507									
Solyc02g086810	LOW QUALITY:DUF1645 family protein (AHRD V3.3 *** G7KIQ4_MEDTR)						IPR012442 (PFAM): mobidb-lite (MOB	13,261	8,497	6,466	4,754	5,716									
Solyc02g086820	chloroplast carbonic anhydrase	ca2	F:GO:0004089; F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001765 (SMART): IPR001765 (PF.	0,600	0,549	0,338	0,248	0,237									
Solyc02g086830	Protease Do-like 1 (AHRD V3.3 *** W9SPU6_9ROSA)		F:GO:0004252; F:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): IPR001478 (SM	27,884	35,530	45,476	46,601	58,451									
Solyc02g086840	Protein KINESIN LIGHT CHAIN-RELATED 3 (AHRD V3.3 *** KLCR3_ARATH)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR019734 (PF.	0,021	0,019	0,022	0,000	0,070									
Solyc02g086860	CASP-like protein (AHRD V3.3 *** K4BBJ3_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006702 (PFAM): mobidb-lite (MOB	10,821	8,904	9,152	8,632	9,259									
Solyc02g086870	farnesyl protein transferase subunit B	ftb	F:GO:0003824; C:G(	F:catalytic activity; C:protein farnesyltransferase complex; P:pro			IPR001330 (PFAM): mobidb-lite (MOB	23,143	21,251	18,311	16,607	18,269									
Solyc02g086880	formate dehydrogenase	fdh	F:GO:0008863; F:G(	F:formate dehydrog	EC:1.2.1.2	Acting on the aldehyc	IPR006140 (PFAM): IPR006139 (PFA	332,230	282,592	416,191	368,237	416,338									
Solyc02g086890	Calcium homeostasis regulator CHoR1 (AHRD V3.3 *** Q5QTN8_SOLTU)		P:GO:0048564	P:photosystem I assembly			IPR037736 (PANTHER)	24,912	34,237	33,835	38,018	58,448			0,785	0,000				up	
Solyc02g086900	HD domain-containing metal-dependent phosphohydrolase family protein (AHRD V3.3 *** AT5G40270.1)		C:GO:0005634; P:G(	C:nucleus; P:dGTP	EC:3.1.5.1	dGTPase	IPR003607 (SMART): IPR006674 (PF.	8,540	11,693	7,086	5,529	6,325									
Solyc02g086910	Peptidyl-prolyl cis-trans isomerase, putative (AHRD V3.3 *** B9RUU4_RICCO)		P:GO:0000413; F:G(	P:protein peptidyl-pr	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PFAM): IPR029000 (G3D	5,284	12,318	3,894	6,087	9,418	1,248	0,000	1,276	0,000			up	up	
Solyc02g086915	Peptidyl-prolyl cis-trans isomerase CYP38 (AHRD V3.3 *** W9SGV3_9ROSA)		P:GO:0000413; F:G(	P:protein peptidyl-pr	EC:5.2.1.8	Peptidylprolyl isomer	G3DSA:1.20.120.290 (GENE3D): PTH	2,870	6,545	2,314	3,544	5,023	1,213	0,014	1,113	0,001			up	up	
Solyc02g086920	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BBJ9_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D): IPF	0,094	0,132	0,025	0,072	0,046									
Solyc02g086930	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072U6Z4_MEDTR	LeHB-1	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR000047 (PRIN_HD-ZIP	273,544	252,840	118,792	137,869	141,559									
Solyc02g086940	ARM repeat superfamily protein (AHRD V3.3 *** AT5G14790.1)						IPR034085 (SMART): IPR024395 (PF.	18,617	16,999	8,053	9,601	8,578									
Solyc02g086950	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FV20_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	0,042	0,018	0,025	0,025	0,000									
Solyc02g086960	LOW QUALITY:Serine-threonine protein kinase, putative (AHRD V3.3 *** A0A061ED60_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,185	0,320	0,168	0,147	0,190									
Solyc02g086970	Aldehyde dehydrogenase (AHRD V3.3 *** Q1AFF6_VITPS)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR015590 (PFAM): IPR016162 (G3D	87,498	81,979	67,726	44,535	51,757					-0,602	0,000			down
Solyc02g086980	LOW QUALITY:Trimeric LpxA-like enzymes superfamily protein (AHRD V3.3 --* AT4G21220.1)							0,478	0,565	0,187	0,147	0,235									
Solyc02g086990	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005249; P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra			IPR003938 (PRINTS): IPR000595 (SM	11,543	8,966	8,991	8,123	7,658									
Solyc02g087000	Potassium transporter (AHRD V3.3 *** Q0MVH0_TOBAC)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (TIGRFAM): IPR003855 (F	32,550	30,298	19,305	23,558	23,615									
Solyc02g087010	LOW QUALITY:NHL repeat-containing family protein (AHRD V3.3 *** B9HJT0_POPTR)		F:GO:0005515	F:protein binding			IPR001258 (PFAM): IPR011042 (G3D	5,408	5,136	4,409	5,850	4,454									
Solyc02g087030	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 *-* A0A061EBN2_THECC)						PTHR13833:SF41 (PANTHER): PTHR	1,051	0,878	1,445	1,800	1,482									
Solyc02g087040	Ring finger protein, putative (AHRD V3.3 *** B9RUC1_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination; F:u			IPR001841 (SMART): IPR013083 (G3	3,136	2,799	1,232	1,146	1,221									
Solyc02g087050	WAT1-related protein (AHRD V3.3 *** K4BBL2_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	0,234	0,388	0,050	0,047	0,117									
Solyc02g087060	WAT1-related protein (AHRD V3.3 *** K4BBL2_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	20,341	11,199	7,359	9,397	10,496	-0,833	0,003					down		
Solyc02g087070	alpha-DOX1		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR019791 (PFAM): IPR037120 (G3D	0,000	0,000	0,047	0,067	0,071									
Solyc02g087110	Alpha-dioxygenase (AHRD V3.3 *** Q5GQ66_PEA)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR037120 (G3DSA:1.10.640.GENE3I	5,764	7,026	81,152	54,339	84,843					-0,578	0,047			down
Solyc02g087120	Trichome birefringence-like 22, putative (AHRD V3.3 *** A0A061EBK7_THECC)		C:GO:0005794; P:G(	C:Golgi apparatus; P:xyloglucan metabolic process; C:integral c			IPR025846 (PFAM): IPR026057 (PFA	0,216	0,290	0,100	0,022	0,000									
Solyc02g087130	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3I	68,718	81,464	43,918	42,088	45,594									
Solyc02g087140	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3I	4,015	3,697	4,093	3,717	3,678									
Solyc02g087150	EG2771 (AHRD V3.3 *-* U3GN03_MANES)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			mobidb-lite (MOBIDB_LITE): PTHR357	9,219	13,612	11,821	14,532	18,140			0,614	0,001				up	
Solyc02g087170	GPI ethanolamine phosphate transferase 1 (AHRD V3.3 *** A0A0B0P6R7_GOSAR)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:GPI anchor biosynthetic			IPR017852 (PFAM): IPR002591 (PFA	18,917	19,492	17,545	18,612	17,543									
Solyc02g087180	Mediator of RNA polymerase II transcription subunit 4 (AHRD V3.3 *** A0A0S2LKP4_REHGL)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR019258 (PFAM): mobidb-lite (MOB	20,942	15,307	13,364	12,154	14,155									

Solyc02g087190	Peroxidase (AHRD V3.3 *** K4BBM6_SOLLC)		F:GO:0004601; P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	48,877	47,373	48,148	69,780	57,149					0,539	0,001			up
Solyc02g087200	U-box domain-containing protein 40 (AHRD V3.3 *** PUB40_ARATH)		F:GO:0004842; F:G	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR003613 (SMART): IPR000225 (SM	20,462	15,629	7,790	8,185	9,334									
Solyc02g087210	Zinc finger AN1 domain-containing stress-associated protein 12 (AHRD V3.3 *** A0A151RAZ5_CAJCA)		F:GO:0008270	F:zinc ion binding			IPR000058 (SMART): IPR000058 (PF	0,042	0,080	0,071	0,097	0,094									
Solyc02g087220	Sterile alpha motif domain-containing family protein (AHRD V3.3 *** A9PGP1_POPTR)		F:GO:0005515	F:protein binding			IPR001660 (SMART): IPR001660 (PF	13,202	10,539	14,393	13,489	13,250									
Solyc02g087230	Ferredoxin-thioredoxin reductase catalytic chain (AHRD V3.3 *** W9SEM5_9ROSA)		F:GO:0016730; P:G	F:oxidoreductase activity, acting on iron-sulfur proteins as donc			IPR024707 (PIRSF): IPR004209 (PFA	34,999	54,466	43,353	41,240	49,268	0,665	0,004					up		
Solyc02g087240	NADH dehydrogenase (AHRD V3.3 *** Q43840_SOLTU)		F:GO:0010181; F:G	F:FMN binding; F:oxidoreductase activity, acting on NAD(P)H; F			IPR019575 (SMART): IPR019554 (PF	126,657	126,831	251,763	214,907	234,960									
Solyc02g087250	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic (AHRD V3.3 *** A0A0B0PGC2_GOSAR		F:GO:0003723; F:G	F:RNA binding; F:cofactor binding			IPR001890 (SMART): IPR012349 (G3	120,801	98,641	92,971	94,112	99,111									
Solyc02g087260	plant viral-response family protein (DUF716) (AHRD V3.3 *** AT3G01360.2)		C:GO:0016021	C:integral component of membrane			IPR006904 (PFAM): mobidb-lite (MOB	28,242	25,059	24,745	34,408	29,693					0,476	0,009			up
Solyc02g087270	F-box family protein (AHRD V3.3 *-* A0A061EN61_THECC)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): IPR001810 (F	1,856	1,203	1,162	1,820	1,532									
Solyc02g087280	Major facilitator superfamily protein (AHRD V3.3 *** AT5G14940.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	6,582	5,638	4,928	5,549	5,601									
Solyc02g087290	Alpha-mannosidase (AHRD V3.3 *** K4BBN6_SOLLC)		F:GO:0004559; P:G	F:alpha-mannosidas	EC:3.2.1.24	Alpha-mannosidase	IPR015341 (SMART): IPR013780 (G3	59,000	44,266	48,922	42,631	48,628									
Solyc02g087300	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G01340.2)		F:GO:0005198; F:G	F:structural molecule activity; F:protein binding; C:COPII vesicle			IPR020472 (PRINTS): IPR001680 (SM	97,817	112,221	108,219	97,378	95,336									
Solyc02g087310	E2F transcription factor-like E2FE (AHRD V3.3 *** W9SXR3_9ROSA)		F:GO:0003700; C:G	F:DNA-binding transcription factor activity; C:transcription facto			IPR003316 (SMAF E2F/DP	6,630	7,526	5,984	5,811	5,419									
Solyc02g087315	Beta-fructofuranosidase, insoluble isoenzyme 1 (AHRD V3.3 --* INV1_ORYSJ)							0,864	0,518	1,755	1,709	1,621									
Solyc02g087320	Homeobox-leucine zipper protein HOX17 (AHRD V3.3 --* HOX17_ORYSJ)							0,273	0,174	0,747	0,807	0,751									
Solyc02g087330	B12D (AHRD V3.3 *** D2XQY6_WOLAR)		C:GO:0016021	C:integral component of membrane			IPR010530 (PFAM): PTHR33417:SF7	10,165	15,421	14,627	20,144	17,235					0,462	0,028			up
Solyc02g087340	Hop-interacting protein THI043 (AHRD V3.3 *** G8Z270_SOLLC)						IPR008479 (PFAM): mobidb-lite (MOB	97,832	97,127	183,385	183,331	180,131									
Solyc02g087360	Paired amphipathic helix SIN3-like protein (AHRD V3.3 *** G7KJX2_MEDTR)		F:GO:0003714; P:G	F:transcription corepressor activity; P:regulation of transcriptior			IPR013194 (SMART): G3DSA:1.20.11	77,828	69,841	87,214	87,314	84,116									
Solyc02g087390	Paired amphipathic helix protein Sin3 (AHRD V3.3 *-* A0A151TFV5_CAJCA)		F:GO:0003714; P:G	F:transcription corepressor activity; P:regulation of transcriptior			G3DSA:1.20.1160.11 (GENE3D): IPR	0,601	0,931	0,050	0,072	0,000									
Solyc02g087400	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A103XGS2_CYNCS)		F:GO:0005515; P:G	F:protein binding; P:response to light stimulus; C:chloroplast; P:			IPR000953 (SMART): IPR002110 (SM	27,190	49,186	14,363	18,822	30,876	0,882	0,009	1,097	0,000			up	up	
Solyc02g087410	ABC transporter B family protein (AHRD V3.3 *** G7KJX5_MEDTR)	ABCB3	F:GO:0005524; C:G	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	3,536	3,228	2,271	1,786	2,365									
Solyc02g087420	spindle assembly checkpoint component (AHRD V3.3 *** AT3G28370.4)						PTHR36001 (PANTHER)	12,186	13,803	10,905	16,169	13,671					0,569	0,007			up
Solyc02g087440	DUF248-1 (AHRD V3.3 --* A0A161CGG5_POPTO)		C:GO:0016021	C:integral component of membrane			PS51257 (PROSITE_PROFILES)	0,058	0,220	0,000	0,000	0,000									
Solyc02g087450	Nuclear mitotic apparatus 1 (AHRD V3.3 *-* A0A0B0NXR3_GOSAR)						PTHR34778:SF2 (PANTHER): PTHR3	2,897	2,799	0,189	0,751	0,682									
Solyc02g087470	Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic (AHRD V3.3 --* FABI_ARATH)							0,820	1,054	0,561	0,836	0,727									
Solyc02g087480	CW14 protein (DUF1336) (AHRD V3.3 *** AT1G59650.1)						IPR009769 (PFAM): mobidb-lite (MOB	57,090	61,727	37,439	61,851	47,102					0,724	0,001			up
Solyc02g087490	Pectinesterase (AHRD V3.3 --* PME_ACTDE)							0,019	0,000	0,022	0,000	0,070									
Solyc02g087500	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** A0A0M4FCN7_9SOLA)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR006620 (SMART): IPR003582 (SM	0,789	0,643	0,581	2,138	1,061					1,860	0,000			up
Solyc02g087510	Protein kinase (AHRD V3.3 *** Q9LUK3_ARATH)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,665	2,487	2,228	3,054	2,151									
Solyc02g087520	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7KK13_MEDTR)						IPR001938 (PRINTS): IPR001938 (SM	0,386	0,446	0,191	0,229	0,210									
Solyc02g087530	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G28610.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): IPR025753 (PF	0,057	0,021	0,022	0,000	0,024									
Solyc02g087540	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G28510.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): IPR003959 (PF	48,098	33,456	24,277	83,594	53,211			1,128	0,000	1,784	0,000		up	up
Solyc02g087550	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061EEC9_T		F:GO:0008375; C:G	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297:SF1	50,289	52,913	64,097	58,849	57,953									
Solyc02g087560	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YHD1_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	13,597	14,599	13,962	13,707	16,658									
Solyc02g087580	Actin cross-linking (AHRD V3.3 *** A0A103Y4S4_CYNCS)						G3DSA:2.80.10.50 (GENE3D): IPR00	2,558	7,695	0,555	0,170	0,421	1,620	0,000					up		
Solyc02g087600	DTW domain-containing protein (AHRD V3.3 *** AT2G41750.1)						IPR005636 (SMART): IPR005636 (PF	3,954	4,480	3,454	2,950	4,042									
Solyc02g087610	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7LM18_ARALL)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	2,542	2,734	2,009	1,723	1,695									
Solyc02g087620	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (AHRD V3.3 *** A0A0B2PX10_G		F:GO:0000829	F:inositol heptakisphosphate kinase activity			G3DSA:3.30.470.100 (GENE3D): G3D	57,924	70,182	51,188	53,561	65,745									
Solyc02g087630	Thioredoxin (AHRD V3.3 *** A0A103YHF4_CYNCS)		P:GO:0006662; F:G	P:glycerol ether metabolic process; F:protein disulfide oxidored			PR00421 (PRINTS): IPR013766 (PFA	33,701	36,499	44,102	44,973	42,525									
Solyc02g087640	NADH dehydrogenase ubiquinone complex I, assembly factor-like protein (DUF185) (AHRD V3.3 *** AT3G28		C:GO:0005739; F:G	C:mitochondrion; F:	EC:2.1.1.125	Transferring one-carl	IPR003788 (PFAM): IPR038375 (G3D	19,617	17,568	19,731	17,813	15,791									
Solyc02g087660	SIPIN8	PIN8	C:GO:0016021; P:G	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): IPR014024 (TIGF	0,425	0,324	0,643	0,647	0,400									
Solyc02g087665	Transmembrane amino acid transporter family protein (AHRD V3.3 --* AT3G30390.3)							0,000	0,019	0,025	0,000	0,046									
Solyc02g087670	Pectate lyase (AHRD V3.3 *** K4BBS3_SOLLC)		F:GO:0030570	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	0,118	0,157	0,025	0,000	0,000									
Solyc02g087680	FACT complex subunit SSRP1 (AHRD V3.3 *-* SSRP1_CATRO)		F:GO:0003677; C:G	F:DNA binding; C:nucleus			IPR000969 (PRINTS): IPR011993 (G3	0,219	0,154	0,274	0,075	0,187									
Solyc02g087690	FACT complex subunit SSRP1 (AHRD V3.3 --* SSRP1_CATRO)		P:GO:0000741; F:G	P:karyogamy; F:DNA binding; C:nucleus; C:chromosome; C:nuclear euchromatin; P:DNA replication; P:I				0,019	0,043	0,025	0,025	0,024									
Solyc02g087700	FACT complex subunit SSRP1 (AHRD V3.3 *-* SSRP1_CATRO)		F:GO:0003677; C:G	F:DNA binding; C:nucleus			IPR000969 (PRINTS): G3DSA:2.30.29	0,101	0,085	0,050	0,098	0,141									
Solyc02g087705	Pectate lyase (AHRD V3.3 *-* M0ZLE8_SOLTU)		C:GO:0016021; F:G	C:integral compone	EC:4.2.2.2	Pectate lyase	IPR012334 (G3DSA:2.160.20.GENE3	3,128	4,389	2,898	3,050	3,604									
Solyc02g087710	FACT complex subunit SSRP1 (AHRD V3.3 *** SSRP1_VICFA)		F:GO:0003677; C:G	F:DNA binding; C:nucleus			IPR000969 (PRINTS): IPR013719 (SM	201,846	285,307	171,586	176,846	208,964									
Solyc02g087720	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G28720.1)		C:GO:0016021	C:integral component of membrane			PTHR31515:SF3 (PANTHER): PTHR3	41,211	43,985	44,330	51,203	46,018									
Solyc02g087730	F-box family protein (AHRD V3.3 *** A0A061EFG6_THECC)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	21,526	33,799	32,254	30,804	32,153									
Solyc02g087740	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B0PVN9_GOSAR)		F:GO:0016702; P:G	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR012864 (PFAM): IPR014710 (G3D	95,610	52,604	120,720	169,051	108,913	-0,837	0,001			0,489	0,002	down		up
Solyc02g087750	Ubiquitin-conjugating enzyme (AHRD V3.3 *** Q5GMM2_CAPCH)		P:GO:0000209; F:G	P:protein polyubiquitination; F:ATP binding; P:DNA repair; P:prot			SM00212 (SMART): IPR016135 (G3D	122,671	105,763	177,248	167,762	154,086									
Solyc02g087760	SUN-like protein 7	SUN7	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR000048 (PF	127,428	118,199	62,494	58,173	64,565									
Solyc02g087770	Aldose 1-epimerase (AHRD V3.3 *** K4BBT3_SOLLC)		F:GO:0016853; P:G	F:isomerase activity; P:hexose metabolic process; F:carbohydr			IPR008183 (PFAM): IPR015443 (PIRS	120,177	118,485	28,556	27,589	37,749									
Solyc02g087780	Aldose 1-epimerase (AHRD V3.3 *** K4BBT4_SOLLC)		F:GO:0016853; P:G	F:isomerase activity; P:hexose metabolic process; F:carbohydr			IPR015443 (PIRSF): IPR014718 (G3D	13,535	14,904	3,034	2,719	5,645			0,888	0,034				up	
Solyc02g087790	Aldose 1-epimerase (AHRD V3.3 *** K4BBT5_SOLLC)		F:GO:0016853; P:G	F:isomerase activity; P:hexose metabolic process; F:carbohydr			IPR008183 (PFAM): IPR014718 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc02g087800	Aldose 1-epimerase (AHRD V3.3 *** K4BBT6_SOLLC)		F:GO:0016853; P:G	F:isomerase activity; P:hexose metabolic process; F:carbohydr			IPR008183 (PFAM): IPR015443 (PIRS	10,497	9,231	1,668	1,379	1,755									
Solyc02g087810	Aldose 1-epimerase (AHRD V3.3 *** K4BBT7_SOLLC)		P:GO:0005975; F:G	P:carbohydrate metabolic process; F:isomerase activity; F:carb			IPR008183 (PFAM): IPR014718 (G3D	2,715	2,664	0,435	0,481	0,753									
Solyc02g087820	LOW QUALITY:Aldose 1-epimerase (AHRD V3.3 *** O48971_TOBAC)		P:GO:0005975; F:G	P:carbohydrate metabolic process; F:isomerase activity; F:carb			IPR014718 (G3DSA:2.70.98.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc02g087830	Kinase family protein (AHRD V3.3 *** B9H0D5_POPTR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	11,515	10,595	0,422	0,297	0,562									
Solyc02g087840	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072U5Q1_MEDTR)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN HD-ZIP	62,669	34,080	3,369	4,171	6,556	-0,850	0,003					down		
Solyc02g087850	Glutaredoxin family protein, putative (AHRD V3.3 *** A0A061EEI9_THECC)		F:GO:0009055; F:G	F:electron transfer activity; F:protein disulfide oxidoreductase a			G3DSA:3.40.30.10 (GENE3D): IPR00	114,799	64,828	11,151	27,703	19,063	-0,800	0,007			1,309	0,000	down		up
Solyc02g087860	Transcription factor protein (AHRD V3.3 *** A0A0B0MSC8_GOSAR)		P:GO:0006355; F:G	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR036638 (G3DS bHLH	0,456	0,502	0,044	0,000	0,047									
Solyc02g087870	ABC transporter B family protein (AHRD V3.3 *** A0A072U6J8_MEDTR)	ABCB4	F:GO:0005524; C:G	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	64,883	38,971	16,543	13,183	17,542	-0,706	0,029					down		
Solyc02g087880	Tubulin alpha chain (AHRD V3.3 *** TBA_PRUDU)		F:GO:0003924; F:G	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002452 (PRINTS): IPR000217 (PF	1,290	1,653	1,993	1,470	1,365									
Solyc02g087900	Cullin family protein (AHRD V3.3 *** B9HV99_POPTR)		P:GO:0006511; F:G	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR019559 (SMART): IPR016158 (SM	82,656	90,322	106,187	97,207	95,848									
Solyc02g087910	Non-specific lipid-transfer protein (AHRD V3.3 *** K4BBU7_SOLLC)		P:GO:0006869; F:G	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	57,211	54,188	0,789	0,702	0,000									
Solyc02g087920	NAC domain protein, (AHRD V3.3 *** A0A061EFK4_THECC)	NAC021	F:GO:0003677; P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,019	0,000	0,000	0,000	0,000									
Solyc02g087935	mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT1G23230.3)							0,000	0,019	0,000	0,000	0,096									
Solyc02g087950	60S ribosomal protein L34, putative (AHRD V3.3 *** A0A061EMA0_THECC)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM): mobidb-lite (MOB	29,699	42,504	15,006	17,685	19,640									
Solyc02g087960	R2R3MYB transcription factor 94	R2R3MYB94	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	14,657	7,224	4,569	3,800	4,348	-0,989	0,004					down		
Solyc02g087970	Mini zinc finger protein (AHRD V3.3 *** A0ZXL1_SOLLC)						IPR006456 (PFAM ZF-HD	583,373	395,434	219,289	145,593	161,271			-0,446	0,009	-0,588	0,000		down	down
Solyc02g087980	Structural maintenance of chromosomes protein (AHRD V3.3 *** K4BBV4_SOLLC)		F:GO:0005515; F:G	F:protein binding; F:ATP binding; C:chromosome; P:chromosom			IPR010935 (SMART): IPR010935 (PF	35,661	15,976	3,614	1,656	1,988	-1,127	0,004			-1,116	0,018	down		down
Solyc02g087990	DUF1666 (AHRD V3.3 *-* A0A075QQN3_BRAOA)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM): PTHR10759:SF1	0,059	0,350	0,000	0,000	0,071									
Solyc02g088000	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *** K4BBV6_SOLLC)	STS6	F:GO:0004373	F:glycogen (starch)	EC:2.4.1.11	Glycogen(starch) syr	G3DSA:3.40.50.2000 (GENE3D): IPR	38,939	50,196	35,288	38,498	41,244									
Solyc02g088010	Defective in cullin neddylation protein (AHRD V3.3 *** K4BBV7_SOLLC)		C:GO:0000151; P:G	C:ubiquitin ligase complex; P:auxin-activated signaling pathway;			IPR005176 (PFAM): G3DSA:1.10.238	13,546	13,556	19,322	19,962	17,132									
Solyc02g088020	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_CUCSA)						PS51257 (PROSITE_PROFILES)	0,000	0,000	0,022	0,000	0,000									
Solyc02g088030	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT1G26800.1)		C:GO:0016021; F:G	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR013083 (G3	0,019	0,000	0,000	0,000	0,000									
Solyc02g088040	LOW QUALITY:Ribosomal protein L34e superfamily protein (AHRD V3.3 *** AT3G01170.1)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR008195 (PANTHER): PTHR10759:	3,333	5,415	4,872	5,282	4,785									
Solyc02g088060	Plasma membrane ATPase (AHRD V3.3 *-* A0A199V3F7_ANACO)		F:GO:0005524; F:G	F:ATP binding; F:pr	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR004014 (SMART): G3DSA:2.70.15	0,061	0,000	0,050	0,145	0,024									
Solyc02g088070	Dof zinc finger protein (AHRD V3.3 *** W9QEV1_9ROSA)		F:GO:0003677; P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	2,506	1,655	3,046	3,868	3,628									
Solyc02g088075	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G17365.2)							0,019	0,000	0,025	0,025	0,047									
Solyc02g088080	Thioredoxin superfamily protein (AHRD V3.3 --* AT3G56420.3)						PTHR37908 (PANTHER)	0,038	0,078	0,000	0,022	0,000									
Solyc02g088090	Calcium-binding EF-hand (AHRD V3.3 *** A0A103YHF0_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	29,777	9,879	5,670	23,177	8,161	-1,566	0,000			2,033	0,000	down		up
Solyc02g088100	expansin precursor 5	EXPA5	C:GO:0005576; P:G	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS): IPR002963 (PF	172,605	102,324	13,366	10,818	17,974									
Solyc02g088110	Polypyrimidine tract-binding protein-like (AHRD V3.3 *-* Q2XTB3_SOLTU)		P:GO:0000381; C:G	P:regulation of alternative mRNA splicing, via spliceosome; C:P			IPR012677 (G3DSA:3.30.70.GENE3D	12,102	12,338	13,142	14,301	13,899									
Solyc02g088113	Polypyrimidine tract-binding protein-like (AHRD V3.3 *-* Q2XTB3_SOLTU)		P:GO:0000381; C:G	P:regulation of alternative mRNA splicing, via spliceosome; C:P			IPR012677 (G3DSA:3.30.70.GENE3D	7,007	6,381	6,603	7,702	7,690									
Solyc02g088115	Polypyrimidine tract-binding protein-like (AHRD V3.3 *-* Q2XTB3_SOLTU)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	8,429	8,330	8,844	9,106	9,412									
Solyc02g088117	RNA-binding KH domain-containing protein (AHRD V3.3 *-* AT5G15270.3)		F:GO:0003723	F:RNA binding			IPR004088 (PFAM): IPR036612 (G3D	1,699	1,397	0,576	0,297	0,399									
Solyc02g088120	RNA-binding KH domain protein (AHRD V3.3 *-* G7KKX1_MEDTR)		F:GO:0003723	F:RNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,035	2,021	0,582	0,482	0,869									
Solyc02g088140	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7M761_ARALL)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,556	0,490	0,629	0,468	0,798									
Solyc02g088150	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9SM34_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	0,274	0,178	0,215	0,189	0,188									
Solyc02g088160	CASP-like protein (AHRD V3.3 *** K4BBX2_SOLLC)		C:GO:0016020; C:G	C:membrane; C:integral component of membrane				0,491	0,588	0,337	0,391	0,681									
Solyc02g088163	Mitochondrial transcription termination factor family protein (AHRD V3.3 --* AT4G19650.2)							0,021	0,000	0,000	0,000	0,000									
Solyc02g088167	CASP-like protein (AHRD V3.3 *** M0ZLJ2_SOLTU)		C:GO:0005886; C:G	C:plasma membrane; C:integral component of membrane			IPR006459 (TIGRFAM): IPR006702 (F	0,433	0,685	0,479	0,379	0,328									
Solyc02g088180	NAC domain-containing protein (AHRD V3.3 *** A0A060A652_BOENI)	ORE1S02	F:GO:0003677; P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,900	1,043	0,288	0,740	0,255									
Solyc02g088190	MYB-related transcription factor (AHRD V3.3 *** A0A059PRK4_SALMI)	R2R3MYB16	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	11,523	10,989	17,777	14,592	14,386									
Solyc02g088200	Activating signal cointegrator 1 complex subunit 1 (AHRD V3.3 *-* A0A0B2NTB9_GLYSO)		C:GO:0016020	C:membrane			IPR019510 (PFAM): G3DSA:3.90.114	2,638	2,215	2,242	1,766	1,630									
Solyc02g088205	Activating signal cointegrator 1 complex subunit 1 (AHRD V3.3 --* A0A1D1XDP2_9ARAE)		F:GO:0003676; F:G	F:nucleic acid binding; F:RNA binding; F:kinase activity; P:phos			G3DSA:3.90.1140.10 (GENE3D)	0,315	0,265	0,254	0,219	0,425									
Solyc02g088210	SPX domain-containing family protein (AHRD V3.3 *** B9IK08_POPTR)		P:GO:0016036	P:cellular response to phosphate starvation			IPR004331 (PFAM): mobidb-lite (MOB	3,051	2,133	1,159	1,099	0,613									
Solyc02g088220	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0MVV1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004331 (PFAM): IPR004342 (PFA	29,803	31,066	2,882	2,760	2,469									
Solyc02g088230	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0MVV1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004342 (PFAM): IPR004331 (PFA	33,508	27,685	2,867	2,171	3,660									
Solyc02g088240	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0MVV1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004331 (PFAM): IPR004342 (PFA	71,478	62,820	15,680	10,820	18,982									
Solyc02g088260	Latex abundant protein 1 (AHRD V3.3 *** B9N9R7_POPTR)		F:GO:0070300	F:phosphatidic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	16,698	22,098	23,350	19,770	20,491									
Solyc02g088270	DUF1997 family protein (AHRD V3.3 *** G7KKZ0_MEDTR)						IPR018971 (PFAM): PTHR34133 (PAN	14,202	14,557	665,733	824,315	674,248									
Solyc02g088280	Chalcone--flavonone isomerase (AHRD V3.3 --* CFI_PHAVU)	CHI						8,108	7,655	7,623	8,969	8,209									
Solyc02g088300	ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *** G7KLA3_MEDTR)		C:GO:0016020	C:membrane			IPR027815 (PFAM): IPR032880 (PFA	37,540	33,823	41,133	44,154	38,776									
Solyc02g088307	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform (AHRD V3.3 --* 2A5B_A		C:GO:0016592	C:mediator complex				0,179	0,298	0,147	0,149	0,309									
Solyc02g088320	DHHC-type zinc finger family protein (AHRD V3.3 --* AT3G56930.2)							0,056	0,134	0,025	0,025	0,024									
Solyc02g088325	DUF1336 family protein (AHRD V3.3 *** A0A072UPS9_MEDTR)						IPR009769 (PFAM): PTHR31558:SF1	1,589	1,873	0,390	0,435	0,427									
Solyc02g088340	WRKY transcription factor 3	WRKY3	F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMAF WRKY	12,154	12,260	5,349	5,817	5,724									
Solyc02g088345	Transcription factor (AHRD V3.3 *** A0A0P0UVC4_SOLTU)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMART): IPR003657 (PF	36,338	23,753	43,464	53,050	52,920	-0,586	0,034					down		
Solyc02g088350	Domain of Uncharacterized protein function isoform 1 (AHRD V3.3 *** A0A061EEX8_THECC)		P:GO:0032955	P:regulation of division septum assembly			IPR012674 (G3DSA:2.40.128.GENE3	42,098	50,912	57,395	60,056	78,064			0,441	0,002				up	
Solyc02g088360	LOW QUALITY:SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *-* A		C:GO:0016020	C:membrane			IPR001972 (PRINTS): IPR001107 (PF	0,513	0,328	0,093	0,337	0,188									
Solyc02g088370	LOW QUALITY:Band 7 stomatin family protein (AHRD V3.3 --* C1MUP6_MICPC)		C:GO:0016020	C:membrane			IPR032435 (PFAM)	0,244	0,119	0,118	0,094	0,117									
Solyc02g088380	Early nodulin-like protein (AHRD V3.3 *** G7J772_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	26,633	14,440	12,749	15,867	17,982	-0,853	0,001					down		
Solyc02g088390	Blue copper protein, putative (AHRD V3.3 *** B9T3T7_RICCO)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	34,733	17,194	21,904	25,251	27,135	-0,985	0,002					down		
Solyc02g088395	mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT1G15772.4)							6,160	3,810	5,946	6,722	6,035									
Solyc02g088400	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 --* A0A0X7YCF6_SOLTU)		P:GO:0006259; F:G	P:DNA metabolic process; F:organic cyclic compound binding; F:heterocyclic compound binding				1,054	0,719	1,295	1,045	1,272									
Solyc02g088420	DNA mismatch repair protein mutL (AHRD V3.3 *-* W9RKQ1_9ROSA)		F:GO:0005524; P:G	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,079	0,039	0,050	0,022	0,000									
Solyc02g088425	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* A0A0B2QGB0_GLYSO)		F:GO:0016787; F:G	F:hydrolase activity; F:organic cyclic compound binding; F:heter			PTHR13710:SF69 (PANTHER): PTHR	1,721	1,237	2,188	2,395	2,785									
Solyc02g088427	RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 *-* AT3G24255.7)		F:GO:0005524; P:G	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				1,768	1,024	2,189	1,450	1,741									
Solyc02g088430	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *-* A0A072VML8_MEDTR)		F:GO:0000166; F:G	F:nucleotide binding	EC:3.6.1.15	Nucleoside-triphosph	IPR036388 (G3DSA:1.10.10.GENE3D	0,037	0,037	0,022	0,050	0,118									
Solyc02g088440	SCAR family protein (AHRD V3.3 --* AT2G34150.5)							0,176	0,062	0,050	0,146	0,143									
Solyc02g088450	phosphatidylinositol-4-phosphate 5-kinase 2 (AHRD V3.3 --* AT1G77740.2)							0,200	0,177	0,201	0,273	0,305									
Solyc02g088460	Chorismate mutase (AHRD V3.3 *** S4VFM2_SALMI)	CM1	F:GO:0004106; P:G	F:chorismate mutas	EC:5.4.99.5	Chorismate mutase	IPR037039 (G3DSA:1.10.590.GENE3	14,439	14,786	17,222	17,570	18,201									
Solyc02g088470	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YHC4_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	8,216	7,500	6,303	5,286	6,924									
Solyc02g088480	T-box transcription factor, putative (DUF863) (AHRD V3.3 *-* AT1G69360.1)						IPR008581 (PFAM): mobidb-lite (MOB	36,324	38,105	40,955	39,344	42,492									
Solyc02g088490	Saccharopine dehydrogenase (AHRD V3.3 *** AT5G39410.1)		F:GO:0016491; P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR005097 (PFAM): G3DSA:3.40.50.7	54,254	57,897	51,409	41,707	44,066									
Solyc02g088510	Saccharopine dehydrogenase (AHRD V3.3 *** AT5G39410.1)		F:GO:0016491; P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR005097 (PFAM): G3DSA:3.40.50.7	13,324	10,679	26,172	22,436	23,505									
Solyc02g088513	Saccharopine dehydrogenase (AHRD V3.3 *-* AT5G39410.1)		C:GO:0005739; C:G	C:mitochondrion; C:lipid droplet; C:plasma membrane; P:glycolic			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,000	2,068	4,415	4,278	3,882									
Solyc02g088517	Glycosyltransferase (AHRD V3.3 *** A0A022RUH0_ERYGU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	5,846	4,421	7,950	8,630	7,918									
Solyc02g088530	3-ketoacyl-CoA synthase 15 (AHRD V3.3 --* AT3G52160.1)							0,284	0,277	0,267	0,388	0,448									
Solyc02g088540	TRNA/rRNA methyltransferase family protein (AHRD V3.3 *** A0A061EEZ7_THECC)		F:GO:0003723; F:G	F:RNA binding; F:RNA methyltransferase activity; P:tRNA methy			IPR001537 (PFAM): IPR029026 (G3D	13,808	17,128	13,618	12,435	14,397									
Solyc02g088550	U-box domain-containing protein (AHRD V3.3 *** AT5G15400.1)		C:GO:0000151; P:G	C:ubiquitin ligase complex; P:ubiquitin-dependent protein catabo			IPR003613 (SMART): IPR019474 (PF	120,495	123,723	173,433	181,649	177,837									
Solyc02g088560	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9T3S5_RICCO)		F:GO:0005216; P:G	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART): IPR000595 (PF	16,257	30,237	46,644	56,866	57,313	0,920	0,037					up		
Solyc02g088570	RING/U-box superfamily protein (AHRD V3.3 *** AT3G29270.2)		C:GO:0016021; F:G	C:integral component of membrane; F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	11,692	13,059	15,984	14,684	14,597									
Solyc02g088590	Plant calmodulin-binding protein-like protein (AHRD V3.3 *-* AT5G39380.5)		F:GO:0005516	F:calmodulin binding			IPR012417 (SMART): IPR012417 (PF	31,517	21,626	28,721	32,211	30,771									
Solyc02g088600	Pentatricopeptide repeat-containing-like protein (AHRD V3.3 *** A0A0B0P8M8_GOSAR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	16,225	14,016	23,147	22,571	22,608									
Solyc02g088610	LeHSP110/ClpB heat shock protein	ClpB3	F:GO:0005524; C:G	F:ATP binding; C:cytoplasm; P:response to heat; P:protein meta			IPR001270 (PRINTS): IPR019489 (SM	145,646	125,953	766,696	671,487	749,098									
Solyc02g088620	Membrane-anchored ubiquitin-fold protein 1 (AHRD V3.3 *** A0A151SZZ4_CAJCA)		F:GO:0005515	F:protein binding			IPR017000 (PIRSF): IPR039540 (PFA	26,135	29,211	52,687	64,789	49,949									

Solyc02g088630	Hexosyltransferase (AHRD V3.3 *** K4BC18_SOLLC)	GAUT14	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	89,183	135,949	28,756	25,514	40,707									
Solyc02g088640	LOW QUALITY:F-box associated ubiquitination effector family protein (AHRD V3.3 --* AT3G10990.1)							0,000	0,057	0,000	0,000	0,000									
Solyc02g088650	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2RWF1_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,645	2,967	1,876	2,044	1,643									
Solyc02g088660	BAG family molecular chaperone regulator 8, chloroplastic (AHRD V3.3 *** A0A0B0MGC2_GOSAR)		F:GO:0005515	F:protein binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	20,467	20,605	32,784	30,883	32,141									
Solyc02g088670	Zinc finger protein, putative (AHRD V3.3 *** B9SJB9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,266	0,869	0,168	0,048	0,096									
Solyc02g088690	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT3G29360.2)		F:GO:0003979: F:G	F:UDP-glucose 6-de	EC:1.1.1.22	UDP-glucose 6-dehy	IPR014027 (SMART): IPR017476 (TIG	247,736	361,180	135,867	131,982	157,699									
Solyc02g088700	Mitochondrial processing peptidase-like (AHRD V3.3 *** Q2V992_SOLTU)		F:GO:0003824: F:G	F:catalytic activity; F:metal ion binding			IPR011765 (PFAM): G3DSA:3.30.830	109,834	114,476	162,351	161,994	157,336									
Solyc02g088705	serine carboxypeptidase-like 41 (AHRD V3.3 --* AT5G42230.2)							13,553	15,796	21,640	22,362	20,592									
Solyc02g088710	4-coumarate:CoA ligase-like (AHRD V3.3 *** Q84K86_NICSY)	4CL-like	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): IPR025110 (PFA	0,019	0,021	0,000	0,072	0,141									
Solyc02g088720	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT4G00830.6)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	43,399	37,834	52,799	49,268	49,203									
Solyc02g088730	F-box family protein-like (AHRD V3.3 *** Q307Y5_SOLTU)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	14,777	10,525	17,298	16,111	16,815									
Solyc02g088740	LOW QUALITY:Transcription factor bHLH151, putative (AHRD V3.3 *** A0A061EF71_THECC)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,639	3,689	2,334	4,623	4,991			1,091	0,006	0,983	0,002		up	up
Solyc02g088750	UDP-glycosyltransferase (AHRD V3.3 *** A0A067XU00_CICAR)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,000	0,000	0,000	0,000	0,023									
Solyc02g088770	Mitochondrial carrier protein, expressed (AHRD V3.3 *** Q6AVS9_ORYSJ)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	0,080	0,165	0,168	0,265	0,117									
Solyc02g088780	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *-* B9GRF3_POPTR)		F:GO:0003735: F:G	F:structural constituent of ribosome; F:protein binding; C:ribosor			IPR001680 (SMART): IPR002885 (PF	87,545	84,133	78,415	66,812	65,308									
Solyc02g088790	RNA-binding protein (AHRD V3.3 *** Q941H9_TOBAC)		F:GO:0003676	F:nucleic acid binding			PR01228 (PRINTS): IPR000504 (SMA	31,873	35,666	44,271	30,771	33,974					-0,522	0,000			down
Solyc02g088800	Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9IK79_POPTR)		C:GO:0000145: P:G	C:exocyst; P:exocytosis			IPR004140 (PFAM): mobidb-lite (MOB	36,234	46,057	34,513	34,707	33,820									
Solyc02g088820	Carboxypeptidase (AHRD V3.3 *** M0ZM60_SOLTU)		F:GO:0004185: P:G	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PRINTS): G3DSA:3.40.50	0,655	0,424	0,071	0,000	0,094									
Solyc02g088830	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *-* AT3G02120.1)						IPR007727 (PFAM): mobidb-lite (MOB	0,308	0,135	0,050	0,000	0,046									
Solyc02g088840	Assimilatory nitrate reductase catalytic subunit (AHRD V3.3 *** A0A0B0NYS4_GOSAR)		F:GO:0016772: P:G	F:transferase activity, transferring phosphorus-containing group			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,039	0,022	0,025	0,000									
Solyc02g088850	Limkain-b1 (AHRD V3.3 *** A0A0B2Q3Y9_GLYSO)		C:GO:0005777: P:G	C:peroxisome; P:regulation of gene expression			IPR021139 (PFAM): mobidb-lite (MOB	1,103	1,461	0,208	0,169	0,187									
Solyc02g088860	Endonuclease or glycosyl hydrolase, putative (AHRD V3.3 *-* G7KWF4_MEDTR)		C:GO:0005777: P:G	C:peroxisome; P:regulation of gene expression			IPR021139 (PFAM): mobidb-lite (MOB	0,080	0,219	0,000	0,025	0,000									
Solyc02g088890	Endonuclease or glycosyl hydrolase, putative (AHRD V3.3 *-* G7KWF4_MEDTR)		C:GO:0005777: P:G	C:peroxisome; P:regulation of gene expression			IPR021139 (PFAM): PTHR14379:SF7	0,000	0,000	0,000	0,022	0,000									
Solyc02g088900	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT3G17430.2)		C:GO:0005768: C:G	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM): mobidb-lite (MOB	1,378	2,333	0,190	0,076	0,211									
Solyc02g088910	Ninja-family protein AFP2 (AHRD V3.3 *** A0A0B0PRX3_GOSAR)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM): IPR012463 (PFA	12,667	12,751	12,138	13,068	14,243									
Solyc02g088920	Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *** A0A061EH36_T		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): G3DSA:3.10.45	17,838	16,207	8,612	7,632	8,789									
Solyc02g088930	furry (AHRD V3.3 *** AT5G08060.1)						PTHR36391 (PANTHER)	33,584	34,566	51,848	45,716	47,090									
Solyc02g088940	CTP synthase family protein (AHRD V3.3 *-* AT1G30820.1)		F:GO:0003883: P:G	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR017926 (PFAM): IPR029062 (G3D	51,392	56,653	55,126	63,521	67,097									
Solyc02g088945	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 --* A0A0X7YCF6_SOLTU)		F:GO:0005524: P:G	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,504	0,790	0,559	0,852	0,515									
Solyc02g088950	Superoxide dismutase [Cu-Zn] (AHRD V3.3 --* A9NTC6_PICSI)		F:GO:0005524: P:G	F:ATP binding; P:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		13,372	11,088	7,381	8,957	9,500									
Solyc02g088954	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		F:GO:0005524: P:G	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,042	0,000	0,000	0,022	0,000									
Solyc02g088956	glucan synthase-like 1 (AHRD V3.3 --* AT4G04970.1)							2,084	2,719	1,125	1,416	1,440									
Solyc02g088958	telomeric repeat binding protein 1 (AHRD V3.3 --* AT5G59430.5)		F:GO:0005524: P:G	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				0,725	0,665	0,687	0,677	0,447									
Solyc02g088980	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT5G56890.1)		F:GO:0005524: P:G	F:ATP binding; P:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		1,706	1,769	1,461	1,594	1,492									
Solyc02g088983	LOW QUALITY:Arginine/serine-rich splicing factor, putative (AHRD V3.3 --* B9RNP5_RICCO)		F:GO:0003676: F:G	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): G3DSA:4.10.60	5,386	4,687	4,506	4,500	4,967									
Solyc02g088987	LOW QUALITY:Arginine/serine-rich splicing factor, putative (AHRD V3.3 --* B9T7V5_RICCO)		F:GO:0003676: F:G	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): G3DSA:4.10.60	4,415	7,443	3,554	4,002	3,569									
Solyc02g089010	Receptor protein kinase, putative (AHRD V3.3 *-* B9RXG1_RICCO)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PTHF	9,881	19,949	8,564	10,972	9,565	1,040	0,002					up		
Solyc02g089020	TCP transcription factor 5	TCP5	F:GO:0003700: C:G	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM_TCP	1,592	1,822	0,665	1,072	0,753									
Solyc02g089040	Unknown protein (AHRD V3.3)							0,101	0,019	0,000	0,075	0,023									
Solyc02g089050	Longifolia protein (AHRD V3.3 *** A0A072UUU5_MEDTR)		P:GO:0051513	P:regulation of monopolar cell growth			IPR025486 (PFAM): mobidb-lite (MOB	0,123	0,081	0,051	0,167	0,047									
Solyc02g089060	methyl esterase 11 (AHRD V3.3 *** AT3G29770.1)		P:GO:0009694: P:G	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	10,599	13,673	16,208	17,485	16,761									
Solyc02g089065	SPIRAL1-like1 (AHRD V3.3 *** AT1G26355.1)		P:GO:0043622	P:cortical microtubule organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	390,441	360,202	94,068	64,544	86,016					-0,541	0,001			down
Solyc02g089070	Eukaryotic translation initiation factor 3 subunit M (AHRD V3.3 *** K4BC61_SOLLC)		F:GO:0003743: C:G	F:translation initiation factor activity; C:eukaryotic translation in			IPR000717 (SMART): SM00753 (SMA	49,672	55,534	50,255	52,849	48,950									
Solyc02g089075	Rapid alkalinization factor 5 (AHRD V3.3 *** Q6DN46_SOLCH)						IPR039252 (PANTHER)	0,038	0,222	0,000	0,000	0,093									
Solyc02g089080	Rapid alkalinization factor 5 (AHRD V3.3 *** Q6DN46_SOLCH)						IPR039252 (PANTHER)	2,879	1,845	1,038	0,906	0,826									
Solyc02g089090	Receptor-like kinase (AHRD V3.3 *** C6ZRN8_SOYBN)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR024788 (PF	92,924	109,267	82,486	75,263	85,405									
Solyc02g089100	TSA: Wollemia nobilis Ref_Wollemi_Transcript_16418_819 transcribed RNA sequence (AHRD V3.3 *** A0A0C9QNI1_9SPER)						IPR019351 (PFAM): mobidb-lite (MOB	29,201	26,643	39,186	32,965	32,519									
Solyc02g089110	Mitochondrial carrier family protein (AHRD V3.3 *** B9H0H4_POPTR)		F:GO:0022857: P:G	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR018108 (PF	12,220	19,869	13,369	14,627	15,286	0,726	0,047					up		
Solyc02g089115	COBRA protein (AHRD V3.3 *-* K4B708_SOLLC)		P:GO:0010215: P:G	P:cellulose microfibril organization; P:cell growth; C:anchored co			IPR006918 (PFAM): PTHR31673:SF3	26,612	15,991	17,993	15,691	22,795	-0,708	0,006					down		
Solyc02g089120	Protein COBRA (AHRD V3.3 *-* A0A151S444_CAJCA)		P:GO:0010215: P:G	P:cellulose microfibril organization; P:cell growth; C:anchored co			PTHR31673:SF7 (PANTHER): IPR006	29,444	19,202	21,839	17,448	25,725	-0,592	0,048					down		
Solyc02g089130	COBRA-like protein (AHRD V3.3 *** L0ATP1_POPTO)		P:GO:0010215: P:G	P:cellulose microfibril organization; P:cell growth; C:anchored co			IPR006918 (PIRSF): IPR006918 (PFA	8,689	5,918	5,898	4,527	6,816									
Solyc02g089140	LOW QUALITY:SIN3-like 1 (AHRD V3.3 --* AT3G01320.2)							0,040	0,093	0,047	0,096	0,024									
Solyc02g089150	PI-PLC X domain-containing protein (AHRD V3.3 *** A0A0B2PWM6_GLYSO)		P:GO:0006629: F:G	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR017946 (G3DSA:3.20.20.GENE3D	3,375	5,193	11,164	12,409	16,087			0,521	0,037				up	
Solyc02g089160	dwarf	d	F:GO:0005506: F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	3,785	8,261	27,801	53,807	32,489	1,148	0,042			0,957	0,000	up		up
Solyc02g089170	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (AHRD V3.3 *** UPTG1_SOLTU)		F:GO:0016866: P:G	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR004901 (PIRSF): IPR037595 (PFA	0,058	0,082	0,125	0,025	0,072									
Solyc02g089175	N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative (AHRD V3.3 *** A0A072U633_MEDTR)		F:GO:0003723: F:G	F:RNA binding; F:tRNA (guanine-N2-)-methyltransferase activity			IPR002905 (PFAM): G3DSA:3.30.56.7	45,296	45,111	37,113	36,611	35,209									
Solyc02g089190	R2R3MYB transcription factor 29	R2R3MYB29	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,021	0,000	0,044	0,025	0,000									
Solyc02g089195	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT5G60310.1)							0,040	0,000	0,000	0,000	0,023									
Solyc02g089200	TM29	TM29	F:GO:0000977: F:G	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	229,530	237,908	194,230	214,321	193,350									
Solyc02g089205	purple acid phosphatase 14 (AHRD V3.3 --* AT2G46880.2)							13,948	13,487	10,611	11,677	11,341									
Solyc02g089210	MADS box transcription factor (AHRD V3.3 *** Q689E7_GENTR)		F:GO:0000977: F:G	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	2,092	4,133	1,358	1,559	2,530	1,011	0,036					up		
Solyc02g089220	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT3G02300.2)						IPR000408 (PRINTS): IPR000408 (PF	11,877	12,424	30,348	29,647	29,257									
Solyc02g089230	DSBA oxidoreductase family protein (AHRD V3.3 *** G7KR19_MEDTR)		F:GO:0015035	F:protein disulfide oxidoreductase activity			G3DSA:3.40.30.10 (GENE3D): IPR00	26,099	25,737	22,488	23,575	24,394									
Solyc02g089240	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EHB8_THECC)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART): IPR013083 (G3	25,282	19,603	43,081	41,887	36,378									
Solyc02g089250	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** A0A061EFL6_THECC)		F:GO:0016301: P:G	F:kinase activity; P:phosphorylation			PF01190 (PFAM): mobidb-lite (MOBID	21,663	53,404	15,357	4,755	5,665	1,331	0,046	-1,439	0,026	-1,688	0,009	up	down	down
Solyc02g089260	Auxin transport protein BIG (AHRD V3.3 *-* W9RHS2_9ROSA)		C:GO:0005829: F:G	C:cytosol; F:zinc ion binding; C:plasmodesma; P:response to fu			PTHR21725 (PANTHER)	50,308	36,571	33,171	49,579	43,833									
Solyc02g089263	auxin transport protein (BIG) (AHRD V3.3 *** AT3G02260.3)		F:GO:0005515: F:G	F:protein binding; F:zinc ion binding			IPR000433 (SMART): IPR003126 (SM	339,827	366,952	315,903	330,214	325,049									
Solyc02g089267	Clathrin heavy chain (AHRD V3.3 --* M0U7T0_MUSAM)							1,306	1,435	1,381	0,983	1,058									
Solyc02g089280	alpha-L RNA-binding motif/ribosomal protein S4 family protein		C:GO:0005622: F:G	C:intracellular; F:rRNA binding			IPR001912 (SMART): IPR002942 (SM	13,159	15,922	16,023	14,176	16,305									
Solyc02g089290	protein kinase superfamily protein		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	30,583	38,105	37,105	39,488	35,761									
Solyc02g089300	root meristem growth factor-like protein (AHRD V3.3 --* AT3G30350.2)		C:GO:0016020: C:G	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	0,019	0,021	0,000	0,000	0,000									
Solyc02g089310	F-box family protein		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR015915 (G3	10,372	9,457	14,992	24,468	16,622					0,709	0,000			up
Solyc02g089320	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G30380.2)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	7,021	11,429	13,673	17,917	16,433									
Solyc02g089330	DNA-directed RNA polymerase (AHRD V3.3 *-* A0A0V0IYF1_SOLCH)		F:GO:0003677: F:G	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR029262 (SMART): IPR029262 (PF	3,451	2,786	4,044	5,159	3,939									
Solyc02g089340	DNA-directed RNA polymerase (AHRD V3.3 *** K4BC86_SOLLC)		F:GO:0003677: F:G	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR029262 (SMART): IPR029262 (PF	15,662	13,876	18,547	18,268	15,152									
Solyc02g089350	Gibberellin-regulated family protein (AHRD V3.3 *** A0A061EVH9_THECC)		C:GO:0005576	C:extracellular region			IPR003854 (PFAM): PTHR23201:SF8	42,410	26,480	13,312	5,895	8,664	-0,652	0,047			-1,175	0,001	down		down
Solyc02g089360	SMAD/FHA domain-containing protein (AHRD V3.3 *** A0A061ENF0_THECC)		F:GO:0005515	F:protein binding			IPR000253 (SMART): G3DSA:2.60.20	58,818	47,888	68,380	68,832	63,896									
Solyc02g089390	Cell morphogenesis related protein (AHRD V3.3 *** F4KB73_ARATH)		P:GO:0000902	P:cell morphogenesis			IPR025481 (PFAM): IPR029473 (PFA	32,174	29,483	37,078	39,740	39,492									
Solyc02g089400	Amino acid transporter, putative (AHRD V3.3 *** B9T738_RICCO)		P:GO:0003333: F:G	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): mobidb-lite (MOB	0,814	0,938	0,692	0,622	0,472									
Solyc02g089410	RING/U-box superfamily protein (AHRD V3.3 *** AT3G02340.2)		C:GO:0005737: P:G	C:cytoplasm; P:protein ubiquitination; F:ubiquitin protein ligase a			IPR001841 (SMART): IPR013083 (G3	9,410	9,365	11,124	10,253	8,888									
Solyc02g089415	Signal transduction histidine kinase, hybrid-type, ethylene sensor (AHRD V3.3 --* AT3G23150.2)							0,518	0,728	0,332	0,249	0,260									
Solyc02g089420	BZIP transcription factor family protein (AHRD V3.3 *** B9NC16_POPTR)		F:GO:0003700: P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	0,698	0,841	0,134	0,164	0,118									
Solyc02g089440	glycosyltransferase family protein	GAUT9	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	164,141	178,611	41,550	42,028	45,787									
Solyc02g089450	Glutamine dumper, putative (AHRD V3.3 *** G7I7K5_MEDTR)		P:GO:0080143	P:regulation of amino acid export			PTHR33228:SF5 (PANTHER): IPR040	0,317	0,290	0,000	0,000	0,000									
Solyc02g089460	Glutamine dumper 2, putative (AHRD V3.3 *** A0A061ENI6_THECC)		P:GO:0080143	P:regulation of amino acid export			PTHR33228:SF5 (PANTHER): IPR040	0,938	1,239	0,961	1,287	1,202									
Solyc02g089470	Glutamine dumper, putative (AHRD V3.3 -** G7I7K5_MEDTR)		P:GO:0080143	P:regulation of amino acid export			mobidb-lite (MOBIDB_LITE): IPR0403	0,792	0,769	0,121	0,315	0,354									
Solyc02g089480	Glutamine dumper 2, putative (AHRD V3.3 *** A0A061ENI6_THECC)		P:GO:0080143	P:regulation of amino acid export			mobidb-lite (MOBIDB_LITE): PTHR332	0,180	0,347	0,119	0,657	0,189									
Solyc02g089490	Plant Tudor-like RNA-binding protein (AHRD V3.3 --* AT4G32440.3)							6,802	4,849	10,278	21,235	11,782					1,048	0,000			up
Solyc02g089493	CONSTANS protein (AHRD V3.3 *-* C0Z3T8_SOLTU)		F:GO:0005515: F:G	F:protein binding; F:zinc ion binding			IPR000315 (SMART): IPR010402 (PF	0,748	0,528	1,641	2,387	2,049									
Solyc02g089495	Eukaryotic translation initiation factor 3 subunit D (AHRD V3.3 --* M8BC43_AEGTA)							2,667	1,813	4,459	8,409	5,228					0,918	0,000			up
Solyc02g089497	Minichromosome maintenance (MCM2/3/5) family protein (AHRD V3.3 --* AT5G46280.4)							2,704	1,963	4,146	5,565	4,527									
Solyc02g089500	CONSTANS protein (AHRD V3.3 *-* C0Z3T8_SOLTU)	BBX2	F:GO:0008270	F:zinc ion binding			IPR000315 (SMAF DBB	1,098	0,835	2,541	3,740	3,114									
Solyc02g089510	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT3G22250.1)							0,040	0,000	0,069	0,074	0,070									
Solyc02g089515	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_NUPAD)						mobidb-lite (MOBIDB_LITE)	0,199	0,197	0,410	0,287	0,165									
Solyc02g089520	CONSTANS protein (AHRD V3.3 *** C0Z3T8_SOLTU)	BBX1	F:GO:0005515: F:G	F:protein binding; F:zinc ion binding			IPR000315 (SMAF CO-like	7,453	6,495	16,986	18,319	14,318									
Solyc02g089530	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT5G35930.3)							1,274	1,241	4,062	5,599	3,407									
Solyc02g089540	CONSTANS 1	BBX3	F:GO:0005515: F:G	F:protein binding; F:zinc ion binding			IPR000315 (SMAF CO-like	5,988	6,395	8,221	8,387	6,620									
Solyc02g089550	NSP-interacting kinase 1 (AHRD V3.3 *** AT5G16000.1)		F:GO:0004672: F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR001611 (PF	13,042	11,322	6,354	6,878	7,163									
Solyc02g089560	Pentatricopeptide repeat (PPR) superfamily protein, putative (AHRD V3.3 *** A0A061DIE6_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	18,126	18,004	22,652	22,279	19,068									
Solyc02g089580	Late embryogenesis abundant protein family protein (AHRD V3.3 *** A0A061EH65_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc02g089590	Late embryogenesis abundant protein family protein (AHRD V3.3 *** A0A061EIU3_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,021	0,047	0,000	0,000									
Solyc02g089600	ribosomal RNA-processing 7 protein (AHRD V3.3 *-* AT5G38720.1)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR024326 (PFAM): mobidb-lite (MOB	40,781	33,714	30,318	29,798	27,227									
Solyc02g089610	S-adenosylmethionine decarboxylase 2		F:GO:0004014: P:G	F:adenosylmethioni	EC:4.1.1.5	Adenosylmethionine	G3DSA:3.60.90.10 (GENE3D): IPR00	301,561	386,757	270,113	366,838	311,243									
Solyc02g089615	S-adenosylmethionine decarboxylase uORF (AHRD V3.3 *-* Q6RUQ6_DAUCA)						IPR012511 (PFAM): PTHR35727 (PAN	71,657	81,915	56,871	88,118	66,537					0,633	0,017			up
Solyc02g089620	proline dehydrogenase	pdh	F:GO:0004657: P:G	F:proline dehydroge	EC:1.5.99.8	Acting on the CH-NH	G3DSA:3.20.20.220 (GENE3D): IPR0	474,823	173,659	45,672	46,580	48,017	-1,422	0,004					down		
Solyc02g089630	Proline dehydrogenase (AHRD V3.3 *** A0A0H4CNX3_BETPL)		F:GO:0004657: P:G	F:proline dehydroge	EC:1.5.99.8	Acting on the CH-NH	G3DSA:3.20.20.220 (GENE3D): IPR0	161,491	168,915	29,688	39,422	37,288									
Solyc02g089640	cellulose-synthase-like		C:GO:0005768: C:G	C:endosome; C:trar	EC:2.4.1.12	Cellulose synthase (U	IPR001173 (PFAM): IPR029044 (G3D	269,972	76,842	94,459	324,662	266,276	-1,789	0,000	1,492	0,000	1,781	0,000	down	up	up
Solyc02g089650	DUF1262 family protein (AHRD V3.3 *** A0A072U7Y1_MEDTR)		C:GO:0016020	C:membrane			IPR010683 (PFAM): PTHR31050 (PAN	2,698	3,212	2,414	2,827	3,394									
Solyc02g089660	Titin (AHRD V3.3 *** A0A0B0NSM2_GOSAR)						PTHR34563 (PANTHER): PTHR34563	1,148	1,457	2,435	5,084	4,399			0,857	0,011	1,071	0,002		up	up
Solyc02g089670	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)		C:GO:0005794: C:G	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	0,598	0,098	0,143	0,168	0,163									
Solyc02g089680	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)		C:GO:0005794: C:G	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFA	80,141	58,002	35,082	50,711	52,292			0,572	0,006	0,532	0,013		up	up
Solyc02g089685	Phytochrome (AHRD V3.3 --* A0A087HFM1_ARAAL)							6,962	3,648	3,176	5,100	5,532			0,791	0,047				up	
Solyc02g089690	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)		C:GO:0005794: C:G	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	11,444	16,279	2,916	2,792	3,277									
Solyc02g089700	Trichome birefringence-like protein (AHRD V3.3 *** A0A072TUJ8_MEDTR)		C:GO:0005794: F:G	C:Golgi apparatus; F:O-acetyltransferase activity			IPR026057 (PFAM): IPR025846 (PFA	0,057	0,054	0,000	0,000	0,094									
Solyc02g089720	Glycoside hydrolase, family 81 (AHRD V3.3 *** A0A103YH72_CYNCS)		F:GO:0052861	F:glucan endo-1,3-b	EC:3.2.1.6	Endo-1,3(4)-beta-glu	G3DSA:2.70.98.30 (GENE3D): PF176	52,769	79,640	66,423	71,713	66,431									
Solyc02g089730	Glycoside hydrolase family 81 protein (AHRD V3.3 *** G8A0L0_MEDTR)		F:GO:0052861	F:glucan endo-1,3-b	EC:3.2.1.6	Endo-1,3(4)-beta-glu	G3DSA:2.70.98.30 (GENE3D): PF176	0,896	2,082	0,698	1,440	1,155	1,236	0,020					up		
Solyc02g089740	RTE1-homolog (AHRD V3.3 --* AT3G51040.3)							0,825	0,905	0,602	1,256	0,995									
Solyc02g089750	Receptor kinase IPR002290 Serine_threonine protein kinase		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	6,268	5,552	3,787	5,251	5,659									
Solyc02g089760	Receptor-like protein kinase At3g21340 IPR001245 Tyrosine protein kinase		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	5,345	4,748	4,267	5,120	5,728									
Solyc02g089770	Dihydroflavonol-4-reductase-binding domain	DFRL1	F:GO:0003854: P:G	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	IPR002225 (PFAM): G3DSA:3.40.50.7	43,358	31,090	194,574	176,596	201,308									
Solyc02g089780	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase isoform 1 (AHRD V3.3 *-* A0A061EI47_THE		C:GO:0016021	C:integral component of membrane			PTHR30603 (PANTHER): PTHR30603	0,139	0,076	5,314	4,334	4,748									
Solyc02g089790	Histone acetyltransferase (AHRD V3.3 *-* A0A087HP23_ARAAL)		F:GO:0003712: F:G	F:transcription core	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR001965 (SMART): IPR013178 (SM	7,785	7,552	6,021	5,698	5,859									
Solyc02g089800	Nuclear matrix constituent-like protein 1 (AHRD V3.3 *** E5GCT1_CUCME)		C:GO:0005634: P:G	C:nucleus; P:nucleus organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	81,807	82,350	97,678	88,199	93,143									
Solyc02g089810	Translation initiation factor eIF-2B subunit delta (AHRD V3.3 *** W9S6A9_9ROSA)		P:GO:0044237	P:cellular metabolic process			IPR000649 (PFAM): G3DSA:3.40.50.1	31,804	38,336	37,605	34,685	35,394									
Solyc02g089820	proteasome maturation factor UMP1-like		P:GO:0043248	P:proteasome assembly			PF05348 (PFAM): IPR008012 (PANTH	67,208	77,906	125,676	115,803	109,886									
Solyc02g089840	Calcium uniporter, mitochondrial (AHRD V3.3 *** A0A0B0PJN2_GOSAR)		P:GO:0051560	P:mitochondrial calcium ion homeostasis			PTHR13462:SF4 (PANTHER): IPR039	11,100	12,266	10,208	9,760	11,314									
Solyc02g089850	Calcium uniporter protein, mitochondrial (AHRD V3.3 *-* A0A0B2RWG8_GLYSO)		P:GO:0051560	P:mitochondrial calcium ion homeostasis			IPR006769 (PFAM): IPR039055 (PAN	8,101	9,141	9,230	9,446	9,305									
Solyc02g089860	GNS1/SUR4 membrane protein (AHRD V3.3 *** A0A124SFB5_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR002076 (PFAM): PTHR11157:SF1	0,292	0,165	0,050	0,099	0,024									
Solyc02g089870	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DGI8_THECC)		P:GO:0006511: C:G	P:ubiquitin-dependent protein catabolic process; C:integral com			IPR001841 (SMART): PF13920 (PFAM	17,173	19,914	22,350	20,140	20,699									
Solyc02g089880	Hexosyltransferase (AHRD V3.3 *** K4BCD9_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR029044 (G3DSA:3.90.550.GENE3	13,390	14,181	16,481	12,868	12,811									
Solyc02g089890	PQ-loop repeat family protein / transmembrane family protein (AHRD V3.3 *** AT4G36850.1)		F:GO:0003824: C:G	F:catalytic activity; C:integral component of membrane; F:coenz			IPR006603 (SMART): IPR006603 (PF	5,201	6,282	9,169	7,247	7,438									
Solyc02g089900	Kinase family protein (AHRD V3.3 *** B9HEM3_POPTR)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR018392 (SMART): IPR000719 (PF	90,442	112,793	21,021	47,526	43,504			1,046	0,000	1,177	0,000		up	up
Solyc02g089920	Kinase family protein (AHRD V3.3 *** B9HEM3_POPTR)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,021	0,121	0,047	0,050	0,071									
Solyc02g089930	Protein DA1-related 1 (AHRD V3.3 *** A0A199UXH9_ANACO)		F:GO:0043130: F:G	F:ubiquitin binding; F:metal ion binding			IPR003903 (SMART): IPR001781 (SM	45,373	38,105	27,075	27,759	28,269									
Solyc02g089940	BIPINNATA (AHRD V3.3 *** B2Y2H0_SOLLC)		F:GO:0003677: P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006563 (SMAF TALE	9,261	6,174	3,438	3,586	3,224									
Solyc02g089950	BTB/POZ domain-containing protein (AHRD V3.3 *** W9R5W8_9ROSA)						G3DSA:3.30.710.10 (GENE3D): mobi	1,824	1,869	0,553	0,383	0,590									
Solyc02g089960	Transmembrane protein 220 (AHRD V3.3 *** A0A1D1Z4L8_9ARAE)		C:GO:0016021	C:integral component of membrane			IPR029377 (PFAM): PTHR34262 (PAN	0,040	0,080	0,047	0,126	0,023									
Solyc02g089970	Histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 *** A0A0B2SA40_GLYSO)		F:GO:0003676: F:G	F:nucleic acid bindi	EC:2.1.1.43	Histone-lysine N-met	IPR013087 (SMART): IPR001214 (SM	37,808	35,281	51,553	59,806	57,855									
Solyc02g089980	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G66600.9)						IPR006869 (PFAM): IPR025757 (PFA	25,938	21,106	10,082	10,580	9,990									
Solyc02g089990	HTH-type transcriptional regulator (AHRD V3.3 *** AT2G23690.1)						IPR025322 (PFAM): mobidb-lite (MOB	4,547	1,991	1,225	8,331	4,611	-1,160	0,048	1,884	0,000	2,736	0,000	down	up	up
Solyc02g090000	CASP-like protein (AHRD V3.3 *** K4BCF1_SOLLC)		C:GO:0005886: C:G	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021:SF2	3,849	4,010	6,168	7,167	6,971									

Solyc02g090010	Molybdopterin synthase sulfur carrier subunit (AHRD V3.3 *** M1AMG8_SOLTU)		C:GO:0005829; P:G(	C:cytosol; P:Mo-molybdopterin cofactor biosynthetic process			IPR012675 (G3DSA:3.10.20.GENE3D	13,358	13,800	14,617	13,969	13,752									
Solyc02g090020	stress regulated protein AY873991		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	PTHR33471 (PANTHER): PTHR33471	8,243	8,358	7,759	5,934	8,672									
Solyc02g090040	CTP synthase family protein (AHRD V3.3 *-* AT4G20320.6)		F:GO:0003883; F:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutamine hydrolyzing)		5,609	4,581	5,213	5,503	6,121									
Solyc02g090043	DNA mismatch repair protein mutL (AHRD V3.3 --* A0A0B2SBZ1_GLYSO)		F:GO:0005524; P:G(	F:ATP binding; P:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,772	0,662	0,738	0,879	0,704									
Solyc02g090070	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G66560.1)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR027356 (PF	39,771	22,866	7,659	8,197	8,256	-0,770	0,004					down		
Solyc02g090090	ethylene responsive proteinase inhibitor 1	er1	F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	50,295	46,474	55,281	49,468	54,081									
Solyc02g090100	LOW QUALITY:Synechocystis YCF37 (AHRD V3.3 *** A0A061DHK7_THECC)		C:GO:0009535	C:chloroplast thylakoid membrane			PTHR36734 (PANTHER)	27,044	34,182	19,509	19,034	27,140			0,475	0,006				up	
Solyc02g090110	WAK-like kinase		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR024171 (PIF	44,067	56,142	29,072	32,752	44,574			0,614	0,003				up	
Solyc02g090120	LOW QUALITY:Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 (AHRD V3.3 -** A0A1D1XL30		P:GO:0008150	P:biological_process			mobidb-lite (MOBIDB_LITE): PTHR353	4,115	4,352	9,235	10,671	14,395			0,633	0,004				up	
Solyc02g090130	vacuolar protein sorting-associated protein, putative (DUF1162) (AHRD V3.3 *** AT3G50380.4)						IPR009543 (PFAM): IPR031645 (PFA	54,286	47,280	53,579	63,726	62,766									
Solyc02g090135	vacuolar protein sorting-associated protein, putative (DUF1162) (AHRD V3.3 *-* AT3G50380.2)						PTHR16166:SF98 (PANTHER): PTHR	15,777	10,065	12,743	19,907	16,660					0,642	0,050			up
Solyc02g090150	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G50390.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,037	0,100	0,000	0,000	0,047									
Solyc02g090160	Guanine nucleotide-binding protein alpha-2 subunit (AHRD V3.3 *** W9QPE6_9ROSA)		F:GO:0003924; P:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001019 (PRINTS): IPR001019 (SM	54,081	43,800	64,710	69,398	66,120									
Solyc02g090170	B3 domain-containing protein (AHRD V3.3 *** A0A199VWS3_ANACO)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	2,130	3,255	0,779	1,152	1,468									
Solyc02g090180	Prolyl oligopeptidase family protein (AHRD V3.3 *** AT5G66960.1)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR002470 (PRINTS): IPR001375 (PF	5,495	5,277	3,489	3,900	3,488									
Solyc02g090190	Molybdenum cofactor sulfurase (AHRD V3.3 *** A0A0B2NTX1_GLYSO)		F:GO:0003824	F:catalytic activity			IPR015422 (G3DSA:3.90.1150.GENE	58,367	48,614	72,512	61,944	63,038									
Solyc02g090200	Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 *-* AT2G23530.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018866 (PFAM): mobidb-lite (MOB	13,904	10,976	9,545	8,928	8,920									
Solyc02g090210	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RJ07_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,176	0,134	0,347	0,507	0,563									
Solyc02g090220	Zinc finger, Dof-type (AHRD V3.3 *** A0A124SC40_CYNCS)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,377	0,514	0,050	0,000	0,046									
Solyc02g090230	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT4G37130.1)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	11,882	11,549	8,670	9,768	9,754									
Solyc02g090240	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S8N5_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,021	0,064	0,022	0,148	0,000									
Solyc02g090260	Golgin candidate 6 isoform 2 (AHRD V3.3 *** A0A061DMU6_THECC)						IPR032794 (PFAM): IPR029415 (PFA	19,568	28,908	10,464	13,903	14,722									
Solyc02g090265	Cytochrome P450 (AHRD V3.3 *-* A0A103Y527_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3	6,691	10,911	4,322	5,046	5,120									
Solyc02g090267	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	14,784	28,505	11,606	10,928	13,720	0,972	0,008					up		
Solyc02g090290	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,021	0,018	0,022	0,000	0,023									
Solyc02g090300	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,489	1,310	0,316	0,395	0,306	1,417	0,026					up		
Solyc02g090310	Dof zinc finger protein (AHRD V3.3 *-* W9QGW0_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	4,117	16,688	10,512	13,208	8,131	2,042	0,000					up		
Solyc02g090315	meiotically up-regulated protein (AHRD V3.3 *** AT5G66930.3)		P:GO:0006914	P:autophagy			IPR012445 (PFAM): IPR012445 (PAN	0,301	0,636	0,000	0,000	0,046									
Solyc02g090330	meiotically up-regulated protein (AHRD V3.3 *** AT5G66930.2)		P:GO:0006914	P:autophagy			IPR012445 (PFAM): IPR012445 (PAN	2,049	1,542	1,721	1,576	1,325									
Solyc02g090350	Cytochrome P450 (AHRD V3.3 *** A0A103Y530_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	30,541	28,946	1,003	0,742	1,870									
Solyc02g090360	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2RUS1_GLYSO)		F:GO:0005507; F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR011707 (PFAM): IPR008972 (G3D	333,584	428,607	185,886	266,568	270,691									
Solyc02g090370	Reticulon-like protein (AHRD V3.3 *** M1AMN6_SOLTU)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): mobidb-lite (MOB	11,527	7,388	0,664	3,304	0,255									
Solyc02g090380	NBS-LRR disease resistance protein (AHRD V3.3 *** G7K839_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR013103 (PFA	189,150	72,897	15,993	47,881	39,008	-1,351	0,000	1,280	0,000	1,579	0,000	down	up	up
Solyc02g090390	Kinase family protein (AHRD V3.3 *** B9N888_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	55,740	70,625	75,583	86,823	82,221									
Solyc02g090395	SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 --* AT2G44980.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,000	0,000	0,000									
Solyc02g090400	Two-component response regulator (AHRD V3.3 *** W9S3N8_9ROSA)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	2,216	6,447	2,353	1,788	1,914	1,557	0,004					up		
Solyc02g090410	ASYMMETRIC LEAVES 2-like 1 (AHRD V3.3 *** A0A061DMY0_THECC)		P:GO:0048827	P:phyllome development			IPR004883 (PFAM LBD	0,704	0,298	0,050	0,050	0,023									
Solyc02g090420	LOW QUALITY:50S ribosomal protein L25, putative (AHRD V3.3 *** B9S8K5_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR020057 (PFAM): IPR037121 (G3D	30,776	25,971	36,133	32,329	33,848									
Solyc02g090430	MAP kinase kinase kinase 20	MAPKKK20	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	11,796	16,218	3,196	2,702	4,430									
Solyc02g090440	ankyrin repeat family protein (AHRD V3.3 --* AT4G05040.7)							0,610	1,128	1,647	1,617	1,174									
Solyc02g090450	Sl Peroxidase		F:GO:0004601; P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,613	0,678	0,158	0,244	0,070									
Solyc02g090470	Peroxidase (AHRD V3.3 *** K4BCJ6_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,096	0,114	0,000	0,000	0,000									
Solyc02g090480	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0V0I8Y4_SOLCH)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomera	IPR002130 (PRINTS): IPR019734 (SM	5,901	7,971	1,291	0,556	1,009									
Solyc02g090490	Patatin (AHRD V3.3 *** K4BCJ8_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM): G3DSA:3.40.109	4,279	14,277	2,438	3,447	3,985	1,758	0,003					up		
Solyc02g090500	Phenylalanine ammonia-lyase (AHRD V3.3 --* D3K195_9ROSA)	PAL						4,548	4,636	1,221	1,050	2,228									
Solyc02g090505	haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *-* AT1G56500.2)		C:GO:0009534; C:G(	C:chloroplast thylakoid; C:chloroplast stroma; P:nonphotochemi			IPR023214 (G3DSA:3.40.50.GENE3D	0,714	0,684	0,197	0,167	0,471									
Solyc02g090510	CDPK-related kinase (AHRD V3.3 *** AT3G50530.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.23	5,860	5,990	0,466	0,766	1,246									
Solyc02g090520	stress regulated protein (AHRD V3.3 --* AT5G27290.1)							0,000	0,018	0,000	0,000	0,000									
Solyc02g090530	SAP domain-containing protein (AHRD V3.3 *** AT5G66840.2)						IPR036361 (G3DSA:1.10.720.GENE3	31,438	32,833	26,646	29,271	27,298									
Solyc02g090540	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061DHS1_THECC)						IPR002347 (PRINTS): G3DSA:3.40.50	0,019	0,059	0,000	0,050	0,000									
Solyc02g090545	Calcium-transporting ATPase (AHRD V3.3 *** M5X6S2_PRUPE)		F:GO:0000166	F:nucleotide binding			IPR006068 (PFAM): IPR023299 (G3D	0,037	0,160	0,000	0,025	0,096									
Solyc02g090560	Calcium-transporting ATPase (AHRD V3.3 *** M5X6S2_PRUPE)		F:GO:0000166	F:nucleotide binding			IPR023214 (G3DSA:3.40.50.GENE3D	3,652	8,308	0,735	1,143	1,262	1,206	0,049					up		
Solyc02g090570	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G50590.2)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	114,127	95,770	93,071	100,146	98,580									
Solyc02g090580	ternary complex factor MIP1 leucine-zipper protein (Protein of unknown function, DUF547) (AHRD V3.3 *** AT4G37080.3)						IPR025757 (PFAM): IPR006869 (PFA	16,305	12,828	4,868	5,750	7,144									
Solyc02g090620	Sulfotransferase (AHRD V3.3 *** K4BCL1_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM): G3DSA:3.40.50.3	17,318	16,351	1,685	1,260	2,002									
Solyc02g090630	Patatin (AHRD V3.3 *** A0A0E0IDC7_ORYNI)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR	1,499	1,499	1,427	1,442	1,227									
Solyc02g090650	Ran-binding protein in the microtubule-organising centre protein (AHRD V3.3 *** AT5G66810.4)						IPR006595 (SMART): mobidb-lite (MO	31,592	24,236	45,815	42,669	39,205									
Solyc02g090660	Patatin (AHRD V3.3 *-* K4BCL5_SOLLC)		P:GO:0016042; F:G(	P:lipid catabolic process; F:hydrolase activity				0,019	0,037	0,118	0,146	0,094									
Solyc02g090665	Patatin (AHRD V3.3 *-* K4BCL5_SOLLC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR	0,038	0,061	0,050	0,000	0,000									
Solyc02g090670	Methionine aminopeptidase 1 (AHRD V3.3 *** M1BAG1_SOLTU)		F:GO:0004177; P:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR001714 (PRINTS): IPR000994 (PF	30,465	42,628	51,997	56,247	61,283									
Solyc02g090680	Cyclin-dependent kinase inhibitor (AHRD V3.3 *** Q8GUA2_TOBAC)		F:GO:0004861; C:G(	F:cyclin-dependent protein serine/threonine kinase inhibitor acti			IPR003175 (PFAM): IPR003175 (PIRS	14,610	16,850	0,461	0,537	0,727									
Solyc02g090690	membrane protein (AHRD V3.3 *** AT4G37030.1)		C:GO:0016021	C:integral component of membrane			PTHR31133:SF4 (PANTHER): IPR040	2,836	1,841	1,248	1,433	1,154									
Solyc02g090710	B3 domain-containing protein (AHRD V3.3 *** W9R6M5_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	56,063	51,476	54,405	47,275	48,708									
Solyc02g090740	Protein DETOXIFICATION (AHRD V3.3 *** K4BCM3_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	3,058	3,688	1,421	0,993	1,454									
Solyc02g090750	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A) (AHRD V3.3 *-* E1ZM95_CHLVA)		F:GO:0003743; F:G(	F:translation initiati	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (PFAM): G3DSA:3.40.50.3	4,489	7,605	4,522	3,442	4,289									
Solyc02g090760	TUDOR-SN protein 1 isoform 2 (AHRD V3.3 *** A0A061DN41_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	231,791	232,855	200,425	204,213	214,905									
Solyc02g090770	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RA19_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,099	0,287	0,025	0,101	0,093									
Solyc02g090780	LOW QUALITY:ubiquitin-specific protease 2 (AHRD V3.3 --* AT1G04860.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,000	0,000	0,000									
Solyc02g090790	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R7J5_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,000	0,000	0,050	0,000									
Solyc02g090800	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R7J5_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,018	0,000	0,076	0,000									
Solyc02g090810	centrin2 (AHRD V3.3 *** AT3G50360.1)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	8,647	4,914	7,520	5,914	6,181	-0,786	0,035					down		
Solyc02g090820	SolycHsfB1	HSF-05	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	80,761	115,320	170,115	210,059	175,343									
Solyc02g090840	DUF1685 family protein (AHRD V3.3 *** G7K6Q0_MEDTR)						IPR012881 (PFAM): mobidb-lite (MOB	421,183	363,080	602,503	524,321	478,569									
Solyc02g090850	CLK4-associating serine/arginine-rich protein (AHRD V3.3 *** AT4G36980.4)						IPR019147 (SMART): IPR019147 (PF	135,523	123,364	192,741	184,618	173,378									
Solyc02g090860	Phenylalanyl-tRNA synthetase alpha chain, putative (AHRD V3.3 *** G7JG63_MEDTR)		F:GO:0000049; F:G(	F:tRNA binding; F:p	EC:6.1.1.2	Phenylalanine--tRNA	IPR004529 (TIGRFAM): G3DSA:1.10.	50,386	52,604	54,775	53,752	50,822									
Solyc02g090870	LOW QUALITY:GTPase-activating protein pac-1 (AHRD V3.3 *** A0A1D1Y9Q3_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	18,660	33,467	25,785	32,879	26,142	0,869	0,009					up		
Solyc02g090890	zeaxanthin epoxidase	zep	F:GO:0005515; C:G(	F:protein binding; C	EC:1.14.13.9; EC:1.	Acting on paired dono	PR00420 (PRINTS): IPR000253 (SMA	87,648	99,409	77,615	85,320	140,545			0,853	0,000				up	
Solyc02g090900	Remorin family protein (AHRD V3.3 *** B9H6G4_POPTR)						IPR005516 (PFAM): mobidb-lite (MOB	8,873	8,617	2,073	1,669	2,018									
Solyc02g090910	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT4G36960.2)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	41,949	42,522	57,007	57,083	54,069									
Solyc02g090920	LOW QUALITY:Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM): IPR029058 (G3D	0,080	0,103	0,022	0,097	0,047									
Solyc02g090930	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM): IPR029058 (G3D	21,108	41,761	1,646	1,422	1,247	1,010	0,010					up		
Solyc02g090940	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	0,042	0,105	0,000	0,000	0,000									
Solyc02g090950	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT3G50330.1)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,000	0,000	0,022	0,000	0,000									
Solyc02g090960	Rapid alkalinization factor 3 (AHRD V3.3 *** Q6TF27_SOLCH)		C:GO:0009506; C:G(	C:plasmodesma; C:membrane; P:calcium-mediated signaling			IPR008801 (PFAM): PTHR33136:SF7	4,124	3,548	0,050	0,000	0,023									
Solyc02g090970	MAP kinase kinase kinase 21	MAPKKK21	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	7,241	12,932	2,186	5,521	1,949					1,348	0,000			up
Solyc02g090980	MAP kinase kinase kinase 22	MAPKKK22	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,322	0,719	0,411	0,456	0,116									
Solyc02g090990	MAP kinase kinase kinase 23	MAPKKK23	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	2,062	2,464	0,517	0,932	0,306									
Solyc02g091000	Late embryogenesis abundant protein (AHRD V3.3 *** G7LCF7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	19,052	35,174	30,991	39,086	34,388	0,909	0,008					up		
Solyc02g091020	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *-* A0A0B0NW09_GOSAR)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural con			IPR007230 (PFAM): IPR036903 (G3D	12,397	27,403	6,499	8,249	9,598	1,169	0,001					up		
Solyc02g091023	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *-* A0A0B0NW09_GOSAR)		C:GO:0005643; F:G(	C:nuclear pore; F:structural constituent of nuclear pore			G3DSA:1.10.10.2360 (GENE3D): mob	1,105	2,106	0,625	0,943	1,104									
Solyc02g091027	polyadenylate-binding protein 1-B-binding protein (AHRD V3.3 --* AT5G44860.2)							5,863	7,069	3,326	3,793	3,648									
Solyc02g091030	Nuclear transcription factor Y subunit C-2 (AHRD V3.3 *-* W9SQ52_9ROSA)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YC	59,366	87,434	39,573	38,953	45,412									
Solyc02g091040	myb domain protein 76 (AHRD V3.3 --* AT5G07700.2)							5,017	4,603	157,131	224,122	186,464					0,517	0,045			up
Solyc02g091050	Protein DETOXIFICATION (AHRD V3.3 *** K4BCQ4_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	0,042	0,018	0,598	0,373	0,450									
Solyc02g091060	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT5G16640.1)							0,159	0,278	0,144	0,098	0,117									
Solyc02g091070	Protein DETOXIFICATION (AHRD V3.3 *** K4BCQ6_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	0,000	0,000	0,000	0,025	0,000									
Solyc02g091080	Protein DETOXIFICATION (AHRD V3.3 *** K4BCQ7_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	0,879	3,837	1,656	1,845	2,218	2,149	0,000					up		
Solyc02g091085	Protein DETOXIFICATION (AHRD V3.3 *-* V4S8W0_9ROSI)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			PTHR11206 (PANTHER): PTHR11206	0,199	0,138	0,583	0,494	0,283									
Solyc02g091090	Receptor-type tyrosine-protein phosphatase U (AHRD V3.3 *** A0A061FRU0_THECC)						PTHR37076 (PANTHER): PTHR37076	10,077	9,490	14,156	11,440	13,121									
Solyc02g091100	Thiamine pyrophosphate dependent pyruvate decarboxylase family protein (AHRD V3.3 *** AT5G17380.1)		F:GO:0000287; F:G(	F:magnesium ion binding; F:catalytic activity; F:thiamine pyroph			G3DSA:3.40.50.1220 (GENE3D): G3D	214,046	199,850	282,184	257,791	262,458									
Solyc02g091110	Histone chaperone (AHRD V3.3 *** A9TVI5_PHYPA)		C:GO:0005634; P:G(	C:nucleus; P:chromatin assembly or disassembly			IPR036747 (G3DSA:2.60.40.GENE3D	4,702	4,919	3,642	3,555	3,530									
Solyc02g091120	DNA ligase (AHRD V3.3 *** K4BCR1_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:Di	EC:6.5.1.1	DNA ligase (ATP)	IPR012310 (PFAM): G3DSA:2.40.50.1	44,534	38,980	36,469	40,687	34,925									
Solyc02g091130	ATP synthase subunit beta (AHRD V3.3 *** A0A0V0IJL8_SOLCH)		C:GO:0000275; F:G(	C:mitochondrial pro	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR004100 (PF	7,603	6,831	8,040	5,416	6,745									
Solyc02g091140	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (AHRD V3.3 *** B9HJH9_POPTR)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM): G3DSA:3.40.50.1	7,932	16,897	19,659	17,840	30,699	1,113	0,024	0,641	0,032			up	up	
Solyc02g091160	Integrin-linked protein kinase family (AHRD V3.3 *-* A0A061GZK1_THECC)		F:GO:0005515	F:protein binding			IPR002110 (SMART): PF13857 (PFAM	1,522	1,179	0,432	0,588	0,443									
Solyc02g091170	Serine-threonine protein kinase, putative (AHRD V3.3 *** B9SPY3_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): PIRSF000654 (P	0,664	1,306	0,501	0,530	0,540									
Solyc02g091180	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IAV0_MEDTR)						IPR025322 (PFAM): PTHR33052:SF3	16,419	2,102	8,725	54,674	11,485	-2,935	0,000			2,644	0,000	down		up
Solyc02g091190	Protein-lysine N-methyltransferase PGSC0003DMG400030596 (AHRD V3.3 *** M1D0F7_SOLTU)		F:GO:0008168	F:methyltransferase activity			IPR025714 (PFAM): G3DSA:3.40.50.1	69,308	72,152	76,698	72,135	74,576									
Solyc02g091210	Eukaryotic translation initiation factor 5 (AHRD V3.3 *** IF5_PHAVU)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; P:transla			IPR002735 (SMART): IPR003307 (SM	30,976	26,093	35,387	29,654	30,775									
Solyc02g091220	Eukaryotic translation initiation factor 5 (AHRD V3.3 *** IF5_PHAVU)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; P:transla			IPR002735 (SMART): IPR003307 (SM	2,788	2,034	4,191	4,574	3,894									
Solyc02g091230	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EGA0_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	4,205	3,057	4,589	4,175	4,288									
Solyc02g091240	Auxin efflux carrier (AHRD V3.3 *** A0A103XKJ3_CYNCS)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): IPR039305 (PAN	67,846	48,529	59,305	59,675	59,602									
Solyc02g091250	LOW QUALITY:mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT2G01300.1)		C:GO:0016021	C:integral component of membrane			PTHR33782 (PANTHER): PTHR33782	21,771	38,787	6,094	6,966	6,247									
Solyc02g091260	LOW QUALITY:mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT2G01300.1)		C:GO:0016021	C:integral component of membrane			PTHR33782 (PANTHER): PTHR33782	0,376	1,090	0,075	0,000	0,048									
Solyc02g091270	ELL-associated factor, putative (AHRD V3.3 *** B9SYJ2_RICCO)		P:GO:0006355; C:G(	P:regulation of transcription, DNA-templated; C:ELL-EAF comple			IPR019194 (PFAM): mobidb-lite (MOB	19,974	22,777	18,404	16,946	18,379									
Solyc02g091280	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4BCS6_SOLLC)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): G3DSA:3.90.22	57,890	78,455	127,855	116,775	125,881									
Solyc02g091290	Protein pigment defective 194 (AHRD V3.3 *** A0A0G2T576_9ROSI)		F:GO:0004479; P:G(	F:methionyl-tRNA fo	EC:2.1.2.9	Methionyl-tRNA form	G3DSA:3.40.50.170 (GENE3D): IPR0	3,374	4,319	3,599	3,466	4,834									
Solyc02g091300	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061EH84_THECC)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	0,019	0,036	0,000	0,022	0,000									
Solyc02g091310	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT1G23000.2)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0	0,399	0,604	0,512	0,374	0,564									
Solyc02g091320	glutamyl-tRNA (Gln) amidotransferase subunit C (AHRD V3.3 *-* AT5G17460.5)						mobidb-lite (MOBIDB_LITE): PTHR383	2,917	3,798	5,234	5,657	5,770									
Solyc02g091330	AAR2 protein family (AHRD V3.3 *** AT1G66510.4)		P:GO:0000244	P:spliceosomal tri-snRNP complex assembly			IPR038514 (G3DSA:1.25.40.GENE3D	39,877	33,953	76,009	68,096	80,675									
Solyc02g091340	Pyridoxal kinase (AHRD V3.3 *** Q4JR84_SOLTU)		F:GO:0008478; P:G(	F:pyridoxal kinase a	EC:2.7.1.35	Pyridoxal kinase	IPR004625 (TIGRFAM): IPR013749 (F	10,692	11,326	11,696	9,731	12,185									
Solyc02g091345	Pyridoxal kinase (AHRD V3.3 *-* Q4JR84_SOLTU)		C:GO:0005829; F:G(	C:cytosol; F:pyrido	EC:2.7.1.35	Pyridoxal kinase		1,498	1,321	1,489	1,481	1,459									
Solyc02g091350	Glycosyltransferase (AHRD V3.3 *** K4BCT3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	5,205	3,937	1,975	1,127	1,413									
Solyc02g091360	Plastid movement impaired protein (AHRD V3.3 *** A0A072VEV4_MEDTR)		C:GO:0005886	C:plasma membrane			IPR025322 (PFAM): PTHR33148 (PAN	1,175	1,125	0,241	0,745	0,658									
Solyc02g091370	Glycosyltransferase (AHRD V3.3 *** K4BCT5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	1,405	1,568	0,025	0,100	0,069									
Solyc02g091390	cold-regulated protein (AHRD V3.3 *** AT3G03341.1)		C:GO:0016021	C:integral component of membrane			PTHR34673 (PANTHER)	5,076	7,792	0,817	2,105	2,146			1,373	0,004	1,348	0,004		up	up
Solyc02g091410	Protease Do-like 7 (AHRD V3.3 *** DEGP7_ARATH)		F:GO:0004252; F:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): IPR001478 (SM	91,656	74,406	102,421	94,444	97,025									
Solyc02g091420	NOD26-like intrinsic protein 4.1	NIP4.1	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	0,000	0,000	0,000	0,000	0,046									
Solyc02g091430	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PMJ3_ZOSMR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	29,601	35,591	30,201	18,247	24,720					-0,726	0,000			down
Solyc02g091460	Double-stranded RNA binding protein, putative (AHRD V3.3 *-* B9T2K0_RICCO)		F:GO:0003723	F:RNA binding			IPR014720 (SMART): G3DSA:3.30.16	21,667	20,258	24,191	26,927	23,789									
Solyc02g091470	Kinase family protein (AHRD V3.3 *** U5GCF1_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	2,060	1,401	0,505	0,461	0,636									
Solyc02g091480	Calcium binding protein (AHRD V3.3 *** B5QST3_PARJU)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	0,084	0,021	0,047	0,025	0,069									
Solyc02g091490	symbol=Frk3	fruc3	F:GO:0016301	F:kinase activity			IPR002139 (PRINTS): IPR011611 (PF	54,032	75,252	123,092	139,477	133,699									
Solyc02g091500	Calcium binding protein (AHRD V3.3 *** Q93YA8_SESRO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	61,415	32,638	32,709	85,185	57,740	-0,888	0,003	0,817	0,004	1,382	0,000	down	up	up
Solyc02g091510	GDP-L-galactose phosphorylase 2	GGP2	F:GO:0080048	F:GDP-D-glucose p	EC:2.4.1.1; EC:2.7.7	Glycogen phosphoryl	mobidb-lite (MOBIDB_LITE): IPR0265	59,267	75,604	133,700	145,225	131,925									
Solyc02g091520	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** F4K8L6_ARATH)						IPR000008 (PRINTS): IPR000008 (SM	11,083	13,110	27,754	25,924	21,954									
Solyc02g091525	5'-AMP-activated protein kinase subunit beta-1 (AHRD V3.3 *** A0A061EHR2_THECC)						IPR013783 (G3DSA:2.60.40.GENE3D	0,000	0,021	0,025	0,000	0,000									
Solyc02g091530	5'-AMP-activated protein kinase subunit beta-1 (AHRD V3.3 *** A0A061EHR2_THECC)						IPR032640 (PFAM): IPR013783 (G3D	0,156	0,239	0,237	0,101	0,117									
Solyc02g091540	Senescence-associated protein, putative (AHRD V3.3 *** A0A072UZQ4_MEDTR)						PTHR33270:SF5 (PANTHER): IPR040	0,078	0,021	0,000	0,025	0,000									
Solyc02g091560	Serine hydroxymethyltransferase (AHRD V3.3 *** A0A0R4J3Y9_SOYBN)		F:GO:0004372; P:G(	F:glycine hydroxym	EC:2.1.2.1	Glycine hydroxymeth	IPR015422 (G3DSA:3.90.1150.GENE	325,422	675,798	84,435	99,608	322,795	1,081	0,001	1,931	0,000			up	up	

Solyc02g091570	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	0,160	0,041	0,050	0,000	0,046									
Solyc02g091580	Oligopeptidase A (AHRD V3.3 *** W9RQH4_9ROSA)		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	G3DSA:1.10.1370.40 (GENE3D): IPR(	79,859	90,535	93,193	93,657	96,525									
Solyc02g091590	symbiosis receptor-like kinase (SYMRK)	SYMRK	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR032675 (G3	2,459	3,087	1,487	3,925	4,352			1,545	0,001	1,402	0,007		up	up
Solyc02g091620	Nuclear pore complex protein (AHRD V3.3 --* AT1G55540.2)		F:GO:0005524; P:G(	F:ATP binding; P:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		8,352	16,911	7,819	7,251	7,074	1,042	0,007					up		
Solyc02g091623	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_PSINU)							0,040	0,135	0,022	0,000	0,024									
Solyc02g091625	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)							0,040	0,079	0,025	0,000	0,024									
Solyc02g091627	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A0B2SBZ1_GLYSO)		P:GO:0006298; P:G(	P:mismatch repair;	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036890 (G3DSA:3.30.565.GENE3	0,040	0,425	0,243	0,195	0,120									
Solyc02g091640	endoribonuclease E-like protein (AHRD V3.3 *** AT4G37920.1)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast envelope			IPR040320 (PANTHER): PTHR31755:	19,066	20,294	39,153	35,878	40,207									
Solyc02g091650	DNA-binding protein, putative (duplicated DUF1399) (AHRD V3.3 *** AT2G22660.3)						IPR009836 (PFAM): PTHR34365 (PAN	1,808	2,686	4,292	6,355	5,050									
Solyc02g091655	Telomerase activating protein Est1 (AHRD V3.3 --* AT1G28260.2)							2,862	2,671	1,825	2,266	1,765									
Solyc02g091660	Transcription factor GTE4 (AHRD V3.3 *** A0A0B2QCM2_GLYSO)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR001487 (SM	12,287	14,171	14,780	15,004	15,384									
Solyc02g091670	Octicosapeptide/Phox/Bem1p domain-containing protein (AHRD V3.3 *-* T2DP86_PHAVU)		F:GO:0005515	F:protein binding			IPR000270 (SMART): IPR000270 (PF	98,690	49,396	45,757	72,431	65,309	-0,972	0,000	0,511	0,008	0,665	0,000	down	up	up
Solyc02g091680	Beta-D-xylosidase (AHRD V3.3 *** A9YWR3_MEDTR)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR026891 (SMART): IPR001764 (PF	26,477	21,549	48,076	45,787	46,592									
Solyc02g091690	bHLH transcription factor 081		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	49,086	34,555	9,449	6,054	7,560									
Solyc02g091700	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)		C:GO:0016021	C:integral component of membrane			IPR037699 (PANTHER)	13,937	14,569	31,418	42,608	37,194					0,444	0,050			up
Solyc02g091710	Zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 *** AT5G49665.1)						IPR002035 (SMART): IPR001841 (SM	1,386	0,984	1,118	2,058	1,806									
Solyc02g091720	LisH/CRA/RING-U-box protein (AHRD V3.3 *** G7LHS6_MEDTR)		F:GO:0005515	F:protein binding			IPR001841 (SMART): IPR006595 (SM	33,733	32,798	46,287	45,017	44,937									
Solyc02g091730	Chromatin SPT2 (AHRD V3.3 *** A0A118JSU1_CYNCS)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	30,979	32,416	15,100	19,884	24,123			0,672	0,003				up	
Solyc02g091733	Chromatin SPT2 (AHRD V3.3 --* A0A118JSU1_CYNCS)						IPR013256 (PFAM): mobidb-lite (MOB	0,198	0,136	0,047	0,192	0,188									
Solyc02g091737	Starch synthase V (AHRD V3.3 *-* B2ZGM7_SOLTU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,074	0,047	0,000									
Solyc02g091740	Kinesin-like protein (AHRD V3.3 *** K4BCX6_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	8,672	7,424	4,539	5,109	5,535									
Solyc02g091750	60S ribosomal protein L17 (AHRD V3.3 --* RL17_MAIZE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	6,893	6,950	3,349	4,290	5,294									
Solyc02g091770	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *-* V7CL87_PHAVU)						G3DSA:3.40.50.2000 (GENE3D): IPR(	1,007	0,653	0,523	0,799	0,613									
Solyc02g091790	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G49660.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	22,374	22,655	30,585	29,847	28,947									
Solyc02g091800	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT4G37850.2)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,161	0,263	0,125	0,191	0,306									
Solyc02g091820	bHLH transcription factor 016		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,000	0,036	0,000	0,025	0,000									
Solyc02g091830	Phosphotransferase (AHRD V3.3 *** K4BCY1_SOLLC)		P:GO:0001678; F:G(	P:cellular glucose h	EC:2.7.1.1	Hexokinase	PR00475 (PRINTS): G3DSA:3.30.420	10,906	5,891	4,658	3,375	4,755									
Solyc02g091840	Non-specific serine/threonine protein kinase (AHRD V3.3 *** F8WS84_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART): IPR000719 (SM	340,910	241,161	469,293	398,122	403,702									
Solyc02g091860	Receptor kinase (AHRD V3.3 *** D9IAP8_GOSHI)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR032675 (G3	30,466	24,638	2,192	2,050	3,190									
Solyc02g091870	Tubulin alpha chain (AHRD V3.3 *** M1D0L4_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002452 (PRINTS): IPR000217 (PF	0,438	0,634	0,118	0,025	0,071									
Solyc02g091880	cytochrome c oxidase-like protein (AHRD V3.3 *-* AT4G37830.1)		F:GO:0004129; C:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR036418 (G3DSA:4.10.95.GENE3D	66,602	72,992	103,995	97,475	101,322									
Solyc02g091890	myb-like protein X (AHRD V3.3 *-* AT4G33740.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	85,929	83,373	18,024	15,160	16,077									
Solyc02g091910	Epidermal patterning factor-like protein (AHRD V3.3 *** G7K151_MEDTR),Pfam:PF17181		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): IPR039455 (PANTH	0,021	0,000	0,000	0,000	0,000									
Solyc02g091920	xyloglucan endotransglucosylase-hydrolase 7	xth7	F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	G3DSA:2.60.120.200 (GENE3D): IPR(	194,144	137,198	0,248	0,072	0,282									
Solyc02g091930	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001356 (SMAF HD-ZIP	24,059	26,893	9,112	7,866	8,382									
Solyc02g091940	Protein TSSC4 (AHRD V3.3 *** A0A0B0PXY2_GOSAR)		F:GO:0005515	F:protein binding			IPR029338 (PFAM): mobidb-lite (MOB	0,826	1,117	0,930	0,560	0,706									
Solyc02g091950	Lysosomal Pro-X carboxypeptidase (AHRD V3.3 *-* Q9FLH1_ARATH)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity			G3DSA:1.20.120.980 (GENE3D): IPR(	7,189	7,979	3,024	3,071	3,891									
Solyc02g091960	Nuclear matrix constituent-like protein, putative (AHRD V3.3 *** A0A072UNX6_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:nucleus organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	74,888	60,580	73,219	66,240	64,106									
Solyc02g091970	SIBCAT3	BCAT3	F:GO:0004084; P:G(	F:branched-chain-a	EC:2.6.1.42	Branched-chain-amir	G3DSA:3.30.470.10 (GENE3D): IPR(	43,900	51,162	55,126	53,398	58,238									
Solyc02g091980	blind-like7	R2R3MYB84	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,000	0,021	0,025	0,051	0,000									
Solyc02g091990	1-aminocyclopropane-1-carboxylate synthase 3	ACS3	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			PR00753 (PRINTS): IPR015421 (G3D	1,696	1,545	0,742	1,120	1,505									
Solyc02g092000	transmembrane protein (AHRD V3.3 *** AT3G49720.3)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D): mobic	80,749	105,563	19,185	19,336	20,725									
Solyc02g092010	GTP-binding protein hflx, putative (AHRD V3.3 *** A0A061DHA7_THECC)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR016496 (TI(	57,448	49,638	70,466	65,855	69,029									
Solyc02g092020	F-box protein SKIP23 (AHRD V3.3 *** A0A151TCP0_CAJCA)						G3DSA:1.20.1280.50 (GENE3D): IPR(	0,326	0,472	0,046	0,047	0,070									
Solyc02g092030	DUF21 domain-containing-like protein (AHRD V3.3 *** A0A0B0NQ32_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM): PTHR12064:SF5	0,178	0,217	0,022	0,092	0,023									
Solyc02g092040	LOW QUALITY:Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** G7K170_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph			PR00019 (PRINTS): IPR032675 (G3D	4,159	3,478	1,569	1,342	1,834									
Solyc02g092045	separase (AHRD V3.3 --* AT4G22970.3)							0,139	0,094	0,025	0,000	0,000									
Solyc02g092050	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VCJ1_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' AP2	2,997	3,214	0,065	0,151	0,094									
Solyc02g092070	Growth-regulating factor (AHRD V3.3 *** A0A072VEY4_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten			IPR014978 (SMAF GRF	4,479	3,976	0,862	1,742	1,271									
Solyc02g092080	60S ribosomal protein L23a (AHRD V3.3 *** RL23A_DAUCA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012677 (G3DSA:3.30.70.GENE3D	7,309	7,319	10,477	10,557	8,434									
Solyc02g092100	LOW QUALITY:E3 ubiquitin ligase (AHRD V3.3 --* AT5G05560.1)						PTHR34061:SF1 (PANTHER): PTHR3	0,019	0,036	0,000	0,000	0,000									
Solyc02g092110	Phytosulfokines 3 family protein (AHRD V3.3 *** B9IBM1_POPTR)		C:GO:0005576; F:G(	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM): IPR009438 (PAN	0,800	4,710	2,650	5,031	3,397	2,573	0,007			0,918	0,040	up		up
Solyc02g092120	Phytosulfokines 3 family protein (AHRD V3.3 *** B9IBM1_POPTR)		C:GO:0005576; F:G(	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM): PTHR33285:SF1	0,058	0,210	2,684	3,378	2,143									
Solyc02g092130	Transmembrane protein, putative (AHRD V3.3 *** G7JF82_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR36815 (PANTHER)	6,480	5,996	9,444	9,213	10,150									
Solyc02g092140	Protein PHLOEM PROTEIN 2-LIKE A10 (AHRD V3.3 *** A0A0B2PZA4_GLYSO)		C:GO:0016021	C:integral component of membrane			PTHR21477:SF12 (PANTHER): PTHR	1,859	1,083	12,936	17,724	11,842									
Solyc02g092150	ACT domain-containing protein (AHRD V3.3 *** D7M3X3_ARALL)						IPR002912 (PFAM): G3DSA:3.30.70.2	0,377	0,135	0,244	0,762	0,444									
Solyc02g092160	BSD domain-containing protein, putative (AHRD V3.3 *** A0A061DP77_THECC)						IPR005607 (SMART): IPR005607 (PF	0,000	0,000	0,025	0,095	0,095									
Solyc02g092180	LOW QUALITY:cell division cycle 48C (AHRD V3.3 --* AT3G01610.2)						IPR016972 (PIRSF): PTHR33526 (PA	0,000	0,000	0,000	0,000	0,023									
Solyc02g092190	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G46450.3)						IPR016972 (PIRSF): PTHR33526 (PA	0,019	0,021	0,000	0,025	0,000									
Solyc02g092200	Histone-lysine N-methyltransferase NSD3, putative (AHRD V3.3 *** A0A061DH30_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,143	2,572	2,797	3,343	2,427									
Solyc02g092210	Alpha-6-galactosyltransferase (AHRD V3.3 *** Q5TIN2_SOLTU)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR008630 (PFAM): IPR029044 (G3D	2,759	3,745	5,819	8,837	6,594									
Solyc02g092215	Galactosyl transferase GMA12/MNN10 family protein (AHRD V3.3 *** AT2G22900.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR008630 (PFAM): IPR029044 (G3D	114,721	84,160	10,622	8,735	9,949									
Solyc02g092220	Flavin-binding monooxygenase family protein (AHRD V3.3 --* AT5G25620.1)							10,640	6,257	1,272	0,837	1,157									
Solyc02g092230	ADIPOR-like receptor protein (AHRD V3.3 *** A0A0B0MUN3_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004254 (PFAM): mobidb-lite (MOB	17,077	17,376	26,590	29,125	30,182									
Solyc02g092240	DUF4228 domain protein (AHRD V3.3 *** G7JF67_MEDTR)		C:GO:0005874	C:microtubule			IPR025322 (PFAM): mobidb-lite (MOB	4,180	6,332	7,619	8,159	6,710									
Solyc02g092250	Cytochrome P450 (AHRD V3.3 *** A0A061FC67_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,198	1,042	0,406	0,253	0,211									
Solyc02g092260	Amino acid acetyltransferase(N-acetylglutamate synthase)-like protein (AHRD V3.3 *** Q8H5K9_ORYSJ)		F:GO:0004042; C:G(	F:acetyl-CoA:L-glut	EC:2.3.1.1; EC:2.3.1	Amino-acid N-acetylt	IPR000182 (PFAM): IPR010167 (TIGF	19,239	21,245	14,828	13,743	15,462									
Solyc02g092270	NADH-ubiquinone oxidoreductase-like protein (AHRD V3.3 *** AT5G67590.1)		F:GO:0016651; P:G(	F:oxidoreductase activity, acting on NAD(P)H; P:electron transp			IPR006885 (PFAM): IPR038532 (G3D	187,074	164,889	313,585	265,875	278,076									
Solyc02g092285	aminophospholipid ATPase 3 (AHRD V3.3 --* AT1G59820.1)							1,371	0,670	1,438	1,871	1,033									
Solyc02g092290	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	11,816	9,131	15,427	17,000	13,197									
Solyc02g092300	Ribosomal protein L12 family protein (AHRD V3.3 *** D7MA23_ARALL)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR013823 (PFAM): IPR014719 (G3D	8,427	9,589	10,761	9,236	9,211									
Solyc02g092310	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0K9PPL5_ZOSMR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	18,453	16,150	36,551	37,577	33,189									
Solyc02g092330	ADP-ribosylation factor-like protein		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00177 (SMA	21,979	17,214	42,879	40,500	40,236									
Solyc02g092350	transmembrane protein (AHRD V3.3 *** AT5G67550.1)		C:GO:0016021	C:integral component of membrane			IPR040283 (PANTHER): PTHR31414:	0,061	0,154	0,331	0,832	0,471									
Solyc02g092353	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT3G07340.1)							1,701	1,544	1,225	1,271	1,364									
Solyc02g092357	Polycomb group protein FERTILIZATION-INDEPENDENT SEED 2 (AHRD V3.3 --* FIS2C_ARATH)							0,038	0,061	0,022	0,000	0,048									
Solyc02g092360	glycosyl hydrolase family protein 43 (AHRD V3.3 *** AT3G49880.1)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR023296 (G3DSA:2.115.10.GENE3	20,147	19,903	16,318	13,915	14,780									
Solyc02g092370	GRAS family transcription factor (AHRD V3.3 *** K7NCY5_QUESU)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:asymm			IPR005202 (PFAM GRAS	0,754	0,966	0,096	0,241	0,165									
Solyc02g092380	Peptidyl-prolyl cis-trans isomerase-like protein (AHRD V3.3 *** G7K2I6_MEDTR)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR003613 (SM	23,929	25,773	26,551	27,726	27,553									
Solyc02g092390	Ribose-5-phosphate isomerase A (AHRD V3.3 *** A0A0B0NVQ3_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,196	5,964	4,838	4,794	5,222									
Solyc02g092400	Late embryogenesis abundant hydroxyproline-rich glycoprotein family, putative (AHRD V3.3 *** A0A061GGT		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): PTHR31852:SF6	0,117	0,114	0,094	0,075	0,070									
Solyc02g092410	Adenylyl-sulfate kinase (AHRD V3.3 *** K4BD37_SOLLC)		P:GO:0000103; F:G(	P:sulfate assimilatic	EC:2.7.1.25	Adenylyl-sulfate kina	IPR002891 (TIGRFAM): G3DSA:3.40.	5,089	6,385	2,476	2,390	2,667									
Solyc02g092420	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT3G49900.1)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR027356 (PF	1,467	2,381	0,234	0,094	0,165									
Solyc02g092440	Outer mitochondrial membrane protein porin (AHRD V3.3 *** B6SS48_MAIZE)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe			IPR023614 (G3DSA:2.40.160.GENE3	187,903	201,162	98,600	96,851	105,512									
Solyc02g092450	Calcium-transporting ATPase (AHRD V3.3 *** M1BXI4_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRI	38,422	39,777	7,469	6,995	10,550									
Solyc02g092460	BTB/POZ and TAZ domain-containing protein (AHRD V3.3 *** A0A0M4JJV3_LONJA)		F:GO:0003712; F:G(	F:transcription core	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR000197 (SMART): IPR000210 (SM	0,350	0,346	0,022	0,069	0,095									
Solyc02g092470	Formin-like protein (AHRD V3.3 *** K4BD43_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (SMART): G3DSA:1.20.58	38,020	33,780	8,337	8,678	12,134									
Solyc02g092480	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** G7K3U5_MEDTR)						IPR027356 (PFAM): mobidb-lite (MOB	49,553	57,951	37,044	34,808	35,655									
Solyc02g092490	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT2G23060.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			G3DSA:3.40.630.30 (GENE3D): IPR(	18,083	51,022	28,665	20,088	23,497	1,523	0,001					up		
Solyc02g092495	Tubby-like F-box protein (AHRD V3.3 --* K3YSM4_SETIT)						mobidb-lite (MOBIDB_LITE)	0,558	0,663	1,029	0,883	0,943									
Solyc02g092500	cysteine/histidine-rich C1 domain protein (AHRD V3.3 --* AT1G60787.4)							0,440	0,377	0,448	0,466	0,565									
Solyc02g092510	UPF0553 protein (AHRD V3.3 *** A0A151SC52_CAJCA)		P:GO:0101030	P:tRNA-guanine transglycosylation			IPR019438 (PFAM): IPR019438 (PAN	4,244	5,600	3,338	4,454	4,317									
Solyc02g092513	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		P:GO:0006259; F:G(	P:DNA metabolic process; F:organic cyclic compound binding; F			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,203	1,504	0,376	0,260	0,212									
Solyc02g092515	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				3,330	2,823	0,568	0,707	0,897									
Solyc02g092517	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination; F:ATPase activity; F:mismatched				3,580	3,368	0,768	1,028	0,849									
Solyc02g092520	Cytochrome P450 81F2 (AHRD V3.3 --* C81F2_ARATH)							1,768	1,821	0,372	0,364	0,635									
Solyc02g092523	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 *-* A0A0X7YCF6_SOLTU)		P:GO:0006298; P:G(	P:mismatch repair;	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR038973 (PANTHER): IPR028830 (I	5,754	7,414	1,191	1,105	1,411									
Solyc02g092527	Cysteine-rich receptor-like protein kinase 38 (AHRD V3.3 --* CRK38_ARATH)							2,754	4,394	0,782	0,370	0,539									
Solyc02g092530	Acetamidase/Formamidase family protein (AHRD V3.3 *** AT4G37560.1)		F:GO:0016811	F:hydrolase activity, acting on carbon-nitrogen (but not peptide)			IPR004304 (PFAM): G3DSA:2.60.120	15,841	14,418	7,255	8,269	5,066									
Solyc02g092537	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_CITSI)							5,506	5,352	2,141	1,691	1,761									
Solyc02g092550	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)						IPR004883 (PFAM LBD	1,652	1,490	0,411	0,796	0,211									
Solyc02g092560	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** A0A061DGZ5_THECC)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR000210 (PF	21,965	20,881	31,080	41,073	39,378					0,406	0,039			up
Solyc02g092570	Transcription factor GRAS (AHRD V3.3 *** A0A103Y551_CYNCS)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	0,021	0,039	0,000	0,000	0,000									
Solyc02g092580	Peroxidase (AHRD V3.3 *** K4BD54_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,572	1,204	4,118	1,726	1,700			-1,276	0,020	-1,234	0,028		down	down
Solyc02g092590	T-box transcription factor, putative (DUF863) (AHRD V3.3 *-* AT1G69360.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,059	0,429	0,115	0,025	0,070									
Solyc02g092600	Phototropic-responsive NPH3 family protein (AHRD V3.3 *-* A0A061DGZ5_THECC)						IPR027356 (PFAM): PTHR32370 (PAN	13,232	10,971	26,322	27,185	23,471									
Solyc02g092610	Phototropic-responsive NPH3 family protein (AHRD V3.3 *-* AT5G67385.5)						IPR027356 (PFAM): PTHR32370:SF1	6,328	4,885	13,043	13,048	11,885									
Solyc02g092620	Phototropic-responsive NPH3 family protein (AHRD V3.3 *-* A0A061DGZ5_THECC)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR000210 (PF	18,945	13,656	37,929	42,454	35,256									
Solyc02g092630	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_LIRMU)							1,092	0,735	1,411	2,393	2,128									
Solyc02g092640	Protein kinase superfamily protein (AHRD V3.3 *** AT2G23080.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	72,703	72,913	173,652	186,569	156,542									
Solyc02g092650	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 --* AT4G00165.2)							6,195	5,489	8,641	8,502	8,320									
Solyc02g092660	Major facilitator superfamily protein (AHRD V3.3 *** AT2G23093.1)		F:GO:0015098; P:G(	F:molybdate ion transmembrane transporter activity; P:molybda			G3DSA:1.20.1250.20 (GENE3D): IPR(	12,630	17,629	10,250	8,788	11,734									
Solyc02g092670	Subtilisin-like protease (AHRD V3.3 *** A9XG40_TOBAC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:2.60.4(	136,003	170,088	151,307	196,821	192,506									
Solyc02g092680	Subtilisin-like protease (AHRD V3.3 *** A9XG40_TOBAC)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	18,328	40,878	2,874	3,630	4,614									
Solyc02g092700	DUF1230 family protein (DUF1230) (AHRD V3.3 *** AT5G67370.1)		C:GO:0016021	C:integral component of membrane			IPR009631 (PFAM): IPR009631 (PAN	28,240	50,908	19,106	25,353	38,720	0,876	0,000	1,013	0,000			up	up	
Solyc02g092710	Prolyl 4-hydroxylase subunit alpha-1 (AHRD V3.3 *** W9RH72_9ROSA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR006620 (SMART): IPR005123 (PF	12,280	10,176	30,438	32,687	27,972									
Solyc02g092730	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (AHRD V3.3 *** K4BD69_SOLLC)		P:GO:0006099; F:G(	P:tricarboxylic acid cycle; F:electron transfer activity; F:iron-sul			IPR009051 (G3DSA:1.10.1060.GENE	4,525	4,973	2,544	3,122	3,082									
Solyc02g092740	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (AHRD V3.3 *-* M1AY79_SOLTU)		C:GO:0005743; P:G(	C:mitochondrial inne	EC:1.3.99.1; EC:1.3.	Deleted entry; Succir	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,019	1,001	0,744	0,537	0,637									
Solyc02g092750	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G33920.1)		F:GO:0004722; F:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	43,535	70,078	25,418	30,191	34,522									
Solyc02g092760	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9SG47_RICCO)		P:GO:0080167	P:response to karrikin			IPR029058 (G3DSA:3.40.50.GENE3D	4,650	17,995	1,520	0,893	1,200	1,977	0,000					up		
Solyc02g092770	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9SG47_RICCO)		P:GO:0009704; P:G(	P:de-etiolation; P:response to karrikin			IPR029058 (G3DSA:3.40.50.GENE3D	2,323	3,485	7,833	8,809	6,158									
Solyc02g092780	Tetratricopeptide repeat protein, tpr, putative (AHRD V3.3 *** B9SG46_RICCO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13432 (PFAM	92,945	115,723	85,019	81,696	83,382									
Solyc02g092783	Tetratricopeptide repeat-containing protein (AHRD V3.3 *** D7MQ06_ARALL)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	0,078	0,185	0,586	0,733	0,375									
Solyc02g092790	Arabinogalactan 1		C:GO:0005886	C:plasma membrane			PR01217 (PRINTS): mobidb-lite (MOB	396,317	325,380	132,053	182,252	254,357			0,942	0,013				up	
Solyc02g092800	metal transporter AY196092		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR001046 (PRINTS): IPR001046 (TI(	42,581	31,582	72,263	80,006	85,098									
Solyc02g092810	RING/U-box superfamily protein (AHRD V3.3 *** AT4G24204.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR013083 (G3	5,954	4,445	3,343	5,333	3,488					0,674	0,041			up
Solyc02g092820	IAA-amido synthetase 3-4	GH3_4					IPR004993 (PFAM): IPR004993 (PAN	6,939	11,479	0,584	0,659	0,538									
Solyc02g092830	caspase-6 protein (AHRD V3.3 *** AT2G15000.7)						PTHR33156 (PANTHER): PTHR33156	6,965	8,293	8,786	7,345	7,485									
Solyc02g092840	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR004263 (PFAM): IPR004263 (PAN	119,390	122,186	38,206	29,716	31,991									
Solyc02g092850	LOW QUALITY:Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2RCM4_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion			PTHR12663:SF3 (PANTHER): IPR039	0,000	0,041	0,000	0,000	0,000									
Solyc02g092870	nucleolar protein gar2-like protein (AHRD V3.3 *** AT2G42320.2)		P:GO:0006913; P:G(	P:nucleocytoplasmic transport; P:nuclear pore organization; F:s			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,725	2,771	6,276	13,733	7,927					1,132	0,000			up
Solyc02g092880	maternal effect embryo arrest 59 (AHRD V3.3 *** AT4G37300.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	35,172	40,407	80,647	72,632	75,414									
Solyc02g092890	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 -** A0A072UNU4_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR34663:SF1 (PANTHER): PTHR3	0,000	0,055	0,168	0,144	0,094									
Solyc02g092910	Mortality factor 4-like protein 1 (AHRD V3.3 *** A0A0B2QZE4_GLYSO)		C:GO:0005634; P:G(	C:nucleus; P:chromatin organization; P:regulation of transcriptio			IPR000953 (SMART): G3DSA:2.30.30	27,765	34,862	31,885	29,223	33,485									
Solyc02g092920	heavy metal atpase 1 (AHRD V3.3 *** AT4G37270.1)		F:GO:0000166; P:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): PF00702 (PFAM)	68,231	52,986	51,450	58,704	58,869									
Solyc02g092940	receptor-like kinase (AHRD V3.3 *** AT5G67280.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS): G3DSA:1.10.510	34,334	26,982	9,137	11,478	13,243									
Solyc02g092950	RP/EB family microtubule-associated protein (AHRD V3.3 *** G7K588_MEDTR)		F:GO:0008017	F:microtubule binding			IPR001715 (PFAM): IPR004953 (PFA	8,503	6,992	2,676	1,208	2,014					-1,142	0,021			down
Solyc02g092960	Phosphoglycerate mutase-like family protein (AHRD V3.3 --* AT5G15070.7)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	0,019	0,043	0,000	0,022	0,000									
Solyc02g092970	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00177 (SMA	0,277	0,140	0,401	0,628	0,685									
Solyc02g092980	cyclin D3.1	cycd3	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	11,229	11,970	2,751	2,005	2,457									
Solyc02g092990	F-box protein (AHRD V3.3 *** W9R4Y4_9ROSA)		F:GO:0005515	F:protein binding			IPR006553 (SMART): G3DSA:1.20.12	41,052	25,957	36,126	52,527	43,162					0,543	0,000			up

Solyc02g093000	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN, puta		F:GO:0004725; C:GO	F:protein tyrosine p EC:3.1.3.16; EC:3.1. Protein-serine/threon	IPR014020 (SMART); IPR029021 (G3	23,498	23,994	22,387	26,655	23,648								
Solyc02g093020	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50120.1)		C:GO:0016021	C:integral component of membrane	IPR004158 (PFAM); PTHR31549:SF2	3,754	8,349	1,652	2,035	1,884	1,175	0,002					up		
Solyc02g093030	Peptidyl-tRNA hydrolase family protein (AHRD V3.3 *** AT5G19830.1)		F:GO:0004045	F:aminoacyl-tRNA h EC:3.1.1.29; EC:3.1. Aminoacyl-tRNA hydr	IPR001328 (TIGRFAM); IPR001328 (F	0,177	0,174	0,173	0,145	0,047									
Solyc02g093040	Cysteine protease, putative (AHRD V3.3 *** B9SFZ3_RICCO)		F:GO:0004045; P:GO	F:aminoacyl-tRNA h EC:3.1.1.29; EC:3.1. Aminoacyl-tRNA hydr	IPR000668 (PRINTS); IPR000668 (SM	1,687	1,720	1,377	1,555	1,417									
Solyc02g093050	WRKY transcription factor 8	WRKY8	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	7,119	14,474	4,053	4,922	4,754	1,048	0,021					up		
Solyc02g093060	tRNA-dihydrouridine(16/17) synthase [NAD (P)(+)]-like protein (AHRD V3.3 *** A0A0B0NB62_GOSAR)		P:GO:0008033; F:GO	P:tRNA processing; F:tRNA dihydrouridine synthase activity; F:1	IPR013785 (G3DSA:3.20.20.GENE3D	32,317	27,092	51,787	46,183	48,205									
Solyc02g093070	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G50210.4)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS); IPR027443 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc02g093080	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G50210.4)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS); IPR027443 (G3D	80,857	70,834	67,032	61,345	67,658									
Solyc02g093090	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G71690.1)		P:GO:0045492	P:xylan biosynthetic process	IPR006514 (TIGRFAM); IPR021148 (F	3,232	2,031	0,230	0,304	0,286									
Solyc02g093100	Receptor protein kinase, putative (AHRD V3.3 *** B9T4U3_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	G3DSA:3.30.200.20 (GENE3D); IPR0	15,213	9,498	3,687	4,688	3,715									
Solyc02g093110	Ubiquitin-conjugating enzyme (AHRD V3.3 *** B3TLZ3_ELAGV)		F:GO:0019789	F:SUMO transferase activity	SM00212 (SMART); IPR000608 (PFAI	21,460	26,781	24,160	23,210	22,450									
Solyc02g093120	RNA binding protein, putative (AHRD V3.3 *** B9T820_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR000504 (PF	20,601	18,093	22,719	22,186	24,512									
Solyc02g093130	AP2/EREBP transcription factor_1		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN' ERF	16,931	34,399	14,920	13,815	12,384	1,049	0,002					up		
Solyc02g093140	CBS domain-containing protein-like (AHRD V3.3 *** B8AP73_ORYSI)		C:GO:0009507; P:GO	C:chloroplast; P:cell redox homeostasis	IPR000644 (SMART); IPR000644 (PF	28,490	28,783	65,427	64,994	66,988									
Solyc02g093150	APETALA2c	AP2c	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN' AP2	28,616	28,195	11,560	11,575	11,493									
Solyc02g093160	Filament-like plant protein (AHRD V3.3 *** A0A072UQ33_MEDTR)				IPR008587 (PFAM); mobidb-lite (MOB	3,308	3,665	1,457	1,611	1,808									
Solyc02g093170	cyclin delta-3 (AHRD V3.3 *** AT4G34090.1)		C:GO:0005739	C:mitochondrion	PTHR35115:SF3 (PANTHER); PTHR3	6,835	8,632	6,914	4,897	8,358									
Solyc02g093180	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3	0,500	0,918	8,595	17,341	23,190			1,425	0,021				up	
Solyc02g093190	Histone-lysine N-methyltransferase MEDEA (AHRD V3.3 *-* MEDEA_ARATH)		C:GO:0031519	C:PcG protein complex	mobidb-lite (MOBIDB_LITE); mobidb-lit	13,640	11,637	13,455	16,470	14,702									
Solyc02g093197	Histone-lysine N-methyltransferase EZ2 (AHRD V3.3 --* EZ2_MAIZE)					0,000	0,000	0,049	0,025	0,000									
Solyc02g093210	PI-PLC X domain-containing protein (AHRD V3.3 *** W9SGY7_9ROSA)		P:GO:0006629; F:GO	P:lipid metabolic process; F:phosphoric diester hydrolase activi	IPR017946 (G3DSA:3.20.20.GENE3D	2,289	1,770	1,396	1,776	1,478									
Solyc02g093220	F-box family protein (AHRD V3.3 *** D7MKT1_ARALL)		F:GO:0005515	F:protein binding	IPR006553 (SMART); IPR001810 (SM	11,616	9,028	12,341	13,926	13,194									
Solyc02g093230	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)		F:GO:0008171	F:O-methyltransferase activity	IPR002935 (PFAM); G3DSA:3.40.50.1	16,438	23,030	2,405	2,006	2,713									
Solyc02g093240	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)		F:GO:0008171	F:O-methyltransferase activity	G3DSA:3.40.50.150 (GENE3D); IPR0	0,000	0,021	0,000	0,000	0,000									
Solyc02g093250	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)		F:GO:0008171	F:O-methyltransferase activity	IPR002935 (PFAM); G3DSA:3.40.50.1	2,534	2,915	0,308	0,218	0,489									
Solyc02g093270	caffeoyl-CoA O-methyltransferase	ccoaomt	F:GO:0008171	F:O-methyltransferase activity	G3DSA:3.40.50.150 (GENE3D); IPR0	46,258	52,072	5,968	4,173	10,452									
Solyc02g093280	LOW QUALITY:bHLH transcription factor 017		P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	4,663	6,008	0,336	0,475	0,586									
Solyc02g093290	Nicotinate phosphoribosyltransferase family protein (AHRD V3.3 *** B9H6H6_POPTR)		F:GO:0004514; F:GO	F:nicotinate-nucleot EC:2.4.2.19; EC:6.3. Nicotinate-nucleotide	IPR007229 (PIRSF); PF17767 (PFAM	45,391	56,562	55,960	71,222	59,996					0,352	0,027			up
Solyc02g093300	DNA polymerase (AHRD V3.3 *** H9E8V2_SOLLC)		F:GO:0000166; F:GO	F:nucleotide binding EC:2.7.7.7 DNA-directed DNA p	IPR006172 (PRINTS); IPR006172 (SM	14,760	11,829	7,495	4,553	7,428					-0,711	0,050			down
Solyc02g093310	PI-PLC X domain-containing protein (AHRD V3.3 *** W9RGD5_9ROSA)		P:GO:0006629; F:GO	P:lipid metabolic process; F:phosphoric diester hydrolase activi	IPR017946 (G3DSA:3.20.20.GENE3D	8,570	15,598	1,103	0,903	1,695	0,889	0,002					up		
Solyc02g093320	DNA binding protein (AHRD V3.3 --* AT3G21430.4)		F:GO:0005524; P:GO	F:ATP binding; P:mismatch repair; P:reciprocal meiotic recombination	F:ATPase activity; F:mismatcher	11,869	9,785	11,114	11,358	10,600									
Solyc02g093330	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *-* A0A0B0NED3_GOSAR)		C:GO:0005643; F:GO	C:nuclear pore; F:structural constituent of nuclear pore	G3DSA:1.10.10.2360 (GENE3D); IPR0	2,776	3,982	2,050	2,813	2,613									
Solyc02g093335	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *** A0A0B0NED3_GOSAR)		C:GO:0005643; P:GO	C:nuclear pore; P:nucleocytoplasmic transport; F:structural con	IPR007230 (PFAM); G3DSA:1.10.10.2	12,454	18,283	9,579	11,543	10,425									
Solyc02g093340	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G40490.1)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	59,777	63,346	40,811	38,417	40,005									
Solyc02g093350	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 (AHRD V3.3 *** A0A1D1XJE4_9ARAE)				mobidb-lite (MOBIDB_LITE); mobidb-lit	3,155	3,825	2,628	3,192	3,615									
Solyc02g093360	Stpk1 protein kinase (AHRD V3.3 *** Q41493_SOLTU)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); IPR000719 (PF	23,786	19,097	11,504	16,685	15,076					0,537	0,013			up
Solyc02g093390	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G40530.1)		C:GO:0005730; F:GO	C:nucleolus; F:methyltransferase activity	IPR007823 (PFAM); G3DSA:3.40.50.1	12,994	15,188	26,534	28,210	25,091									
Solyc02g093400	Protein MurJ (AHRD V3.3 *-* A0A1D1XN27_9ARAE)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane	IPR004268 (PRINTS); IPR004268 (PF	1,421	1,662	0,581	0,437	0,398									
Solyc02g093410	MAP kinase kinase kinase 24	MAPKKK24	F:GO:0003677; F:GO	F:DNA binding; F:protein kinase activity; F:ATP binding; P:regul	IPR001245 (PRINTS); IPR000719 (SM	27,979	47,188	14,374	14,521	15,732	0,781	0,008					up		
Solyc02g093420	Plant invertase/pectin methylesterase inhibitor superfamily (AHRD V3.3 --* AT5G09_NAC023				mobidb-lite (MOBI NAC	0,063	0,037	0,072	0,050	0,024									
Solyc02g093430	Beta-1,4-N-acetylglucosaminyltransferase-like protein (AHRD V3.3 *** A0A072U8D1_MEDTR)		F:GO:0003830; P:GO	F:beta-1,4-mannos EC:2.4.1.144 Beta-1,4-mannosyl-g	IPR006813 (PFAM); IPR006813 (PAN	19,435	13,275	15,648	28,411	22,271			0,507	0,008	0,863	0,000		up	up
Solyc02g093440	Glucuronokinase 1 (AHRD V3.3 *** GLAK1_ARATH)		F:GO:0005524	F:ATP binding	PR00959 (PRINTS); IPR006204 (PFA	32,362	31,467	17,274	22,177	20,494									
Solyc02g093443	negative regulator of systemic acquired resistance (SNI1) (AHRD V3.3 --* AT4G18470.1)				mobidb-lite (MOBIDB_LITE)	0,040	0,138	0,025	0,022	0,000									
Solyc02g093447	choice-of-anchor C domain protein, putative (Protein of unknown function, DUF642) (AHRD V3.3 --* AT2G34510.2)				mobidb-lite (MOBIDB_LITE); PTHR357	0,334	0,243	0,096	0,223	0,209									
Solyc02g093450	Cryptic loci regulator protein 1, putative (AHRD V3.3 *** A0A061GBM7_THECC)				PTHR35737 (PANTHER)	1,131	1,044	0,760	0,870	0,916									
Solyc02g093460	tRNA-pseudouridine synthase, putative (AHRD V3.3 *** B9S669_RICCO)		P:GO:0001522; F:GO	P:pseudouridine synthesis; F:RNA binding; P:RNA processing; F	IPR002501 (PFAM); mobidb-lite (MOB	11,170	11,810	17,563	16,772	18,588									
Solyc02g093470	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		C:GO:0016021	C:integral component of membrane	IPR007877 (PFAM); PTHR31210:SF3	47,667	46,814	34,796	33,938	37,001									
Solyc02g093480	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		C:GO:0016021	C:integral component of membrane	IPR007877 (PFAM); IPR007877 (PAN	2,561	2,313	0,093	0,144	0,258									
Solyc02g093490	SGF29 tudor-like domain-containing protein (AHRD V3.3 *** AT3G27460.1)		C:GO:0000124	C:SAGA complex	G3DSA:2.30.30.140 (GENE3D); G3DS	47,379	33,803	64,079	58,727	60,712									
Solyc02g093500	GDSL esterase/lipase family (AHRD V3.3 *** A0A151SPB5_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	1,666	1,455	0,727	1,249	1,337									
Solyc02g093510	Surfeit locus protein 2 (AHRD V3.3 *** A0A1D1ZKN6_9ARAE)				PF05477 (PFAM); mobidb-lite (MOBID	12,933	15,989	13,437	13,273	12,818									
Solyc02g093520	E3 ubiquitin-protein ligase RGLG2 (AHRD V3.3 *** A0A0B0MQU5_GOSAR)		F:GO:0016874	F:ligase activity	IPR002035 (SMART); PF13920 (PFAM	92,663	101,399	145,749	222,523	184,957					0,613	0,000			up
Solyc02g093530	Ras-related protein (AHRD V3.3 *** W9QSD6_9ROSA)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS); SM00175 (SMAR	14,031	12,073	23,189	23,426	21,952									
Solyc02g093540	Cytochrome P450, putative (AHRD V3.3 *** B9SLV1_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS); IPR001128 (PF	2,569	1,962	3,726	5,470	4,307									
Solyc02g093550	S-adenosyl-L-methionine-dependent methyltransferase (AHRD V3.3 *** I0YKX8_COCSC)		F:GO:0008168	F:methyltransferase activity	IPR013216 (PFAM); G3DSA:3.40.50.1	7,913	9,850	7,749	9,624	11,925			0,618	0,010				up	
Solyc02g093580	Tomato 9612 mRNA		C:GO:0005576; F:GO	C:extracellular regic EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS); IPR002022 (SM	0,510	0,750	1,187	2,255	1,049									
Solyc02g093590	Zinc finger CONSTANS-LIKE 7-like protein (AHRD V3.3 *** A0A0B0PB06_GOSAR)		F:GO:0005515	F:protein binding	IPR010402 (PFAM); mobidb-lite (MOB	7,222	8,241	3,868	4,517	7,523			0,958	0,000				up	
Solyc02g093600	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	Hsp15.6	P:GO:0006457; P:GO	P:protein folding; P:response to heat; P:response to salt stress;	IPR002068 (PFAM); IPR008978 (G3D	10,176	7,699	75,871	80,183	103,464									
Solyc02g093610	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** A0A0B0PLU4_GOSAR)		F:GO:0005515	F:protein binding	IPR000626 (PFAM); G3DSA:3.10.20.9	0,977	1,532	0,172	0,025	0,143									
Solyc02g093620	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IJL3_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	16,688	16,368	18,848	17,184	20,937									
Solyc02g093630	transmembrane protein (AHRD V3.3 *** AT5G40640.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	53,968	49,468	46,931	57,050	53,220									
Solyc02g093640	Short-chain dehydrogenase/reductase (AHRD V3.3 *** U5TZJ9_PHAVU)		C:GO:0005783; C:GO	C:endoplasmic reticulum; C:integral component of membrane; F	IPR002347 (PRINTS); IPR002347 (PF	1,212	1,084	0,701	0,861	0,938									
Solyc02g093650	Early nodulin-like protein (AHRD V3.3 *** A0A072U7R7_MEDTR)		F:GO:0009055	F:electron transfer activity	IPR008972 (G3DSA:2.60.40.GENE3D	0,180	0,199	0,051	0,293	0,212									
Solyc02g093670	RPM1-interacting protein 4 family protein, putative (AHRD V3.3 *** A0A061FYM4_THECC)		C:GO:0005886; P:GO	C:plasma membrane; P:defense response signaling pathway, re	IPR008700 (PFAM); mobidb-lite (MOB	0,785	0,569	0,293	0,659	0,357									
Solyc02g093680	succinate dehydrogenase	sucdh	P:GO:0006099; F:GO	P:tricarboxylic acid cycle; F:electron transfer activity; F:iron-sul	IPR012675 (G3DSA:3.10.20.GENE3D	5,416	4,906	11,377	9,411	10,841									
Solyc02g093690	ATP synthase mitochondrial F1 complex assembly factor 2 (AHRD V3.3 *** V5N8F3_PHAVU)		P:GO:0043461	P:proton-transporting ATP synthase complex assembly	IPR023335 (G3DSA:1.10.3580.GENE	9,375	10,653	11,174	9,578	10,588									
Solyc02g093695	BnaC07g24270D protein (AHRD V3.3 *** A0A078D3I8_BRANA)					0,021	0,018	0,044	0,022	0,023									
Solyc02g093700	Cystinosin like (AHRD V3.3 *** A0A0B2R1J2_GLYSO)		C:GO:0005774; F:GO	C:vacuolar membrane; F:L-cystine transmembrane transporter a	IPR006603 (SMART); G3DSA:1.20.12	2,777	3,737	3,190	5,321	4,598									
Solyc02g093710	LOW QUALITY:Hop-interacting protein THI031 (AHRD V3.3 *** G8Z260_SOLLC)				mobidb-lite (MOBIDB_LITE); PTHR342	8,141	11,098	14,387	13,850	11,917									
Solyc02g093720	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *** A0A072U7R9_MEDTR)				IPR027329 (PFAM); mobidb-lite (MOB	3,208	4,629	0,025	0,000	0,162									
Solyc02g093730	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_ANEMR)				IPR038492 (G3DSA:3.30.2020.GENE	9,278	7,883	10,360	10,505	10,091									
Solyc02g093740	R2R3MYB transcription factor 99	R2R3MYB99	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,061	0,039	0,000	0,050	0,000									
Solyc02g093750	C3H4 type zinc finger protein (DUF23) (AHRD V3.3 *** AT5G40720.3)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity	IPR008166 (PFAM); PTHR21461:SF1	9,615	5,962	11,257	12,376	10,878									
Solyc02g093760	C3HC4-type RING zinc finger protein (AHRD V3.3 *** A0A072TYL1_MEDTR)		F:GO:0016874; F:GO	F:ligase activity; F:metal ion binding	IPR013083 (G3DSA:3.30.40.GENE3D	0,243	0,408	0,025	0,172	0,118									
Solyc02g093770	GPI inositol-deacylase (AHRD V3.3 *** A0A0B2PP36_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR012908 (PFAM); mobidb-lite (MOB	95,752	91,525	62,477	71,994	64,453									
Solyc02g093790	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G27320.1)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM); mobidb-lite (MOB	17,715	12,802	4,928	5,292	6,076									
Solyc02g093800	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9HTC9_POPTR)		C:GO:0000159; P:GO	C:protein phosphatase type 2A complex; P:signal transduction;	IPR011989 (G3DSA:1.25.10.GENE3D	55,911	48,949	37,280	38,167	36,700									
Solyc02g093810	HAUS augmin-like complex subunit 6 (AHRD V3.3 *** A0A061ECN9_THECC)		P:GO:0051225; C:GO	P:spindle assembly; C:HAUS complex	IPR028163 (PFAM); mobidb-lite (MOB	28,987	19,916	18,729	19,975	18,235									
Solyc02g093820	plant UBX domain-containing protein 1 (AHRD V3.3 *** AT3G27310.1)		F:GO:0005515	F:protein binding	G3DSA:3.10.20.90 (GENE3D); IPR0	36,966	34,038	55,069	56,095	51,221									
Solyc02g093830	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** K4BDH9_SOLLC)	G6PD	F:GO:0004345; P:GO	F:glucose-6-phosph EC:1.1.1.49 Glucose-6-phosphate	IPR001282 (PRINTS); IPR001282 (TI	177,608	166,440	245,097	233,845	235,504									
Solyc02g093840	F-box family protein (AHRD V3.3 *** B9HTC6_POPTR)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	24,520	29,993	19,330	18,905	19,957									
Solyc02g093850	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9RBN5_RICCO)		F:GO:0005515	F:protein binding	IPR002110 (SMART); PF13637 (PFAM	2,946	4,075	2,886	3,957	3,852									
Solyc02g093860	Amino acid transporter, putative (AHRD V3.3 *** B9RBN4_RICCO)		P:GO:0003333; C:GO	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM); PTHR22950:SF2	3,172	14,922	3,576	9,357	9,318	2,250	0,032	1,375	0,002	1,390	0,000	up	up	up
Solyc02g093870	Amino acid transporter, transmembrane (AHRD V3.3 *** A0A124SF94_CYNCS)		C:GO:0016021	C:integral component of membrane	IPR013057 (PFAM); PTHR22950:SF2	0,042	0,039	0,000	0,000	0,000									
Solyc02g093880	Transcription factor GTE8 (AHRD V3.3 *** A0A0B2PTJ0_GLYSO)		F:GO:0005515	F:protein binding	IPR001487 (PRINTS); IPR001487 (SM	57,039	60,127	87,786	80,754	81,268									
Solyc02g093890	Emb|CAB62340.1 (AHRD V3.3 *** Q9FKS6_ARATH)				PTHR33595:SF4 (PANTHER); PTHR3	0,237	0,642	1,090	2,517	2,377			1,120	0,013	1,203	0,018		up	up
Solyc02g093900	Cytochrome c1, heme protein (AHRD V3.3 *** G7KN99_MEDTR)		F:GO:0009055; F:GO	F:electron transfer activity; F:heme binding	IPR002326 (PRINTS); IPR002326 (PF	174,900	190,517	221,981	206,873	208,299									
Solyc02g093910	Kelch repeat-containing protein family (AHRD V3.3 *** A0A151RD96_CAJCA)		F:GO:0005515	F:protein binding	IPR006652 (SMART); IPR015915 (G3	2,788	2,757	2,617	3,161	3,043									
Solyc02g093930	COP9 signalosome complex subunit 3 (AHRD V3.3 *** A0A151RB05_CAJCA)		C:GO:0008180	C:COP9 signalosome	IPR000717 (SMART); SM00753 (SMA	35,333	31,302	52,161	57,602	52,185									
Solyc02g093935	Sister chromatid cohesion 1 protein 2 (AHRD V3.3 *** U5FJA7_POPTR)		F:GO:0005515; P:GO	F:protein binding; P:sister chromatid cohesion; C:cohesin comp	IPR006910 (PFAM); mobidb-lite (MOB	11,283	10,520	0,939	1,077	0,868									
Solyc02g093940	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT4G14605.2)		F:GO:0003690; P:GO	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (SMART); IPR038538 (G3	15,174	15,701	17,904	17,731	21,495									
Solyc02g093950	Ankyrin repeat (AHRD V3.3 *** A0A061EKD2_THECC)		F:GO:0005515	F:protein binding	IPR002110 (SMART); IPR036770 (G3	0,554	0,716	0,270	0,464	0,682									
Solyc02g093960	Endosomal targeting BRO1-like domain-containing protein (AHRD V3.3 *** A0A061EKR8_THECC)		C:GO:0005773	C:vacuole	IPR004328 (PFAM); IPR038499 (G3	0,185	0,460	1,830	0,472	0,742									
Solyc02g093970	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT5G14210.2)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS); G3DSA:3.30.200	8,377	10,534	4,181	2,289	3,322					-0,861	0,042			down
Solyc02g093975	Receptor protein kinase-like protein (AHRD V3.3 *-* Q9FMT0_ARATH)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); G3DSA:1.10.510	8,179	7,628	3,892	2,215	3,007									
Solyc02g093980	nucleolar protein gar2-like protein (AHRD V3.3 *-* AT2G42320.2)		C:GO:0005886; P:GO	C:plasma membrane; P:nucleocytoplasmic transport; P:nuclear	IPR019448 (PFAM); mobidb-lite (MOB	81,310	62,430	14,686	12,546	13,860									
Solyc02g093990	Adenylate kinase family-like protein (AHRD V3.3 *** Q38JG0_SOLTU)		F:GO:0005524; P:GO	F:ATP binding; P:nucleobase-containing compound metabolic pr	IPR000850 (PRINTS); PF00406 (PFAI	0,021	0,000	0,047	0,000	0,000									
Solyc02g094010	Kinase family protein (AHRD V3.3 *** B9GJR7_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR018392 (SMART); G3DSA:3.30.20	1,520	0,783	0,435	0,876	0,680									
Solyc02g094030	DSR6 (AHRD V3.3 *** A0A076V4W1_CAPAN)				mobidb-lite (MOBIDB_LITE); mobidb-lit	84,837	76,781	61,358	79,017	80,478									
Solyc02g094040	Lipase (AHRD V3.3 *** K4BDK0_SOLLC)		P:GO:0006629; F:GO	P:lipid metabolic process; F:hydrolase activity, acting on ester l	IPR029058 (G3DSA:3.40.50.GENE3D	0,252	0,489	0,099	0,403	0,235									
Solyc02g094060	Chloride channel protein (AHRD V3.3 *** Q9XF71_TOBAC)		F:GO:0005247; P:GO	F:voltage-gated chloride channel activity; P:chloride transport; C	IPR002251 (PRINTS); IPR001807 (PF	4,071	3,116	1,767	2,653	3,195									
Solyc02g094080	LOW QUALITY:F-box family protein (AHRD V3.3 *-* D7M128_ARALL)				IPR017451 (TIGRFAM); PTHR31790 (	0,000	0,000	0,075	0,073	0,000									
Solyc02g094090	Vacuolar protein sorting-associated protein 52 like (AHRD V3.3 *** A0A0B2S8X6_GLYSO)		C:GO:0000938; C:GO	C:GARP complex; C:cytosol; P:Golgi to vacuole transport; F:Ra	IPR007258 (PFAM); PTHR14190:SF1	105,090	100,961	102,646	103,681	104,144									
Solyc02g094100	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *-* KTNA1_ARATH)		F:GO:0005524	F:ATP binding	IPR003593 (SMART); PF17862 (PFAM	6,878	5,950	3,935	2,214	2,816									
Solyc02g094110	Cytochrome P450, putative (AHRD V3.3 *** B9RBJ0_RICCO)		F:GO:0004497; F:GO	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR001128 (PRINTS); IPR002403 (PF	0,213	0,162	0,025	0,025	0,000									
Solyc02g094120	sulfite oxidase	sulox	F:GO:0016491; F:GO	F:oxidoreductase activity; F:molybdenum ion binding; P:nitrate a	IPR008335 (PRINTS); IPR005066 (PF	443,984	469,150	529,538	487,672	434,898									
Solyc02g094130	DCD (Development and Cell Death) domain protein (AHRD V3.3 *** AT3G27090.3)				IPR013989 (SMART); IPR013989 (PF	433,863	398,325	387,302	393,734	426,040									
Solyc02g094140	Mitochondrial import receptor subunit TOM20 (AHRD V3.3 *** TOM20_SOLTU)		F:GO:0005515; C:GO	F:protein binding; C:mitochondrial outer membrane translocase	PF06552 (PFAM); IPR011990 (G3DSA	27,400	30,752	36,687	34,548	34,069									
Solyc02g094150	DHBP synthase RibB-like alpha/beta domain-containing protein (AHRD V3.3 *** AT3G01920.1)		F:GO:0003725	F:double-stranded RNA binding	IPR006070 (TIGRFAM); G3DSA:3.90.1	10,234	10,436	28,584	28,108	31,154									
Solyc02g094170	Zinc finger protein (AHRD V3.3 *** A0A0B0N9T8_GOSAR)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	16,771	15,647	28,366	29,934	27,064									
Solyc02g094180	Peroxidase (AHRD V3.3 *** K4BDL3_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,439	0,990	0,538	0,828	1,435									
Solyc02g094200	Nuclear transport factor 2 (AHRD V3.3 *** NTF2_ARATH)		F:GO:0005515; C:GO	F:protein binding; C:nucleolus; C:cytosol; C:plasma membrane;	G3DSA:3.10.450.50 (GENE3D); IPR0	84,371	88,159	129,134	106,736	109,641									
Solyc02g094210	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT5G08391.1)		C:GO:0016021	C:integral component of membrane	IPR021775 (PFAM); PTHR33128:SF1	0,887	0,767	0,724	0,795	0,497									
Solyc02g094220	transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT3G48660.1)		C:GO:0016021	C:integral component of membrane	IPR021775 (PFAM); IPR021775 (PAN	20,599	20,498	26,601	24,996	23,635									
Solyc02g094230	LOW QUALITY:Dynein heavy chain 1, axonemal (AHRD V3.3 -** A0A1D1Z9S0_9ARAE)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,063	0,170	0,406	0,438	0,355									
Solyc02g094240	LOW QUALITY:Dynein heavy chain 1, axonemal (AHRD V3.3 -** A0A1D1Z9S0_9ARAE)				PTHR36030 (PANTHER)	0,100	0,176	0,000	0,022	0,000									
Solyc02g094250	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 --* A8I000_CHLRE)				mobidb-lite (MOBIDB_LITE); PTHR351	5,961	5,760	5,188	4,985	5,299									
Solyc02g094255	Leucine-rich repeat (LRR) family protein (AHRD V3.3 --* AT4G06744.1)					1,400	1,012	2,035	1,620	1,509									
Solyc02g094260	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT5G11250.3)		P:GO:0000184	P:nuclear-transcribed mRNA catabolic process, nonsense-medi	G3DSA:3.40.50.300 (GENE3D); IPR0	14,083	13,721	19,496	16,704	17,436									
Solyc02g094270	WRKY transcription factor (AHRD V3.3 *** H9XSZ5_GOSBA)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	0,000	0,000	0,022	0,000	0,000									
Solyc02g094280	Yellow stripe-like transporter 12 (AHRD V3.3 *** A0A0K9NNE9_ZOSMR)		P:GO:0055085	P:transmembrane transport	IPR004813 (PFAM); IPR004813 (TIGF	49,142	43,539	82,562	92,399	83,811									
Solyc02g094290	TCP transcription factor 27	TCP27			IPR017887 (PFAM TCP	0,259	0,696	0,147	0,439	0,448									
Solyc02g094300	ACT domain-containing protein (AHRD V3.3 *-* A0A103Y4L4_CYNCS)				IPR002912 (PFAM); G3DSA:3.30.70.2	6,863	6,447	3,425	3,525	4,324									
Solyc02g094310	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2R834_GLYSO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR011990 (G3D	2,982	3,145	2,358	2,776	1,482									
Solyc02g094320	Actin (AHRD V3.3 *** M4QSQ0_9ERIC)		F:GO:0005524; C:GO	F:ATP binding; C:Arp2/3 protein complex; P:Arp2/3 complex-mec	IPR004000 (PRINTS); IPR004000 (SM	14,369	11,552	7,722	4,304	6,512					-0,845	0,008			down
Solyc02g094330	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *-* A0A103XVX8_CYNCS).Pfam:PF01190				PF01190 (PFAM); PTHR31614:SF3 (F	0,608	0,307	0,240	0,193	0,214									
Solyc02g094340	GRAS family transcription factor (AHRD V3.3 *** A0A061ECZ9_THECC)	GRAS	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; F:sequen	IPR005202 (PFAM GRAS	0,040	0,059	0,022	0,000	0,024									
Solyc02g094350	Membrane-anchored ubiquitin-fold protein (AHRD V3.3 *** F4YBD3_SOLNI)		F:GO:0005515	F:protein binding	IPR039540 (PFAM); G3DSA:3.10.20.9	10,488	10,722	12,226	14,134	13,062									
Solyc02g094360	Regulation of nuclear pre-mRNA domain-containing 1B (AHRD V3.3 *** A0A0B0P6N1_GOSAR)		F:GO:0000993; C:GO	F:RNA polymerase II complex binding; C:RNA polymerase II, ho	IPR006569 (SMART); IPR006903 (PF	28,574	25,663	35,859	35,958	35,110									
Solyc02g094380	Protein kinase-like protein (AHRD V3.3 *** C6ZRY1_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); G3DSA:1.10.51	0,019	0,057	0,051	0,050	0,047									
Solyc02g094390	S-acyltransferase (AHRD V3.3 *** K4BDN4_SOLLC)		C:GO:0016021; F:GO	C:integral compone EC:2.3.1.225 Protein S-acyltransfe	IPR001594 (PFAM); mobidb-lite (MOB	52,626	43,315	13,461	8,510	11,394					-0,659	0,005			down
Solyc02g094400	Glycerophosphodiester phosphodiesterase, putative (AHRD V3.3 *** B9RH28_RICCO)		P:GO:0006629; F:GO	P:lipid metabolic process; F:phosphoric diester hydrolase activi	IPR017946 (G3DSA:3.20.20.GENE3D	50,624	26,293	35,399	78,673	47,968	-0,920	0,002			1,153	0,000	down		up
Solyc02g094410	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** A0A061ED78_THECC)		C:GO:0005737	C:cytoplasm	IPR027267 (G3DSA:1.20.1270.GENE	38,265	43,286	37,862	39,400	35,519									
Solyc02g094420	Shikimate kinase family protein (AHRD V3.3 *** B9N0W2_POPTR)		F:GO:0000287; F:GO	F:magnesium ion bi EC:2.7.1.71 Shikimate kinase	PR01100 (PRINTS); IPR031322 (PFA	8,640	11,882	12,768	11,511	14,415									
Solyc02g094430	Esterase/lipase/thioesterase family protein (AHRD V3.3 *** G7KW54_MEDTR)	PES2	F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR007130 (PFAM); PTHR22753 (PAN	28,056	25,612	34,029	34,453	33,197									
Solyc02g094435	Esterase/lipase/thioesterase family protein (AHRD V3.3 *-* AT5G41130.3)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	PTHR22753 (PANTHER); PTHR22753	5,883	5,857	7,639	7,503	8,181									
Solyc02g094440	Translocon-associated protein subunit beta (AHRD V3.3 *** K4BDN9_SOLLC).Pfam:PF05753		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:integral component of m	PF05753 (PFAM); PTHR12861:SF5 (F	50,169	55,507	55,345	50,098	47,713									
Solyc02g094445	Cytochrome c oxidase subunit 2 (AHRD V3.3 --* A0A172NE61_9BRYO)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,120	0,188	0,119	0,025	0,094									
Solyc02g094450	LOW QUALITY:BnaC08g29070D protein (AHRD V3.3 *** A0A078C4W0_BRANA)		F:GO:0004180; P:GO	F:carboxypeptidase activity; P:proteolysis	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,610	0,515	0,221	0,123	0,116									
Solyc02g094460	B3 domain transcription factor (AHRD V3.3 *** Q2HUJ5_MEDTR)		F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	2,156	1,838	0,148	0,251	0,048									
Solyc02g094470	Phosphate carrier, mitochondrial (AHRD V3.3 *** A0A0B0NBL8_GOSAR)		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	234,985	274,193	286,847	251,841	262,988									

Solyc02g094480	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K5K5_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	3,479	4,610	3,373	2,873	2,738									
Solyc02g094485	X4 (AHRD V3.3 *** B2LS35_SILLA)						IPR013078 (SMART): IPR017070 (PIF	26,569	34,604	21,348	22,604	23,439									
Solyc02g094500	sialyltransferase-like	stv3	P:GO:0006486: F:G(	P:protein glycosylat	EC:2.4.99	Glycosyltransferases	IPR001675 (PFAM): IPR038578 (G3D	42,534	37,356	46,415	43,643	42,427									
Solyc02g094510	RING finger protein (AHRD V3.3 *** G7KX94_MEDTR)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR018957 (PF	92,827	91,902	143,419	142,195	132,533									
Solyc02g094520	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4-like protein (AHRD V3.3 *** A0A0B0P721_(		F:GO:0005515: C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR003105 (SMART): IPR001214 (SM	14,348	16,114	11,498	11,240	11,516									
Solyc02g094540	nuclear factor kappa-B-binding protein (AHRD V3.3 *-* AT5G13950.4)		C:GO:0031011	C:Ino80 complex			mobidb-lite (MOBIDB_LITE): mobidb-lit	81,448	74,451	102,833	98,709	97,138									
Solyc02g094560	Aminopeptidase (AHRD V3.3 *** G7KXA9_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR022227 (PFAM): PTHR33645:SF6	36,618	34,841	34,087	36,823	35,441									
Solyc02g094570	Kinase family protein (AHRD V3.3 *** B9GNF8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): PIRSF000654 (P	2,981	2,318	1,131	1,567	1,131									
Solyc02g094580	Kinase family protein (AHRD V3.3 *-* B9GNF8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PTHF	2,755	2,079	1,001	1,064	0,987									
Solyc02g094590	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RGU4_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding; P:DNA repair			IPR014001 (SMART): IPR001650 (SM	23,108	21,363	27,849	27,537	30,271									
Solyc02g094620	Transportin-3 (AHRD V3.3 *** A0A151QYH4_CAJCA)		C:GO:0005634	C:nucleus			IPR011989 (G3DSA:1.25.10.GENE3D	29,312	28,419	37,473	37,306	36,704									
Solyc02g094630	Transportin-3, putative (AHRD V3.3 *-* B9RGS4_RICCO)		C:GO:0005634: C:G(	C:nucleus; C:integral component of membrane			IPR011989 (G3DSA:1.25.10.GENE3D	9,065	7,068	10,028	10,349	10,643									
Solyc02g094635	Glutamate formiminotransferase 1 (AHRD V3.3 --* A0A140E7Z0_MAIZE)		F:GO:0005542: F:G(	F:folic acid binding; F:transferase activity			IPR012886 (PFAM): IPR037064 (G3D	0,179	0,285	0,000	0,047	0,116									
Solyc02g094640	Acetyl-coenzyme A synthetase (AHRD V3.3 *** K4BDQ9_SOLLC)		F:GO:0003987: F:G(	F:acetate-CoA ligas	EC:6.2.1.1	Acetate--CoA ligase	IPR000873 (PFAM): G3DSA:3.30.300.	99,479	111,143	134,417	128,215	144,590									
Solyc02g094740	LOW QUALITY:TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *-* AT5G15510.1)		C:GO:0005819: C:G(	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027329 (PFAM): mobidb-lite (MOB	0,164	0,057	0,025	0,000	0,023									
Solyc02g094750	LOW QUALITY:TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT5G15510.2)		C:GO:0005819: C:G(	C:spindle; C:microtubule; P:activation of protein kinase activity;			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,049	0,000	0,000									
Solyc02g094751	LOW QUALITY:Sucrase/ferredoxin-like family protein (AHRD V3.3 *** AT4G26620.1)		C:GO:0016021	C:integral component of membrane			IPR009737 (PFAM): IPR026960 (PFA	1,628	1,470	2,238	2,099	1,951									
Solyc02g094755	Protein yippee-like (AHRD V3.3 *-* K4CGX1_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding				0,038	0,021	0,093	0,100	0,070									
Solyc02g094758	B3 domain-containing protein (AHRD V3.3 --* R7WFN7_AEGTA)		F:GO:0003677	F:DNA binding			IPR015300 (G3DSA:2.40.330.GENE3	0,038	0,019	0,025	0,000	0,047									
Solyc02g094770	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G49240.1)						mobidb-lite (MOBIDB_LITE)	0,000	0,019	0,000	0,000	0,000									
Solyc02g094860	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	2,748	5,223	0,187	0,048	0,024									
Solyc03g005000	Peptidase family M48 family protein (AHRD V3.3 *** AT3G27110.3)		F:GO:0004222: P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR001915 (PFAM): G3DSA:3.30.201	0,000	0,000	0,000	0,025	0,000									
Solyc03g005010	RNA methyltransferase (AHRD V3.3 *** A0A0B0MZJ0_GOSAR)		P:GO:0006396: F:G(	P:RNA processing; F:RNA methyltransferase activity			PF03602 (PFAM): PTHR11061:SF29 (	9,965	11,125	14,175	14,107	15,969									
Solyc03g005015	Peptidase family M48 family protein (AHRD V3.3 *-* AT3G27110.2)		F:GO:0008233: P:G(	F:peptidase activity; P:CAAX-box protein processing			PTHR10120:SF21 (PANTHER): IPR02	0,474	0,599	0,514	0,460	0,728									
Solyc03g005020	Lipase (AHRD V3.3 *** K4BDS6_SOLLC)		P:GO:0006629: F:G(	P:lipid metabolic process; F:hydrolase activity, acting on ester b			IPR022742 (PFAM): IPR025483 (PIRS	19,150	15,016	646,836	788,201	606,205									
Solyc03g005030	DSR6 (AHRD V3.3 *** A0A076V4W1_CAPAN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	13,850	10,320	53,157	63,431	43,869									
Solyc03g005040	Calcium-binding protein (AHRD V3.3 *** A0A199V9T9_ANACO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	0,102	0,100	0,199	0,835	0,071									
Solyc03g005050	Adenylate kinase family-like protein (AHRD V3.3 *** Q38JG0_SOLTU)		F:GO:0005524: P:G(	F:ATP binding; P:nucleobase-containing compound metabolic pr			IPR000850 (PRINTS): G3DSA:3.40.5(	44,755	50,318	39,405	40,260	33,947									
Solyc03g005060	nucleolar protein gar2-like protein (AHRD V3.3 *-* AT2G42320.2)		P:GO:0006913: P:G(	P:nucleocytoplasmic transport; P:nuclear pore organization; F:s			IPR019448 (PFAM): mobidb-lite (MOB	8,373	6,868	0,695	0,487	0,469									
Solyc03g005070	ubiquitin-specific protease 16 (AHRD V3.3 --* AT4G24560.1)							1,592	1,898	5,885	4,422	5,476									
Solyc03g005080	4-coumarate CoA ligase (AHRD V3.3 *** L7Z9J1_LONJA)	4CL	F:GO:0004729: P:G(	F:oxygen-depender	EC:1.3.3.4	Protoporphyrinogen (	G3DSA:1.10.3110.10 (GENE3D): IPR(	72,733	61,586	225,237	239,025	231,677									
Solyc03g005090	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9RBN5_RICCO)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	18,912	13,482	5,693	5,151	6,275									
Solyc03g005100	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G27320.1)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): mobidb-lite (MOB	20,816	18,749	22,750	19,939	18,283									
Solyc03g005120	Cystinosin like (AHRD V3.3 *** A0A0B2R1J2_GLYSO)		C:GO:0005774: F:G(	C:vacuolar membrane; F:L-cystine transmembrane transporter a			IPR006603 (SMART): IPR005282 (TIC	17,413	14,392	9,320	12,606	11,719									
Solyc03g005130	Serine/threonine-protein kinase (AHRD V3.3 *** K4BDT7_SOLLC)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): G3DSA:1.10.51	17,262	32,864	14,834	18,515	16,864	0,955	0,000					up		
Solyc03g005140	Sugar transporter protein 7	STP7	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI(	0,037	0,115	0,305	0,809	0,398									
Solyc03g005160	Amine oxidase (AHRD V3.3 *** K4BDU0_SOLLC)		F:GO:0005507: F:G(	F:copper ion bindin(	EC:1.4.3.21	Primary-amine oxida:	IPR015802 (PFAM): G3DSA:3.10.450	0,040	0,000	0,000	0,000	0,024									
Solyc03g005170	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein, putative (AHRD V3.3 *** A0A061[		F:GO:0046872	F:metal ion binding			IPR001965 (SMART): IPR032308 (PF	32,539	27,068	33,958	34,288	35,260									
Solyc03g005180	Ribosomal protein L18/L5 (AHRD V3.3 *** A0A103UVK9_CYNCS)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005484 (PFAM): G3DSA:3.30.420	1,220	1,711	1,267	1,395	1,129									
Solyc03g005190	Phosphoinositide phosphatase family protein (AHRD V3.3 --* AT3G43220.3)							0,496	0,357	0,491	0,630	0,446									
Solyc03g005200	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SN	0,000	0,037	0,000	0,022	0,000									
Solyc03g005210	Alpha-amylase inhibitor, lipid transfer and seed storage protein (AHRD V3.3 *** A0A075BNW0_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR016140 (SMART): G3DSA:1.10.11	0,019	0,037	0,261	0,123	0,331									
Solyc03g005227	Histone H2A (AHRD V3.3 *** K4BDU6_SOLLC)		C:GO:0000786: F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR002119 (SN	44,185	49,876	41,526	31,393	34,648					-0,401	0,023			down
Solyc03g005230	Methyl-6-phytyl-1,4-benzoquinone methyltransferase 2 (AHRD V3.3 *** F1BPW0_S(	VTE3b	P:GO:0032259	P:methylation			PF13649 (PFAM): G3DSA:3.40.50.15(	91,100	140,422	104,065	107,997	137,519	0,651	0,010	0,399	0,015			up	up	
Solyc03g005240	Calmodulin, putative (AHRD V3.3 *** B9RTI5_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	0,019	0,000	0,000	0,045	0,023									
Solyc03g005250	ATP-sulfurylase (AHRD V3.3 *** Q1W2K0_CAMSI)		P:GO:0000103: F:G(	P:sulfate assimilatic	EC:2.7.7.4	Sulfate adenylyltrans	G3DSA:3.10.400.10 (GENE3D): IPR(	11,836	9,823	12,051	13,182	12,187									
Solyc03g005260	ATP-sulfurylase (AHRD V3.3 *** Q1W2K0_CAMSI)		P:GO:0000103: F:G(	P:sulfate assimilatic	EC:2.7.7.4	Sulfate adenylyltrans	IPR014729 (G3DSA:3.40.50.GENE3D	25,224	30,178	47,671	46,926	48,006									
Solyc03g005270	Transmembrane emp24 domain-containing protein p24beta3 (AHRD V3.3 *** P24B3_ARATH)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:endoplasmic reticulum-Golgi interme			IPR009038 (SMART): IPR009038 (PF	38,494	39,500	78,941	84,639	72,214									
Solyc03g005280	Aspartic proteinase (AHRD V3.3 *** A0A151SSN8_CAJCA)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR033121 (PF	0,098	0,151	0,116	0,301	0,117									
Solyc03g005290	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 --* AT3G02930.3)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			PR01217 (PRINTS): mobidb-lite (MOB	0,192	0,328	0,074	0,125	0,046									
Solyc03g005300	ADP-ribosylation factor, putative (AHRD V3.3 *** B9RTH6_RICCO)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00175 (SMA	19,813	22,782	22,556	21,502	19,954									
Solyc03g005310	Armadillo repeat-containing protein LFR (AHRD V3.3 *** LFR_ARATH)		P:GO:0006338: C:G(	P:chromatin remodeling; C:SWI/SNF superfamily-type complex			IPR011989 (G3DSA:1.25.10.GENE3D	6,716	6,169	5,508	4,635	4,594									
Solyc03g005315	Translation initiation factor IF-1, chloroplastic (AHRD V3.3 --* IF1C_PLAOC)		P:GO:0006338: C:G(	P:chromatin remodeling; C:SWI/SNF superfamily-type complex			IPR021906 (PANTHER): PTHR12656::	1,934	1,342	1,409	1,631	1,391									
Solyc03g005320	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1A6B6_SOLTU)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR016039 (G3D	0,474	1,000	0,566	0,559	0,282									
Solyc03g005330	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BDV7_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,336	1,377	4,049	4,219	3,275									
Solyc03g005340	Acylamino-acid-releasing enzyme (AHRD V3.3 *** A0A151R6E1_CAJCA)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity			IPR029058 (G3DSA:3.40.50.GENE3D	69,409	59,063	105,328	95,716	103,045									
Solyc03g005350	bHLH transcription factor 018		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	13,212	9,485	23,120	20,753	20,207									
Solyc03g005355	Auxin-responsive protein (AHRD V3.3 *** G9HPW7_SOLLC)		F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-(			IPR033389 (PFAM): G3DSA:3.10.20.(	0,216	0,209	0,315	0,222	0,283									
Solyc03g005380	Protein transport protein sec23, putative (AHRD V3.3 *** B9RTF3_RICCO)		P:GO:0006886: F:G(	P:intracellular protein transport; F:zinc ion binding; C:COPII vesi			IPR012990 (PFAM): IPR006900 (PFA	18,449	14,019	20,631	21,221	19,554									
Solyc03g005390	Magnesium transporter MRS2-like protein (AHRD V3.3 *** G7I479_MEDTR)		C:GO:0016020: P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR002523 (PFAM): G3DSA:2.40.128	65,638	61,909	118,971	115,735	108,303									
Solyc03g005410	Phosphatidate cytidylyltransferase (AHRD V3.3 *** K4BDW5_SOLLC)		F:GO:0004605: C:G(	F:phosphatidate cyt	EC:2.7.7.41	Phosphatidate cytidy	IPR016720 (PIRSF): PF01148 (PFAM	43,855	40,549	43,761	44,658	40,810									
Solyc03g005420	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT5G25260.1)						IPR001107 (PFAM): G3DSA:3.30.479	1,858	3,001	1,447	1,329	1,174									
Solyc03g005430	MATH domain-containing protein (AHRD V3.3 *** A0A0B2RFR3_GLYSO)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR002083 (PF	117,629	94,518	123,593	118,999	121,428									
Solyc03g005440	Agenet domain protein (AHRD V3.3 *** G7JN46_MEDTR)						IPR014002 (SMART): IPR008395 (PF	5,462	5,788	7,010	6,120	6,944									
Solyc03g005450	Cellulose synthase-like protein (AHRD V3.3 *** L0AUE4_POPTO)		C:GO:0016020: F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR029044 (G3DSA:3.90.550.GENE3	63,532	58,794	96,807	149,701	125,540					0,633	0,000			up
Solyc03g005460	Helicase protein with RING/U-box domain-containing protein (AHRD V3.3 *** AT5G43530.1)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding; F:zinc ion binding; F:hydro			IPR001650 (SMART): IPR001841 (SM	1,270	1,144	0,311	0,218	0,283									
Solyc03g005470	HR-like lesion-inducing protein-like protein (AHRD V3.3 *** AT4G14420.1)		C:GO:0016021	C:integral component of membrane			IPR008637 (PFAM): PTHR31474:SF1	71,201	73,375	77,270	111,371	92,495					0,530	0,002			up
Solyc03g005480	WAT1-related protein (AHRD V3.3 *** K4BDX2_SOLLC)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	6,025	4,466	1,794	1,773	1,276									
Solyc03g005490	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EMD3_THECC)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	0,021	0,041	0,025	0,000	0,000									
Solyc03g005510	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R427_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN ERF	0,000	0,018	0,000	0,000	0,000									
Solyc03g005520	Ethylene-responsive transcription factor (AHRD V3.3 *** F2Y9E9_COFAR)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN ERF	0,000	0,000	0,050	0,000	0,000									
Solyc03g005530	Phosphate transporter (AHRD V3.3 *** Q9AYT2_TOBAC)		F:GO:0005315: P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph			IPR004738 (TIGRFAM): IPR005828 (F	0,099	0,164	0,000	0,000	0,023									
Solyc03g005570	MYB family protein (AHRD V3.3 *** A0A067KW19_JATCU)	R2R3MYB0	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	1,309	0,454	0,240	0,225	0,279									
Solyc03g005580	11S storage globulin (AHRD V3.3 *** P93079_COFAR)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS): IPR006045 (SN	2309,984	2036,458	36,041	73,665	9,500									
Solyc03g005590	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT4G14368.3)		F:GO:0046872	F:metal ion binding			IPR000408 (PRINTS): IPR000306 (SN	0,423	0,718	0,243	0,215	0,359									
Solyc03g005600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G04430.3)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	95,115	95,644	33,906	29,442	36,094									
Solyc03g005620	Kinesin like protein (AHRD V3.3 *** A0A0K9Q2Z4_ZOSMR)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SN	0,504	0,673	0,147	0,193	0,119									
Solyc03g005630	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *** A0A103Y0Q9_CYNCS)						PF05664 (PFAM): mobidb-lite (MOBID	0,619	0,255	0,000	0,022	0,095									
Solyc03g005640	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50150.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): mobidb-lite (MOB	0,019	0,043	0,022	0,000	0,023									
Solyc03g005650	CC-NBS-LRR class disease resistance protein, putative (AHRD V3.3 *** A0A061F8A3_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,000	0,018	0,000	0,000	0,000									
Solyc03g005660	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	14,390	9,193	10,364	9,018	9,991									
Solyc03g005670	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** G7IID2_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,040	0,155	0,069	0,050	0,117									
Solyc03g005680	RNA-binding protein-like (AHRD V3.3 *** Q9FJ56_ARATH)		F:GO:0003723	F:RNA binding			IPR000504 (SMART): IPR012677 (G3	42,608	48,486	45,267	41,954	44,411									
Solyc03g005690	Cysteine-rich repeat secretory protein 3 (AHRD V3.3 *** A0A0B2QTT4_GLYSO)		C:GO:0009506: P:G(	C:plasmodesma; P:plasmodesmata-mediated intercellular transı			IPR002902 (PFAM): IPR038408 (G3D	15,914	16,893	20,223	19,427	17,389									
Solyc03g005700	Mitochondrial import receptor subunit TOM22 family protein (AHRD V3.3 *** B9GRD7_POPTR)		C:GO:0005741: P:G(	C:mitochondrial outer membrane; P:intracellular protein transpo			IPR017411 (PIRSF): IPR005683 (PFA	0,082	0,146	0,046	0,025	0,023									
Solyc03g005730	Aconitate hydratase (AHRD V3.3 *** A0A059LL79_9CHLO)		F:GO:0003861: P:G(	F:3-isopropylmalate	EC:4.2.1.33	3-isopropylmalate de	IPR001030 (PRINTS): IPR006251 (TI(	138,199	151,345	299,271	285,774	290,912									
Solyc03g005740	Microsomal signal peptidase 12 kDa subunit family protein (AHRD V3.3 *** B9HT84_POPTR)		C:GO:0005787: P:G(	C:signal peptidase complex; P:signal peptide processing; F:pept			IPR009542 (PFAM): IPR009542 (PAN	70,961	73,062	98,049	84,073	84,478									
Solyc03g005750	RNA polymerase II degradation factor-like protein (DUF1296) (AHRD V3.3 *** AT1G29370.1)		F:GO:0005515	F:protein binding			IPR009719 (PFAM): mobidb-lite (MOB	120,012	111,962	112,623	102,960	110,628									
Solyc03g005760	chlorophyll a/b-binding protein		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	736,307	1535,132	309,432	280,136	646,277	1,088	0,001	1,059	0,003			up	up	
Solyc03g005770	chlorophyll a/b-binding protein		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	94,309	360,439	30,930	41,869	83,474	1,963	0,000	1,427	0,000			up	up	
Solyc03g005780	chlorophyll a/b-binding protein Cab-3C		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	41,053	270,689	8,947	18,678	32,661	2,749	0,000	1,861	0,000	1,064	0,004	up	up	up
Solyc03g005790	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4BE02_SOLLC)		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	0,000	0,062	0,025	0,025	0,000									
Solyc03g005800	UDP-N-acetylglucosamine transferase subunit ALG14 (AHRD V3.3 *** A0A0B0PIX5_GOSAR)		P:GO:0006488	P:dolichol-linked oligosaccharide biosynthetic process			IPR013969 (PFAM): IPR013969 (PAN	8,336	6,920	9,469	9,237	9,295									
Solyc03g005810	Purine permease family protein (AHRD V3.3 *** D7MCV2_ARALL)		F:GO:0005215: C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): PTHR31376:SF17 (	0,118	0,124	0,240	0,320	0,331									
Solyc03g005820	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)		F:GO:0005215: C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	0,317	0,247	0,097	0,488	0,142									
Solyc03g005830	O-acetyltransferase family protein (AHRD V3.3 *** AT5G46340.1)		C:GO:0016021	C:integral component of membrane			IPR012419 (PFAM): PTHR13533 (PAN	13,114	10,111	16,170	19,294	17,267									
Solyc03g005850	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 --* AT3G63090.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,039	0,000	0,025	0,095									
Solyc03g005860	ABC transporter B family protein (AHRD V3.3 *** G7ILW7_MEDTR)	ABCB5	F:GO:0005524: C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	0,040	0,167	0,000	0,047	0,000									
Solyc03g005870	eukaryotic translation initiation factor 4E	eif4e	F:GO:0003743: C:G(	F:translation initiation factor activity; C:cytoplasm; P:translation			IPR023398 (G3DSA:3.30.760.GENE3	46,026	42,059	57,749	51,889	53,257									
Solyc03g005880	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BE11_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004316 (PFAM): G3DSA:1.20.128	0,641	0,315	0,858	0,800	0,754									
Solyc03g005890	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *** AT2G34340.1)						IPR007608 (PFAM): PTHR33083:SF7	0,077	0,057	0,100	0,458	0,210									
Solyc03g005900	GDSL-lipase protein (AHRD V3.3 *** Q08ET5_CAPAN)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,294	0,250	0,000	0,000	0,000									
Solyc03g005910	Lipase, GDSL (AHRD V3.3 *** A0A103XTV4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,000	0,000	0,022	0,000	0,024									
Solyc03g005920	Protein kinase, putative (AHRD V3.3 *** B9S8G7_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PRINTS): IPR002110 (SN	16,620	15,544	21,235	24,459	22,685									
Solyc03g005930	RNA ligase/cyclic nucleotide phosphodiesterase family protein (AHRD V3.3 *** A0A061GEN8_THECC)		F:GO:0004112	F:cyclic-nucleotide phosphodiesterase activity			IPR012386 (PFAM): IPR012386 (PIRS	6,231	6,426	5,474	4,677	5,545									
Solyc03g005940	histone acetyltransferase (DUF1264) (AHRD V3.3 *** AT5G45690.1)						IPR010686 (PFAM): mobidb-lite (MOB	5,923	11,471	2,791	5,877	0,440									
Solyc03g005950	Major facilitator superfamily protein (AHRD V3.3 *** A0A061GLA6_THECC)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,019	0,106	0,000	0,173	0,000									
Solyc03g005960	protein kinase LESK1	lesk1	F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:2.60.120.430 (GENE3D): IPR(	1,145	1,514	0,047	0,317	0,474									
Solyc03g005970	RING/U-box superfamily protein (AHRD V3.3 *** AT3G53690.1)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR002867 (SMART): G3DSA:1.20.12	1,620	1,286	2,284	2,264	2,126									
Solyc03g005980	NOD26-like intrinsic protein 1.1	NIP1.1	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	1,567	0,574	0,072	0,025	0,047									
Solyc03g005990	Brassinazole-resistant 1 protein (AHRD V3.3 *** A0A059CDQ1_EUCGR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:transcription, DNA			IPR008540 (PFAM BES1	16,457	14,660	6,924	10,276	8,137					0,576	0,032			up
Solyc03g006000	SolycHsfA4a	HSF-20	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	20,224	29,244	56,622	50,320	41,523									
Solyc03g006010	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)		C:GO:0016021	C:integral component of membrane			PTHR33916 (PANTHER): PTHR33916	22,891	13,549	59,645	59,568	46,000									
Solyc03g006020	Ubiquitin domain-containing protein (AHRD V3.3 *** AT1G53400.1)						IPR038169 (G3DSA:1.20.225.GENE3	6,012	3,952	9,275	10,737	10,473									
Solyc03g006030	LRR receptor-like kinase (AHRD V3.3 *** A0A072V4N4_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			SM00365 (SMART): IPR003591 (SMA	3,057	5,605	0,757	1,195	2,457	0,900	0,035	1,668	0,002			up	up	
Solyc03g006040	Transcription factor bHLH35-like protein (AHRD V3.3 *** A0A0B0MJP3_GOSAR)						PTHR31945 (PANTHER): PTHR31945	0,082	0,036	0,000	0,000	0,023									
Solyc03g006050	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A142CCY8_9LAMI)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	5,361	3,839	2,740	4,600	3,535					0,748	0,023			up
Solyc03g006060	RING/FYVE/PHD zinc finger superfamily protein, putative (AHRD V3.3 *** A0A061GDI8_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR011016 (PF	5,976	5,704	3,674	4,014	3,834									
Solyc03g006070	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	46,685	50,524	62,391	69,339	60,270									
Solyc03g006080	LRR receptor-like kinase (AHRD V3.3 *** A0A072V4N4_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR000719 (SMA	17,367	34,094	4,334	3,493	5,418									
Solyc03g006090	PAS/LOV protein B (AHRD V3.3 --* AT2G02710.4)		F:GO:0003676: F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis				0,640	0,789	0,741	0,708	0,353									
Solyc03g006100	Receptor-kinase, putative (AHRD V3.3 *** B9RVA8_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	16,998	15,025	3,970	5,611	7,458			0,900	0,023				up	
Solyc03g006110	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IH06_SOLCH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,768	0,972	0,984	0,826	0,844									
Solyc03g006120	transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351: F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM): PTHR22952:SF2	0,334	0,138	0,975	1,651	1,036									
Solyc03g006130	Receptor protein kinase, putative (AHRD V3.3 *** B9T7R3_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:3.30.200.20 (GENE3D): G3DS	48,053	62,172	39,984	47,660	51,147									
Solyc03g006140	Neutral ceramidase (AHRD V3.3 *** NCASE_ARATH)		C:GO:0005576: C:G(	C:extracellular regic	EC:3.5.1.23	Ceramidase	IPR031329 (PFAM): IPR031331 (PFA	231,659	245,537	262,550	307,233	255,139									
Solyc03g006150	LOW QUALITY:MYB-like transcription factor family protein (AHRD V3.3 *** A0A072TT31_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(G2-like	0,000	0,000	0,000	0,025	0,023									
Solyc03g006160	6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** AT2G30230.1)		C:GO:0009507	C:chloroplast			IPR025322 (PFAM): mobidb-lite (MOB	0,715	0,453	0,000	0,000	0,000									
Solyc03g006173	LOW QUALITY:DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)						IPR007493 (PFAM): IPR036758 (G3D	3,579	3,381	3,414	3,069	2,876									
Solyc03g006177	Transcription initiation factor IIB (AHRD V3.3 *** A0A0B2P0T2_GLYSO)		P:GO:0006355: P:G(	P:regulation of transcription, DNA-templated; P:transcription pre			G3DSA:1.10.472.10 (GENE3D): G3DS	5,909	5,294	6,186	5,905	6,517									
Solyc03g006190	Cytochrome b6-f complex subunit 8, chloroplastic (AHRD V3.3 --* PETN_CHLRE)		F:GO:0001093: F:G(	F:TFIIB-class transcription factor binding; F:double-stranded DNA binding; C:nucleus; P:regulation of tra				0,786	0,498	0,658	0,554	0,871									
Solyc03g006210	Cysteine protease (AHRD V3.3 *** J7GPZ5_SOLCI)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): IPR013201 (SN	0,196	0,249	0,150	0,500	0,469									
Solyc03g006220	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)						IPR026057 (PFAM): IPR029962 (PAN	0,397	0,792	0,144	0,097	0,094									
Solyc03g006240	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2QCD5_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	1,796	2,278	0,022	0,025	0,140									
Solyc03g006250	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2QGL7_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	5,944	4,600	1,707	2,613	3,096									
Solyc03g006260	Calcium-binding EF-hand (AHRD V3.3 *-* A0A103XMB0_CYNCS)		F:GO:0005509: C:G(	F:calcium ion binding; C:integral component of membrane; P:tra			IPR002048 (SMART): G3DSA:1.10.23	2,458	1,793	1,819	0,933	1,822									
Solyc03g006270	Rab family GTPase (AHRD V3.3 *** D8RE14_SELML)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	0,098	0,078	0,022	0,094	0,094									
Solyc03g006280	F1K23.23, putative isoform 1 (AHRD V3.3 *** A0A061GM10_THECC)		C:GO:0009507: P:G(	C:chloroplast; P:thylakoid membrane organization; P:granum as			PTHR35694 (PANTHER)	5,537	5,793	6,022	5,973	6,124									
Solyc03g006290	transmembrane protein%2C putative (Protein of unknown function%2C DUF599) (AHRD V3.3 *** AT3G1821		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31168 (PAN	0,000	0,018	0,000	0,025	0,000									
Solyc03g006300	Receptor-like protein kinase HSL1 (AHRD V3.3 *** HSL1_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR013210 (PFA	1,269	1,966	0,164	0,076	0,259									
Solyc03g006310	nuclear fusion defective 6 (AHRD V3.3 *** AT2G20585.7)		P:GO:0000741	P:karyogamy			PTHR33156 (PANTHER): IPR033251 (	9,455	10,556	8,245	7,267	7,532									

Solyc03g006320	Ethylene-responsive transcription factor, putative (AHRD V3.3 *-* B9RVV2_RICCO)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRINT ERF	1,894	2,564	0,578	0,395	0,235									
Solyc03g006330	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** A0A0K9NYE0_ZOSMR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	19,207	18,291	52,664	60,441	49,538									
Solyc03g006350	Zinc finger transcription factor 23	C3H23	F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIL C3H	22,990	19,980	22,228	21,515	21,157									
Solyc03g006360	Auxin-repressed protein (AHRD V3.3 *** K7VPG9_SOLTU)						IPR008406 (PFAM): mobidb-lite (MOB	0,099	0,425	0,144	1,094	0,400									
Solyc03g006370	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G02780.3)							0,877	0,967	1,731	1,589	1,557									
Solyc03g006375	Maturase K (AHRD V3.3 --* Q9GI40_LAMIN)							0,040	0,019	0,050	0,074	0,095									
Solyc03g006380	Transcriptional corepressor LEUNIG (AHRD V3.3 *-* A0A151S5T0_CAJCA)		F:GO:0005515	F:protein binding			IPR006594 (PFAM): mobidb-lite (MOB	2,967	2,463	3,261	3,347	3,462									
Solyc03g006385	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G36570.1)							1,196	0,894	1,390	1,614	1,345									
Solyc03g006390	Transcriptional corepressor LEUNIG-like protein (AHRD V3.3 *-* A0A0B0MGV8_GOSAR)		F:GO:0005515	F:protein binding			IPR006594 (SMART): IPR006594 (PF	1,709	1,962	2,135	2,087	2,168									
Solyc03g006400	MAP kinase kinase kinase 25	MAPKKK25	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	5,463	7,583	76,556	91,848	79,695									
Solyc03g006410	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (F	2,130	2,765	0,115	0,072	0,093									
Solyc03g006420	Origin recognition complex subunit 1 (AHRD V3.3 *** A0A0B2RND7_GLYSO)		F:GO:0003682; F:GO	F:chromatin binding; F:ATP binding			IPR001965 (SMART): IPR003593 (SM	27,259	24,230	15,580	15,678	15,032									
Solyc03g006430	DUF616 family protein (AHRD V3.3 *** G7IPT3_MEDTR)		P:GO:0006672; C:GO	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): mobidb-lite (MOB	35,104	22,503	12,376	12,622	13,392									
Solyc03g006440	Thioesterase family protein (AHRD V3.3 *** D7KCZ7_ARALL)		C:GO:0005777; C:GO	C:peroxisome; C:cytosol; P:phylloquinone biosynthetic process;			IPR003736 (TIGRFAM): IPR006683 (F	0,040	0,000	0,025	0,025	0,000									
Solyc03g006450	Thioesterase family protein (AHRD V3.3 *** D7KCZ7_ARALL)		C:GO:0005777; C:GO	C:peroxisome; C:cytosol; P:phylloquinone biosynthetic process;			G3DSA:3.10.129.10 (GENE3D): IPR0	0,099	0,039	0,025	0,025	0,094									
Solyc03g006460	Altered inheritance rate of mitochondria protein 25 (AHRD V3.3 *** A0A0B2SIA0_GLYSO)		C:GO:0005739; C:GO	C:mitochondrion; C:plastid; P:plasma membrane phospholipid sc			IPR005552 (PFAM): PTHR23248:SF9	34,064	28,033	40,151	39,188	39,792									
Solyc03g006470	CBS domain-containing protein (AHRD V3.3 *** A0A061GEK1_THECC)						IPR000644 (PFAM): G3DSA:3.10.580	0,121	0,136	0,022	0,025	0,023									
Solyc03g006480	TPR and ankyrin repeat-containing 1 (AHRD V3.3 *** A0A0B0MRR0_GOSAR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,019	0,000	0,000	0,000	0,000									
Solyc03g006490	glutaminase domain-containing protein						IPR024286 (SMART): IPR024286 (PF	14,751	18,594	1,992	5,927	5,797			1,522	0,002	1,553	0,000		up	up
Solyc03g006500	Kinase family protein (AHRD V3.3 *** B9IG83_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	32,963	33,929	31,618	30,916	33,687									
Solyc03g006510	Clathrin light chain (AHRD V3.3 *** A0A103XF03_CYNCS)		F:GO:0005198; P:GO	F:structural molecule activity; P:intracellular protein transport; P			IPR000996 (PFAM): mobidb-lite (MOB	41,071	45,873	61,874	59,238	54,009									
Solyc03g006520	Splicing factor 3B subunit 2 (AHRD V3.3 *** A0A151SEI3_CAJCA)		C:GO:0005634	C:nucleus			IPR006568 (SMART): IPR006568 (PF	37,746	33,520	40,556	38,123	38,542									
Solyc03g006530	Hydroxyproline-rich glycoprotein (AHRD V3.3 *-* B9HYL6_POPTR)		C:GO:0009707; C:GO	C:chloroplast outer membrane; C:integral component of membra			PR01217 (PRINTS): mobidb-lite (MOB	0,103	0,078	0,000	0,045	0,047									
Solyc03g006540	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (AHRD V3.3 *-* N1QXW8_AEGTA)						PTHR36729 (PANTHER)	0,114	0,726	0,000	0,000	0,023									
Solyc03g006550	Terpene synthase (AHRD V3.3 *** A0A076GH23_POPTR)		F:GO:0000287; F:GO	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM): G3DSA:1.50.10.1	0,019	0,000	0,000	0,000	0,000									
Solyc03g006560	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G11090.1)		C:GO:0005783; C:GO	C:endoplasmic retic	EC:3.1.1.23; EC:3.1.	Acylglycerol lipase; C	IPR022742 (PFAM): IPR029058 (G3D	6,222	5,868	6,482	6,265	5,803									
Solyc03g006570	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD		F:GO:0005524	F:ATP binding			IPR001841 (SMART): IPR001650 (SM	65,163	92,608	52,095	48,375	59,153									
Solyc03g006580	LisH and RanBPM domains containing protein (AHRD V3.3 *** AT1G61150.11)		F:GO:0005515	F:protein binding			IPR006594 (SMART): IPR006595 (SM	33,711	34,567	40,706	40,520	39,367									
Solyc03g006590	Multidrug resistance 3 (AHRD V3.3 *** A0A0B0MAA3_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,162	0,175	0,025	0,075	0,024									
Solyc03g006600	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G64110.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,916	0,730	0,180	0,075	0,093									
Solyc03g006610	Arf GTPase activating protein (AHRD V3.3 *** A0A103YJY6_CYNCS)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (SM	4,418	4,270	11,150	32,003	17,426			0,641	0,008	1,522	0,000		up	up
Solyc03g006620	Cotton fiber expressed protein (AHRD V3.3 *** A0A0D2VH61_GOSRA)		C:GO:0016021	C:integral component of membrane			IPR008480 (PFAM): IPR025520 (PFA	33,476	33,904	19,231	27,527	19,364					0,518	0,016			up
Solyc03g006630	Sphingosine kinase, putative (AHRD V3.3 *** B9SFA5_RICCO)		F:GO:0003951	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR001206 (SMART): IPR001206 (PF	3,204	3,222	14,469	16,566	13,851									
Solyc03g006640	F-box family protein (AHRD V3.3 *** B9H220_POPTR)		F:GO:0005515	F:protein binding			PTHR34049:SF1 (PANTHER): PTHR3	11,199	10,586	15,666	14,403	13,441									
Solyc03g006650	Sugar transporter protein 10	STP10	C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	0,717	0,853	0,327	0,858	0,352									
Solyc03g006660	Protein kinase-like (AHRD V3.3 *** Q2HTV1_MEDTR)		C:GO:0016021; F:GO	C:integral component of membrane; F:kinase activity; P:phosph			IPR004147 (PFAM): PTHR10566:SF9	14,003	11,414	17,543	20,456	17,179									
Solyc03g006670	cyclinD6_2	CycD6_2	C:GO:0005634; P:GO	C:nucleus; P:regulation of cell cycle			IPR013763 (SMART): G3DSA:1.10.47	0,324	0,337	0,000	0,000	0,023									
Solyc03g006680	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)		C:GO:0005829; C:GO	C:cytosol; C:plasma membrane			IPR006015 (PRINTS): IPR006016 (PF	54,424	51,311	49,275	41,091	44,623									
Solyc03g006690	LOW QUALITY:FAD-binding Berberine family protein (AHRD V3.3 *-* AT5G44380.2)		F:GO:0016491; F:GO	F:oxidoreductase activity; F:flavin adenine dinucleotide binding;			IPR012951 (PFAM): G3DSA:3.30.465	0,000	0,018	0,000	0,000	0,000									
Solyc03g006700	Peroxidase (AHRD V3.3 *** K4BE93_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,394	0,300	2,385	1,699	1,900									
Solyc03g006710	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	0,098	0,175	0,000	0,025	0,000									
Solyc03g006713	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,000	0,022	0,023									
Solyc03g006715	IQ-domain 2 (AHRD V3.3 --* AT5G03040.3)							0,038	0,000	0,000	0,000	0,024									
Solyc03g006720	Serine/threonine-protein kinase (AHRD V3.3 *** A0A059C900_EUCGR)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,000	0,000	0,000	0,025	0,000									
Solyc03g006730	Serine/threonine-protein kinase (AHRD V3.3 *** A0A059C900_EUCGR)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR003609 (SM	0,042	0,062	0,000	0,000	0,000									
Solyc03g006740	Disease resistance protein (AHRD V3.3 *-* Q1RU52_MEDTR)		F:GO:0043531	F:ADP binding			PF18052 (PFAM): PTHR23155 (PANT	0,501	0,634	0,047	0,000	0,000									
Solyc03g006750	CC-NBS-LRR disease resistance protein (AHRD V3.3 *-* A0A067XSV0_CICAR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,000	0,019	0,000	0,000	0,000									
Solyc03g006760	NBS-LRR disease resistance-like protein (AHRD V3.3 *-* Q2LED2_9ROSI)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	4,128	4,533	0,473	0,317	0,354									
Solyc03g006770	Serine/threonine-protein kinase (AHRD V3.3 *** M1A226_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,094	0,057	0,291	0,478	0,304									
Solyc03g006780	Serine/threonine-protein kinase (AHRD V3.3 *** M1B363_SOLTU)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001480 (SMART): IPR000858 (PF	0,077	0,062	0,071	0,094	0,046									
Solyc03g006790	Protein kinase (AHRD V3.3 *** C6ZRP8_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,000	0,000	0,022	0,025	0,000									
Solyc03g006800	TCP transcription factor 21	TCP21	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	1,242	1,524	0,049	0,025	0,023									
Solyc03g006810	Peroxidase (AHRD V3.3 *** K4BEA4_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	1,056	0,939	0,731	0,649	0,521									
Solyc03g006820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G51880.1)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR006620 (SMART): G3DSA:2.60.12	7,628	6,566	12,595	12,432	12,113									
Solyc03g006830	MADS-box transcription factor FYFL (AHRD V3.3 *** W5S185_SOLLC)		F:GO:0000977; F:GO	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINT MIKC_MADS	14,381	10,534	12,423	11,595	10,651									
Solyc03g006840	LOW protein: M-phase inducer phosphatase-like protein (AHRD V3.3 *** AT5G62170.1)						IPR025486 (PFAM): IPR032795 (PFA	0,837	1,204	0,025	0,025	0,023									
Solyc03g006850	Actin cytoskeleton-regulatory complex PAN1 (AHRD V3.3 *** A0A0B0N2N4_GOSAR)						IPR007033 (PFAM): mobidb-lite (MOB	13,068	11,452	13,968	11,103	13,087									
Solyc03g006860	fructokinase	frk1	F:GO:0016301	F:kinase activity			IPR002139 (PRINTS): IPR011611 (PF	23,162	27,983	25,757	23,756	23,826									
Solyc03g006870	phosphoglucomutase (AHRD V3.3 *** AT5G51820.1)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:intramolecular transferase			IPR005841 (PRINTS): G3DSA:3.30.31	27,907	43,698	12,199	9,605	14,531									
Solyc03g006880	gibberellin 20-oxidase-1		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR005123 (PFA	2,529	9,483	0,000	0,022	0,046	1,927	0,000					up		
Solyc03g006890	Kinase superfamily protein (AHRD V3.3 *** A0A061G0U3_THECC)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,000	0,043	0,047	0,000	0,000									
Solyc03g006900	Kinase superfamily protein isoform 1 (AHRD V3.3 *** A0A061G7K8_THECC)						G3DSA:1.10.510.1 Trihelix	0,363	0,801	0,190	0,321	0,351									
Solyc03g006910	bHLH transcription factor 019		F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription by RNA polymerase			IPR011598 (PFAM bHLH	3,577	1,321	0,090	0,047	0,140	-1,407	0,016					down		
Solyc03g006920	Kinase family protein (AHRD V3.3 *** B9ICZ2_POPTR)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR000719 (PF	21,361	17,427	38,728	30,639	30,783									
Solyc03g006930	Protein phosphatase 2c, putative (AHRD V3.3 *** B9R9K8_RICCO)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	1,013	0,983	0,025	0,025	0,000									
Solyc03g006940	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G51760.2)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	1,311	1,140	0,000	0,025	0,000									
Solyc03g006950	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G51760.2)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	0,314	0,350	0,000	0,000	0,000									
Solyc03g006960	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G51760.1)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	5,893	7,505	51,186	54,247	55,281									
Solyc03g006970	serine protease SBT2	sbt2	F:GO:0004252; P:GO	F:serine-type endop	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	16,274	13,858	5,145	4,938	6,272									
Solyc03g006980	Alpha-L-fucosidase 1 (AHRD V3.3 *** W9SQK3_9ROSA)		F:GO:0004560; P:GO	F:alpha-L-fucosidas	EC:3.2.1.51	Alpha-L-fucosidase	IPR000933 (SMART): IPR008979 (G3	4,178	5,244	1,132	0,455	0,755									
Solyc03g006990	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2QQF9_GLYSO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	2,409	2,400	2,406	2,096	1,626									
Solyc03g007000	Mitochondrial metalloendopeptidase OMA1 (AHRD V3.3 *** W9S9F8_9ROSA)		F:GO:0004222; P:GO	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR001915 (PFAM): PTHR22726:SF1	22,205	22,126	55,132	61,785	52,774									
Solyc03g007010	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9R9L5_RICCO)		F:GO:0003723; F:GO	F:RNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART): IPR014001 (SM	9,628	6,900	5,210	5,089	5,442									
Solyc03g007030	CDGSH iron-sulfur domain-containing protein		C:GO:0043231; F:GO	C:intracellular membrane-bounded organelle; F:2 iron, 2 sulfur c			IPR018967 (SMART): G3DSA:3.40.5.9	4,963	9,008	0,490	0,237	1,478	0,887	0,021					up		
Solyc03g007040	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NL94_ZOSMR)		P:GO:0006812; F:GO	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	15,887	12,860	11,493	13,413	12,175									
Solyc03g007050	ERECTA-like 1 (AHRD V3.3 *** AT5G62230.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	1,896	1,404	0,559	0,688	0,539									
Solyc03g007060	Cell cycle regulated microtubule-associated protein (AHRD V3.3 *** A0A072UNM9_MEDTR)		C:GO:0005819; C:GO	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027330 (PFAM): mobidb-lite (MOB	1,009	0,803	0,526	0,411	0,683									
Solyc03g007070	1-aminocyclopropane-1-carboxylate synthase (AHRD V3.3 *** G8E0Q0_GOSHI)	ACS11	F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			PR00753 (PRINTS): IPR004839 (PFA	11,604	8,510	16,079	14,075	16,511									
Solyc03g007080	Hydroxyproline-rich glycoprotein (AHRD V3.3 *** B9ICX5_POPTR)						PTHR37767 (PANTHER)	0,000	0,000	0,000	0,025	0,023									
Solyc03g007090	LOW QUALITY:DUF3475 domain protein (AHRD V3.3 *** A0A072TFG5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR021864 (PFAM): IPR007700 (PFA	0,193	0,231	0,212	0,117	0,119									
Solyc03g007100	Cleavage and polyadenylation specificity factor subunit 1 (AHRD V3.3 *** W9SC01_9ROSA)		F:GO:0003676; F:GO	F:nucleic acid binding; F:protein binding; C:nucleus			PF10433 (PFAM): IPR015943 (G3DSA	72,054	61,847	57,659	57,005	57,872									
Solyc03g007110	ATP-dependent clp protease, putative (AHRD V3.3 *** B9R9N1_RICCO)		P:GO:0019538	P:protein metabolic process			IPR004176 (PFAM): IPR036628 (G3D	23,541	31,289	36,987	37,323	41,000									
Solyc03g007120	Trichome birefringence-like protein (AHRD V3.3 *** A0A072VN16_MEDTR)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	51,581	42,393	40,199	38,263	37,285									
Solyc03g007130	65-kDa microtubule-associated 3-like protein (AHRD V3.3 *** A0A0B0NAV0_GOSAR)		P:GO:0000226; F:GO	P:microtubule cytoskeleton organization; F:microtubule binding			PF03999 (PFAM): G3DSA:1.20.58.152	0,471	0,441	0,022	0,072	0,024									
Solyc03g007140	B3 domain-containing protein (AHRD V3.3 *-* W9S5V1_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	18,273	20,960	11,283	9,459	12,266									
Solyc03g007150	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072VXL7_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): G3DSA:3.30.133	2,260	2,787	5,889	7,310	5,587									
Solyc03g007160	LOW QUALITY:Lysine-specific histone demethylase 1 homolog 1 (AHRD V3.3 *-* LDL1_ORYSJ)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR036188 (G3DSA:3.50.50.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc03g007170	Peptidyl-prolyl cis-trans isomerase FKBP53 (AHRD V3.3 *** W9QW00_9ROSA)		P:GO:0000413; F:GO	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	G3DSA:3.10.50.40 (GENE3D): IPR02	23,937	26,683	8,574	5,957	8,179									
Solyc03g007180	F5O11.10, putative isoform 1 (AHRD V3.3 *** A0A061G0M8_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	27,470	22,489	6,759	5,391	6,827									
Solyc03g007190	Hypersensitive-induced response protein (AHRD V3.3 *** A0A068F6N1_CAPAN)		C:GO:0005774; C:GO	C:vacuolar membrane; C:Golgi apparatus; C:plasma membrane;			IPR001107 (SMART): G3DSA:3.30.47	47,000	49,080	100,988	104,383	91,961									
Solyc03g007200	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): G3DSA:3.90.180	2,548	1,797	1,477	2,376	0,945									
Solyc03g007210	Receptor-like protein kinase (AHRD V3.3 *** A0A061EYK6_THECC)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR032872 (PF	40,098	61,950	30,077	33,497	32,698									
Solyc03g007220	Membrane receptor-like protein 1 (AHRD V3.3 *-* B3TJG2_CAPAN)		C:GO:0016021; F:GO	C:integral component of membrane; F:polysaccharide binding				7,751	14,898	2,364	3,661	4,654	0,969	0,017	0,966	0,034			up	up	
Solyc03g007230	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	68,498	34,881	138,712	138,292	127,695	-0,945	0,000					down		
Solyc03g007240	spermine synthase	spm1	F:GO:0003824; P:GO	F:catalytic activity; P:polyamine metabolic process			IPR037163 (G3DSA:2.30.140.GENE3	26,440	23,122	28,086	29,713	29,361									
Solyc03g007250	Cyclic nucleotide gated channel CNGC6 (AHRD V3.3 *-* A0A0B4U3H6_SOLLC)		F:GO:0005216; C:GO	F:ion channel activity; C:integral component of membrane; P:ior			IPR000595 (SMART): IPR014710 (G3	16,844	23,619	12,992	12,266	14,027									
Solyc03g007260	Cyclic nucleotide gated channel CNGC6 (AHRD V3.3 *** A0A0B4U3H6_SOLLC)		F:GO:0005216; P:GO	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR005821 (PFAM): PTHR10217 (PAN	18,343	24,414	14,578	14,154	15,480									
Solyc03g007270	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G53140.2)		F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	62,783	47,588	63,115	58,960	53,840									
Solyc03g007280	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103XXZ0_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	18,414	21,292	16,458	17,839	16,655									
Solyc03g007290	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4BEF2_SOLLC)		F:GO:0003824; P:GO	F:catalytic activity; P:trehalose biosynthetic process			IPR023214 (G3DSA:3.40.50.GENE3D	1,182	1,128	0,568	0,299	0,333									
Solyc03g007300	LOW QUALITY:ribosomal protein L16 (AHRD V3.3 *** ATMG00080.1)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR000114 (PRINTS): IPR016180 (PF	0,019	0,000	0,000	0,025	0,000									
Solyc03g007310	Abscisic acid receptor PYL8-like protein (AHRD V3.3 *** A0A0B0PTU4_GOSAR)		F:GO:0004864; C:GO	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm			IPR023393 (G3DSA:3.30.530.GENE3	6,434	6,588	5,863	4,770	4,893									
Solyc03g007320	Polypyrimidine tract-binding protein (AHRD V3.3 *** A0A0H5DID0_RHOSS)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR023393 (G3	44,744	45,358	58,103	59,165	53,869									
Solyc03g007330	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** A0A072VFQ6_MEDTR)		F:GO:0004222; F:GO	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): G3DSA:1.20.58	30,054	34,968	19,782	19,844	28,176			0,505	0,027				up	
Solyc03g007340	polypyrimidine tract-binding-like protein (AHRD V3.3 *** AT5G24130.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR349	7,233	6,273	5,951	5,227	3,832									
Solyc03g007360	Nodulin MtN3		C:GO:0016021	C:integral component of membrane			IPR004316 (PFAM): G3DSA:1.20.128	6,279	5,445	2,343	1,740	2,500									
Solyc03g007370	Sigma factor (AHRD V3.3 *** A0A0G2STU5_9ROSI)	SIG5	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:DNA-templated tra			IPR000943 (PRINTS): IPR007627 (PF	29,271	32,105	56,644	60,899	71,200									
Solyc03g007380	WRKY transcription factor 52	WRKY52	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF WRKY	0,205	0,557	0,044	0,073	0,047									
Solyc03g007390	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S636_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	4,740	3,838	3,859	4,963	4,786									
Solyc03g007395	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 --* PSAA_MORIN)							2,298	2,141	2,705	2,106	2,823									
Solyc03g007400	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT2G29780.2)							2,263	1,949	2,591	1,204	2,093					-1,107	0,021			down
Solyc03g007410	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT5G53210.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,040	0,019	0,000	0,000	0,000									
Solyc03g007420	Homeobox-leucine zipper HOX24 (AHRD V3.3 *** A0A0B0P867_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	13,920	10,650	13,226	12,897	12,754									
Solyc03g007430	Mitochondrial carrier protein, putative (AHRD V3.3 *** B9RIM4_RICCO)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	18,463	17,144	84,599	97,569	76,659									
Solyc03g007440	Plastid division protein PDV1 (AHRD V3.3 *** A0A061G8R9_THECC)		P:GO:0010020	P:chloroplast fission			mobidb-lite (MOBIDB_LITE): mobidb-lit	23,787	23,154	24,329	24,687	23,246									
Solyc03g007460	Solanum lycopersicum Cytokinin Response Factor 4	CRF4	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRINT ERF	3,351	2,189	3,086	7,255	3,754					1,234	0,000			up
Solyc03g007470	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A0K9PK38_ZOSMR)		F:GO:0005524; P:GO	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART): IPR016135 (G3D	233,259	186,065	164,914	140,138	137,601									
Solyc03g007480	myosin heavy chain-like protein (AHRD V3.3 *** AT5G53310.1)		F:GO:0003774; C:GO	F:motor activity; C:i	EC:3.6.1.15	Nucleoside-triphosph	IPR010926 (PFAM): PTHR34969 (PAN	101,184	77,179	104,043	101,629	103,588									
Solyc03g007490	cytochrome C oxidase assembly protein (AHRD V3.3 *** AT4G14145.1)		C:GO:0031966	C:mitochondrial membrane			IPR020164 (PFAM): mobidb-lite (MOB	4,050	4,522	4,701	4,929	5,228									
Solyc03g007500	Plastid division protein PDV1 (AHRD V3.3 *** A0A061G8R9_THECC)		P:GO:0010020	P:chloroplast fission			mobidb-lite (MOBIDB_LITE): PTHR336	11,911	12,990	20,830	20,477	18,098									
Solyc03g007510	hAT transposon superfamily (AHRD V3.3 *** AT1G79740.4)		F:GO:0003677	F:DNA binding			IPR003656 (PFAM): IPR007021 (PFA	3,117	2,571	4,434	5,411	4,592									
Solyc03g007520	Proline-rich cell wall-like protein (AHRD V3.3 *** G7J680_MEDTR)		C:GO:0000813; F:GO	C:ESCRT I complex; F:ubiquitin binding; P:ubiquitin-dependent p			G3DSA:1.20.120.1920 (GENE3D): mo	78,913	74,261	67,416	70,554	71,724									
Solyc03g007530	ABC transporter family protein (AHRD V3.3 *** U5FPJ5_POPTR)	ABCC2	F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	27,815	13,754	14,250	16,166	17,557	-0,985	0,001					down		
Solyc03g007550	LIM domain-containing protein A, putative isoform 1 (AHRD V3.3 *** A0A061G8M8_THECC)		C:GO:0005634; P:GO	C:nucleus; P:DNA replication; P:response to ionizing radiation; I			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,614	2,592	0,337	0,148	0,328									
Solyc03g007560	LOW QUALITY:Crooked neck protein, putative (AHRD V3.3 *** B9RCP3_RICCO)		F:GO:0005515; P:GO	F:protein binding; P:RNA processing			IPR003107 (SMART): IPR011990 (G3	2,870	3,122	1,323	1,380	1,366									
Solyc03g007580	DUF21 domain-containing protein (AHRD V3.3 *-* A0A199V808_ANACO)		C:GO:0016021	C:integral component of membrane			PTHR12064:SF36 (PANTHER): PTHR	0,038	0,145	0,000	0,048	0,023									
Solyc03g007590	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *-* AT3G49140.1)						IPR037119 (G3DSA:3.20.180.GENE3	11,401	12,997	16,579	13,638	16,346									
Solyc03g007600	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YJF0_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	44,402	40,757	67,817	61,515	68,062									
Solyc03g007610	DnaJ domain-containing protein (AHRD V3.3 *** A0A124SIC1_CYNCS)		P:GO:0031204	P:posttranslational protein targeting to membrane, translocation			IPR001623 (PRINTS): IPR004179 (SM	38,234	37,082	51,745	49,345	49,486									
Solyc03g007620	Tic22-like family protein (AHRD V3.3 *** AT5G62650.1)		P:GO:0015031	P:protein transport			IPR007378 (PFAM): G3DSA:3.40.135	20,454	19,758	40,332	41,070	41,417									
Solyc03g007640	LOW QUALITY:WRKY transcription factor 68	WRKY68	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF WRKY	0,000	0,039	0,025	0,000	0,000									
Solyc03g007650	LOW QUALITY:DnaJ like protein (AHRD V3.3 *** Q9FEW7_SOLLC)		P:GO:0006457; F:GO	P:protein folding; F:unfolded protein binding			IPR002939 (PFAM): G3DSA:2.60.260	9,864	7,173	18,283	16,653	14,705									
Solyc03g007660	NADH-ubiquinone oxidoreductase-like protein (AHRD V3.3 *** AT5G52840.1)		C:GO:0005747; P:GO	C:mitochondrial respiratory chain complex I; P:respiratory electr			IPR006806 (PFAM): mobidb-lite (MOB	100,647	86,369	156,462	131,800	144,835									
Solyc03g007670	defense signal transduction Sgt1-2	Sgt1-2	F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR007699 (PF	136,766	132,773	102,328	85,803	100,278									
Solyc03g007680	Trafficking protein particle complex subunit-like protein (AHRD V3.3 *** B7FHC8_MEDTR)		P:GO:0016192; C:GO	P:vesicle-mediated transport; C:TRAPP complex			IPR007233 (SMART): G3DSA:3.30.45	16,038	16,570	19,210	22,294	18,872									
Solyc03g007690	ABC transporter family protein (AHRD V3.3 *** U5FQ57_POPTR)	ABCG4	F:GO:0005524; C:GO	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	1,846	2,645	1,338	0,987	0,988									
Solyc03g007695	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycofamily protein, putative (AHRD V3.3		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	0,102	0,021	0,000	0,000	0,000									
Solyc03g007700	LOW QUALITY:Membrane-associated kinase regulator, putative (AHRD V3.3 *** G7IDX6_MEDTR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,889	3,852	0,711	0,287	0,775	1,053	0,012					up		
Solyc03g007710	Membrane-associated kinase regulator, putative (AHRD V3.3 *** G7IDX6_MEDTR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,115	1,129	0,995	1,801	1,225									
Solyc03g007720	Membrane-associated kinase regulator, putative (AHRD V3.3 *** G7IDX6_MEDTR)		C:GO:0005886	C:plasma membrane			PTHR33929:SF1 (PANTHER): IPR039	0,276	0,140	0,068	0,176	0,000									
Solyc03g007740	Reticulon-like protein (AHRD V3.3 *** K4BEJ6_SOLLC)		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994 (PAN	371,576	292,349	191,627	167,985	183,447									

Solyc03g007750	F-box protein family (AHRD V3.3 *** A0A151U6A0_CAJCA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	8,926	8,800	12,671	11,313	12,383								
Solyc03g007760	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G28000.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:1.10.8.6	26,995	30,211	10,139	14,478	9,551					0,518	0,040			up
Solyc03g007770	S-type anion channel (AHRD V3.3 *** A0A098GMQ9_9ROSI)		P:GO:0006873; F:G(	P:cellular ion homeostasis; F:voltage-gated anion channel activ			IPR038665 (G3DSA:1.50.10.GENE3D	104,689	61,012	146,223	168,882	155,645	-0,753	0,001					down		
Solyc03g007775	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_SORBI)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			PTHR34576:SF2 (PANTHER): PTHR3	0,019	0,041	0,000	0,000	0,000									
Solyc03g007780	LOW QUALITY:Ovule Secreted Protein							0,042	0,099	0,396	0,809	1,195									
Solyc03g007790	Serine/threonine-protein kinase (AHRD V3.3 *** K4BEK1_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,138	1,239	0,737	0,862	0,865									
Solyc03g007800	Protein timeless like (AHRD V3.3 *** A0A0B2QAC2_GLYSO)		P:GO:0000076; C:G(	P:DNA replication checkpoint; C:nuclear chromatin; F:DNA bindi			IPR006906 (PFAM): IPR007725 (PFA	5,176	3,873	2,610	1,513	1,650									
Solyc03g007810	Pyruvate kinase (AHRD V3.3 *** K4BEK3_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS): IPR001697 (TI(	158,635	152,570	181,987	203,116	209,997									
Solyc03g007820	casein kinase I-like 3 (AHRD V3.3 --* AT4G28880.4)							0,472	0,281	0,222	0,171	0,284									
Solyc03g007825	Acidic endochitinase (AHRD V3.3 *** CHIA_ARATH)		P:GO:0005975	P:carbohydrate metabolic process			IPR001223 (PFAM): G3DSA:3.20.20.8	0,000	0,018	0,025	0,000	0,000									
Solyc03g007830	Protein curvature thylakoid chloroplastic-like (AHRD V3.3 *-* A0A061SMW2_9CHLO)		C:GO:0009579	C:thylakoid			IPR025564 (PFAM): PTHR33222:SF4	4,039	3,571	16,698	20,811	18,307									
Solyc03g007840	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RIP1_RICCO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (TIGF	1,401	2,165	2,405	2,382	2,048									
Solyc03g007850	Crooked neck protein, putative (AHRD V3.3 *** B9RCP3_RICCO)		F:GO:0005515; P:G(	F:protein binding; P:RNA processing			IPR003107 (SMART): IPR003107 (PF	3,607	3,439	2,357	1,822	2,282									
Solyc03g007860	Protein PAM68, chloroplastic (AHRD V3.3 *-* PAM68_ARATH)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			IPR021855 (PFAM): mobidb-lite (MOB	5,820	8,819	14,854	15,196	21,210			0,513	0,030				up	
Solyc03g007870	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A072TW71_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	134,631	97,064	86,090	115,760	87,950					0,431	0,028			up
Solyc03g007880	Heat shock protein 83 (AHRD V3.3 --* A0A1D1YL00_9ARAE)						PTHR34802 (PANTHER)	0,082	0,059	0,220	0,118	0,047									
Solyc03g007890	class 2 small heat shock protein Le-HSP17.6	hsp17.6	F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS): IPR003594 (SM	128,261	72,941	223,669	224,730	222,844	-0,787	0,012					down		
Solyc03g007900	Glutaminyl-peptide cyclotransferase-like protein (AHRD V3.3 *** A0A0B0P3U3_GOSAR)		F:GO:0005515; F:G(	F:protein binding; F:	EC:2.3.2.5	Glutaminyl-peptide c	IPR015943 (G3DSA:2.130.10.GENE3	17,846	23,298	33,501	32,305	30,700									
Solyc03g007910	Protein kinase family protein (AHRD V3.3 *** C6ZRW5_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,000	0,000	0,000	0,025	0,000									
Solyc03g007940	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G23500.1)	PG56-2	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	23,010	6,831	5,455	2,152	3,535	-1,717	0,000					down		
Solyc03g007950	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G23500.1)	PG56-3	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	0,195	0,096	0,047	0,022	0,046									
Solyc03g007960	beta-carotene hydroxylase-2	BCH2	F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR31899:SF7	14,759	25,166	108,370	124,220	93,050									
Solyc03g007970	UDP-N-acetylmuramate-alanine ligase (AHRD V3.3 *** Q3LHF7_PHYPA)		F:GO:0005524; F:G(	F:ATP binding; F:UD	EC:6.3.2.8	UDP-N-acetylmuram	IPR036565 (G3DSA:3.40.1190.GENE	11,601	21,843	3,749	4,135	5,592	0,939	0,005					up		
Solyc03g007980	Site-determining protein (AHRD V3.3 *** A0A0V0I2C9_SOLCH)	MinD	F:GO:0016887	F:ATPase activity	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR010223 (TIGRFAM): G3DSA:3.40.	20,650	12,178	32,840	35,046	32,095	-0,733	0,036					down		
Solyc03g007990	Conserved peptide upstream open reading frame 14 (AHRD V3.3 *** B3H629_ARATH)							46,875	37,790	110,369	102,032	90,447									
Solyc03g008010	PPPDE putative thiol peptidase family protein (AHRD V3.3 *** AT4G25660.1)						IPR008580 (SMART): IPR008580 (PF	61,387	71,090	30,581	36,087	37,171									
Solyc03g013030	Small ubiquitin-related modifier (AHRD V3.3 *** A0A1D1Y0Z5_9ARAE)						G3DSA:3.10.20.90 (GENE3D): IPR02	26,917	24,678	27,059	26,633	26,994									
Solyc03g013160	Amino acid transporter, putative (AHRD V3.3 *** B9T0U1_RICCO)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): PTHR22950 (PAN	0,539	1,089	0,094	0,070	0,094									
Solyc03g013170	LOW QUALITY:ABC-2 type transporter family protein (AHRD V3.3 --* AT3G55110.1)							1,538	1,397	0,971	1,080	1,199									
Solyc03g013240	lysine-tRNA ligase (AHRD V3.3 *** AT3G01060.1)						IPR025638 (PFAM): IPR025638 (PAN	15,155	15,923	9,543	13,036	18,600			0,953	0,000				up	
Solyc03g013250	Imidazole glycerol phosphate synthase subunit HisH (AHRD V3.3 *** A0A1D1ZHQ6_9ARAE)						PTHR37738 (PANTHER)	8,339	12,687	13,170	12,384	13,775									
Solyc03g013260	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 *-* B6U4N2_MAIZE)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D): PTHF	0,096	0,139	0,000	0,025	0,071									
Solyc03g013270	AT hook motif-containing protein, putative, expressed (AHRD V3.3 *-* Q2QZU2_ORYSJ)						PTHR10492 (PANTHER): PTHR10492	0,021	0,000	0,000	0,025	0,000									
Solyc03g013304	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 *-* B6U4N2_MAIZE)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D): PTHF	0,079	0,021	0,025	0,000	0,047									
Solyc03g013306	Replication A 70 kDa DNA-binding subunit (AHRD V3.3 *-* A0A0B0N129_GOSAR)		F:GO:0003677; C:G(	F:DNA binding; C:membrane; C:integral component of membran			G3DSA:2.40.50.140 (GENE3D): IPR0(	0,243	0,243	0,146	0,173	0,047									
Solyc03g013308	Charged multivesicular body protein 7 (AHRD V3.3 *-* A0A0B2SF15_GLYSO)		P:GO:0007034; C:G(	P:vacuolar transport; C:integral component of membrane			PTHR22761 (PANTHER): PTHR22761	0,255	0,195	0,071	0,145	0,119									
Solyc03g013320	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 --* NU1C_OLIPU)							0,000	0,057	0,000	0,000	0,024									
Solyc03g013340	NOD26-like intrinsic protein 2.1	NIP2.1	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	55,927	33,536	0,156	0,098	0,117									
Solyc03g013430	Transcription factor IIS family protein (AHRD V3.3 --* AT5G27310.1)							3,386	3,517	4,288	3,567	4,191									
Solyc03g013440	Amino acid transporter, putative (AHRD V3.3 *** B9T0U1_RICCO)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): PTHR22950 (PAN	0,000	0,000	0,025	0,000	0,000									
Solyc03g013455	BZIP transcription factor family protein (AHRD V3.3 *-* B9IHM4_POPTR)		C:GO:0016020	C:membrane			PTHR37616 (PANTHER)	0,000	0,000	0,025	0,000	0,000									
Solyc03g013460	Cytochrome c oxidase subunit 3 (AHRD V3.3 *** K4BER7_SOLLC)		F:GO:0004129; C:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR013833 (G3DSA:1.20.120.GENE3	0,019	0,000	0,000	0,000	0,000									
Solyc03g013600	NAD(P)H-quinone oxidoreductase subunit 6, chloroplastic (AHRD V3.3 *** NU6C_SOLLC)		F:GO:0008137; P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001457 (PFAM): G3DSA:1.20.120	0,021	0,332	0,072	0,273	0,116									
Solyc03g013605	30S ribosomal protein S18, chloroplastic (AHRD V3.3 *-* RR18_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001648 (PRINTS): IPR001648 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc03g013610	50S ribosomal protein L32, chloroplastic (AHRD V3.3 *** RK32_TOBAC)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR002677 (PFAM): PTHR36083 (PAN	0,000	0,021	0,000	0,097	0,023									
Solyc03g013615	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 *** NDHI_SOLBU)		F:GO:0008137; C:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR010226 (TIGRFAM): G3DSA:3.30.	0,164	0,573	0,050	0,371	0,257									
Solyc03g013620	LOW QUALITY:NADH dehydrogenase subunit (AHRD V3.3 *-* Q8HSC3_9SOLN)		F:GO:0008137; P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	PR01434 (PRINTS): IPR018393 (PRI	0,040	0,190	0,025	0,050	0,023									
Solyc03g013630	Hexosyltransferase (AHRD V3.3 *** K4BET4_SOLLC)		F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	11,731	12,271	14,029	14,582	13,952									
Solyc03g019630	LOW QUALITY:DnaJ domain-containing protein (AHRD V3.3 *-* A0A103YDI9_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	0,362	0,055	0,000	0,000	0,023									
Solyc03g019640	LOW QUALITY:DnaJ domain-containing protein (AHRD V3.3 *** A0A103XXZ0_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	0,503	0,293	0,408	0,363	0,328									
Solyc03g019650	Major facilitator superfamily protein (AHRD V3.3 *** AT5G14120.1)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1250.20 (GENE3D): IPR(	205,061	155,450	90,214	65,063	109,632									
Solyc03g019660	Thylakoid lumenal 17.9 kDa protein (AHRD V3.3 *** G7J3V7_MEDTR)		C:GO:0009543	C:chloroplast thylakoid lumen			IPR037734 (PANTHER)	0,138	0,241	0,345	0,248	0,495									
Solyc03g019670	Non-hemolytic phospholipase C (AHRD V3.3 *** A0A0B2RKR1_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR017849 (G3DSA:3.40.720.GENE3	31,762	24,514	2,400	1,729	1,895									
Solyc03g019680	CBS domain-containing protein (AHRD V3.3 *** W9QLL8_9ROSA)		F:GO:0005515	F:protein binding			IPR000270 (SMART): IPR000644 (SM	46,353	61,377	41,904	39,544	45,110									
Solyc03g019690	Kunitz-type protease inhibitor (AHRD V3.3 *** Q3S481_SOLTU)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS): IPR002160 (SM	0,058	0,202	7,860	4,671	2,870									
Solyc03g019700	transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT5G63500.1)		C:GO:0016021	C:integral component of membrane			IPR021775 (PFAM): PTHR33128:SF1	9,598	11,066	5,219	5,145	4,892									
Solyc03g019710	TDR8	tdr8	F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	7,206	2,380	42,653	67,657	29,145			-0,552	0,003	0,668	0,004		down	up
Solyc03g019720	Carnitine operon protein caiE (AHRD)						G3DSA:2.160.10.10 (GENE3D): IPR0(	58,505	55,574	68,235	60,337	64,194									
Solyc03g019730	Ubiquitin activating enzyme (AHRD V3.3 *** O82692_SOLLC)		F:GO:0008641	F:ubiquitin-like modifier activating enzyme activity			IPR000594 (PFAM): G3DSA:3.40.50.7	19,861	19,255	31,006	29,140	27,971									
Solyc03g019740	LOW QUALITY:BRI1 suppressor 1 (BSU1)-like 2 (AHRD V3.3 --* AT1G08420.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,019	0,018	0,022	0,000	0,000									
Solyc03g019750	Alpha-1,4-glucan-protein synthase [UDP-forming] (AHRD V3.3 *** UPTG_PEA)		F:GO:0016866; P:G(	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR004901 (PIRSF): IPR037595 (PFA	0,386	2,744	0,068	0,022	0,023									
Solyc03g019760	ABC transporter G family member (AHRD V3.3 *** A0A0K9NYG1_ZOSMR)	ABCG5	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	42,594	30,943	37,639	35,650	36,969									
Solyc03g019770	Testis-expressed sequence 2 protein (AHRD V3.3 *** A0A0B2Q462_GLYSO)		F:GO:0008289	F:lipid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,139	3,856	3,174	2,869	2,588									
Solyc03g019780	40S ribosomal protein SA (AHRD V3.3 *** K4BEV0_SOLLC)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001865 (PRINTS): IPR005707 (TI(	390,144	394,972	199,138	167,251	186,551									
Solyc03g019790	alpha-galactosidase	agal	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR002241 (PRINTS): IPR013785 (G3	110,252	95,297	4,287	5,930	3,358									
Solyc03g019800	Myb domain-containing protein (AHRD V3.3 *-* W9SD24_9ROSA)		F:GO:0003677	F:DNA binding			IPR001005 (SMART): G3DSA:1.10.10	24,187	30,780	19,374	18,353	18,688									
Solyc03g019810	Ser/thr phosphatase family protein (AHRD V3.3 *** G7KPP7_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR004843 (PFAM): PTHR36492:SF2	7,703	7,061	13,213	11,685	11,739									
Solyc03g019830	Receptor kinase (AHRD V3.3 *** B6SWV2_MAIZE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR013210 (PFAM): G3DSA:3.30.200	0,000	0,000	0,000	0,050	0,024									
Solyc03g019840	DNA binding protein (AHRD V3.3 *-* AT3G52170.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,546	6,932	15,206	16,347	13,394									
Solyc03g019850	MAP kinase kinase 5	MAPKK5	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	8,458	6,640	10,754	11,082	10,504									
Solyc03g019860	minichromosome maintenance (MCM2/3/5) family protein (AHRD V3.3 --* AT5G44635.2)							0,000	0,062	0,022	0,050	0,000									
Solyc03g019870	Cytochrome P450 family protein (AHRD V3.3 *** U5FM31_POPTR)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR001128 (PRINTS): IPR002403 (PF	0,021	0,036	0,025	0,025	0,094									
Solyc03g019873	ankyrin repeat protein (AHRD V3.3 --* AT1G73350.2)						mobidb-lite (MOBIDB_LITE): PTHR372	2,823	2,427	2,402	2,252	2,264									
Solyc03g019877	TSL-kinase interacting protein 1 (AHRD V3.3 --* AT2G36960.3)							0,000	0,018	0,000	0,000	0,000									
Solyc03g019880	UPF0426 protein, chloroplastic (AHRD V3.3 *** A0A0B2Q4P7_GLYSO)						mobidb-lite (MOBIDB_LITE): PTHR359	51,133	58,337	51,116	44,878	56,939									
Solyc03g019890	beta-galactosidase 7	tbg7	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): IPR031330 (PF	17,504	36,863	7,320	13,370	11,794	1,100	0,000	0,682	0,016			up	up	
Solyc03g019900	phytochrome-associated serine/threonine-protein phosphatase 3-like		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	28,647	28,313	34,688	33,793	32,613									
Solyc03g019910	Translation initiation factor IF-2, putative isoform 2 (AHRD V3.3 *** A0A061DJU8_THECC)						PTHR37248 (PANTHER)	14,341	12,422	13,795	17,274	15,887									
Solyc03g019930	UPF0415 protein C7orf25 like (AHRD V3.3 *-* A0A0B2QSR0_GLYSO)						IPR010733 (PFAM): IPR010733 (PAN	23,213	18,853	32,569	28,344	27,586									
Solyc03g019940	Asparaginyl-tRNA synthetase family protein (AHRD V3.3 *** U5FL49_POPTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:aminoacyl-tRNA ligase activity; F:ATP			IPR002312 (PRINTS): IPR004364 (PF	44,982	54,221	73,417	66,100	77,004									
Solyc03g019950	Endosomal targeting BRO1-like domain-containing protein (AHRD V3.3 *** AT1G73390.7)						IPR004328 (SMART): IPR038499 (G3	50,746	55,350	84,700	90,592	80,372									
Solyc03g019960	CDT1-like protein a, chloroplastic (AHRD V3.3 *** A0A0B2NWY1_GLYSO)						IPR014939 (SMART): IPR014939 (PF	3,894	3,639	2,672	2,491	2,115									
Solyc03g019970	LOW QUALITY:WAS/WASL-interacting family protein (AHRD V3.3 --* AT1G55160.2)							0,040	0,083	0,022	0,000	0,000									
Solyc03g019980	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR000719 (SMA	0,019	0,000	0,000	0,000	0,000									
Solyc03g020010	miraculin		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS): IPR002160 (SM	0,021	0,078	0,025	0,125	0,094									
Solyc03g020015	Respiratory burst oxidase homolog protein C (AHRD V3.3 --* RBOHC_ARATH)						mobidb-lite (MOBIDB_LITE)	0,061	0,061	0,022	0,022	0,047									
Solyc03g020020	Embryo defective 2016, putative (AHRD V3.3 *** A0A061ETU7_THECC)		P:GO:0009793; C:G(	P:embryo development ending in seed dormancy; C:nuclear spe			IPR031801 (PFAM): mobidb-lite (MOB	93,434	66,621	64,312	72,198	71,301									
Solyc03g020030	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): IPR00	0,059	0,356	5,589	2,348	1,934									
Solyc03g020035	Miraculin-like protein 1 (AHRD V3.3 --* G0WPQ9_9ROSI)		F:GO:0004866; P:G(	F:endopeptidase inhibitor activity; P:negative regulation of endopeptidase activity				0,019	0,000	0,000	0,000	0,023									
Solyc03g020040	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): G3DS	0,084	0,021	0,000	0,000	0,096									
Solyc03g020050	VIROID-INDUCIBLE PROTEINASE INHIBITOR II		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): G3DS	2,137	2,197	0,491	0,368	0,071									
Solyc03g020060	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): G3DS	593,583	258,139	33,042	10,613	29,093					-1,633	0,000			down
Solyc03g020070	Proteinase inhibitor II (AHRD V3.3 *-* A0A075EZT7_TOBAC)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): IPR00	0,572	0,806	0,122	0,255	0,164									
Solyc03g020080	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity			G3DSA:3.30.60.30 (GENE3D): IPR00	0,194	0,276	0,101	0,123	0,166									
Solyc03g025100	Peroxidase superfamily protein (AHRD V3.3 --* AT1G68850.1)							0,059	0,019	0,000	0,119	0,140									
Solyc03g025150	Dentin sialophosphoprotein-related, putative isoform 1 (AHRD V3.3 *-* A0A061G268_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	90,257	116,620	94,007	93,137	91,804									
Solyc03g025160	Translational activator gcn1 (AHRD V3.3 *** A0A0B0PG07_GOSAR)		P:GO:0007346	P:regulation of mitotic cell cycle			mobidb-lite (MOBIDB_LITE): mobidb-lit	15,400	15,663	17,524	14,950	14,434									
Solyc03g025170	gras10	GRAS10	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; C:cytopla			IPR005202 (PFAM GRAS	110,567	65,121	104,285	127,708	110,781	-0,737	0,002					down		
Solyc03g025180	LOW QUALITY:Isoflavone-7-O-methyltransferase 8 (AHRD V3.3 --* 7OMT8_MEDSA)							0,117	0,105	0,118	0,047	0,163									
Solyc03g025190	anthocyanin permease		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (TIGRFAM): IPR002528 (F	0,097	1,115	0,050	0,000	0,023	3,392	0,000					up		
Solyc03g025200	Multidrug resistance protein mdtK (AHRD V1 **-- MDTK_PHOLL)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (TIGRFAM): IPR002528 (F	10,523	11,002	5,578	4,532	4,760									
Solyc03g025210	Mate efflux family protein (AHRD V1 **-- D7M5Q2_ARALY)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (PFAM): IPR002528 (TIGF	0,488	0,504	0,146	0,269	0,375									
Solyc03g025220	Multidrug resistance protein mdtK (AHRD V1 *--- MDTK_PHOLL)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (PFAM): IPR002528 (TIGF	4,969	6,101	2,114	1,893	1,935									
Solyc03g025230	Multidrug resistance protein mdtK (AHRD V1 *--- MDTK_YERE8)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (TIGRFAM): IPR002528 (F	21,235	13,130	10,426	7,152	9,141									
Solyc03g025240	Protein DETOXIFICATION (AHRD V3.3 *-* K4BEZ6_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (PFAM): PTHR11206 (PAN	0,117	0,099	0,000	0,000	0,023									
Solyc03g025250	Protein DETOXIFICATION (AHRD V3.3 *** K4BEZ8_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (PFAM): PTHR11206 (PAN	0,213	0,286	2,199	3,962	2,876									
Solyc03g025255	Protein DETOXIFICATION (AHRD V3.3 *-* K4BEZ8_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (PFAM): PTHR11206:SF1	0,094	0,242	2,321	2,972	2,164									
Solyc03g025270	fibrillarin 2 (AHRD V3.3 *** AT4G25630.1)		F:GO:0003723; P:G(	F:RNA binding; P:rRNA processing; F:methyltransferase activity			IPR000692 (PRINTS): IPR000692 (SM	69,881	81,690	57,356	50,924	47,852									
Solyc03g025280	RNA recognition motif (RRM)-containing protein (AHRD V3.3 *** AT5G25060.1)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing			IPR006569 (SMART): IPR000061 (SM	62,243	55,986	69,697	67,814	69,284									
Solyc03g025290	Hydroxyproline-rich glycoprotein (AHRD V3.3 *** B9I470_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	44,088	41,939	32,057	33,846	39,577									
Solyc03g025310	Sec-independent translocase protein TatA (AHRD V3.3 *** A0A0B0PZ99_GOSAR)		C:GO:0005886; F:G(	C:plasma membrane; F:protein transporter activity; P:protein se			IPR006312 (TIGRFAM): IPR003369 (F	13,699	18,251	19,004	18,622	20,061									
Solyc03g025320	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** A0A061G131_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	196,088	145,916	6,744	8,119	6,844									
Solyc03g025330	UPF0496 plant-like protein (AHRD V3.3 *** A0A072VNT1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR007749 (PFAM): PTHR31113:SF6	0,536	0,339	0,211	0,293	0,189									
Solyc03g025340	Calcium-dependent lipid-binding family protein (AHRD V3.3 *** A0A061G8B6_THECC)		C:GO:0016020	C:membrane			IPR000008 (SMART): IPR000008 (PF	287,408	309,673	314,633	322,275	338,425									
Solyc03g025350	Divalent ion symporter (AHRD V3.3 *** AT1G02260.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004680 (PFAM): PTHR43302 (PAN	2,866	1,235	1,123	0,500	0,864									
Solyc03g025360	MAP kinase kinase kinase 26	MAPKKK26	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	79,727	74,799	70,654	60,310	68,901									
Solyc03g025370	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G23420.2)						IPR002347 (PRINTS): IPR002347 (PF	0,021	0,039	0,000	0,000	0,000									
Solyc03g025380	Peroxidase (AHRD V3.3 *** K4BF11_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	1,522	1,178	1,014	1,113	1,105									
Solyc03g025390	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G23420.2)						IPR002347 (PRINTS): IPR002347 (PF	3,432	3,235	2,118	1,584	2,147									
Solyc03g025400	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G23430.2)						IPR002347 (PRINTS): G3DSA:3.40.50	2,753	3,245	2,551	2,378	2,947									
Solyc03g025410	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT4G23430.2)						IPR002347 (PRINTS): IPR002347 (PF	12,868	19,595	5,564	5,861	11,596	0,632	0,031	1,049	0,003			up	up	
Solyc03g025420	SKP1 family protein (AHRD V3.3 *** B9I474_POPTR)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR001232 (SMART): G3DSA:3.30.71	15,262	14,153	12,614	13,379	12,116									
Solyc03g025440	Zinc finger, C2H2 (AHRD V3.3 *** A0A103YJ68_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	40,531	30,701	34,335	32,455	33,635									
Solyc03g025450	Kinase family protein (AHRD V3.3 *** B9I476_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity			IPR003613 (SMART): G3DSA:3.30.20	19,262	20,077	15,825	17,366	19,037									
Solyc03g025455	U-box domain-containing family protein (AHRD V3.3 *-* B9I8K1_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity			PTHR27003 (PANTHER): PTHR27003	4,203	4,289	3,315	3,356	3,653									
Solyc03g025460	ATP binding protein, putative (AHRD V3.3 *** A0A061G233_THECC)						IPR040300 (PANTHER): PTHR34937:	1,313	1,512	0,196	0,331	0,494									
Solyc03g025470	Kinesin-like protein (AHRD V3.3 *** E5GCU2_CUCME)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,400	0,584	0,050	0,073	0,143									
Solyc03g025480	Ribosomal RNA small subunit methyltransferase E (AHRD V3.3 *** A0A061G880_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,908	4,488	8,047	7,845	8,116									
Solyc03g025490	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G23340.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,019	0,000	0,000	0,022	0,000									
Solyc03g025500	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9RIW8_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR003582 (SMART): IPR006620 (SM	9,907	7,935	8,486	8,251	8,698									
Solyc03g025510	Calmodulin-binding heat-shock protein, putative (AHRD V3.3 *** B9RIW9_RICCO)		P:GO:0016042	P:lipid catabolic process			IPR002921 (PFAM): IPR029058 (G3D	40,489	38,872	56,051	62,046	57,508									
Solyc03g025520	60S ribosomal protein L36 (AHRD V3.3 *** K4BF25_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000509 (PFAM): IPR038097 (G3D	168,614	199,486	171,971	145,342	150,111									
Solyc03g025530	Oxidoreductase/transition metal ion-binding protein, putative (AHRD V3.3 *** A0A072UAG3_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	162,713	148,841	183,185	162,951	180,291									
Solyc03g025540	Cleavage and polyadenylation specificity factor subunit 2 (AHRD V3.3 *** CPSF2_ARATH)		C:GO:0005847; P:G(	C:mRNA cleavage and polyadenylation specificity factor comple			IPR022712 (SMART): IPR001279 (SM	27,570	27,527	22,675	20,118	23,071									
Solyc03g025550	Signal peptide peptidase family protein (AHRD V3.3 *** B9I483_POPTR)		F:GO:0004190; C:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR006639 (SMART): IPR007369 (PF	56,791	51,485	78,733	70,214	67,674									
Solyc03g025560	cis-prenyltransferase 3		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR001441 (TIGRFAM): IPR036424 ((	5,826	5,411	3,473	2,942	3,555									
Solyc03g025570	DNA-directed RNA polymerase II, putative (AHRD V3.3 *** B9RKM1_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p	IPR000783 (PFAM): IPR035913 (G3D	0,473	0,507	0,919	1,793	1,833									
Solyc03g025580	LOW QUALITY:Pectinacetylesterase family protein (AHRD V3.3 *-* AT5G23870.3)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): PTHR21562:SF2	0,040	0,057	0,022	0,000	0,024									
Solyc03g025585	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A0B0NVF8_GOSAR)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21; EC:3.4.1	Acting on peptide bor	PTHR43806:SF14 (PANTHER): PTHR	13,560	11,513	10,169	10,521	10,979									
Solyc03g025600	Pectinacetylesterase family protein (AHRD V3.3 *** AT5G23870.3)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): PTHR21562:SF2	33,092	34,087	25,251	27,017	28,756									
Solyc03g025610	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A151T4Q0_CAJCA)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	59,456	50,599	45,709	46,493	47,572									

Solyc03g025613	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A0B0NVF8_GOSAR)		F:GO:0004252; P:G(	F:serine-type endoc	EC:3.4.21; EC:3.4.1	Acting on peptide bor	PTHR43806:SF14 (PANTHER); PTHR	13,913	12,023	12,673	10,320	11,700									
Solyc03g025617	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A0B2QPH0_GLYSO)		F:GO:0004252; C:G(	F:serine-type endoc	EC:3.4.21; EC:3.4.1	Acting on peptide bonds (peptidases); Acting on peptide bond		0,081	0,078	0,046	0,073	0,046									
Solyc03g025630	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A0B0NVF8_GOSAR)		F:GO:0004252; P:G(	F:serine-type endoc	EC:3.4.21; EC:3.4.1	Acting on peptide bor	G3DSA:1.25.40.710 (GENE3D)	9,057	8,599	7,079	6,328	6,866									
Solyc03g025650	Beta-1,3-glucanase (AHRD V3.3 *** Q8S2G6_ORYSJ)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM); G3DSA:3.20.20.8	0,042	0,018	0,000	0,025	0,000									
Solyc03g025660	LOW QUALITY:Plant self-incompatibility S1 (AHRD V3.3 *** A0A118JZS1_CYNCS)						IPR010264 (PFAM); PTHR31232:SF5	0,059	0,000	0,000	0,000	0,000									
Solyc03g025670	PAR1 protein (AHRD V3.3 *** AT5G52390.1)						IPR009489 (PFAM); PTHR33649:SF2	0,021	0,859	0,444	1,014	0,914									
Solyc03g025700	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** V5QPJ4_GOSHI)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	0,965	1,247	2,351	2,444	2,024									
Solyc03g025710	Acyl-CoA N-acyltransferases-like protein (AHRD V3.3 *** Q9C7G6_ARATH)		P:GO:0007064; F:G(	P:mitotic sister chrc	EC:2.3.1.5	Arylamine N-acetyltra	G3DSA:3.40.630.30 (GENE3D); IPR0(	1,547	1,745	0,334	0,291	0,820									
Solyc03g025720	4-coumarate:CoA ligase-like protein (AHRD V3.3 *** A0A0A1ETC4_ALBBR)	4CL-like	F:GO:0003824	F:catalytic activity			IPR025110 (PFAM); IPR000873 (PFA	107,218	76,353	165,729	155,788	150,182									
Solyc03g025740	Actin-depolymerizing factor (AHRD V3.3 *** A0A199VAH1_ANACO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:actin binding; F:zinc ion binding; C:acti			IPR002108 (SMART); IPR001878 (SM	5,277	6,075	3,353	3,191	3,223									
Solyc03g025760	Protein O-glucosyltransferase 1 (AHRD V3.3 *** A0A199V2E0_ANACO)		C:GO:0016021; F:G(	C:integral component of membrane; F:glucosyltransferase activ			IPR006598 (SMART); IPR006598 (PF	4,852	2,836	0,190	0,167	0,142									
Solyc03g025780	O-glucosyltransferase rumi like (AHRD V3.3 *** A0A0B2SCL3_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:glucosyltransferase activ			IPR006598 (SMART); IPR006598 (PF	0,037	0,000	0,000	0,000	0,000									
Solyc03g025790	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A072UJW0_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM); G3DSA:3.30.70.1	0,115	0,060	0,000	0,025	0,000									
Solyc03g025795	Heavy-metal-associated domain-containing protein, putative, expressed (AHRD V3.3 *** Q109F9_ORYSJ)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); IPR0(	0,000	0,000	0,025	0,000	0,000									
Solyc03g025800	Heavy metal-associated domain, putative (AHRD V3.3 *-* Q7G2B2_ORYSJ)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); mobic	0,384	0,217	0,331	0,311	0,281									
Solyc03g025810	Low-temperature-induced 65 kDa-like protein (AHRD V3.3 *-* A0A0B0MRR8_GOSAR)		P:GO:0009737	P:response to abscisic acid			IPR012418 (PFAM); mobidb-lite (MOB	1,157	1,734	4,305	5,760	4,520									
Solyc03g025820	Shortage in chiasmata 1, putative (AHRD V3.3 *** A0A061G1E9_THECC)		P:GO:0007131	P:reciprocal meiotic recombination			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,301	0,959	0,352	0,404	0,355									
Solyc03g025830	Myosin heavy chain-related protein (AHRD V3.3 *** AT5G52280.1)						IPR019448 (PFAM); mobidb-lite (MOB	4,326	4,171	4,248	11,149	5,749					1,392	0,001			up
Solyc03g025840	Cytochrome b561 (AHRD V3.3 *** Q3LGX5_CITLA)		C:GO:0016021; F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR006593 (SMART); IPR006593 (PF	26,277	29,155	59,889	75,468	86,427			0,526	0,001				up	
Solyc03g025850	remorin 1	REM1	C:GO:0005886; P:G(	C:plasma membrane; P:cell-cell signaling; F:galacturonate bindi			IPR005516 (PFAM); IPR005518 (PFA	171,809	126,561	137,523	144,670	136,242									
Solyc03g025855	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G17365.1)							0,061	0,019	0,072	0,022	0,024									
Solyc03g025860	25.3 kDa vesicle transport protein (AHRD V3.3 *** A0A151U6D5_CAJCA)		C:GO:0000139; F:G(	C:Golgi membrane; F:SNAP receptor activity; C:endoplasmic re			IPR010908 (SMART); G3DSA:3.30.45	0,424	0,361	0,047	0,215	0,118									
Solyc03g025870	R2R3MYB transcription factor 19	R2R3MYB19	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,216	0,648	0,025	0,025	0,000									
Solyc03g025880	Cleavage and polyadenylation specificity factor subunit 5 (AHRD V3.3 *** A0A0K9P6H8_ZOSMR)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cleavage factor complex; P:mRNA po			G3DSA:3.90.79.10 (GENE3D); IPR01(	20,783	25,050	26,512	29,177	27,888									
Solyc03g025890	DNA mismatch repair protein (AHRD V3.3 *** Q6DQL5_PETHY)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			IPR007696 (SMART); IPR000432 (SM	35,019	32,180	36,916	38,962	40,877									
Solyc03g025900	Flap endonuclease GEN-like protein (AHRD V3.3 *** G7KLZ3_MEDTR)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR006084 (PRINTS); IPR006086 (SM	8,656	9,088	7,568	6,675	6,784									
Solyc03g025910	transmembrane protein (AHRD V3.3 *** AT4G00585.1)		C:GO:0016021	C:integral component of membrane			PTHR34286 (PANTHER); PTHR34286	57,981	59,629	111,003	88,841	99,782									
Solyc03g025920	F-box family protein (AHRD V3.3 *** B9I4C3_POPTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); IPR(	9,499	8,008	12,581	11,020	10,299									
Solyc03g025923	Membrane steroid-binding 2-like protein (AHRD V3.3 --* A0A0B0NCY7_GOSAR)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:membrane; C:integral component of membrane				5,242	4,217	7,602	7,883	5,944									
Solyc03g025925	F-box family protein (AHRD V3.3 --* D7LS19_ARALL)							3,606	3,505	4,788	6,272	5,223									
Solyc03g025927	membrane steroid binding protein 1 (AHRD V3.3 --* AT5G52240.2)							2,329	1,855	2,719	2,909	2,832									
Solyc03g025930	F-box family protein (AHRD V3.3 *** B9I4C3_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	7,033	7,860	10,191	10,787	9,922									
Solyc03g025933	F-box/LRR-repeat protein (AHRD V3.3 *-* A0A0B2QK07_GLYSO)						PTHR44918 (PANTHER)	0,000	0,018	0,000	0,000	0,024									
Solyc03g025935	F-box family protein (AHRD V3.3 *-* D7LS19_ARALL)		F:GO:0005515	F:protein binding			PTHR44918 (PANTHER); IPR036047 (	0,019	0,021	0,025	0,000	0,000									
Solyc03g025937	Membrane steroid-binding protein (AHRD V3.3 --* G5DXK7_SILLA)							2,439	2,911	2,498	2,659	2,731									
Solyc03g025940	F-box family protein (AHRD V3.3 *** B9ID45_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	7,242	10,492	7,794	8,018	8,474									
Solyc03g025950	Membrane steroid-binding protein (AHRD V3.3 *** G5DXK7_SILLA)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			IPR001199 (SMART); IPR001199 (PF	165,251	158,189	364,167	356,715	342,674									
Solyc03g025960	LOW QUALITY:CLAVATA3/ESR (CLE)-related protein 2 (AHRD V3.3 -** CLE14_ARATH)							0,375	0,776	3,437	5,250	3,543									
Solyc03g025970	Methyl-CpG-binding domain-containing 13-like protein (AHRD V3.3 *** A0A0B0PUU8_GOSAR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			G3DSA:3.30.890.10 (GENE3D); IPR0(	18,909	20,299	74,997	109,388	72,589					0,548	0,004			up
Solyc03g025980	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NN67_ZOSMR)		F:GO:0004864; P:G(	F:protein phosphatase inhibitor activity; P:regulation of signal tr			IPR007062 (PFAM); mobidb-lite (MOB	33,148	31,865	40,947	39,154	39,291									
Solyc03g026000	cold regulated protein 27 (AHRD V3.3 --* AT5G42900.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,893	1,650	0,629	1,126	1,783									
Solyc03g026010	Transmembrane protein (AHRD V3.3 *-* A0A0B0NIL8_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR13624:SF6 (PANTHER); IPR019	6,650	6,540	5,594	6,707	6,293									
Solyc03g026020	SolycHsfB2a	HSF-03	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	117,633	92,145	172,703	179,631	157,221									
Solyc03g026030	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	0,000	0,018	0,000	0,000	0,000									
Solyc03g026040	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072VNY9_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS); SM00365 (SMAR	0,637	1,036	0,050	0,000	0,069									
Solyc03g026050	Terminal flower 1 (AHRD V3.3 *** G7ZV36_MEDTR)		C:GO:0005737; P:G(	C:cytoplasm; P:flower development; P:vegetative to reproductiv			IPR008914 (PFAM); IPR036610 (G3D	4,016	9,946	0,280	0,358	0,569	1,335	0,005					up		
Solyc03g026060	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9R9E4_RICCO)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS); IPR002110 (SM	13,273	20,181	7,847	7,472	8,361	0,630	0,040					up		
Solyc03g026070	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			IPR001356 (SMAF HD-ZIP	5,412	4,997	2,675	2,410	2,911									
Solyc03g026080	Rhomboid-like protein (AHRD V3.3 *** K4BF81_SOLLC)		F:GO:0004252; P:G(	F:serine-type endoc	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM); IPR035952 (G3D	0,594	1,004	0,170	0,396	0,189									
Solyc03g026090	Non-specific lipid-transfer protein (AHRD V3.3 *** B8LRP3_PICSI)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS); G3DSA:1.10.11	1,523	2,074	2,817	2,564	2,072									
Solyc03g026100	LOW QUALITY:Cytidine/deoxycytidylate deaminase family protein (AHRD V3.3 *** AT5G24670.4)		F:GO:0003824	F:catalytic activity			IPR002125 (PFAM); PTHR44418 (PAN	8,157	7,546	12,218	12,381	10,833									
Solyc03g026110	SUN-like protein 8	SUN8	F:GO:0005515	F:protein binding			IPR000048 (PFAM); IPR025064 (PFA	27,896	17,342	10,162	8,594	9,028									
Solyc03g026120	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G00750.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	6,273	8,695	0,093	0,541	0,355									
Solyc03g026130	Cytochrome P450 (AHRD V3.3 *** A0A0N9HM28_9MAGN)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	8,787	7,799	10,580	6,402	8,078									
Solyc03g026140	Cytochrome P450 (AHRD V3.3 *** A0A0N9HM28_9MAGN)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	6,851	7,107	2,252	1,326	2,281									
Solyc03g026150	RING/U-box superfamily protein (AHRD V3.3 *** AT3G63530.2)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			IPR001841 (SMART); IPR001841 (PF	14,086	14,691	2,804	2,306	2,442									
Solyc03g026155	inositol transporter 1 (AHRD V3.3 --* AT2G43330.1)							0,138	0,037	0,000	0,000	0,000									
Solyc03g026170	F-box protein (AHRD V3.3 *** A0A0B2QYU7_GLYSO)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR025886 (PFA	12,651	12,209	17,539	20,050	19,745									
Solyc03g026180	DNA-directed RNA polymerases II and IV subunit 5A (AHRD V3.3 --* A0A199VH08_ANACO)							10,132	9,567	14,987	14,167	14,919									
Solyc03g026190	Transcriptional corepressor SEUSS-like protein (AHRD V3.3 *** A0A0B0NMV7_GOSAR)						IPR029005 (PFAM); mobidb-lite (MOB	51,267	38,808	62,121	63,230	63,172									
Solyc03g026200	Protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB2, chloroplastic (AHRD V3.3 *** CCB2_ARATH)						IPR021325 (PFAM); PTHR36403 (PAN	10,945	10,127	5,751	6,541	6,692									
Solyc03g026210	Dihydrodipicolinate reductase-like protein (AHRD V3.3 *** A0A0F7GZT6_9ROSI)		F:GO:0008839; P:G(	F:4-hydroxy-tetrahy	EC:1.17.1.8	4-hydroxy-tetrahydro	G3DSA:3.40.50.720 (GENE3D); IPR0(	17,988	21,960	1,716	1,574	3,988			1,204	0,008				up	
Solyc03g026220	BAG family molecular chaperone regulator-like protein (AHRD V3.3 *** A0A072TGZ0_MEDTR)		F:GO:0051087	F:chaperone binding			IPR003103 (SMART); G3DSA:3.10.20	166,243	180,182	65,749	59,861	66,054									
Solyc03g026230	Protein DETOXIFICATION (AHRD V3.3 *** K4BF96_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); IPR002528 (TIGF	7,110	9,322	2,919	2,125	4,365									
Solyc03g026240	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *** B9R9G7_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spli			IPR000504 (SMART); IPR000504 (PF	29,529	36,593	21,021	21,577	23,765									
Solyc03g026250	Two-component response regulator (AHRD V3.3 *-* W9QMB4_9ROSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding			IPR001789 (SMAF ARR-B	12,474	12,536	7,928	8,993	10,348									
Solyc03g026260	TraB family protein (AHRD V3.3 *** AT5G52030.2)						IPR002816 (PFAM); PTHR21530 (PAN	24,009	34,043	10,733	12,851	20,237			0,912	0,000				up	
Solyc03g026270	CBF		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	12,804	3,789	4,694	15,285	12,400	-1,732	0,000	1,394	0,003	1,699	0,000	down	up	up
Solyc03g026280	CBF	CBF1	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	32,578	1,401	10,415	72,717	26,827	-4,510	0,000	1,360	0,001	2,801	0,000	down	up	up
Solyc03g026290	Post-GPI attachment-like factor-protein (AHRD V3.3 *** A0A072UAB4_MEDTR)		C:GO:0000139; P:G(	C:Golgi membrane; P:GPI anchor biosynthetic process; C:integ			IPR007217 (PFAM); PTHR13148:SF5	12,028	6,137	17,756	18,238	17,327	-0,940	0,001					down		
Solyc03g026300	Post-GPI attachment-like factor-protein (AHRD V3.3 *** A0A072UAB4_MEDTR)		C:GO:0000139; P:G(	C:Golgi membrane; P:GPI anchor biosynthetic process; C:integ			IPR007217 (PFAM); IPR007217 (PAN	6,709	7,500	6,414	7,231	8,540									
Solyc03g026310	ABC transporter family protein (AHRD V3.3 *-* B9ID16_POPTR)	ABCB20	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	11,365	11,782	18,424	23,422	21,269									
Solyc03g026315	ABC transporter family protein (AHRD V3.3 *** A0A072UL65_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR011527 (PF	26,689	30,924	44,115	50,569	48,821									
Solyc03g026320	ABC transporter family protein (AHRD V3.3 *-* A0A072U9U8_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); PTHF	0,078	0,019	0,022	0,120	0,024									
Solyc03g026330	ATP-dependent Clp protease ATP-binding subunit (AHRD V3.3 *** AT5G62140.1)						PTHR35320 (PANTHER)	0,201	0,387	0,125	0,245	0,354									
Solyc03g026340	Calcium-dependent protein kinase, putative (AHRD V3.3 *-* B9R9H6_RICCO)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	PTHR24349:SF111 (PANTHER); PTHF	24,426	22,458	22,411	24,736	20,104									
Solyc03g026345	Kinase family protein (AHRD V3.3 *** B9GW56_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	49,901	38,616	39,209	41,297	38,180									
Solyc03g026350	Zinc finger transcription factor 24	C3H24	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding			IPR020472 (PRIN C3H	35,866	32,193	49,828	48,858	47,656									
Solyc03g026370	LOW QUALITY:Peptidoglycan-binding LysM domain-containing protein (AHRD V3.3 *** A0A061G7P2_THEC		C:GO:0016021	C:integral component of membrane			IPR018392 (PFAM); PTHR33648 (PAN	3,500	2,533	3,250	3,110	3,335									
Solyc03g026400	F-box family protein (AHRD V3.3 *** B9I4C3_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc03g031420	LOW QUALITY:Molybdenum cofactor sulfurase (AHRD V3.3 *** A0A0B2Q7C8_GLYSO)		F:GO:0003824	F:catalytic activity			IPR015421 (G3DSA:3.40.640.GENE3	46,944	56,913	10,984	18,041	17,019			0,630	0,019	0,718	0,003		up	up
Solyc03g031430	urease accessory protein F	uref	P:GO:0006807; F:G(	P:nitrogen compound metabolic process; F:nickel cation binding			IPR038277 (G3DSA:1.10.4190.GENE	0,096	0,062	0,287	0,750	0,450									
Solyc03g031440	Quinone reductase family protein (AHRD V3.3 *** AT4G27270.1)		F:GO:0003955; F:G(	F:NAD(P)H dehydrc	EC:1.6.5.2	NAD(P)H dehydroger	IPR029039 (G3DSA:3.40.50.GENE3D	1,312	1,431	7,355	13,738	5,715					0,908	0,000			up
Solyc03g031450	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G61660.7)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,000	0,019	0,000	0,000	0,071									
Solyc03g031470	Anthocyanidin reductase (AHRD V3.3 *** D5LMJ0_CAMSI)		F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM); G3DSA:3.40.50.7	0,701	0,793	0,136	0,101	0,189									
Solyc03g031490	Metallocarboxypeptidase inhibitor (AHRD V3.3 -** O24639_SOLTU)		F:GO:0004866; P:G(	F:endopeptidase inhibitor activity; P:negative regulation of endc			IPR009632 (PRODOM)	0,000	0,000	0,000	0,025	0,000									
Solyc03g031530	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT1G61740.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM); PTHR14255:SF3	0,019	0,058	0,025	0,025	0,000									
Solyc03g031560	Trimeric LpxA-like enzymes superfamily protein, putative isoform 3 (AHRD V3.3 *** A0A061GGP4_THECC)		P:GO:0009245; F:G(	P:lipid A biosynthetic process; F:N-acyltransferase activity			G3DSA:2.160.10.10 (GENE3D); IPR0(	2,373	2,418	1,929	0,959	1,693									
Solyc03g031570	Auxin induced-like protein (AHRD V3.3 *-* E0Z5W7_PICSI)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART); IPR017214 (PIF	0,076	0,021	0,000	0,000	0,000									
Solyc03g031600	Peroxisomal membrane protein PMP22 (AHRD V3.3 *** A0A0B0NRG7_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM); PTHR11266:SF7	22,387	29,691	15,181	15,090	20,263									
Solyc03g031620	5'-adenylylsulfate reductase (AHRD V3.3 *** A0A072V4H5_MEDTR)		F:GO:0016671; P:G(	F:oxidoreductase activity, acting on a sulfur group of donors, di			IPR014729 (G3DSA:3.40.50.GENE3D	16,363	20,712	42,838	48,616	45,531									
Solyc03g031630	Calcium-binding EF-hand family protein (AHRD V3.3 *** A0A061DTS7_THECC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,037	0,082	0,044	0,047	0,093									
Solyc03g031650	Autophagy-related protein (AHRD V3.3 *** K4Q337_PETHY)		C:GO:0005737; P:G(	C:cytoplasm; P:autophagy; P:cellular response to nitrogen starv			IPR004241 (PFAM); G3DSA:3.10.20.9	12,583	8,328	15,979	16,210	12,094									
Solyc03g031655	Far1-related sequence 11 isoform 3 (AHRD V3.3 --* A0A061EWP7_THECC)							0,021	0,039	0,000	0,050	0,000									
Solyc03g031660	LOW QUALITY:Homer protein isoform 2 (AHRD V3.3 *-* A0A061GHT7_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,039	0,097	0,000	0,047									
Solyc03g031670	calcium-dependent protein kinase	cpk1	F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (SMART); IPR000719 (SM	57,290	69,705	80,805	80,586	77,469									
Solyc03g031680	GPI-anchored protein (AHRD V3.3 *** AT2G30700.2)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			PTHR33831:SF2 (PANTHER); IPR040	7,960	6,367	3,097	3,096	3,676									
Solyc03g031690	DNA-directed RNA polymerases I, II, and III subunit RPABC3 (AHRD V3.3 *** A0A1D1YZS2_9ARAE)		P:GO:0006351	P:transcription, DNA-templated			IPR005570 (SMART); G3DSA:2.40.50	34,046	30,388	59,405	59,167	50,759									
Solyc03g031700	ATP-binding-cassette transporter family protein (AHRD V3.3 *** B9H1C6_POPTR)		P:GO:0016226	P:iron-sulfur cluster assembly			IPR010231 (TIGRFAM); IPR000825 (F	29,651	27,932	52,489	48,103	58,046									
Solyc03g031720	RNA-binding family protein (AHRD V3.3 *** A0A061FD24_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR000504 (PF	37,868	37,029	26,963	25,032	25,628									
Solyc03g031730	Beta-glucosidase, putative (AHRD V3.3 *** B9RXP7_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); G3DSA:3.20.2(	0,255	0,181	0,022	0,000	0,023									
Solyc03g031740	Glucose-6-phosphate/phosphate-translocator family protein (AHRD V3.3 *-* U5GXN4_POPTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:hydrolase activity, hydrolyzing O-glyco			IPR000504 (SMART); IPR004696 (TIG	0,242	0,138	0,261	0,216	0,281									
Solyc03g031750	Vacuolar protein sorting-associated protein VPS28 family protein (AHRD V3.3 *** AT4G05000.3)		C:GO:0000813; P:G(	C:ESCRT I complex; P:endosome transport via multivesicular bo			IPR038358 (G3DSA:1.20.1440.GENE	36,395	44,140	60,002	70,712	64,837									
Solyc03g031755	26S proteasome non-ATPase regulatory subunit 6 homolog (AHRD V3.3 --* PSMD6_ARATH)							0,019	0,021	0,025	0,000	0,023									
Solyc03g031760	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GU68_POPTR)		F:GO:0008289	F:lipid binding			IPR002913 (SMART); IPR023393 (G3	1,792	1,933	0,211	0,441	0,118									
Solyc03g031780	50S ribosomal protein L2, chloroplastic (AHRD V3.3 --* RK2_ILLOL)		P:GO:0007142	P:male meiosis II			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,339	0,480	0,212	0,144	0,071									
Solyc03g031790	Oligosaccharyltransferase complex/magnesium transporter family protein (AHRD V3.3 *** AT1G61790.2)		F:GO:0004579; C:G(	F:dolichyl-diphosph	EC:2.4.1.119	Glycosyltransferases	IPR021149 (PFAM); G3DSA:3.40.30.1	84,222	94,701	94,296	89,153	85,706									
Solyc03g031800	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4BFF2_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR008264 (PRINTS); IPR010713 (PF	48,384	54,535	1,177	0,412	0,471									
Solyc03g031820	tyrosyl-DNA phosphodiesterase-like protein (AHRD V3.3 *** AT5G15170.1)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; C:nucleu			G3DSA:3.30.870.10 (GENE3D); G3DS	17,040	11,906	22,819	21,902	20,702									
Solyc03g031830	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03965.1)						IPR001841 (SMART); IPR013083 (G3	0,746	0,750	1,108	1,333	0,939									
Solyc03g031840	expansin precursor 3	EXPA3	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS); IPR002963 (PF	232,320	134,040	118,349	68,829	85,680	-0,765	0,003	-0,469	0,002	-0,778	0,000	down	down	down
Solyc03g031850	LOW QUALITY:Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein (AHRD V3.3 *** AT3G03210.1)		C:GO:0016021	C:integral component of membrane			PTHR13533 (PANTHER); PTHR13533	4,577	3,888	22,247	22,098	16,340									
Solyc03g031860	Phytoene synthase 1	PSY1	F:GO:0004310; P:G(	F:farnesyl-diphosph	EC:2.5.1.29; EC:2.5.	Geranylgeranyl diphc	PF00494 (PFAM); IPR008949 (G3DS/	55,419	69,948	6126,691	6217,249	5306,645									
Solyc03g031870	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)		F:GO:0003824	F:catalytic activity			IPR025110 (PFAM); G3DSA:3.30.300	0,000	0,064	0,000	0,000	0,000									
Solyc03g031880	Amine oxidase family protein (AHRD V3.3 *** B9H3J5_POPTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001613 (PRINTS); IPR002937 (PF	0,334	0,264	0,243	0,249	0,330									
Solyc03g031890	Oxidative stress 3, putative isoform 2 (AHRD V3.3 *** A0A061GIQ6_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,664	1,852	1,556	3,626	2,153					1,223	0,002			up
Solyc03g031900	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061E		F:GO:0004386; F:G(	F:helicase activity;	EC:3.6.1.15	Nucleoside-triphosph	PF13087 (PFAM); G3DSA:3.40.50.30(	0,019	0,043	0,000	0,000	0,000									
Solyc03g031910	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061E		F:GO:0004386; F:G(	F:helicase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D); PF13	7,655	49,996	3,870	8,691	5,439	2,729	0,000			1,172	0,000	up		up
Solyc03g031920	Oligopeptide transporter, putative (AHRD V3.3 *** B9SIR4_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (TIGRFAM); IPR004813 (F	17,663	32,902	118,730	192,164	132,693	0,922	0,020			0,699	0,001	up		up
Solyc03g031940	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT1G21540.1)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM); G3DSA:3.30.300	4,894	2,536	0,545	0,047	0,048									
Solyc03g031950	transmembrane protein (AHRD V3.3 *** AT1G65720.1)		C:GO:0016021	C:integral component of membrane			PTHR35107:SF2 (PANTHER); PTHR3!	198,334	185,020	309,839	307,135	282,718									
Solyc03g031970	Auxin response factor (AHRD V3.3 *** A0A191T8S7_SALMI)	ARF8A	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF ARF	115,402	114,898	67,443	66,840	73,194									
Solyc03g031980	Clade XVI lectin receptor kinase (AHRD V3.3 *** K4BFG9_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR001245 (PF	0,255	1,865	0,097	0,267	0,446									
Solyc03g031990	Auxin efflux carrier family protein (AHRD V3.3 *** AT1G20925.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM); mobidb-lite (MOB	0,272	0,649	0,115	0,192	0,165									
Solyc03g032000	Thioredoxin reductase (AHRD V3.3 *** K4BFH1_SOLLC)		F:GO:0004791; C:G(	F:thioredoxin-disulfi	EC:1.8.1.9	Thioredoxin-disulfide	IPR000103 (PRINTS); PR00368 (PRIN	27,213	27,172	31,147	24,347	26,855									
Solyc03g032010	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3 (AHRD V3.3 *** HMDH3_SOLTU)		F:GO:0004420; P:G(	F:hydroxymethylglut	EC:1.1.1.34	Hydroxymethylglutary	IPR002202 (PRINTS); IPR009023 (G3	14,005	14,285	32,330	36,591	34,531									
Solyc03g032020	3-hydroxy-3-methylglutaryl coenzyme A reductase (AHRD V3.3 *** K4BFH3_SOLLC)		F:GO:0004420; P:G(	F:hydroxymethylglut	EC:1.1.1.34	Hydroxymethylglutary	IPR002202 (PRINTS); IPR004554 (TI(	3,866	4,380	14,639	19,562	17,580									
Solyc03g032030	Phosphate carrier protein, mitochondrial (AHRD V3.3 *** A0A0B2RN43_GLYSO)		F:GO:0022857	F:transmembrane transporter activity			IPR018108 (PFAM); IPR023395 (G3D	3,046	3,352	3,322	4,019	2,468									
Solyc03g032035	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD V3.3 --* AT1G11100.5)							0,140	0,149	0,462	1,045	0,493									
Solyc03g032040	Tonoplast monosaccharide transporter 1	TMT1	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); G3DSA:1.20.12	46,045	44,943	29,823	58,061	34,016					0,965	0,000			up
Solyc03g032050	GTP binding protein (AHRD V3.3 *** AT5G65960.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001806 (PFAM); PF10199 (PFAM)	22,702	20,306	24,491	23,732	25,368									
Solyc03g032060	RING/U-box superfamily protein (AHRD V3.3 *** AT1G20823.1)		C:GO:0016021	C:integral component of membrane			SM01197 (SMART); IPR001841 (SMA	8,783	5,536	12,978	9,441	11,570									
Solyc03g032070	RuvB-like helicase (AHRD V3.3 *** K4BFH8_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:In	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR010339 (PF	52,935	42,319	57,943	47,297	49,471									
Solyc03g032080	Auxin efflux carrier family protein (AHRD V3.3 *** AT2G17500.4)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM); PTHR31651:SF3	0,239	0,223	0,290	0,433	0,257									
Solyc03g032090	Amino acid transporter, putative (AHRD V3.3 *** B9S6V9_RICCO)		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM); PTHR22950:SF4(	11,251	11,326	50,099	66,457	51,148					0,409	0,029			up
Solyc03g032100	Phosphoenolpyruvate carboxylase 1 (AHRD V3.3 --* CAPP1_MAIZE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	5,310	5,192	6,217	7,034	6,090									
Solyc03g032110	RB1-inducible coiled-coil protein 1, putative isoform 1 (AHRD V3.3 *** A0A061DFH3_THECC)		F:GO:0098519	F:nucleotide phosphatase activity, acting on free nucleotides			IPR025486 (PFAM); IPR032795 (PFA	0,019	0,036	0,046	0,025	0,000									
Solyc03g032120	Cancer-related nucleoside-triphosphatase-like protein (AHRD V3.3 *** G7K184_MEDTR)		F:GO:0098519	F:nucleotide phosphatase activity, acting on free nucleotides			G3DSA:3.40.50.300 (GENE3D); IPR0(	2,203	1,634	1,292	1,693	1,484									
Solyc03g032130	High mobility group protein (AHRD V3.3 *-* O49948_SOLTU)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR036910 (G3DSA:1.10.30.GENE3D	351,811	359,493	386,354	342,831	353,562									
Solyc03g032140	Heterogeneous nuclear ribonucleoprotein, putative (AHRD V3.3 *** B9S6U9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR012677 (G3	21,488	21,777	21,629	18,806	20,158									
Solyc03g032150	Kinase family protein (AHRD V3.3 *** U5GGQ9_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); IPR000719 (F	87,066	103,619	34,916	42,453	45,235									

Solyc03g032160	Ubiquitin 1, related protein (AHRD V3.3 *** G7K017_MEDTR)		F:GO:0005515	F:protein binding	IPR015940 (SMART): IPR000626 (SM	81,241	71,973	121,217	113,424	115,618									
Solyc03g032170	Potassium channel AKT2/3 (AHRD V3.3 --* AKT2_ARATH)		F:GO:0016740	F:transferase activity		0,175	0,169	0,329	0,571	0,259									
Solyc03g032180	Poly(A) polymerase, putative (AHRD V3.3 *** B9S6T6_RICCO)		F:GO:0003723; P:GO	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti	IPR002646 (PFAM): IPR032828 (PFA	11,125	10,712	15,209	17,184	15,740									
Solyc03g032190	cyclinB2_7	CycB2_7	C:GO:0005634	C:nucleus	IPR013763 (SMART): IPR004367 (SM	0,400	0,402	0,000	0,025	0,000									
Solyc03g032210	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity	IPR000873 (PFAM): G3DSA:3.40.50.1	5,142	5,076	2,316	2,211	3,147									
Solyc03g032220	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** A2PZD5_IPONI)		F:GO:0008171	F:O-methyltransferase activity	G3DSA:3.40.50.150 (GENE3D): IPR0	0,176	0,119	0,071	0,050	0,000									
Solyc03g032230	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA86_MEDTR)				IPR004320 (PFAM): mobidb-lite (MOB	0,037	0,000	0,000	0,000	0,000									
Solyc03g032240	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NYV5_ZOSMR)		P:GO:0006812; F:GO	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR038770 (G3DSA:1.20.1530.GENE	2,392	3,726	3,629	4,331	5,294									
Solyc03g033245	embryo defective 2737 (AHRD V3.3 --* AT5G53860.3)					0,019	0,039	0,025	0,025	0,116									
Solyc03g033260	Maltose excess protein 1 (AHRD V3.3 *-* A0A0C5DIX1_CAMSI)		F:GO:0005363; C:GO	F:maltose transmembrane transporter activity; C:chloroplast env	IPR034628 (PANTHER)	0,838	0,652	0,449	0,474	0,779									
Solyc03g033270	Maltose excess protein 1-like protein (AHRD V3.3 *** S8DX10_9LAMI)		F:GO:0005363; C:GO	F:maltose transmembrane transporter activity; C:chloroplast env	IPR034628 (PANTHER)	1,850	1,245	1,518	1,438	1,785									
Solyc03g033280	LOW QUALITY:tracheary element differentiation-related 6 (AHRD V3.3 *** AT1G43790.1)		P:GO:0009834; C:GO	P:plant-type secondary cell wall biogenesis; C:integral compone	PTHR35697 (PANTHER): PTHR35697	0,100	0,156	0,000	0,000	0,047									
Solyc03g033290	LOW QUALITY:tracheary element differentiation-related 6 (AHRD V3.3 *** AT1G43790.1)		C:GO:0016021	C:integral component of membrane	PTHR35697:SF1 (PANTHER): PTHR3	0,000	0,021	0,000	0,000	0,000									
Solyc03g033310	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT4G35785.2)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	22,722	24,777	38,649	34,289	35,013									
Solyc03g033320	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9SXB7_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR006620 (SMART): IPR005123 (PF	25,303	22,904	22,205	20,018	21,842									
Solyc03g033330	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DF87_THECC)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART): IPR025693 (PF	9,617	9,226	5,418	3,104	6,209					-0,795	0,027			down
Solyc03g033340	Phosphatase 2C family protein (AHRD V3.3 *** A9PFH7_POPTR)		F:GO:0004722; P:GO	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	29,223	30,035	50,346	54,950	51,268									
Solyc03g033350	Aspartyl protease family protein (AHRD V3.3 *-* S8EJ88_9LAMI)		F:GO:0004190; P:GO	F:aspartic-type end EC:3.4.23 Acting on peptide bor	PTHR13683:SF232 (PANTHER): IPR0	1,417	1,045	0,696	0,802	0,567									
Solyc03g033360	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT2G17760.1)		F:GO:0004190; P:GO	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR032799 (PFAM): IPR021109 (G3D	0,495	0,467	0,209	0,286	0,190									
Solyc03g033370	Protein preY, mitochondrial, putative (AHRD V3.3 *** B9SYS9_RICCO)		C:GO:0000506; C:GO	C:glycosylphosphatidylinositol-N-acetylglucosaminyltransferase	IPR005651 (PFAM): G3DSA:2.20.25.1	1,981	1,683	1,425	1,394	1,295									
Solyc03g033380	SPla/RYanodine receptor (SPRY) domain-containing protein (AHRD V3.3 *** AT1G35470.2)		F:GO:0005515	F:protein binding	IPR006595 (SMART): IPR013144 (SM	26,490	22,909	34,292	34,256	32,066									
Solyc03g033390	F-box family protein (AHRD V3.3 *** A0A061DGH5_THECC)		F:GO:0005515	F:protein binding	mobidb-lite (MOBIDB_LITE): PTHR340	4,521	4,180	1,336	0,493	0,776					-1,385	0,026			down
Solyc03g033400	Vacuolar protein sorting-associated protein 35 (AHRD V3.3 *** K4BFL2_SOLLC)		P:GO:0015031; C:GO	P:protein transport; C:retromer, cargo-selective complex; P:retro	G3DSA:1.25.40.660 (GENE3D): IPR0	41,057	46,070	46,384	48,733	48,773									
Solyc03g033410	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A172S1R1_NICBE)		F:GO:0005524; P:GO	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e	SM00212 (SMART): IPR000608 (PFAI	2,531	1,836	4,408	2,698	3,862									
Solyc03g033420	ROP GTPases family protein		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	28,862	27,527	22,834	22,512	24,551									
Solyc03g033440	LOW QUALITY:ATP synthase subunit alpha (AHRD V3.3 *-* U5HSR4_SILVU)		F:GO:0005524; C:GO	F:ATP binding; C:mi EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): mobic	0,000	0,207	0,050	0,152	0,163									
Solyc03g033450	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *** A0A097PSE7_TI		F:GO:0008168	F:methyltransferase activity	IPR023269 (PRINTS): IPR023267 (PF	17,184	16,209	20,472	25,768	19,830									
Solyc03g033460	Oligopeptide transporter, putative (AHRD V3.3 *** B9SUI4_RICCO)		P:GO:0055085	P:transmembrane transport	IPR004648 (TIGRFAM): IPR004813 (T	1,863	2,010	0,913	1,701	1,808									
Solyc03g033470	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G35987.1)		C:GO:0005737; F:GO	C:cytoplasm; F:calr EC:2.1.1.6 Calmodulin-lysine N-(	G3DSA:3.40.50.150 (GENE3D): IPR0	0,000	0,082	0,075	0,098	0,257									
Solyc03g033480	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G35987.1)		C:GO:0005737; F:GO	C:cytoplasm; F:calr EC:2.1.1.6 Calmodulin-lysine N-(	G3DSA:3.40.50.150 (GENE3D): IPR0	4,595	3,526	6,414	5,699	6,217									
Solyc03g033490	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** O65638_ARATH)		C:GO:0016021	C:integral component of membrane	IPR001938 (PRINTS): IPR001938 (SM	0,122	0,191	0,143	0,170	0,212									
Solyc03g033500	Zinc knuckle family protein (AHRD V3.3 *-* A0A061FDW4_THECC)		F:GO:0003676; F:GO	F:nucleic acid binding; F:zinc ion binding	IPR001878 (SMART): G3DSA:4.10.60	9,533	12,887	14,589	11,348	11,016									
Solyc03g033510	Armadillo repeat only (AHRD V3.3 *** W0TQK6_ACAMN)		F:GO:0005515	F:protein binding	IPR000225 (SMART): IPR011989 (G3	23,296	12,417	8,795	8,124	9,876	-0,879	0,001					down		
Solyc03g033520	LOW QUALITY:Maturase-like protein (AHRD V3.3 *** Q9LZA5_ARATH)		P:GO:0006397	P:mRNA processing	IPR024937 (PFAM): PTHR33642:SF1	4,565	4,389	5,844	4,943	5,330									
Solyc03g033530	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *** A0A0V0IEZ0_SOLCH)		F:GO:0004518; P:GO	F:nuclease activity; P:DNA repair; F:zinc ion binding	IPR005135 (PFAM): IPR010666 (PFA	3,054	2,325	3,528	4,016	4,003									
Solyc03g033535	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *-* A0A0V0IEZ0_SOLCH)		F:GO:0004518; P:GO	F:nuclease activity; P:DNA repair	IPR005135 (PFAM): IPR036691 (G3D	1,409	1,065	1,320	1,851	1,392									
Solyc03g033540	calcium-dependent protein kinase2	LeCPK2	F:GO:0004672; F:GO	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR000719 (SMART): IPR002048 (SM	237,779	387,005	51,675	57,335	76,961									
Solyc03g033550	WEB family protein (AHRD V3.3 *** A0A0B2SGS1_GLYSO)		C:GO:0005829; P:GO	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac	PTHR32054 (PANTHER): PTHR32054	0,119	0,380	0,122	0,025	0,070									
Solyc03g033560	Zinc finger family protein (AHRD V3.3 *** B9MXH1_POPTR)		F:GO:0003723; C:GO	F:RNA binding; C:nucleus; P:response to abscisic acid; F:metal	IPR001876 (SMART): IPR001876 (PF	60,577	53,645	55,492	51,927	56,600									
Solyc03g033580	polyamine-modulated factor 1-binding protein (AHRD V3.3 *** AT2G17990.3)		P:GO:0009639; P:GO	P:response to red or far red light; P:negative gravitropism	IPR040225 (PANTHER): PTHR31161:	31,491	35,740	36,991	39,508	38,778									
Solyc03g033590	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G34760.1)		P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	0,000	0,082	0,000	0,022	0,048									
Solyc03g033600	Small nuclear ribonucleoprotein (AHRD V3.3 *** G7LBD3_MEDTR)		P:GO:0000387; C:GO	P:spliceosomal snRNP assembly; C:spliceosomal complex	IPR001163 (SMART): IPR001163 (PF	18,066	19,406	30,188	28,708	26,088									
Solyc03g033610	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BFN3_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR003591 (SMART): IPR000719 (SM	1,428	1,006	0,319	0,959	0,564									
Solyc03g033620	Serine carboxypeptidase S28 family protein (AHRD V3.3 *** AT4G36195.3)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity	IPR008758 (PFAM): IPR029058 (G3D	37,602	32,408	57,579	58,551	59,540									
Solyc03g033630	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *** A0A0B2RNF7_GLYSO)		F:GO:0005515	F:protein binding	IPR003169 (SMART): IPR001965 (SM	53,541	55,334	71,477	66,289	62,726									
Solyc03g033640	Transmembrane and coiled-coil domain-containing protein 4 (AHRD V3.3 *** A0A151R318_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR029058 (G3DSA:3.40.50.GENE3D	40,353	39,024	111,436	109,311	103,523									
Solyc03g033650	altered inheritance of mitochondria protein (AHRD V3.3 *** AT3G51100.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	22,728	18,490	28,568	29,637	28,827									
Solyc03g033660	GATA transcription factor (AHRD V3.3 *** K4BFN8_SOLLC)		F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ion	IPR000679 (SMAF GATA	6,106	6,218	0,115	0,336	0,143									
Solyc03g033690	Peroxidase (AHRD V3.3 *** K4BFP1_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	3,363	2,100	0,118	0,613	0,188									
Solyc03g033720	HECT-like ubiquitin-conjugating enzyme (E2)-binding protein (AHRD V3.3 *** AT3G26750.1)				IPR019193 (PFAM): IPR019193 (PAN	3,417	3,009	1,879	2,068	1,936									
Solyc03g033730	LOW QUALITY:BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc	IPR004827 (SMAF bZIP	0,644	0,153	0,047	0,072	0,070									
Solyc03g033740	Proteasome subunit beta type (AHRD V3.3 *-* M1C263_SOLTU)		F:GO:0004298; C:GO	F:threonine-type en EC:3.4.25 Acting on peptide bor	PTHR11599 (PANTHER): IPR035202	1,895	1,324	1,698	1,474	1,907									
Solyc03g033745	Proteasome subunit beta type (AHRD V3.3 *-* M1C263_SOLTU)		F:GO:0004298; C:GO	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	1,109	0,707	0,701	0,956	0,798									
Solyc03g033770	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT3G50940.1)		F:GO:0000166; F:GO	F:nucleotide binding; F:ATP binding	IPR025753 (PFAM): PTHR23070:SF8	0,021	0,018	0,000	0,000	0,000									
Solyc03g033790	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): IPR003959 (PF	0,285	1,037	0,050	0,217	0,235									
Solyc03g033810	F-box/RNI-like superfamily protein (AHRD V3.3 --* AT3G03040.1)					0,510	0,566	0,682	0,668	0,638									
Solyc03g033813	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT5G57480.1)		F:GO:0005524	F:ATP binding	PTHR23070 (PANTHER): PTHR23070	0,000	0,000	0,000	0,025	0,024									
Solyc03g033815	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G17760.2)		F:GO:0000166; F:GO	F:nucleotide binding; F:ATP binding		0,158	0,177	0,243	0,116	0,095									
Solyc03g033817	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT3G50940.1)		F:GO:0000166	F:nucleotide binding	IPR025753 (PFAM): PTHR23070:SF8	0,000	0,000	0,000	0,000	0,023									
Solyc03g033820	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): IPR003959 (PF	0,315	0,187	0,115	0,361	0,235									
Solyc03g033825	Ubiquitin-related modifier 1 homolog (AHRD V3.3 --* URM1_ORYSJ)					0,515	0,546	0,458	0,590	0,707									
Solyc03g033830	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 *-* G7I744_MEDTR)				IPR025558 (PFAM): PTHR34427 (PAN	0,855	0,821	0,644	0,508	1,129									
Solyc03g033835	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT3G50940.1)		F:GO:0000166; F:GO	F:nucleotide binding; F:ATP binding	IPR025753 (PFAM): PTHR23070 (PAN	0,117	0,165	0,091	0,075	0,000									
Solyc03g033840	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): G3DSA:3.40.50	0,925	4,455	0,824	1,808	1,527	2,279	0,000					up		
Solyc03g033850	Syntaxin-81-like protein (AHRD V3.3 *** A0A0B0PVL2_GOSAR)		C:GO:0016020; P:GO	C:membrane; P:vesicle-mediated transport	G3DSA:1.20.5.110 (GENE3D): IPR01	6,689	7,123	7,854	8,285	7,323									
Solyc03g033860	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072TTD0_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR33640:SF1 (PANTHER): PTHR3	0,019	0,039	0,000	0,000	0,000									
Solyc03g033910	LOW QUALITY:Thylakoid lumenal 17.9 kDa protein, chloroplastic (AHRD V3.3 --* TL1Y_ARATH)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc03g033920	LOW QUALITY:Signal transduction histidine kinase, hybrid-type, ethylene sensor (AHRD V3.3 --* AT3G04580.2)					0,037	0,000	0,000	0,000	0,000									
Solyc03g033950	pre-mRNA-splicing factor of RES complex protein (AHRD V3.3 *** AT1G31870.2)		C:GO:0005634; C:GO	C:nucleus; C:cytosol	IPR018609 (PFAM): mobidb-lite (MOB	147,219	135,099	101,755	94,845	98,391									
Solyc03g033980	Tubby-like F-box protein (AHRD V3.3 *** K4BFS0_SOLLC)		F:GO:0005515	F:protein binding	IPR000007 (PRINTS): IPR001810 (PF	24,275	24,489	15,064	12,442	14,544									
Solyc03g033990	Cytochrome c-type biogenesis protein CcmE (AHRD V3.3 *** A0A1D1XQ32_9ARAE)		C:GO:0005886; P:GO	C:plasma membrane; P:protein-heme linkage; P:cytochrome com	IPR004329 (PFAM): G3DSA:2.40.50.1	10,821	10,905	13,235	12,987	12,656									
Solyc03g034000	bHLH transcription factor 020		P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,078	0,249	0,100	0,256	0,259									
Solyc03g034010	U-box domain-containing family protein (AHRD V3.3 *-* U5GHQ7_POPTR)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination	PTHR22849:SF40 (PANTHER): PTHR2	0,768	1,011	2,102	2,246	2,042									
Solyc03g034020	U-box domain-containing family protein (AHRD V3.3 *** U5GHQ7_POPTR)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR003613 (SMART): IPR003613 (PF	4,124	17,756	2,988	3,302	3,794	2,131	0,000					up		
Solyc03g034030	Late embryogenesis abundant (LEA) protein (AHRD V3.3 -** AT4G36600.2)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,194	0,230	0,173	0,350	0,023									
Solyc03g034050	MIP18 family protein (AHRD V3.3 *** A0A0B2SB63_GLYSO)		P:GO:0016226	P:iron-sulfur cluster assembly	IPR034904 (G3DSA:3.30.300.GENE3	9,530	10,894	12,747	10,582	11,279									
Solyc03g034057	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G08450.2)					0,019	0,000	0,047	0,097	0,046									
Solyc03g034060	Kinase family protein (AHRD V3.3 *** U5GFC9_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR001245 (PF	0,154	0,463	0,050	1,430	0,678									
Solyc03g034080	Acidic leucine-rich nuclear phosphoprotein 32-related protein (AHRD V3.3 *** W9RLR5_9ROSA)		F:GO:0005515	F:protein binding	PF14580 (PFAM): IPR032675 (G3DSA	117,111	147,579	129,337	127,375	127,574									
Solyc03g034090	Sugar transporter, putative (AHRD V3.3 *** A0A061DGB7_THECC)		C:GO:0016021	C:integral component of membrane	IPR010608 (PFAM): PTHR34358:SF2	4,999	4,904	4,179	4,698	4,309									
Solyc03g034100	ovate family protein 6	OFP6	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (TIGRFAM): IPR006458 (F	0,237	0,410	0,693	1,232	0,758									
Solyc03g034120	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MXR7_POPTR)		F:GO:0003677	F:DNA binding	IPR000047 (PRIN HD-ZIP	0,000	0,000	0,025	0,000	0,000									
Solyc03g034140	Quinone reductase family protein (AHRD V3.3 *** AT4G36750.1)		F:GO:0003955; F:GO	F:NAD(P)H dehydrc EC:1.6.5.2 NAD(P)H dehydroger	IPR029039 (G3DSA:3.40.50.GENE3D	1,405	1,449	23,668	24,829	17,642									
Solyc03g034150	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MXR7_POPTR)		F:GO:0003677	F:DNA binding	IPR000047 (PRIN HD-ZIP	0,000	0,000	0,000	0,000	0,024									
Solyc03g034160	fanconi anemia group D2 protein (AHRD V3.3 --* AT4G14970.6)				mobidb-lite (MOBIDB_LITE)	0,136	0,142	0,169	0,097	0,069									
Solyc03g034165	downstream target of AGL15-4 (AHRD V3.3 --* AT1G79760.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,276	0,204	0,507	0,288	0,308									
Solyc03g034170	acclimation of photosynthesis to environment (AHRD V3.3 *** AT5G38660.1)		C:GO:0016021	C:integral component of membrane	IPR021275 (PFAM): IPR021275 (PAN	8,313	14,220	5,695	6,627	14,588	0,802	0,041	1,346	0,000			up	up	
Solyc03g034180	14-3-3-like protein (AHRD V3.3 *** 14331_SOLTU)		F:GO:0019904	F:protein domain specific binding	IPR000308 (PRINTS): IPR023410 (SM	37,718	42,077	63,715	57,726	60,565									
Solyc03g034190	30S ribosomal protein 3 (AHRD V3.3 *** W9SB90_9ROSA)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038447 (G3DSA:1.20.58.GENE3D	7,448	8,702	13,003	14,888	14,808									
Solyc03g034200	RNA-binding KH domain-containing protein (AHRD V3.3 *** AT5G15270.3)		F:GO:0003723	F:RNA binding	IPR004087 (SMART): IPR036612 (G3	66,589	66,371	80,485	81,033	76,395									
Solyc03g034206	BZIP domain class transcription factor (AHRD V3.3 --* D9ZIP9_MALDO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,474	0,547	0,047	0,000	0,070									
Solyc03g034208	Heat shock protein 70 (Hsp 70) family protein (AHRD V3.3 --* AT3G09440.4)					0,019	0,021	0,000	0,000	0,000									
Solyc03g034220	Tomato RuBP carboxylase small subunit	RBCS2a	F:GO:0004497; F:GO	F:monooxygenase a EC:4.1.1.39 Ribulose-bisphospha	IPR024681 (PRINTS): IPR000894 (SM	434,502	1380,688	155,610	238,732	577,666	1,695	0,000	1,889	0,000	0,622	0,017	up	up	up
Solyc03g034230	translocase subunit seca (AHRD V3.3 *** AT1G13390.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	2,638	0,858	0,482	0,480	0,610	-1,557	0,007					down		
Solyc03g034240	Abscisic acid-deficient 4 (AHRD V3.3 *** A0A061EPF5_THECC)		C:GO:0016021	C:integral component of membrane	IPR025461 (PFAM): IPR025461 (PAN	0,119	0,000	0,165	0,578	0,400									
Solyc03g034250	peptidase M50B-like protein (AHRD V3.3 *** AT1G67060.1),Pfam:PF13398		C:GO:0005886; C:GO	C:plasma membrane; C:integral component of membrane	PF13398 (PFAM): PTHR33979 (PANT	12,378	19,156	8,675	8,705	9,311									
Solyc03g034270	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G38220.3)		F:GO:0016787	F:hydrolase activity	IPR022742 (PFAM): IPR029058 (G3D	6,857	7,423	8,952	7,045	7,155									
Solyc03g034300	LOW QUALITY:50S ribosomal protein-related, putative (AHRD V3.3 *** A0A061EGK7_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,417	1,644	0,384	0,223	0,424									
Solyc03g034320	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)		F:GO:0016787	F:hydrolase activity	IPR029062 (G3DSA:3.40.50.GENE3D	0,322	0,444	0,245	0,478	0,469									
Solyc03g034330	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)		P:GO:0006869	P:lipid transport	IPR016140 (SMART): IPR016140 (PF	0,548	1,143	0,497	0,403	0,357									
Solyc03g034370	plasma membrane H+-ATPase (AHRD V3.3 --* AT2G24520.4)					3,878	3,281	0,453	0,400	0,821									
Solyc03g034375	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)		P:GO:0006869	P:lipid transport	IPR016140 (SMART): G3DSA:1.10.11	53,099	44,772	6,151	5,796	10,235									
Solyc03g034395	Glutamate receptor (AHRD V3.3 *-* M1CHN3_SOLTU)		F:GO:0004970; C:GO	F:ionotropic glutamate receptor activity; C:plasma membrane; P:ion transport; C:membrane; C:integral c		0,437	0,430	0,465	0,168	0,213									
Solyc03g034400	Protein DETOXIFICATION (AHRD V3.3 *** K4BFW0_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (PFAM): IPR002528 (TIGF	5,043	4,232	0,022	0,000	0,000									
Solyc03g034410	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IAV0_MEDTR)				IPR025322 (PFAM): PTHR33052:SF3	0,102	0,098	0,187	0,788	0,471									
Solyc03g034417	cAMP-regulated phosphoprotein 19-related protein (AHRD V3.3 -** AT5G64130.2)					11,435	10,786	14,311	15,955	13,467									
Solyc03g034430	Eukaryotic translation initiation factor 5 (AHRD V3.3 *** IF5_PHAVU)		F:GO:0003743; F:GO	F:translation initiation factor activity; F:protein binding; P:transla	IPR002735 (SMART): IPR003307 (SM	79,270	80,552	102,847	100,283	98,559									
Solyc03g034440	Eukaryotic translation initiation factor 5 (AHRD V3.3 *** A0A0B2QDQ1_GLYSO)		F:GO:0003743; F:GO	F:translation initiation factor activity; F:protein binding; P:transla	IPR002735 (SMART): IPR003307 (SM	170,211	142,694	169,191	197,241	174,572									
Solyc03g034450	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BFW5_SOLLC)		F:GO:0005515; C:GO	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR018121 (PFAM): IPR013083 (G3D	9,470	11,022	7,223	5,682	6,752									
Solyc03g034453	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT5G11650.2)					3,855	3,005	1,949	2,027	2,589									
Solyc03g034457	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BFW6_SOLLC)		F:GO:0005515; C:GO	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR013083 (G3DSA:3.30.40.GENE3D	4,309	3,741	1,916	2,789	3,317									
Solyc03g036460	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BFX6_SOLLC)		F:GO:0005515; C:GO	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR018121 (PFAM): IPR013083 (G3D	0,113	0,101	0,000	0,000	0,024									
Solyc03g036470	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL1_SOLLC)	PAL	C:GO:0005737; P:GO	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l	G3DSA:1.20.200.10 (GENE3D): IPR0	63,224	33,658	3,476	13,514	12,334			1,826	0,000	1,961	0,000		up	up
Solyc03g036473	Phenylalanine ammonia-lyase (AHRD V3.3 *-* PAL1_SOLLC)	PAL	F:GO:0003824	F:catalytic activity	IPR023144 (G3DSA:1.10.274.GENE3	2,500	2,049	0,147	1,143	0,641									
Solyc03g036477	B3 domain-containing protein family (AHRD V3.3 *** A0A151S4J0_CAJCA)		F:GO:0003677	F:DNA binding	IPR003340 (SMART): IPR015300 (G3	0,019	0,019	0,000	0,000	0,000									
Solyc03g036480	Phenylalanine ammonia-lyase (AHRD V3.3 *-* PAL1_SOLLC)	PAL	F:GO:0003824	F:catalytic activity	G3DSA:1.20.200.10 (GENE3D): IPR0	0,021	0,019	0,000	0,000	0,000									
Solyc03g042520	LOW QUALITY:E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BFW6_SOLLC)		C:GO:0005634; P:GO	C:nucleus; P:ubiquitin-dependent protein catabolic process; P:n	IPR013083 (G3DSA:3.30.40.GENE3D	0,038	0,039	0,025	0,000	0,023									
Solyc03g042528	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BFX6_SOLLC)		C:GO:0005634; P:GO	C:nucleus; P:ubiquitin-dependent protein catabolic process; P:n	IPR004162 (PANTHER): PTHR10315:	0,000	0,021	0,000	0,000	0,000									
Solyc03g042560	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL1_SOLLC)	PAL	C:GO:0005737; P:GO	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l	IPR023144 (G3DSA:1.10.274.GENE3	59,188	42,080	4,686	11,942	18,020			1,942	0,000	1,352	0,008		up	up
Solyc03g043577	B3 domain-containing protein family (AHRD V3.3 *** A0A151S4J0_CAJCA)		F:GO:0003677	F:DNA binding	IPR003340 (SMART): IPR015300 (G3	0,000	0,041	0,000	0,000	0,000									
Solyc03g043580	B3 domain-containing transcription factor VRN1 (AHRD V3.3 *** A0A0B0MJI2_GOSAR)		F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	0,019	0,000	0,000	0,000	0,000									
Solyc03g043600	E3 ubiquitin-protein ligase (AHRD V3.3 *-* M1BDY9_SOLTU)		F:GO:0005515; C:GO	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR009071 (SMART): IPR036910 (G3	28,618	24,538	29,371	25,585	27,701									
Solyc03g043620	LOW QUALITY:Agenet and bromo-adjacent homology (BAH) domain-containing protein (AHRD V3.3 --* AT1G68580.5)					0,568	0,681	0,692	0,790	0,781									
Solyc03g043630	LOW QUALITY:Nucleotidylyl transferase superfamily protein (AHRD V3.3 --* AT3G27610.8)		C:GO:0005739	C:mitochondrion		0,000	0,019	0,022	0,000	0,000									
Solyc03g043640	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G17450.1)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D): IPR0	0,158	0,190	0,965	1,262	0,869									
Solyc03g043660	Protease Do-like 7 (AHRD V3.3 *** DEGP7_ARATH)		F:GO:0004252; F:GO	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR001940 (PRINTS): IPR001478 (SM	75,071	62,422	113,448	110,698	109,570									
Solyc03g043665	LOW QUALITY:Agamous-like MADS-box protein AGL80 (AHRD V3.3 *** A0A151U9H4_CAJCA)		F:GO:0000981; F:GO	F:DNA-binding transcription factor activity, RNA polymerase II-s	IPR002100 (PRINTS): IPR002100 (SM	0,061	0,059	0,000	0,050	0,000									
Solyc03g043700	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PMJ3_ZOSMR)		F:GO:0005515	F:protein binding	IPR000225 (SMART): IPR011989 (G3	19,284	24,633	1,835	1,995	2,995									
Solyc03g043710	Clade IX lectin receptor kinase (AHRD V3.3 *** K4BFZ2_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	0,021	0,000	0,000	0,000	0,000									
Solyc03g043715	Protein BRICK 1 (AHRD V3.3 *** BRK1_ARATH)		P:GO:0007015; C:GO	P:actin filament organization; C:SCAR complex; F:protein-conta	G3DSA:1.20.5.110 (GENE3D): IPR03	0,357	0,395	0,452	0,485	0,566									
Solyc03g043720	Protein BRICK 1 (AHRD V3.3 *** BRK1_ARATH)		P:GO:0007015; C:GO	P:actin filament organization; C:SCAR complex; F:protein-conta	G3DSA:1.20.5.110 (GENE3D): IPR03	0,021	0,057	0,072	0,050	0,071									
Solyc03g043740	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)		C:GO:0016021	C:integral component of membrane	IPR037699 (PANTHER)	2,435	5,142	4,205	3,734	2,101	1,099	0,010	-0,999	0,019			up	down	
Solyc03g043750	NAD(P)H dehydrogenase C1 (AHRD V3.3 *** AT5G08740.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	PR00411 (PRINTS): PR00368 (PRINT	26,845	34,770	92,541	91,737	114,660									
Solyc03g043760	Chromatin SPT2 (AHRD V3.3 *** A0A118JSU1_CYNCS)				IPR013256 (SMART): IPR013256 (PF	80,591	87,063	90,732	83,890	84,293									
Solyc03g043770	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IVW5_SOLCH)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR003591 (SMART): IPR000719 (SM	11,817	14,352	0,289	0,048	0,235									
Solyc03g043790	LOW QUALITY:Protein TIC 214 (AHRD V3.3 --* TI214_NASOF)				mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,000	0,000									
Solyc03g043850	cytochrome c oxidase-like protein (AHRD V3.3 *** AT4G37830.1)		F:GO:0004129; C:GO	F:cytochrome-c oxi EC:1.9.3.1 Cytochrome-c oxidas	IPR036418 (G3DSA:4.10.95.GENE3D	37,067	39,655	226,376	195,499	219,410									
Solyc03g043870	zinc ion binding protein (AHRD V3.3 *** AT5G65740.2)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:interstrand cross-link r	SM01197 (SMART): IPR019162 (PFAI	0,954	1,054	1,152	1,210	1,080									
Solyc03g043880	SIBCAT4	BCAT4	F:GO:0004084; P:GO	F:branched-chain-a EC:2.6.1.42 Branched-chain-amir	IPR001544 (PFAM): IPR005786 (TIGF	0,948	0,960	0,656	2,194	2,187			1,725	0,001	1,742	0,000		up	up
Solyc03g043890	1-aminocyclopropane-1-carboxylate synthase	ACS8	F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process; F:pyridoxal phosphe	PR00753 (PRINTS): IPR015422 (G3D	0,019	0,039	0,000	0,000	0,000									
Solyc03g043900	Basic-leucine zipper (BZIP) transcription factor family (AHRD V3.3 *-* A0A0K9NZH2_ZOSMR)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc	IPR004827 (SMAF bZIP	0,626	4,266	7,901	15,815	11,670	2,781	0,000			1,008	0,000	up		up

Solyc03g043910	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic (AHRD V3.3 --* NDHJ_PHYPA)						IPR005607 (SMART): IPR005607 (PF	4,995	4,626	1,704	0,880	1,129									
Solyc03g043920	Xyloglucan alpha-1,6-xylosyltransferase (AHRD V3.3 *** X2CZ83_PINRA)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR008630 (PFAM): IPR029044 (G3D	0,239	0,140	0,234	0,097	0,258									
Solyc03g043930	ADIPOR-like receptor protein (AHRD V3.3 *** A0A0B0MUN3_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004254 (PFAM): PTHR20855:SF5	7,400	5,434	6,243	5,882	5,479									
Solyc03g043940	O-methyltransferase, putative (AHRD V3.3 *-* B9SGP1_RICCO)		F:GO:0008171	F:O-methyltransferase activity			IPR001077 (PFAM): G3DSA:3.40.50.1	2,207	1,043	4,716	4,199	3,727									
Solyc03g043950	Amino acid acetyltransferase(N-acetylglutamate synthase)-like protein (AHRD V3.3 *** Q8H5K9_ORYSJ)		F:GO:0004042; C:G(	F:acetyl-CoA:L-glut	EC:2.3.1.1; EC:2.3.1	Amino-acid N-acetylt	IPR001048 (PFAM): G3DSA:3.40.630	66,173	49,964	27,832	28,309	31,466									
Solyc03g043960	ADP-ribosylation factor, putative (AHRD V3.3 *** B9T2F5_RICCO)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00178 (SMA	30,993	29,335	33,940	30,717	32,890									
Solyc03g044000	60S ribosomal protein L26-1 (AHRD V3.3 *** RL261_ARATH)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005824 (SMART): IPR014722 (G3	396,128	421,654	246,270	254,956	238,053									
Solyc03g044010	Outer mitochondrial membrane protein porin (AHRD V3.3 *** B6SS48_MAIZE)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe			IPR027246 (PFAM): IPR001925 (PAN	25,651	31,967	51,007	48,526	46,789									
Solyc03g044020	Condensin-2 complex subunit G2, putative (AHRD V3.3 *** G7K2J6_MEDTR)		C:GO:0005634	C:nucleus			IPR024741 (PFAM): IPR011989 (G3D	3,093	2,433	0,694	0,656	0,822									
Solyc03g044026	DEA(D/H)-box RNA helicase family protein (AHRD V3.3 --* AT1G51380.1)		C:GO:0005739	C:mitochondrion				0,179	0,175	0,050	0,025	0,117									
Solyc03g044028	Oxygen-evolving enhancer protein 2-2, chloroplastic (AHRD V3.3 --* PSBP2_TOBAC)							0,446	0,432	0,237	0,288	0,237									
Solyc03g044030	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 --* A0A0K9NTW4_ZOSM		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:catalytic step 2 spliceoso			PTHR11246:SF5 (PANTHER); PTHR1	0,000	0,000	0,000	0,000	0,024									
Solyc03g044040	LOW QUALITY:Pre-mRNA-splicing factor SYF1 (AHRD V3.3 *-* W9QRC5_9ROSA)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,158	0,025	0,000	0,070									
Solyc03g044050	alpha-soluble NSF attachment protein 2 (AHRD V3.3 --* AT3G56190.2)						G3DSA:2.40.50.140 (GENE3D)	0,399	0,535	0,315	0,382	0,353									
Solyc03g044060	Formin-like protein (AHRD V3.3 *** K4BG26_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (SMART): G3DSA:1.20.58	38,710	34,809	38,278	36,088	39,922									
Solyc03g044080	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein (AHRD V3.3 --* AT1G76580.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	10,640	12,335	11,945	11,683	11,735									
Solyc03g044085	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SGZ4_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR012946 (PF	0,393	0,803	0,047	0,152	0,000									
Solyc03g044090	Phototropic-responsive NPH3 family protein						IPR027356 (PFAM): mobidb-lite (MOB	1,843	2,038	0,584	0,596	1,011									
Solyc03g044093	Homeobox-leucine zipper protein HOX10 (AHRD V3.3 --* HOX10_ORYSJ)							0,058	0,059	0,025	0,050	0,000									
Solyc03g044100	Peroxidase (AHRD V3.3 *** K4BG30_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc03g044120	Tyrosine decarboxylase (AHRD V3.3 *** W5XTE8_SOLTU)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:carboxy-lyase activi			IPR010977 (PRINTS): IPR015421 (G3	0,019	0,000	0,000	0,000	0,000									
Solyc03g044140	Protein kinase superfamily protein (AHRD V3.3 *** AT2G23080.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	92,717	85,047	124,363	122,091	110,063									
Solyc03g044150	Subtilisin-like protease (AHRD V3.3 *** A9XG40_TOBAC)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.30	209,815	166,225	12,523	14,021	17,742			0,497	0,048				up	
Solyc03g044160	protein kinase family protein (AHRD V3.3 *-* AT5G54380.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:2.60.12	7,098	8,058	3,425	2,928	3,007									
Solyc03g044180	Transmembrane protein, putative (AHRD V3.3 *-* A0A072UNU4_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR346	0,021	0,268	0,112	0,047	0,069									
Solyc03g044190	FAD-dependent oxidoreductase family protein (AHRD V3.3 *** AT5G67290.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR036188 (G3DSA:3.50.50.GENE3D	58,607	48,855	92,386	76,430	88,946									
Solyc03g044200	Alcohol dehydrogenase (AHRD V3.3 *** Q43169_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.90.18	22,375	21,967	66,250	71,943	54,123									
Solyc03g044210	Vicilin-like protein (AHRD V3.3 *** A0A0S3B0K0_COCNU)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR014710 (G3	0,100	0,163	0,025	0,050	0,047									
Solyc03g044220	F-box protein (AHRD V3.3 *** W9R4Y4_9ROSA)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001810 (PF	22,215	25,649	13,487	12,785	13,937									
Solyc03g044245	F-box protein At1g59680 (AHRD V3.3 --* FB67_ARATH)							0,056	0,018	0,000	0,000	0,000									
Solyc03g044250	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 --* NU4C_TOBAC)							0,360	0,261	0,165	0,173	0,164									
Solyc03g044260	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** A9PAA6_POPTR)		F:GO:0019789	F:SUMO transferase activity			SM00212 (SMART): IPR016135 (G3D	38,081	37,304	67,112	66,720	67,832									
Solyc03g044270	tRNA-dihydrouridine(16/17) synthase [NAD (P)(+)]-like protein (AHRD V3.3 *** A0A0B0NB62_GOSAR)		P:GO:0008033; F:G(	P:tRNA processing; F:tRNA dihydrouridine synthase activity; F:I			IPR013785 (G3DSA:3.20.20.GENE3D	19,263	15,227	32,759	30,800	29,868									
Solyc03g044277	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G42940.2)		C:GO:0016020	C:membrane			IPR001841 (SMART): IPR001841 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc03g044300	APETALA2a	AP2a	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' AP2	22,559	17,918	228,939	293,752	173,110									
Solyc03g044330	Acetolactate synthase (AHRD V3.3 *** A0A0V0IYE7_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.2.1.6	Acetolactate synthas	IPR012000 (PFAM): IPR011766 (PFA	457,446	479,043	368,706	339,437	369,915									
Solyc03g044350	Transcription elongation factor-related family protein (AHRD V3.3 *-* B9H8S4_POPTR)		C:GO:0005634	C:nucleus			IPR001623 (PRINTS): IPR001623 (SM	0,438	0,163	2,638	0,050	1,321									
Solyc03g044370	OTU domain-containing protein, putative (AHRD V3.3 *** B9SCB5_RICCO)						IPR003323 (PFAM): IPR004027 (PFA	13,977	11,235	14,664	15,026	13,858									
Solyc03g044380	Histone-lysine N-methyltransferase MEDEA (AHRD V3.3 *-* MEDEA_ARATH)	EZ2	F:GO:0005515; C:G(	F:protein binding; C:PcG protein complex			IPR001005 (SMART): IPR033467 (SM	21,225	18,298	3,746	3,852	4,860									
Solyc03g044420	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 --* AT5G22870.1)							1,827	1,822	2,048	1,855	2,284									
Solyc03g044430	Nicotinate phosphoribosyltransferase family protein (AHRD V3.3 *** B9H6H6_POPTR)		F:GO:0004514; F:G(	F:nicotinate-nucleot	EC:2.4.2.19; EC:6.3.	Nicotinate-nucleotide	IPR013785 (G3DSA:3.20.20.GENE3D	16,738	15,355	32,815	32,115	35,729									
Solyc03g044440	50S ribosomal protein L22 (AHRD V3.3 *** A0A1D1Z3I2_9ARAE)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR036394 (G3DSA:3.90.470.GENE3	0,310	0,240	0,000	0,000	0,000									
Solyc03g044460	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT3G50330.1		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,000	0,000	0,000	0,000	0,024									
Solyc03g044470	red chlorophyll catabolite reductase	rccr	F:GO:0051743	F:red chlorophyll catabolite reductase activity			IPR009439 (PFAM): G3DSA:3.40.150	20,533	21,175	23,479	23,353	26,836									
Solyc03g044480	Cyclin-dependent kinase inhibitor family protein (AHRD V3.3 *-* AT2G23430.1)		F:GO:0004861; C:G(	F:cyclin-dependent protein serine/threonine kinase inhibitor acti			G3DSA:4.10.365.10 (GENE3D); IPR0(	1,542	0,851	0,047	0,022	0,094									
Solyc03g044510	Sulfotransferase (AHRD V3.3 *** K4BG70_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM): G3DSA:3.40.50.3	3,330	3,086	3,468	4,211	3,256									
Solyc03g044520	LOW QUALITY:Phospholipid/glycerol acyltransferase family protein (AHRD V3.3 --* AT3G11325.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,046									
Solyc03g044590	transmembrane protein, putative (DUF1279) (AHRD V3.3 *** AT2G20940.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR009688 (PFAM): PTHR21377:SF0	0,000	0,000	0,025	0,050	0,000									
Solyc03g044600	multidrug resistance-associated protein 6 (AHRD V3.3 --* AT3G21250.6)						mobidb-lite (MOBIDB_LITE)	0,503	0,488	3,341	3,275	2,586									
Solyc03g044620	Transmembrane protein 131-like (AHRD V3.3 *** A0A0B2S5T7_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR022113 (PFAM): mobidb-lite (MOB	40,147	32,998	45,539	48,127	46,323									
Solyc03g044625	PLATZ transcription factor family protein (AHRD V3.3 *** AT4G17900.2)						IPR006734 (PFAM): IPR006734 (PAN	0,906	0,488	1,783	2,238	1,673									
Solyc03g044630	DUF309 domain protein (AHRD V3.3 *** AT2G41120.1)						IPR005500 (PFAM): G3DSA:1.10.345	0,122	0,446	0,022	0,047	0,139									
Solyc03g044660	4-hydroxy-tetrahydrodipicolinate synthase (AHRD V3.3 *** K4D398_SOLLC)		F:GO:0008840; P:G(	F:4-hydroxy-tetrahy	EC:4.3.3.7	4-hydroxy-tetrahydro	IPR002220 (PRINTS): IPR002220 (SM	10,415	19,215	10,641	12,475	11,486	0,911	0,003					up		
Solyc03g044670	LOW QUALITY:D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** A0A0B2QT46_GLYSO)		F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D); IPR0(	3,738	3,950	17,156	17,292	15,070									
Solyc03g044673	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061FID3_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			PTHR23272 (PANTHER)	0,277	0,309	0,482	0,609	0,308									
Solyc03g044710	Patatin (AHRD V3.3 *** K4BG88_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM): G3DSA:3.40.109	0,080	0,275	0,441	0,050	0,168									
Solyc03g044720	Isoflavone reductase family protein (AHRD V3.3 *** B9HRL8_POPTR)						IPR008030 (PFAM): G3DSA:3.90.25.1	6,652	6,382	6,492	6,304	6,641									
Solyc03g044740	Methyl esterase 10, putative (AHRD V3.3 *** A0A061DG36_THECC)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	0,790	2,003	0,025	0,196	0,259	1,364	0,043					up		
Solyc03g044747	Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 --* AT5G28010.2)							4,856	4,946	5,590	6,093	5,447									
Solyc03g044790	methylesterase AY455313		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.78; EC:3.1.	Polyneuridine-aldehy	IPR029058 (G3DSA:3.40.50.GENE3D	2,347	4,056	3,710	4,469	5,757									
Solyc03g044800	Methyl jasmonate esterase (AHRD V3.3 *** Q56SE1_SOLTU)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,758	1,127	2,008	2,816	1,718									
Solyc03g044810	Methyl jasmonate esterase (AHRD V3.3 *** Q56SE1_SOLTU)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	0,416	0,676	0,653	1,715	0,897					1,378	0,005			up
Solyc03g044820	Methyl jasmonate esterase (AHRD V3.3 *** Q56SE1_SOLTU)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	2,772	2,852	4,906	4,439	4,940									
Solyc03g044830	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G18950.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,000	0,021	0,000	0,000	0,023									
Solyc03g044850	LOW QUALITY:Dehydrin family protein, expressed (AHRD V3.3 --* Q40711_ORYSJ)						mobidb-lite (MOBIDB_LITE)	0,238	0,467	0,143	0,419	0,190									
Solyc03g044860	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7K9H8_MEDTR)						IPR025322 (PFAM): mobidb-lite (MOB	0,000	0,000	0,049	0,045	0,000									
Solyc03g044880	Exostosin family protein (AHRD V3.3 *** AT1G67410.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM): PTHR11062:SF4	9,519	11,275	12,543	12,223	11,392									
Solyc03g044910	GNS1/SUR4 membrane protein family (AHRD V3.3 *** AT4G36830.1)		C:GO:0016021	C:integral component of membrane			IPR002076 (PFAM): PTHR11157:SF1	45,125	61,824	18,976	20,740	19,896									
Solyc03g044960	Calcium uniporter protein, mitochondrial (AHRD V3.3 *** A0A0B2SA24_GLYSO)		P:GO:0051560	P:mitochondrial calcium ion homeostasis			IPR006769 (PFAM): PTHR13462:SF4	0,021	0,018	0,046	0,000	0,023									
Solyc03g044980	LOW QUALITY:aluminum activated malate transporter family protein (AHRD V3.3 --* AT5G46610.2)						mobidb-lite (MOBIDB_LITE)	0,670	0,470	0,563	0,366	0,566									
Solyc03g044990	LOW QUALITY:Ferredoxin (AHRD V3.3 --* FER_SAMNI)							0,000	0,000	0,000	0,000	0,024									
Solyc03g045000	Drought responsive protein 2 (AHRD V3.3 *** V5J389_9POAL)						IPR026939 (G3DSA:4.10.1050.GENE	0,000	0,021	0,075	0,025	0,000									
Solyc03g045030	TCP transcription factor 26	TCP26	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	0,019	0,000	0,000	0,000	0,000									
Solyc03g045050	Nuclear matrix constituent-like protein 1 (AHRD V3.3 *** E5GCT1_CUCME)		C:GO:0005634; P:G(	C:nucleus; P:nucleus organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	80,241	93,004	91,282	95,687	92,317									
Solyc03g045060	Proline-rich spliceosome-associated family protein / zinc knuckle (CCHC-type) family protein (AHRD V3.3 ***		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR006568 (SMART): IPR001878 (SM	31,429	28,148	33,172	31,999	32,584									
Solyc03g045070	ammonium transporter AF118858		F:GO:0008519; C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR001905 (TIGRFAM): IPR029020 ((	3,055	4,913	0,065	0,050	0,303									
Solyc03g045080	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT4G08850.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:kinase acti			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc03g045090	dihydroflavonol 4-reductase/flavanone protein (AHRD V3.3 *** AT3G02420.1)	DFR	C:GO:0016021	C:integral component of membrane			IPR005344 (PFAM): mobidb-lite (MOB	50,287	48,517	73,077	72,955	71,052									
Solyc03g045100	LOW QUALITY:adenosine kinase 2 (AHRD V3.3 --* AT5G03300.1)							0,517	0,621	0,189	0,050	0,331									
Solyc03g045110	30S ribosomal protein S7, chloroplastic (AHRD V3.3 --* A0A0A0QFY6_9FABA)		P:GO:0006412	P:translation			IPR036823 (G3DSA:1.10.455.GENE3	6,390	7,439	9,119	8,607	9,951									
Solyc03g045120	jacalin-related lectin 22 (AHRD V3.3 --* AT2G39310.4)							0,691	0,361	1,039	0,745	0,613									
Solyc03g045123	D111/G-patch domain-containing protein (AHRD V3.3 --* AT5G08535.1)		F:GO:0003676	F:nucleic acid binding			IPR000467 (PFAM): IPR000467 (PRC	0,687	0,485	0,658	0,881	0,685									
Solyc03g045127	D111/G-patch domain-containing protein (AHRD V3.3 --* A0A061E228_THECC)		F:GO:0003676	F:nucleic acid binding				1,300	1,385	1,641	1,810	1,951									
Solyc03g045140	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *** AT3G23530.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			G3DSA:3.30.70.1990 (GENE3D); PF0	0,000	0,000	0,050	0,000	0,046									
Solyc03g046200	LOW QUALITY:Glycoside hydrolase, family 81 (AHRD V3.3 *** A0A103YH72_CYNCS)		F:GO:0052861	F:glucan endo-1,3-b	EC:3.2.1.6	Endo-1,3(4)-beta-glu	G3DSA:2.70.98.30 (GENE3D); PF176	0,460	0,476	0,025	0,025	0,164									
Solyc03g046207	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072VIR5_MEDTR)		F:GO:0005515; F:G(	F:protein binding; F:ADP binding			PR00364 (PRINTS): IPR003593 (SMA	5,965	4,170	4,026	4,540	5,044									
Solyc03g046250	Pectin lyase-like superfamily protein (AHRD V3.3 --* AT2G26620.1)							0,225	0,140	0,193	0,094	0,261									
Solyc03g046270	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	0,098	0,118	0,025	0,000	0,047									
Solyc03g046275	DNA-directed RNA polymerase subunit (AHRD V3.3 --* A0A068TZY7_COFCA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,600	0,438	0,339	0,440	0,352									
Solyc03g046340	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** W9RE71_9ROSA)		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): PF17862 (PFAM	14,472	17,577	30,803	28,560	31,495									
Solyc03g046350	ribosomal RNA-processing 7 protein (AHRD V3.3 *-* AT5G38720.3)		P:GO:0000028; P:G(	P:ribosomal small subunit assembly; P:rRNA processing; C:CUF			IPR024326 (PFAM): mobidb-lite (MOB	24,778	24,174	20,160	21,621	20,355									
Solyc03g046380	LOW QUALITY:Seed maturation protein PM41 (AHRD V3.3 *** Q9SWB2_SOYBN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,347	3,723	2,134	5,583	3,000									
Solyc03g046390	LOW QUALITY:Vacuolar-processing enzyme beta-isozyme 1 (AHRD V3.3 --* VPE1_ORYSJ)							0,265	0,074	0,068	0,000	0,071									
Solyc03g046410	LOW QUALITY:myosin heavy chain, cardiac protein (AHRD V3.3 --* AT5G26770.6)							0,874	1,014	0,952	1,312	1,181									
Solyc03g046420	LOW QUALITY:RUN/FYVE domain protein (AHRD V3.3 --* AT1G10417.4)		F:GO:0043531	F:ADP binding				0,019	0,000	0,000	0,000	0,000									
Solyc03g046450	Cell morphogenesis related protein (AHRD V3.3 *** F4KB73_ARATH)		P:GO:0000902	P:cell morphogenesis			IPR025481 (PFAM): IPR029473 (PFA	85,643	67,508	80,901	85,419	88,493									
Solyc03g046470	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G30300.2)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; P:fucose metabolic proces			IPR024709 (PIRSF): IPR019378 (PFA	38,809	40,398	23,279	23,065	26,176									
Solyc03g046515	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR036396 (G3	0,000	0,021	0,000	0,000	0,000									
Solyc03g046547	BHLH transcription factor (AHRD V3.3 --* C6THG7_SOYBN)		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): mobidb-lit	5,709	4,810	7,468	6,050	5,795									
Solyc03g046570	Transcription factor BIM2-like protein (AHRD V3.3 *** A0A0B0NVI3_GOSAR)		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,673	15,467	18,759	15,599	16,017									
Solyc03g046590	AUGMIN subunit 5 (AHRD V3.3 *** AUG5_ARATH)		P:GO:0051225; C:G(	P:spindle assembly; C:HAUS complex			IPR029131 (PFAM): mobidb-lite (MOB	29,925	29,380	22,096	21,856	24,552									
Solyc03g051590	LOW QUALITY:Protein Ycf2 (AHRD V3.3 --* YCF2_LEMMI)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,046									
Solyc03g051645	Alcohol dehydrogenase (AHRD V3.3 --* G0Z9K9_MALDO)							0,038	0,018	0,000	0,000	0,000									
Solyc03g051660	Sister-chromatide cohesion protein 3 (AHRD V3.3 --* D7LHE4_ARALL)							0,179	0,224	0,050	0,172	0,164									
Solyc03g051690	Alcohol dehydrogenase (AHRD V3.3 --* A0A0H3TZ81_9POAL)							0,078	0,039	0,050	0,022	0,000									
Solyc03g051780	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G57790.2)		F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	32,350	36,693	47,557	44,886	45,260									
Solyc03g051785	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061EX66_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	0,497	0,864	0,358	0,371	0,493									
Solyc03g051790	Nucleolar gar2-like protein (AHRD V3.3 *** A2Q3E1_MEDTR)		P:GO:0006913; P:G(	P:nucleocytoplasmic transport; P:nuclear pore organization; F:s			mobidb-lite (MOBIDB_LITE): mobidb-lit	199,970	221,744	62,962	52,793	63,784									
Solyc03g051810	Homogentisate phytyltransferase (AHRD V3.3 *** A0A072VUE3_MEDTR)	HST	C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR000537 (PFAM): G3DSA:1.10.357	14,249	17,869	20,064	22,233	25,557									
Solyc03g051885	WD repeat-containing protein RUP1 (AHRD V3.3 --* RUP1_ARATH)							3,340	4,410	2,582	2,178	3,002									
Solyc03g051900	Protein RRP5-like protein (AHRD V3.3 *** W9QKL3_9ROSA)		F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; C:nucleus; P:mRNA pro			IPR003107 (SMART): IPR022967 (SM	66,090	67,313	44,902	43,986	42,539									
Solyc03g051920	lipase (DUF620) (AHRD V3.3 *** AT5G06610.1)						IPR006873 (PFAM): mobidb-lite (MOB	13,763	13,941	15,785	14,699	14,772									
Solyc03g051930	Histone-lysine N-methyltransferase (AHRD V3.3 *-* W9S3I1_9ROSA)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			PTHR12197:SF262 (PANTHER); PTHF	0,000	0,000	0,047	0,025	0,024									
Solyc03g051950	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9S3I1_9ROSA)		F:GO:0005515	F:protein binding			IPR001214 (SMART): G3DSA:2.170.2	2,584	2,495	3,167	3,858	3,516									
Solyc03g051970	Dihydrosphingosine 1-phosphate phosphatase (AHRD V3.3 *** W9S3H5_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR000326 (SMART): IPR000326 (PF	29,540	38,375	17,222	19,690	19,058									
Solyc03g052970	LOW QUALITY:Maturase K (AHRD V3.3 --* M4WAG0_9POAL)							0,081	0,055	0,119	0,047	0,095									
Solyc03g052980	RNA helicase DEAD11	DEAD11	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	110,075	119,623	139,807	131,810	128,205									
Solyc03g053000	Peptide upstream ORF protein (AHRD V3.3 *** G7KWB8_MEDTR)		C:GO:0005739; P:G(	C:mitochondrion; P:mitochondrial respiratory chain complex I as			IPR034595 (PANTHER)	2,832	2,637	4,643	5,551	4,622									
Solyc03g053010	Colon cancer-associated Mic1-like protein (AHRD V3.3 *** G7KWB7_MEDTR)		P:GO:0010506; C:G(	P:regulation of autophagy; C:Mon1-Ccz1 complex			IPR009755 (PFAM): mobidb-lite (MOB	52,025	47,110	76,480	85,110	76,174									
Solyc03g053023	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** AT2G41950.1)		C:GO:0009505; C:G(	C:plant-type cell wall; C:chloroplast stroma			PTHR37217 (PANTHER); IPR029063 (	4,240	3,970	7,326	6,619	7,435									
Solyc03g053025	Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 *** A0A151SH12_CAJCA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR000477 (PFAM): PTHR44484 (PAN	0,390	0,098	0,000	0,000	0,000									
Solyc03g053027	Ribonuclease 3-like protein 2 (AHRD V3.3 --* RTL2_ORYSJ)		F:GO:0003676	F:nucleic acid binding				10,230	11,344	4,415	3,866	4,526									
Solyc03g053040	nucleolar RNA-binding Nop10p family protein (AHRD V3.3 -** AT2G20490.3)						mobidb-lite (MOBIDB_LITE)	2,053	2,246	0,904	0,793	0,940									
Solyc03g053060	Cell differentiation, Rcd1-like protein (AHRD V3.3 --* Q8RWV5_ARATH)							0,254	0,058	0,101	0,000	0,024									
Solyc03g053080	Kinesin-like protein (AHRD V3.3 *-* K4BGL0_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (SMART): IPR036961 (G3	10,580	9,328	7,779	6,921	6,863									
Solyc03g053100	Kinesin-like protein (AHRD V3.3 *** A0A0V0IXU5_SOLCH)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PFAM): G3DSA:1.20.58.1	32,805	32,647	21,182	20,448	21,541									
Solyc03g053105	Ribonuclease 3-like protein 2 (AHRD V3.3 *-* RTL2_ARATH)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR000999 (PFAM): IPR036389 (G3D	33,101	27,822	21,313	20,247	18,236									
Solyc03g053110	Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 *** AT2G42220.1)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			IPR001763 (SMART): IPR036873 (G3	27,733	55,191	25,770	32,306	49,660	1,020	0,000	0,942	0,000			up	up	
Solyc03g053120	LOW QUALITY:TBCC domain-containing protein 1 (AHRD V3.3 *-* W9SIC9_9ROSA)		P:GO:0000902	P:cell morphogenesis			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc03g053130	Strictosidine synthase family protein (AHRD V3.3 *** B9HGZ9_POPTR)		P:GO:0009058; F:G(	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR011042 (G3DSA:2.120.10.GENE3	12,926	8,963	1,054	0,289	0,330									
Solyc03g058160	Zinc finger family protein (AHRD V3.3 *** B9HA00_POPTR)		F:GO:0003676	F:nucleic acid binding			PTHR26374 (PANTHER); PTHR26374	0,138	0,135	0,000	0,000	0,000									
Solyc03g058190	elongation factor family protein (AHRD V3.3 *** AT5G13650.2)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR000640 (SM	88,182	100,779	89,065	90,458	118,729			0,412	0,008				up	
Solyc03g058213	50S ribosomal protein L16, chloroplastic (AHRD V3.3 *** RK16_GUIAB)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036920 (SUPERFAMILY)	0,019	0,043	0,000	0,222	0,069									
Solyc03g058243	Protein Ycf2 (AHRD V3.3 *-* YCF2_VITVI)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PANTHER)	0,000	0,000	0,000	0,000	0,024									
Solyc03g058330	Seed maturation protein LEA 4 (AHRD V3.3 *** Q9FNW3_GLYTO)		P:GO:0009793	P:embryo development ending in seed dormancy			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,341	0,455	0,197	0,727	0,024									
Solyc03g058340	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 --* AT5G10100.3)		P:GO:0006979; C:G(	P:response to oxidative stress; C:integral component of membra			PTHR37223 (PANTHER)	9,274	10,940	13,831	15,171	14,036									
Solyc03g058350	Translation initiation factor (AHRD V3.3 *-* G7ID01_MEDTR)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004161 (PF	99,389	87,281	80,303	74,455	73,764									
Solyc03g058370	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR(	4,754	1,628	0,025	0,025	0,143									
Solyc03g058380	Translation initiation factor (AHRD V3.3 *** G7ID01_MEDTR)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR005225 (TI(	110,739	103,802	119,818	110,510	113,768									
Solyc03g058390	eukaryotic translation initiation factor 2 (eIF-2) family protein (AHRD V3.3 --* AT1G76810.1)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:GTPase activity; F:GTP			mobidb-lite (MOBIDB_LITE): mobidb-lit	45,872	35,921	42,455	43,190	39,622									
Solyc03g058430	Fatty acid desaturase (AHRD V3.3 *** M4QSE6_9ERIC)		P:GO:0006629; F:G(	P:lipid metabolic pro	EC:1.14.19	Acting on paired don	IPR021863 (PFAM): IPR005804 (PFA	8,788	24,839	0,411	0,521	1,240	1,523	0,000					up		

Solyc03g058450	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SHH6_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012946 (SMART): IPR000490 (PF	0,000	0,000	0,000	0,047	0,000									
Solyc03g058470	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT2G43490.8)				IPR000195 (SMART): IPR000195 (PF	11,819	11,395	14,825	14,948	13,994									
Solyc03g058510	aluminum activated malate transporter family protein (AHRD V3.3 --* AT5G46610.3)					0,057	0,099	0,144	0,092	0,072									
Solyc03g058860	3-dehydroquinate synthase (AHRD V3.3 *** AT3G28760.2)		F:GO:0003856; P:G(	F:3-dehydroquinate EC:4.2.3.4 3-dehydroquinate sy	IPR002812 (PIRSF): IPR002812 (PFA	33,641	44,163	43,340	46,944	48,123									
Solyc03g058880	Translation factor GUF1 homolog, mitochondrial (AHRD V3.3 *** K4BGT6_SOLLC)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.30.7(	23,145	20,727	31,461	28,384	29,796									
Solyc03g058910	Pectate lyase (AHRD V3.3 *** M1A3P9_SOLTU)		F:GO:0030570; P:G(	F:pectate lyase act EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	0,059	0,096	1,358	1,418	1,383									
Solyc03g058917	Photosystem I assembly protein Ycf4 (AHRD V3.3 --* YCF4_PSEAK)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,081	0,566	0,605	0,867	0,519									
Solyc03g058920	Mitochondrial outer membrane porin (AHRD V3.3 *** VDAC1_WHEAT)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe	IPR023614 (G3DSA:2.40.160.GENE3I	0,000	0,000	0,022	0,000	0,023									
Solyc03g058930	Hypersensitive-induced response protein (AHRD V3.3 *** Q6UNT3_CUCSA)				IPR001107 (SMART): IPR001107 (PF	0,300	0,254	0,097	0,146	0,118									
Solyc03g058950	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (AHRD V3.3 *** A0A0B2PX10_G		F:GO:0000829	F:inositol heptakisphosphate kinase activity	IPR000560 (PFAM): mobidb-lite (MOB	13,827	20,635	10,882	10,961	14,411	0,605	0,041					up		
Solyc03g058970	Alkaline alpha-galactosidase seed imbibition protein (AHRD V3.3 *** Q8H6N3_SOLLC)		F:GO:0003824	F:catalytic activity	IPR008811 (PFAM): IPR013785 (G3D	148,896	116,176	306,975	279,910	280,533									
Solyc03g058990	60S ribosomal protein L38 (AHRD V3.3 *** RL38_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038464 (G3DSA:3.30.720.GENE3I	3,753	3,982	2,138	1,808	2,136									
Solyc03g059010	Carbon catabolite repressor 4-like protein (AHRD V3.3 *** A0A0B0P8G6_GOSAR)				IPR005135 (PFAM): IPR036691 (G3D	17,169	16,247	23,480	24,742	22,697									
Solyc03g059020	Receptor protein kinase CLAVATA1, putative (AHRD V3.3 *** B9T272_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): IPR0(	0,038	0,000	0,000	0,000	0,024									
Solyc03g059030	CDK5RAP3-like protein (AHRD V3.3 *** A0A061EXQ0_THECC)		P:GO:0000079; P:G(	P:regulation of cyclin-dependent protein serine/threonine kinase	IPR008491 (PFAM): IPR008491 (PAN	49,876	44,348	75,597	68,435	69,780									
Solyc03g059035	30S ribosomal protein S4, chloroplastic (AHRD V3.3 --* RR4_COFAR)					0,000	0,000	0,000	0,025	0,000									
Solyc03g059060	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G22330.1)					0,061	0,080	0,000	0,025	0,047									
Solyc03g059070	Kinase family protein (AHRD V3.3 *** U5FGJ0_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR024788 (PF	14,105	11,890	10,779	10,582	12,356									
Solyc03g059090	Ribosomal protein L32e (AHRD V3.3 -** AT5G46430.2)					0,609	0,875	0,340	0,338	0,330									
Solyc03g059100	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G43770.1)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR001680 (SM	43,619	40,145	53,735	48,013	48,168									
Solyc03g059110	LOW QUALITY:AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT3G11580.3)					1,824	1,924	0,960	1,443	1,154									
Solyc03g059140	Ion channel CASTOR (AHRD V3.3 *-* A0A1D1ZL57_9ARAE)		C:GO:0016021	C:integral component of membrane	PTHR31563:SF9 (PANTHER): PTHR3	0,559	0,380	0,527	0,392	0,566									
Solyc03g059150	Ion channel DMI1 (AHRD V3.3 *** DMI1_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR010420 (PFAM): PTHR31563:SF9	7,625	6,813	7,842	7,927	7,446									
Solyc03g059155	Pathogenesis-related thaumatin superfamily protein (AHRD V3.3 --* AT1G77700.1)					0,080	0,059	0,148	0,125	0,071									
Solyc03g059160	Ion channel CASTOR (AHRD V3.3 *-* CASTO_LOTJA)		C:GO:0016021	C:integral component of membrane	PTHR31563:SF9 (PANTHER): PTHR3	0,000	0,021	0,000	0,000	0,047									
Solyc03g059180	Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 *** AT3G59780.1)		C:GO:0009507	C:chloroplast	IPR001763 (SMART): IPR036873 (G3	47,490	70,838	92,514	118,475	119,467	0,604	0,022	0,366	0,039			up	up	
Solyc03g059190	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G59710.3)		F:GO:0050221; P:G(	F:prostaglandin-E2 EC:1.1.1.189 Prostaglandin-E(2) 9-	IPR002347 (PRINTS): IPR002347 (PF	0,175	0,229	0,000	0,097	0,047									
Solyc03g059230	LOW QUALITY:HhH-GPD base excision DNA repair family protein (AHRD V3.3 --* AT5G04560.3)					0,059	0,021	0,122	0,050	0,072									
Solyc03g059235	Zinc finger protein CONSTANS-LIKE 3 (AHRD V3.3 --* COL3_ARATH)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,019	0,000	0,025	0,000									
Solyc03g059250	Kinase family protein (AHRD V3.3 *-* B9GW98_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	23,276	19,768	16,236	17,589	20,018									
Solyc03g059260	Carboxyl-terminal-processing protease (AHRD V3.3 *** A0A151QQ57_CAJCA)		F:GO:0005515; P:G(	F:protein binding; P:proteolysis; F:serine-type peptidase activity	IPR005151 (SMART): IPR001478 (SM	227,031	271,734	126,556	166,434	199,303			0,653	0,007				up	
Solyc03g059270	Protein TRANSPARENT TESTA 1 (AHRD V3.3 *** A0A0B2PI42_GLYSO)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	1,386	0,842	0,420	0,437	0,474									
Solyc03g059300	LOW QUALITY:NAC transcription factor (AHRD V3.3 *** B3VK72_TOBAC)	NAC024	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAN NAC	0,000	0,018	0,000	0,000	0,000									
Solyc03g059310	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G18140.1)		F:GO:0005515; C:G(	F:protein binding; C:TORC1 complex; C:TORC2 complex; P:pos	IPR020472 (PRINTS): IPR001680 (SM	56,687	66,019	109,758	104,148	115,076									
Solyc03g059314	squamosa promoter-like 11 (AHRD V3.3 --* AT1G27360.4)					3,587	2,842	1,815	1,797	1,905									
Solyc03g059350	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0005388; F:G(	F:calcium-transporti EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	G3DSA:1.20.1110.10 (GENE3D): IPR(	0,539	1,137	0,506	0,454	0,540									
Solyc03g059360	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0000166	F:nucleotide binding	PF13246 (PFAM): IPR023299 (G3DS/	1,138	1,887	0,682	1,181	1,201									
Solyc03g059390	Tetraspanin (AHRD V3.3 *** A0A103XNJ6_CYNCS)		C:GO:0016021	C:integral component of membrane	IPR000301 (PRINTS): IPR018499 (PF	1,415	1,461	0,764	0,685	1,060									
Solyc03g059420	Sister-chromatid cohesion protein 2 (AHRD V3.3 *** F4K9U3_ARATH)		F:GO:0003682; P:G(	F:chromatin binding; P:regulation of gene expression	IPR001965 (SMART): IPR026003 (PF	60,630	48,481	65,963	72,688	68,360									
Solyc03g059430	prenylated RAB acceptor 1.A2 (AHRD V3.3 --* AT5G05987.1)					0,000	0,000	0,022	0,000	0,000									
Solyc03g059490	Leucine rich repeat receptor protein kinase 2 (AHRD V3.3 *** F8WS89_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	60,385	56,181	47,683	69,204	59,948					0,539	0,001			up
Solyc03g059500	Casein kinase 1-like protein 5 (AHRD V3.3 --* CKL5_ARATH)					0,375	0,393	0,140	0,117	0,235									
Solyc03g060510	keratin-associated protein (DUF819) (AHRD V3.3 *** AT5G24000.1)		C:GO:0016021	C:integral component of membrane	IPR008537 (PFAM): PTHR34289:SF4	0,748	1,459	0,904	0,744	1,150									
Solyc03g061540	LOW QUALITY:NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A0C5B2A9_HYONI)		C:GO:0005739; F:G(	C:mitochondrion; F: EC:1.6.99.5; EC:1.6. Acting on NADH or N	PTHR22773:SF102 (PANTHER): PTHI	0,037	0,000	0,025	0,025	0,023									
Solyc03g061550	LOW QUALITY:poly ADP-ribose polymerase 3 (AHRD V3.3 --* AT5G22470.1)				mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,000	0,000									
Solyc03g061590	Cell division cycle protein 27 homolog B (AHRD V3.3 *-* CD27B_ARATH),Pfam:PF12895		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	7,149	5,182	6,199	6,266	6,857									
Solyc03g061600	Cell division cycle protein 27/anaphase promoting complex subunit3 (AHRD V3.3 *** A0A0K9NSQ6_ZOSMR		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR001440 (PF	35,799	27,899	31,589	31,753	32,190									
Solyc03g061620	Zinc finger family protein (AHRD V3.3 *** B9H0F7_POPTR)				IPR006456 (TIGRI ZF-HD	0,102	0,230	0,000	0,000	0,000									
Solyc03g061650	LOW QUALITY:F-box family protein (AHRD V3.3 *-* B9HWR1_POPTR)		F:GO:0005515	F:protein binding	IPR006566 (SMART): IPR032675 (G3	0,021	0,062	0,000	0,000	0,000									
Solyc03g061655	Ribosomal protein S12 (AHRD V3.3 -** A0A0K0Q6T6_9CARY)					0,019	0,000	0,000	0,000	0,000									
Solyc03g062650	thyroid adenoma-associated-like protein (AHRD V3.3 *** AT3G55160.3)		C:GO:0005829; P:G(	C:cytosol; P:cold acclimation; P:tRNA methylation; P:regulation	IPR019442 (PFAM): PTHR14387 (PAI	34,932	27,616	42,107	44,716	40,025									
Solyc03g062660	Protein kinase (AHRD V3.3 *** C6FF71_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	6,719	4,682	3,482	3,833	2,403									
Solyc03g062670	LOW QUALITY:NAC transcription factor (AHRD V3.3 *** B3VK72_TOBAC)	NAC025	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAN NAC	0,115	0,143	0,072	0,000	0,069									
Solyc03g062680	Serine/threonine-protein phosphatase 4 regulatory subunit 2 (AHRD V3.3 *** A0A061FUH5_THECC)		F:GO:0019888; C:G(	F:protein phosphatase regulator activity; C:protein phosphatase	IPR015267 (PFAM): mobidb-lite (MOB	16,805	16,073	23,770	23,974	24,215									
Solyc03g062700	ARM repeat superfamily protein (AHRD V3.3 *** A0A061F2F3_THECC)		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:nucleus; C:cytoplasm; C:in	IPR011989 (G3DSA:1.25.10.GENE3D	0,000	0,000	0,000	0,022	0,000									
Solyc03g062710	NDH-dependent cyclic electron flow 5 (AHRD V3.3 *** A0A0F7CYY3_9ROSI)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol	PTHR11122 (PANTHER): PTHR11122	0,019	0,021	0,000	0,000	0,000									
Solyc03g062720	Photosynthetic NDH subcomplex B 2 (AHRD V3.3 *** A0A0F7GZL7_9ROSI)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol	IPR014718 (G3DSA:2.70.98.GENE3D	0,380	1,429	0,000	0,000	0,000									
Solyc03g062740	acyl-activating enzyme 17 (AHRD V3.3 --* AT5G23050.1)					0,344	0,283	0,146	0,222	0,234									
Solyc03g062745	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *-* AT1G03330.1)		P:GO:0006397	P:mRNA processing	IPR001163 (SMART): IPR001163 (PF	0,061	0,000	0,000	0,000	0,000									
Solyc03g062780	LOW QUALITY:30S ribosomal protein S7, chloroplastic (AHRD V3.3 --* RR7_TOBAC)		P:GO:0000028; F:G(	P:ribosomal small subunit assembly; F:RNA binding; F:mRNA binding; F:structural constituent of ribosom		0,021	0,000	0,000	0,050	0,000									
Solyc03g062790	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT2G42130.4)				IPR006843 (PFAM): PTHR31906:SF1	20,563	32,245	16,687	15,612	21,155	0,675	0,006					up		
Solyc03g062820	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *** AT1G72350.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR002100 (PRIN M-type_MADS	0,019	0,021	0,000	0,000	0,047									
Solyc03g062830	Nudix hydrolase-like protein (AHRD V3.3 *** G7KVE3_MEDTR)		F:GO:0016787	F:hydrolase activity	G3DSA:3.90.79.10 (GENE3D): G3DS/	11,088	14,994	16,615	20,663	19,145									
Solyc03g062880	Unknown protein (AHRD V3.3)					0,019	0,000	0,000	0,000	0,000									
Solyc03g062890	Superoxide dismutase [Cu-Zn] (AHRD V3.3 *** K4BH38_SOLLC)		P:GO:0006801; F:G(	P:superoxide metabolic process; F:metal ion binding	IPR001424 (PRINTS): IPR001424 (PF	81,460	92,618	243,007	202,036	227,858									
Solyc03g062900	Elongation factor 4 (AHRD V3.3 *** A0A0B0NVN0_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	7,031	5,557	1,175	1,237	1,032									
Solyc03g062910	Copia protein (AHRD V3.3 *-* A0A151SBM2_CAJCA)					1,636	0,891	0,625	0,757	0,732									
Solyc03g062915	5'-3' exonuclease family protein (AHRD V3.3 *-* AT3G52050.2)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.7 DNA-directed DNA p(	IPR020046 (PFAM): G3DSA:3.40.50.1	1,518	1,482	1,089	1,007	1,320									
Solyc03g062930	5\'-3\' exonuclease family protein isoform 1 (AHRD V3.3 *-* A0A061EJA7_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.7 DNA-directed DNA p(	IPR008918 (SMART): IPR002421 (SM	3,947	3,691	3,505	2,966	3,812									
Solyc03g062940	peroxisomal targeting signal type 2 receptor		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR001680 (SM	135,293	109,314	185,245	163,603	162,392									
Solyc03g062950	LOW QUALITY:Chaperonin-60 beta subunit (AHRD V3.3 *-* P93570_SOLTU)		P:GO:0009987	P:cellular process	IPR027410 (G3DSA:3.30.260.GENE3I	0,537	0,418	0,333	0,430	0,307									
Solyc03g063030	Transmembrane amino acid transporter family protein (AHRD V3.3 *** AT2G39130.2)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:vacuolar membrane;	IPR013057 (PFAM): mobidb-lite (MOB	14,964	15,658	11,455	10,155	13,548									
Solyc03g063040	Amino acid transporter family protein (AHRD V3.3 *-* B9HLH9_POPTR)		C:GO:0016021	C:integral component of membrane	PTHR22950 (PANTHER): PTHR22950	3,365	3,550	2,270	2,221	2,405									
Solyc03g063053	phytochelatin synthase 2 (AHRD V3.3 --* AT1G03980.3)		C:GO:0016021	C:integral component of membrane		0,220	0,110	0,150	0,262	0,117									
Solyc03g063057	Ycf20-like protein (AHRD V3.3 *** YC20L_ARATH)		C:GO:0016021	C:integral component of membrane	IPR007572 (PFAM): IPR007572 (PAN	0,000	0,043	0,000	0,022	0,023									
Solyc03g063090	LOW QUALITY:Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 --* PFPB_SOLTU)					0,079	0,037	0,072	0,025	0,047									
Solyc03g063100	single flower truss		F:GO:0008429; P:G(	F:phosphatidylethanolamine binding; P:regulation of flower deve	IPR008914 (PFAM): IPR036610 (G3D	0,040	0,154	0,637	1,933	1,271					1,596	0,004			up
Solyc03g063110	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** K0A7N8_SOLAC)		P:GO:0006631; F:G(	P:fatty acid metabo EC:1.14.19.2; EC:1.' Stearoyl-[acyl-carrier	IPR005067 (PIRSF): IPR005067 (PFA	79,333	75,798	118,361	100,739	119,075									
Solyc03g063140	Asymmetric leaves 2 (AHRD V3.3 *** A0A1C9U0Z1_9FABA)		C:GO:0005654; P:G(	C:nucleoplasm; P:specification of symmetry; P:polarity specifica	IPR004883 (PFAN LBD	0,056	0,000	0,000	0,048	0,000									
Solyc03g063150	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2SJP2_GLYSO)		F:GO:0005507; F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red	IPR008972 (G3DSA:2.60.40.GENE3D	0,770	0,817	1,151	0,968	0,918									
Solyc03g063200	Zinc finger transcription factor 25	C3H25	F:GO:0003723; F:G(	F:RNA binding; F:metal ion binding	IPR000571 (SMAF C3H	13,898	15,088	14,942	13,558	14,429									
Solyc03g063210	Helicase, putative (AHRD V3.3 *-* B9SBN6_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:ATP binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	15,184	16,365	15,679	15,057	15,411									
Solyc03g063220	RNA helicase DEAH-box8	DEAH8	F:GO:0005524	F:ATP binding	IPR001650 (SMART): IPR014001 (SM	25,539	21,472	24,892	27,831	24,698									
Solyc03g063240	Pyridoxamine 5'-phosphate oxidase-related FMN-binding protein (AHRD V3.3 *** A0A0K9PSN3_ZOSMR)		F:GO:0048037	F:cofactor binding	IPR019595 (PFAM): IPR012349 (G3D	32,413	35,751	69,372	62,931	70,778									
Solyc03g063260	Class II aminoacyl-tRNA and biotin synthetases superfamily protein (AHRD V3.3 --* AT4G17300.2)					1,026	1,115	0,920	0,893	0,948									
Solyc03g063280	Emsy N terminus domain-containing family protein (AHRD V3.3 *** B9HPS6_POPTR)		P:GO:0050832	P:defense response to fungus	IPR005491 (SMART): IPR005491 (PF	35,825	35,820	38,649	37,001	39,458									
Solyc03g063290	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G19630.1)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	10,230	9,762	12,473	11,335	10,444									
Solyc03g063300	LOW QUALITY:heat shock protein 70 (Hsp 70) family protein (AHRD V3.3 --* AT1G11660.4)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,037	0,000	0,000	0,000									
Solyc03g063320	Metal tolerance-like protein (AHRD V3.3 *** G7KVE4_MEDTR)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;	IPR027469 (G3DSA:1.20.1510.GENE	10,391	9,297	13,041	15,244	14,896									
Solyc03g063340	DNA polymerase delta small subunit (AHRD V3.3 *** AT2G42120.2)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.7 DNA-directed DNA p(	G3DSA:2.40.50.430 (GENE3D): PF18	57,803	53,944	103,876	105,356	98,759									
Solyc03g063350	DNAJ/Hsp40 domain-containing protein				IPR001623 (PRINTS): IPR001623 (SM	16,159	19,034	26,016	26,230	26,496									
Solyc03g063370	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A0B2RWF1_GLYSO)		P:GO:0009451	P:RNA modification	PTHR24015:SF1059 (PANTHER): PTH	0,822	0,601	0,384	0,197	0,355									
Solyc03g063380	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2RWF1_GLYSO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	0,903	0,899	0,290	0,340	0,401									
Solyc03g063390	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT4G19650.2)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (SMART): IPR003690 (PF	4,369	3,255	3,811	4,996	4,363									
Solyc03g063420	Proteasome subunit beta type (AHRD V3.3 *** K4C2U0_SOLLC)		F:GO:0004298; C:G(	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR001353 (PFAM): IPR029055 (G3D	0,000	0,000	0,046	0,000	0,000									
Solyc03g063450	Proteasome subunit beta type (AHRD V3.3 *-* K4C2U0_SOLLC)		F:GO:0004298; C:G(	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	0,040	0,000	0,050	0,076	0,000									
Solyc03g063470	Mitovirus RNA-dependent RNA polymerase (AHRD V3.3 *** AT2G07749.1)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane	IPR008686 (PFAM): PTHR34456:SF3	0,000	0,043	0,071	0,176	0,072									
Solyc03g063480	LOW QUALITY:high chlorophyll fluorescent 107 (AHRD V3.3 --* AT3G17040.2)		C:GO:0005739	C:mitochondrion	PTHR34890 (PANTHER)	0,852	0,836	1,782	1,634	1,695									
Solyc03g063500	NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A068BCT0_BRAOB)		C:GO:0005739; F:G(	C:mitochondrion; F: EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001750 (PFAM): PTHR22773 (PAI	0,000	0,021	0,000	0,000	0,000									
Solyc03g063510	NADH dehydrogenase subunit 2 (AHRD V3.3 --* A0A1C9I9Q6_9ROSI)					0,000	0,043	0,000	0,000	0,000									
Solyc03g063525	RNA-binding family protein (AHRD V3.3 *-* A0A061FBT9_THECC)		F:GO:0003676	F:nucleic acid binding	PTHR45276 (PANTHER)	0,000	0,019	0,000	0,000	0,000									
Solyc03g063550	LOW QUALITY:cotton fiber protein (AHRD V3.3 *** AT3G57950.1)				IPR008480 (PFAM): PTHR33450 (PAI	0,000	0,021	0,000	0,000	0,000									
Solyc03g063560	Glutamate synthase, putative (AHRD V3.3 *** B9SLP5_RICCO)		P:GO:0006537; F:G(	P:glutamate biosynthetic process; F:glutamate synthase activity	IPR002489 (PFAM): IPR002932 (PFA	238,146	297,780	269,018	290,017	371,405			0,462	0,001				up	
Solyc03g063580	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)				IPR012876 (PFAM): IPR012876 (PAN	0,159	0,160	0,197	0,164	0,140									
Solyc03g063585	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic (AHRD V3.3 --* ISPF_ORYSJ)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding; C:membrane; C:integral comp	mobidb-lite (MOBIDB_LITE)	0,000	0,018	0,194	0,050	0,046									
Solyc03g063600	Guanylate kinase (AHRD V3.3 *** W9QSK2_9ROSA)		F:GO:0004385; F:G(	F:guanylate kinase EC:2.7.4.4; EC:2.7.4 Nucleoside-phosphat	IPR008145 (SMART): IPR017665 (TI(	131,413	216,961	402,225	495,142	374,113									
Solyc03g063640	HEAT repeat-containing protein (AHRD V3.3 --* AT1G67140.3)					0,122	0,300	0,047	0,124	0,093									
Solyc03g063650	Serine/threonine-protein kinase (AHRD V3.3 *** K4BHA7_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR001480 (SMART): IPR003609 (SM	3,319	5,449	2,871	3,218	2,590									
Solyc03g063680	Zinc finger transcription factor 26	C3H26	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding	IPR002110 (SMART): IPR000571 (SM	7,503	6,403	2,831	2,161	2,914									
Solyc03g063690	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MS71_ARALL)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (TIGRFAM): IPR002885 (F	2,040	3,131	2,635	2,999	2,730									
Solyc03g063700	ARM repeat superfamily protein (AHRD V3.3 *-* AT3G57570.1)				PTHR37743 (PANTHER): IPR016024 (	0,000	0,000	0,022	0,000	0,000									
Solyc03g063710	two-pore channel 1 (AHRD V3.3 --* AT4G03560.1)					0,000	0,019	0,025	0,000	0,000									
Solyc03g063720	RING/FYVE/PHD zinc finger superfamily protein, putative (AHRD V3.3 *-* A0A061GYX1_THECC)		F:GO:0046872	F:metal ion binding	IPR001965 (SMART): IPR013083 (G3	2,125	1,481	0,452	0,360	0,353									
Solyc03g063730	Protein DETOXIFICATION (AHRD V3.3 *** M1AVC8_SOLTU)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp(	IPR002528 (TIGRFAM): IPR002528 (F	3,981	7,525	4,824	9,430	12,549	0,940	0,029	1,370	0,000	0,967	0,002	up	up	up
Solyc03g063750	exostosin family protein (AHRD V3.3 *** AT3G57630.3)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyc(	IPR013111 (PFAM): IPR004263 (PFA	44,027	40,917	164,086	165,670	142,425									
Solyc03g063760	DNA-binding protein SMUBP-2 (AHRD V3.3 *** A0A0B2PI38_GLYSO)		F:GO:0003677; F:G(	F:DNA binding; F:ATP binding	IPR014001 (SMART): IPR003593 (SM	33,516	31,601	25,722	22,736	27,426									
Solyc03g063765	LOW QUALITY:Polyprotein, putative (AHRD V3.3 *-* Q0KIN7_SOLDE)		F:GO:0046983	F:protein dimerization activity	IPR008906 (PFAM): IPR012337 (SUP	0,021	0,041	0,000	0,000	0,000									
Solyc03g063880	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** Q2Z1Y8_PRUMU)		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR002123 (SMART): IPR002123 (PF	59,359	63,187	75,942	77,377	71,717									
Solyc03g063900	LOW QUALITY:Mitochondrial transcription termination factor family protein (AHRD V3.3 --* AT4G09620.3)					0,000	0,041	0,022	0,025	0,023									
Solyc03g063970	Cornichon (AHRD V3.3 *** A0A103YMW6_CYNCS)		P:GO:0016192	P:vesicle-mediated transport	IPR003377 (SMART): IPR003377 (PF	2,111	1,634	4,020	4,935	3,749									
Solyc03g064010	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** A0A061EWF2_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): G3DS	0,787	1,073	0,164	0,095	0,189									
Solyc03g064020	Ras-related protein RABA4d (AHRD V3.3 *** RAA4D_ARATH)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	0,037	0,000	0,000	0,025	0,000									
Solyc03g064030	alpha/beta hydrolase family protein (AHRD V3.3 *** AT3G12150.1)				IPR019149 (PFAM): IPR029058 (G3D	16,867	16,640	34,511	33,771	31,148									
Solyc03g064040	LOW QUALITY:ubiquitin-specific protease 16 (AHRD V3.3 --* AT4G24560.1)					0,019	0,060	0,075	0,025	0,070									
Solyc03g064047	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G22490.2)				IPR015410 (PFAM)	0,000	0,000	0,000	0,000	0,024									
Solyc03g065050	Ribosomal protein S12 (AHRD V3.3 *-* A0A0S2M9Q3_9GENT)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:chloroplast	G3DSA:2.40.50.140 (GENE3D): IPR0	0,021	0,043	0,000	0,098	0,047									
Solyc03g065205	DUF1336 family protein, putative (DUF1336) (AHRD V3.3 *** AT5G39430.1)				IPR009769 (PFAM): PTHR31558:SF1	0,000	0,000	0,000	0,000	0,024									
Solyc03g065230	LOW QUALITY:Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q7G3C6_ORYSJ)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	PTHR33499 (PANTHER): PTHR33499	0,000	0,021	0,149	0,000	0,000									
Solyc03g065250	Fatty acid hydroxylase superfamily protein (AHRD V3.3 *** A0A072TKE8_MEDTR)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas	IPR006694 (PFAM): IPR021940 (PFA	13,284	13,233	117,547	139,950	105,029									
Solyc03g065320	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_TOBAC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA p(	IPR007120 (PFAM): IPR037033 (G3D	0,000	0,021	0,025	0,051	0,023									
Solyc03g065340	Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** K4BHG4_SOLLC)	PHO1/PHS1	P:GO:0005975; F:G(	P:carbohydrate met EC:2.4.1.1 Glycogen phosphoryl	IPR000811 (PIRSF): G3DSA:3.40.50.:	922,891	571,797	288,641	157,866	231,580	-0,662	0,010			-0,869	0,002	down		down
Solyc03g065350	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT5G15490.1)		P:GO:0000271; F:G(	P:polysaccharide bi EC:1.1.1.22 UDP-glucose 6-dehy	IPR014027 (SMART): IPR014027 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc03g070380	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:G(	P:jasmonic acid me EC:3.1.1.1 Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,069	0,071									
Solyc03g070390	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (AHRD V3.3 *** UPTG1_SOLTU)		F:GO:0016866; P:G(	F:intramolecular transferase activity; P:plant-type cell wall orgai	IPR004901 (PIRSF): IPR037595 (PFA	9,731	9,351	1,611	1,465	1,990									
Solyc03g070430	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G14170.2)					0,527	0,417	0,438	0,923	0,683									
Solyc03g070440	COBRA-like protein (AHRD V3.3 *** L0ATP1_POPTO)		P:GO:0010215; P:G(	P:cellulose microfibril organization; P:cell growth; C:anchored cc	IPR006918 (PIRSF): IPR006918 (PFA	1,746	1,182	0,065	0,263	0,236									
Solyc03g070450	Protein COBRA, putative (AHRD V3.3 *-* B9RLL0_RICCO)		P:GO:0010215; P:G(	P:cellulose microfibril organization; P:cell growth; C:anchored cc	IPR006918 (PANTHER): IPR006918 (I	0,000	0,000	0,025	0,000	0,000									
Solyc03g071520	LOW QUALITY:Hexosyltransferase (AHRD V3.3 *** K4BHI2_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR001079 (PFAM): G3DSA:2.60.120	0,042	0,018	0,000	0,025	0,023									
Solyc03g071533	catalase 3 (AHRD V3.3 --* AT1G20620.6)					0,907	0,805	0,338	0,517	0,352									
Solyc03g071540	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_PORAR)					1,477	1,134	1,217	1,573	1,270									
Solyc03g071550	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *-* G7K198_MEDTR)		F:GO:0046872	F:metal ion binding	IPR001965 (SMART): G3DSA:3.40.63	9,266	8,209	11,257	11,688	10,782									

Solyc03g071555	RNA binding protein (AHRD V3.3 --* A0A0K9NY52_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	3,618	2,897	5,406	6,168	5,823									
Solyc03g071560	Glycine-rich RNA-binding family protein (AHRD V3.3 *** B9HUL0_POPTR)		F:GO:0003676: F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR000504 (PF.	0,135	0,282	0,280	0,422	0,567									
Solyc03g071570	Pectate lyase (AHRD V3.3 *** K4BHI7_SOLLC)		C:GO:0016021: F:GC	C:integral compone	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	0,446	0,440	0,747	1,109	0,659									
Solyc03g071590	chloroplast malate dehydrogenase	chmdh	P:GO:0005975: P:GC	P:carbohydrate met	EC:1.1.1.82	Malate dehydrogenas	IPR022383 (PFAM): IPR011273 (TIGF	24,308	46,684	17,474	20,509	34,953	0,967	0,000	0,994	0,000			up	up	
Solyc03g071620	Histone H2B (AHRD V3.3 *** K4BHJ2_SOLLC)		C:GO:0000786: F:GC	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	38,576	39,691	46,609	38,039	37,311									
Solyc03g071630	LOW QUALITY:RNA-binding protein 39 (AHRD V3.3 *-* W9QGD1_9ROSA)		F:GO:0003729: C:GC	F:mRNA binding; C:nucleus; P:mRNA processing; C:cytoplasmic			PTHR44425 (PANTHER): PTHR44425	0,038	0,000	0,000	0,000	0,000									
Solyc03g071640	RNA-binding protein 39 (AHRD V3.3 *-* W9QGD1_9ROSA)		F:GO:0003723: C:GC	F:RNA binding; C:nucleus; P:mRNA processing			PTHR44425:SF1 (PANTHER): PTHR4	0,042	0,021	0,025	0,070	0,046									
Solyc03g071650	LOW QUALITY:TRICHOME BIREFRINGENCE-LIKE 11 (AHRD V3.3 *-* AT5G19160.2)		C:GO:0005794: C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR029962 (PAN	5,816	3,835	3,313	4,646	3,958									
Solyc03g071660	LOW QUALITY:Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *-* W9QQU0_9ROSA)		C:GO:0000932: P:GC	C:P-body; P:deadenylation-independent decapping of nuclear-tr			PTHR15598:SF7 (PANTHER): PTHR1	0,138	0,101	0,097	0,050	0,000									
Solyc03g071670	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** A0A061FPQ4_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc03g071680	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** A0A061FPQ4_THECC)						IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,019	0,000	0,000	0,024									
Solyc03g071690	Non-symbiotic hemoglobin 1 (AHRD V3.3 *** A0A199VNT0_ANACO)		F:GO:0019825: F:GC	F:oxygen binding; F:heme binding			IPR001032 (PRINTS): IPR000971 (PF	3,791	10,248	2,134	2,663	5,342	1,454	0,000	1,321	0,002			up	up	
Solyc03g071700	LOW QUALITY:Photosystem I iron-sulfur center (AHRD V3.3 --* PSAC_PINTH)							0,895	0,489	0,097	0,097	0,069									
Solyc03g071710	Cyclin-dependent protein kinase inhibitor Siamese (AHRD V3.3 *** M4M6N3_GOSAR)		P:GO:0032875	P:regulation of DNA endoreduplication			PTHR33142:SF13 (PANTHER): IPR04	30,021	18,271	30,679	32,653	28,900									
Solyc03g071720	Phytol kinase (AHRD V3.3 *** D2D1G4_LACSA)	VTE5	C:GO:0009507: P:GC	C:chloroplast; P:vitamin E biosynthetic process; F:phytol kinase			PTHR32523:SF7 (PANTHER): IPR039	11,541	14,672	7,672	8,778	9,670									
Solyc03g071730	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT1G31600.3)		F:GO:0004869: P:GC	F:cysteine-type endopeptidase inhibitor activity; P:negative reg			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,162	0,000	0,000	0,072	0,096									
Solyc03g071750	3-phosphoinositide-dependent protein kinase (AHRD V3.3 *** AT3G10540.1)		F:GO:0004674: F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): PIRSF000654 (	3,109	2,968	1,300	1,357	1,269									
Solyc03g071770	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLLC)		F:GO:0003677: F:GC	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	SSF64484 (SUPERFAMILY)	0,000	0,019	0,000	0,000	0,000									
Solyc03g071790	Defective in meristem silencing 3 (AHRD V3.3 *** A0A061G2F1_THECC)						PTHR33566 (PANTHER): PTHR33566	1,030	0,708	0,534	0,290	0,305									
Solyc03g071795	Defective in meristem silencing 3 (AHRD V3.3 --* A0A061G2F1_THECC)						PTHR33566 (PANTHER): PTHR33566	0,164	0,313	0,050	0,092	0,000									
Solyc03g071800	Gamma-irradiation and mitomycin c induced 1, putative isoform 3 (AHRD V3.3 *-* A0A061G1V8_THECC)						PTHR33566 (PANTHER): PTHR33566	0,000	0,018	0,000	0,000	0,023									
Solyc03g071850	Glycosyltransferase (AHRD V3.3 *** K4BHL4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,038	0,018	0,143	0,116	0,000									
Solyc03g071857	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL1_TOBAC)	PAL	F:GO:0003824	F:catalytic activity			IPR001106 (PFAM): IPR023144 (G3D	0,203	0,354	0,025	0,047	0,118									
Solyc03g071870	Phenylalanine ammonia-lyase (AHRD V3.3 *-* PAL5_SOLLC)		F:GO:0003824	F:catalytic activity			IPR001106 (PFAM): IPR024083 (G3D	0,136	0,099	0,000	0,072	0,070									
Solyc03g077910	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061EEC9_T		F:GO:0008375: C:GC	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297:SF1	7,042	7,280	1,847	1,801	1,737									
Solyc03g077920	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT5G06850.1)		F:GO:0008565: C:GC	F:protein transporter activity; C:plasmodesmatal endoplasmic re			IPR000008 (SMART): IPR013583 (PF.	10,001	10,422	10,221	13,522	12,476									
Solyc03g077925	40S ribosomal protein S9, putative (AHRD V3.3 *** Q60CZ2_SOLDE)		F:GO:0003723: F:GC	F:RNA binding; F:structural constituent of ribosome; C:ribosome			G3DSA:3.40.50.150 (GENE3D): PF02	0,319	0,625	0,291	0,265	0,612									
Solyc03g077930	40S ribosomal protein s9 (AHRD V3.3 *-* F4YFG2_CAMSI)		F:GO:0003735: F:GC	F:structural constituent of ribosome; F:rRNA binding; C:cytosolic			PTHR11831:SF5 (PANTHER): IPR022	0,021	0,000	0,000	0,000	0,000									
Solyc03g077950	O-fucosyltransferase family protein (AHRD V3.3 *** AT2G01480.1)		P:GO:0006004: C:GC	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	2,370	2,363	1,594	1,358	1,579									
Solyc03g077960	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 --* AT2G35720.1)							1,375	1,197	0,870	0,814	0,940									
Solyc03g077970	LOW QUALITY:RNA-directed DNA polymerase (Reverse transcriptase) (AHRD V3.3 *** A2Q1A3_MEDTR)						PTHR45245 (PANTHER)	0,000	0,000	0,025	0,000	0,000									
Solyc03g078000	Vacuolar glucose transporter 1	VGT1	C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	72,388	79,558	68,999	73,469	91,319			0,402	0,023				up	
Solyc03g078005	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_ENCLE)		C:GO:0009522: P:GC	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM): IPR036408 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc03g078010	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524: C:GC	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,022	0,100	0,024									
Solyc03g078015	Peptide chain release factor 1 (AHRD V3.3 *-* AT2G47020.5)		F:GO:0004371: P:GC	F:glycerone kinase	EC:2.7.1.29	Glycerone kinase	IPR004006 (PFAM): G3DSA:3.40.50.1	2,710	3,273	2,868	3,140	3,201									
Solyc03g078020	Peptide chain release factor 1 (AHRD V3.3 *-* A0A0B2SGE7_GLYSO)		P:GO:0006415	P:translational termination			IPR005139 (SMART): G3DSA:3.30.70	2,853	2,475	2,850	3,149	3,485									
Solyc03g078025	Peptide chain release factor, putative (AHRD V3.3 *-* B9RN56_RICCO)		F:GO:0003747: P:GC	F:translation release factor activity; P:translational termination			G3DSA:3.30.70.1660 (GENE3D): G3D	5,250	5,291	7,097	6,409	6,150									
Solyc03g078030	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* AT3G60290.1)							1,351	2,175	1,407	1,552	1,558									
Solyc03g078050	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)						IPR012876 (PFAM): IPR012876 (PAN	0,218	0,178	0,148	0,378	0,164									
Solyc03g078055	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT1G26850.3)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): PTHR10108:SF1	1,679	1,592	1,004	1,364	1,180									
Solyc03g078060	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT1G26850.3)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): PTHR10108:SF1	2,881	3,082	2,266	2,096	2,288									
Solyc03g078080	Uridylate kinase (AHRD V3.3 *** W9QLW7_9ROSA)		C:GO:0005737: P:GC	C:cytoplasm; P:pyri	EC:2.7.4.4: EC:2.7.4	Nucleoside-phosphat	IPR015963 (TIGRFAM): IPR036393 (	29,758	34,223	35,181	35,389	41,437									
Solyc03g078090	Pectinesterase (AHRD V3.3 *** K4BHN9_SOLLC)		F:GO:0004857: F:GC	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR012334 (G3	0,453	0,925	0,146	0,194	0,186									
Solyc03g078100	Pectinesterase (AHRD V3.3 *** K4BHP0_SOLLC)		F:GO:0004857: F:GC	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR000070 (PF.	39,847	26,890	18,714	15,945	19,659									
Solyc03g078120	NAC domain protein, (AHRD V3.3 *-* A0A061FNG1_THECC)	NAC027	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM: NAC	25,959	63,736	31,732	33,943	30,207	1,322	0,000					up		
Solyc03g078150	Amino acid transporter family protein (AHRD V3.3 *** D7LGK0_ARALL)		F:GO:0003333: C:GC	P:amino acid transmembrane transport; C:vacuolar membrane;			IPR013057 (PFAM): mobidb-lite (MOB	28,432	22,137	31,619	26,213	32,763									
Solyc03g078160	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT3G07470.1)						IPR007493 (PFAM): IPR036758 (G3D	7,032	3,929	3,348	4,137	4,089									
Solyc03g078190	LOW QUALITY:Protein phosphatase 2A regulatory B subunit family protein (AHRD V3.3 --* AT3G21650.2)		F:GO:0005488: C:GC	F:binding; C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc03g078200	Subtilisin-like protease (AHRD V3.3 *-* W9RY25_9ROSA)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	PF17766 (PFAM): IPR036852 (G3DSA	1,765	0,464	0,047	0,050	0,119									
Solyc03g078203	Subtilisin-like protease (AHRD V3.3 *-* W9RY25_9ROSA)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	0,675	0,231	0,000	0,000	0,000									
Solyc03g078207	Subtilisin-like protease (AHRD V3.3 *-* W9RY25_9ROSA)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,953	0,134	0,000	0,000	0,000									
Solyc03g078210	En/Spm-like transposon protein, putative (AHRD V3.3 --* Q9C6X8_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,548	3,815	2,547	3,092	2,652									
Solyc03g078230	RING/U-box superfamily protein (AHRD V3.3 *** AT1G47570.1)		F:GO:0016874: F:GC	F:ligase activity; F:metal ion binding			IPR001841 (SMART): IPR001841 (PF.	3,703	3,876	3,098	2,981	3,062									
Solyc03g078240	Glycosyltransferase (AHRD V3.3 *** K4BHQ3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,038	0,021	0,000	0,000	0,000									
Solyc03g078280	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL5_SOLLC)	PAL	F:GO:0003824	F:catalytic activity			IPR001106 (PFAM): G3DSA:1.20.200	0,782	0,673	0,271	0,216	0,423									
Solyc03g078290	Ribosomal protein S13 (AHRD V3.3 *** A0A103XPA4_CYNCS)		F:GO:0003723: F:GC	F:RNA binding; F:structural constituent of ribosome; C:ribosome			G3DSA:1.10.8.50 (GENE3D): IPR001	59,813	71,469	50,720	48,782	46,607									
Solyc03g078300	Disease resistance protein (AHRD V3.3 *** A0A068EUA8_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	33,056	34,097	26,081	29,669	31,631									
Solyc03g078310	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *-* A0A0K9P2Z4_ZOSMR)		F:GO:0003824	F:catalytic activity			PTHR43272:SF9 (PANTHER): PTHR4	0,161	0,399	0,197	0,248	0,258									
Solyc03g078320	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *-* A0A0G2SJB5_SALMI)		F:GO:0003824	F:catalytic activity			PTHR43272 (PANTHER): PTHR43272	0,158	0,132	0,068	0,172	0,188									
Solyc03g078330	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4BHR2_SOLLC)		P:GO:0006633: C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR016039 (G3DSA:3.40.47.GENE3D	0,000	0,021	0,025	0,000	0,000									
Solyc03g078350	UPF0235 protein C15orf40 like (AHRD V3.3 *** A0A0B2R9A9_GLYSO)						IPR003746 (SMART): IPR003746 (PF.	8,513	7,312	9,313	9,264	8,459									
Solyc03g078360	Serine/threonine-protein kinase (AHRD V3.3 *** K4BHR5_SOLLC)		F:GO:0004674: F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): G3DSA:1.10.51	34,023	22,236	41,927	91,048	58,395			0,475	0,005	1,122	0,000		up	up
Solyc03g078370	Serine/threonine-protein kinase (AHRD V3.3 *** K4BHR6_SOLLC)		F:GO:0004674: F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	55,230	41,880	11,452	15,622	17,251			0,590	0,025				up	
Solyc03g078380	Glutaredoxin family protein (AHRD V3.3 *** AT5G13810.1)		F:GO:0009055: F:GC	F:electron transfer activity; F:protein disulfide oxidoreductase a			G3DSA:3.40.30.10 (GENE3D): IPR00	47,526	40,433	125,505	128,594	116,092									
Solyc03g078390	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** G7JCB7_MEDTR)		F:GO:0004843: P:GC	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR006615 (SMART): G3DSA:3.90.70	50,443	42,648	44,244	45,676	44,882									
Solyc03g078400	actin	act	F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): IPR004000 (SM	1961,947	1425,953	885,749	737,587	813,842									
Solyc03g078403	RING/U-box superfamily protein (AHRD V3.3 --* AT3G02290.5)		F:GO:0004842: C:GC	F:ubiquitin-protein transferase activity; C:nucleus; P:DNA repair			mobidb-lite (MOBIDB_LITE)	0,019	0,037	0,000	0,000	0,000									
Solyc03g078405	Eukaryotic translation initiation factor 6 (AHRD V3.3 --* IF6_BETVU)							0,115	0,000	0,022	0,076	0,070									
Solyc03g078430	Cinnamyl-alcohol dehydrogenase (AHRD V3.3 *-* Q53X16_MEDSA)		P:GO:0008152: F:GC	P:metabolic process; F:oxidoreductase activity, acting on the C			G3DSA:3.90.180.10 (GENE3D): PTHF	0,000	0,018	0,000	0,000	0,000									
Solyc03g078440	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9SVQ2_RICCO)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.40.50	17,746	13,624	1,117	0,386	0,730									
Solyc03g078490	Glycosyltransferase (AHRD V3.3 *** K4BHS7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,370	0,343	0,533	0,873	1,101									
Solyc03g078510	LOW QUALITY:Fatty acid hydroxylase superfamily (AHRD V3.3 --* AT1G02205.2)							0,000	0,043	0,000	0,000	0,047									
Solyc03g078520	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9P3X9_ZOSMR)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR003591 (SM	16,375	19,055	28,580	35,743	33,381									
Solyc03g078570	Ras-related protein (AHRD V3.3 *** W9QNC0_9ROSA)		F:GO:0003924: F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	11,215	19,532	4,790	4,135	4,423	0,825	0,005					up		
Solyc03g078580	LOW QUALITY:Unknown protein (AHRD V3.3)							0,000	0,043	0,000	0,000	0,000									
Solyc03g078590	LOW QUALITY:Protein argonaute (AHRD V3.3 *-* A0A151T3S6_CAJCA)		F:GO:0003676: P:GC	F:nucleic acid binding; P:gene silencing by RNA			G3DSA:3.40.50.2300 (GENE3D): G3D	0,077	0,061	0,044	0,216	0,094									
Solyc03g078610	N-lysine methyltransferase (AHRD V3.3 *** AT1G78150.2)						IPR025131 (PFAM): mobidb-lite (MOB	22,226	23,696	25,377	20,099	21,754									
Solyc03g078620	LOW QUALITY:Nitric oxide synthase-interacting protein, putative (AHRD V3.3 *** A0A061DQB5_THECC)						PTHR35503 (PANTHER): PTHR35503	0,000	0,018	0,047	0,051	0,048									
Solyc03g078630	Polyubiquitin (AHRD V3.3 *-* UBI2P_PETCR)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): IPR000626 (SM	15,507	53,793	9,210	9,178	7,585	1,820	0,000					up		
Solyc03g078640	LOW QUALITY:Mediator of RNA polymerase II transcription subunit 26, putative (AHRD V3.3 *** A0A061DI3		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	49,461	64,008	7,290	8,528	9,151									
Solyc03g078650	Lipase (AHRD V3.3 *** G7JAK3_MEDTR)						IPR006873 (PFAM): IPR006873 (PAN	0,942	1,779	0,293	0,237	0,259									
Solyc03g078710	Glycosyltransferase (AHRD V3.3 *** M1C4J3_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,613	0,635	0,321	0,292	0,353									
Solyc03g078720	Glycosyltransferase (AHRD V3.3 *** K4BHV3_SOLLC)		F:GO:0008194: F:GC	F:UDP-glycosyltransferase activity; F:transferase activity, trans			G3DSA:3.40.50.2000 (GENE3D): G3D	3,271	2,198	2,130	1,776	1,979									
Solyc03g078730	Glycosyltransferase (AHRD V3.3 *-* K4BHV3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	12,144	9,137	6,484	5,095	6,768									
Solyc03g078770	Glycosyltransferase (AHRD V3.3 *** K4BHV3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,000	0,000	0,000	0,000	0,023									
Solyc03g078780	UDP-glycosyltransferase (AHRD V3.3 *** A0A164TMY6_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	2,436	10,325	1,376	3,754	6,034	2,104	0,000	2,123	0,000	1,443	0,000	up	up	up
Solyc03g078800	Glycosyltransferase (AHRD V3.3 *** K4BHV3_SOLLC)		F:GO:0016740	F:transferase activity			G3DSA:3.40.50.2000 (GENE3D): PTH	0,552	0,873	0,000	0,000	0,000									
Solyc03g078810	UDP-glycosyltransferase (AHRD V3.3 *** A0A164TMY6_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,171	0,429	0,000	0,000	0,024									
Solyc03g078813	F-box family protein (AHRD V3.3 --* AT1G25211.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,350	2,353	2,981	2,987	2,641									
Solyc03g078830	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50120.1)		C:GO:0016020	C:membrane			IPR004158 (PFAM): PTHR31549:SF6	0,021	0,192	0,000	0,000	0,024									
Solyc03g079850	guanylyl cyclase						IPR018616 (PFAM): IPR018616 (PAN	10,348	9,242	16,181	15,697	14,426									
Solyc03g079860	DUF616 family protein (AHRD V3.3 *-* G7IPT3_MEDTR)		P:GO:0006672: C:GC	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): IPR008901 (PAN	0,058	0,000	0,050	0,000	0,024									
Solyc03g079865	Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 --* A0A151SL68_CAJCA)		F:GO:0003677: F:GC	F:DNA binding; F:endonuclease activity; P:DNA repair; P:nucleic			acid phosphodiester bond hydrolysis	2,520	2,126	2,727	2,776	2,373									
Solyc03g079880	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9HHI8_POPTR)		F:GO:0005504: P:GC	F:fatty acid binding; P:systemic acquired resistance			G3DSA:1.10.110.10 (GENE3D): IPR0	0,321	0,863	0,119	0,000	0,070									
Solyc03g079890	Subtilisin-like serine protease (AHRD V3.3 *** A0A072U8N9_MEDTR)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,000	0,000	0,125	0,000	0,094									
Solyc03g079910	Protein DA1-related 1 (AHRD V3.3 *** A0A199UXH9_ANACO)		F:GO:0046872	F:metal ion binding			IPR001781 (SMART): IPR001781 (PF	1,530	1,410	0,535	0,486	0,587									
Solyc03g079920	WD40 repeat-containing protein (AHRD V3.3 *** A0A103Y9A7_CYNCS)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	18,500	15,475	21,746	22,787	20,977									
Solyc03g079930	Mitochondrial glycoprotein (AHRD V3.3 *** A0A103YDB4_CYNCS)		C:GO:0005759	C:mitochondrial matrix			IPR003428 (PFAM): IPR036561 (G3D	0,084	0,181	0,211	0,116	0,143									
Solyc03g079940	Mitochondrial import inner membrane translocase subunit Tim17-like protein (AHRD V3.3 *** A0A0B0N7E3_(		F:GO:0005515: C:GC	F:protein binding; C:TIM22 mitochondrial import inner membrane			G3DSA:1.10.150.50 (GENE3D): IPR0(	151,453	148,538	135,637	124,385	130,807									
Solyc03g079950	double-stranded DNA binding protein (AHRD V3.3 *-* AT5G24630.9)		F:GO:0003690: C:GC	F:double-stranded DNA binding; C:DNA topoisomerase complex			mobidb-lite (MOBIDB_LITE): mobidb-lit	21,118	19,078	26,341	26,972	22,157									
Solyc03g079960	Pathogenesis-related thaumatin superfamily protein (AHRD V3.3 *** AT5G24620.3)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS): IPR001938 (SM	0,140	0,329	0,047	0,050	0,024									
Solyc03g079970	F-box SKIP31-like protein (AHRD V3.3 *** A0A0B0N9S3_GOSAR)						PTHR36372 (PANTHER)	0,273	0,060	0,025	0,070	0,093									
Solyc03g079980	transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT3G18215.1)		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31168:SF3	0,511	0,613	0,386	0,617	0,374									
Solyc03g080000	LOW QUALITY:transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31168:SF3	0,021	0,018	0,000	0,000	0,071									
Solyc03g080010	DNA mismatch repair protein MutS2-like (AHRD V3.3 *** Q9LVW1_ARATH)		F:GO:0004519: F:GC	F:endonuclease act	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR000432 (SMART): IPR000432 (PF.	16,767	15,370	11,405	13,234	16,735			0,547	0,018				up	
Solyc03g080020	UNC93-like protein (AHRD V3.3 *** A0A0B2SHJ9_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR010291 (PFAM): G3DSA:1.20.125	3,277	3,644	34,247	47,623	30,889					0,481	0,028			up
Solyc03g080030	PGPS/D3 (AHRD V3.3 *** Q9ZTN4_PETHY)		P:GO:0044237	P:cellular metabolic process			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,059	0,098	0,000	0,000	0,000									
Solyc03g080040	Serine protease inhibitor, Kazal-type family protein (AHRD V3.3 *** F4JG23_ARATH)		C:GO:0016021	C:integral component of membrane			PTHR34376 (PANTHER)	2,520	3,322	2,855	2,462	2,430									
Solyc03g080050	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT4G27585.1)		C:GO:0016020	C:membrane			IPR001972 (PRINTS): IPR001107 (SM	33,521	34,050	62,520	59,617	55,399									
Solyc03g080060	LOW QUALITY:Clade XV lectin receptor kinase (AHRD V3.3 *** A0A0K1U1X9_SOLLC)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	74,884	28,242	54,006	39,292	51,130	-1,377	0,000					down		
Solyc03g080070	WAT1-related protein (AHRD V3.3 *-* K4BHY3_SOLLC)		C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport			PTHR31218:SF26 (PANTHER): IPR03	0,236	0,170	0,000	0,000	0,023									
Solyc03g080075	WAT1-related protein (AHRD V3.3 *** K4BHY3_SOLLC)		C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	2,937	3,798	0,147	0,173	0,447									
Solyc03g080080	Calcium-binding endonuclease/exonuclease/phosphatase family (AHRD V3.3 *** AT5G54130.2)		F:GO:0005509	F:calcium ion binding			IPR036691 (G3DSA:3.60.10.GENE3D	9,243	9,874	3,345	3,459	3,915									
Solyc03g080090	Nam-like protein 1	NAC028	F:GO:0003677: P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	372,911	407,820	210,356	320,185	320,806			0,606	0,006	0,607	0,009		up	up
Solyc03g080100	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G24580.4)		P:GO:0030001: F:GC	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): G3DS	53,253	43,230	12,296	26,448	21,385			0,797	0,014	1,110	0,000		up	up
Solyc03g080110	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061G9N4_THECC)		P:GO:0030001: F:GC	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	0,392	0,236	1,024	1,548	1,159									
Solyc03g080120	LOW QUALITY:holocarboxylase synthetase 2 (AHRD V3.3 --* AT1G37150.8)							2,055	4,234	1,645	2,390	1,891									
Solyc03g080140	Hexokinase type 1 (AHRD V3.3 *** A0A0B0MXR5_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	110,896	100,055	116,976	128,397	119,317									
Solyc03g080150	Peroxidase (AHRD V3.3 *** K4BHZ1_SOLLC)		F:GO:0004601: P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,222	1,157	0,166	0,270	0,235									
Solyc03g080160	Nascent polypeptide associated complex alpha subunit, putative (AHRD V3.3 *** B9S5M4_RICCO)		C:GO:0005854	C:nascent polypeptide-associated complex			IPR002715 (SMART): G3DSA:1.10.8.1	208,540	185,825	138,108	113,365	125,856									
Solyc03g080170	28 kDa ribonucleoprotein, chloroplastic (AHRD V3.3 *-* R7VZU8_AEGTA)						PTHR33443 (PANTHER)	5,321	4,339	6,118	5,184	5,088									
Solyc03g080180	Caffeic acid O-methyltransferase (AHRD V3.3 *** A0A0G4DCV8_CAPCH)		F:GO:0008171: F:GC	F:O-methyltransferase activity; F:protein dimerization activity			IPR016461 (PIRSF): IPR036388 (G3D	22,811	21,567	6,959	7,421	11,323									
Solyc03g080190	2-oxoglutarate Fe(II) dependent oxygenase superfamily protein		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	9,173	41,523	5,338	7,593	9,645	2,204	0,000					up		
Solyc03g081190	LOW QUALITY:9-cis-epoxycarotenoid dioxygenase NCED3, chloroplastic (AHRD V3.3 --* NCED3_ARATH)							1,759	1,648	2,336	1,634	1,739									
Solyc03g081200	WD40 repeat protein (AHRD V3.3 *** L7T9S0_SOLTU)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	3,706	4,820	3,905	4,128	3,981									
Solyc03g081203	WD40 repeat protein (AHRD V3.3 --* L7T9S0_SOLTU)							0,318	0,456	0,474	0,446	0,448									
Solyc03g081207	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT5G67385.5)							0,144	0,217	0,118	0,245	0,236									
Solyc03g081210	WD40 repeat protein (AHRD V3.3 *** L7T9S0_SOLTU)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	1,495	1,097	0,760	0,880	0,683									
Solyc03g081220	LOW QUALITY:RING-H2 zinc finger protein (AHRD V3.3 *** AT5G24460.1)		C:GO:0005618: F:GC	C:cell wall; F:hydrolase activity			PTHR36395 (PANTHER)	28,550	42,927	32,416	29,352	31,671	0,614	0,023					up		
Solyc03g081230	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT5G53730.1)		C:GO:0009506: C:GC	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM): PTHR31415:SF2	0,466	0,279	0,670	0,342	0,261									
Solyc03g081240	Two-component response regulator-like protein (AHRD V3.3 *** W9RA17_9ROSA)		P:GO:0000160: F:GC	P:phosphorelay signal transduction system; F:protein binding			IPR001789 (SMART): IPR010402 (PF.	9,139	9,804	10,917	8,404	13,164									
Solyc03g081253	Subtilisin-like protease (AHRD V3.3 *-* A0A151SMH1_CAJCA)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	0,040	0,000	0,049	0,025	0,047									
Solyc03g081260	Subtilisin-like protease (AHRD V3.3 *** W9RY09_9ROSA)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	33,435	29,003	16,448	15,263	18,171									
Solyc03g081270	Pseudo response regulator (AHRD V3.3 *-* A0A087GCX2_ARAAL)		F:GO:0004252: P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR010402 (PFAM): IPR036852 (G3D	0,391	0,490	0,708	0,396	0,658									
Solyc03g081290	LOW QUALITY:Mitotic spindle checkpoint protein MAD2 (AHRD V3.3 --* MAD2_ARATH)						mobidb-lite (MOBIDB_LITE)	0,226	0,018	0,144	0,022	0,118									
Solyc03g081300	Mitochondrial transcription termination factor-related family protein (AHRD V3.3 *** B9IDI0_POPTR)		F:GO:0003690: P:GC	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR003690 (PF.	41,372	24,347	19,110	26,111	26,344	-0,739	0,021	0,458	0,038	0,449	0,024	down	up	up
Solyc03g081310	BnaA02g32530D protein (AHRD V3.3 *** A0A078F0S3_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	17,277	18,671	17,181	17,452	17,398									
Solyc03g081320	StAR-related lipid transfer protein (AHRD V3.3 *** T2DNH6_PHAVU)		F:GO:0008289	F:lipid binding			IPR002913 (PFAM): IPR023393 (G3D	18,436	18,132	10,182	11,533	12,346									
Solyc03g081330	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 65 (AHRD V3.3 *** Q9FQZ0_TOBAC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,353	3,508	2,386	4,871	2,539					1,024	0,042			up
Solyc03g081335	delta 1-pyrroline-5-carboxylate synthase 2 (AHRD V3.3 --* AT3G55610.1)							0,079	0,080	0,047	0,025	0,023									
Solyc03g082350	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 65 (AHRD V3.3 *** Q9FQZ0_TOBAC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,555	0,467	0,559	0,630	0,497									

Solyc03g082355	Mitochondrial import inner membrane translocase subunit TIM16 (AHRD V3.3 --* A0A0K9Q5B1_ZOSMR)		C:GO:0005744: P:G(	C:TIM23 mitochondrial import inner membrane translocase complex: P:protein import into mitochondrial		0,220	0,200	0,612	0,349	0,757									
Solyc03g082360	LOW QUALITY:delta1-pyrroline-5-carboxylate synthase 1 (AHRD V3.3 --* AT2G39800.2)					0,000	0,000	0,000	0,025	0,000									
Solyc03g082363	60S acidic ribosomal protein P1 (AHRD V3.3 *** A0A199VEQ5_ANACO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translationa	IPR038716 (G3DSA:1.10.10.GENE3D	0,000	0,021	0,196	0,240	0,094									
Solyc03g082367	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G02840.1)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF.	10,931	9,774	12,440	11,688	10,337									
Solyc03g082380	Pre-mRNA splicing factor-like protein (AHRD V3.3 *** Q3HRY5_SOLTU)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF.	77,582	86,973	76,979	74,848	75,821									
Solyc03g082390	RNA-binding protein, putative (AHRD V3.3 *** B9T1D4_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF.	1,120	1,157	1,266	1,191	1,041									
Solyc03g082400	heat shock protein 21	hsp21	F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF.	14,187	14,472	21,407	20,024	19,569									
Solyc03g082410	Heat shock induced transcript 2 (AHRD V3.3 *-* Q96486_SOLLC)					0,021	0,055	0,065	0,047	0,047									
Solyc03g082420	Heat shock protein (AHRD V3.3 *** A9QVH3_9FABA)	Hsp26.2	C:GO:0009507	C:chloroplast	IPR002068 (PFAM): IPR008978 (G3D	22,957	35,507	1654,007	1964,566	2457,358									
Solyc03g082430	LOW QUALITY:Growth-regulating factor (AHRD V3.3 *** G7J891_MEDTR)		F:GO:0005524: C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten	IPR014978 (SMAF GRF	0,459	0,665	0,124	0,050	0,047									
Solyc03g082440	LOW QUALITY:Lung seven transmembrane receptor family protein (AHRD V3.3 *** AT5G42090.1)		C:GO:0016021	C:integral component of membrane	IPR009637 (PFAM): IPR009637 (PAN	92,727	92,475	87,174	85,228	75,056									
Solyc03g082450	Receptor-like protein kinase (AHRD V3.3 *** M8BN66_AEGTA)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR000719 (SMA	1,625	2,191	1,357	1,614	1,310									
Solyc03g082470	Receptor-like protein kinase (AHRD V3.3 *** M8BN66_AEGTA)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	1,718	1,310	0,644	0,532	1,084									
Solyc03g082480	GRF1-interacting factor-like protein (AHRD V3.3 *-* A0A072TYG4_MEDTR)		F:GO:0003713	F:transcription coactivator activity	IPR007726 (PFAM): mobidb-lite (MOB	1,452	1,430	1,150	1,496	1,700									
Solyc03g082490	Reticulocyte-binding 2 a (AHRD V3.3 *** A0A0B0N4X3_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	219,672	195,098	241,707	226,082	231,749									
Solyc03g082500	serine/threonine protein kinase pk23	pk23	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF.	34,697	66,970	36,007	33,933	42,814									
Solyc03g082510	Small auxin up-regulated RNA35	SAUR35	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374:SF1	0,161	0,360	0,097	0,126	0,023									
Solyc03g082520	Small auxin up-regulated RNA36	SAUR36	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	0,339	0,491	0,980	1,459	1,179									
Solyc03g082530	Small auxin up-regulated RNA37	SAUR37	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374 (PAN	3,521	2,963	2,148	7,441	2,843					1,788	0,000			up
Solyc03g082540	Triose phosphate/phosphate translocator, chloroplastic (AHRD V3.3 --* A0A1D1YFA4_9ARAE)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	PTHR34116 (PANTHER): PTHR34116	31,792	25,360	13,607	12,066	15,511									
Solyc03g082550	Homeobox leucine zipper (AHRD V3.3 *-* J7FWS7_ROSRU)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR000047 (PRINT HD-ZIP	1,129	0,686	0,403	0,387	0,475									
Solyc03g082560	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT5G53580.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020471 (PRINTS): IPR023210 (PF	7,677	7,908	2,560	2,331	4,578			0,830	0,032				up	
Solyc03g082575	Transcriptional factor B3 family protein (AHRD V3.3 --* AT4G31650.1)					0,000	0,018	0,000	0,000	0,000									
Solyc03g082580	6-phosphogluconolactonase, putative (AHRD V3.3 *** B9RWU5_RICCO)		P:GO:0005975: P:G(	P:carbohydrate met EC:3.1.1.31; EC:3.1. 6-phosphogluconolac	IPR005900 (TIGRFAM): G3DSA:3.40.!	0,203	0,241	0,241	0,164	0,233									
Solyc03g082590	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT3G49350.1)		P:GO:0005975: P:G(	P:carbohydrate met EC:3.1.1.31; EC:3.1. 6-phosphogluconolac	IPR000195 (SMART): G3DSA:1.10.47	63,745	55,437	131,119	133,501	105,567									
Solyc03g082600	Cytochrome b5 (AHRD V3.3 *** A0A0C5DKP2_CATRO)		C:GO:0016021: F:G(	C:integral component of membrane; F:heme binding; F:metal ior	IPR001199 (PRINTS): IPR001199 (SM	248,060	254,336	189,478	160,048	176,099									
Solyc03g082610	senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *-* AT3G15040.1)				IPR007608 (PFAM): PTHR33083 (PAN	20,184	16,358	20,767	17,985	19,999									
Solyc03g082620	Yellow stripe 1A transporter (AHRD V3.3 *** A0A0K9P9K5_ZOSMR)		P:GO:0055085	P:transmembrane transport	IPR004813 (PFAM): IPR004813 (TIGF	59,880	90,872	24,523	21,511	34,769	0,628	0,025	0,499	0,014			up	up	
Solyc03g082630	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G53540.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): PF17862 (PFAM	10,537	12,055	8,152	8,444	9,851									
Solyc03g082640	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G46620.1)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): IPR003959 (PF.	9,192	9,778	2,777	3,481	4,045									
Solyc03g082660	Major facilitator superfamily domain (AHRD V3.3 *** J7G577_ROSRU)		F:GO:0015098: P:G(	F:molybdate ion transmembrane transporter activity; P:molybda	G3DSA:1.20.1250.20 (GENE3D): IPR(	425,079	531,287	136,493	113,393	166,798									
Solyc03g082670	F-box-like protein (AHRD V3.3 *** G7J857_MEDTR)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR001810 (PF.	1,168	0,657	1,999	2,538	2,311									
Solyc03g082680	Neuroblastoma-amplified protein (AHRD V3.3 *** B2Z6N3_NICBE)		P:GO:0006890	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r	IPR013244 (PFAM): mobidb-lite (MOB	27,626	22,590	28,640	29,195	28,582									
Solyc03g082685	Neuroblastoma-amplified protein (AHRD V3.3 *-* B2Z6N3_NICBE)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3I	8,914	6,033	6,493	9,901	7,852									
Solyc03g082690	U-box domain-containing protein 43 (AHRD V3.3 *** W9S1U9_9ROSA)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR000225 (SMART): IPR003613 (SM	7,223	18,628	3,557	6,411	6,303	1,392	0,000	0,813	0,031			up	up	
Solyc03g082700	Oligopeptide transporter, putative (AHRD V3.3 *** B9RYS3_RICCO)		P:GO:0055085	P:transmembrane transport	IPR004648 (TIGRFAM): IPR004813 (T	0,040	0,064	0,000	0,050	0,023									
Solyc03g082710	RNA-binding protein with multiple splicing (AHRD V3.3 *** K9P2M2_9ROSI)		P:GO:0000398: F:G(	P:mRNA splicing, via spliceosome; F:snRNA stem-loop binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	8,083	7,229	6,199	5,810	6,316									
Solyc03g082720	Protein yippee-like (AHRD V3.3 *** K4BI48_SOLLC)		F:GO:0046872	F:metal ion binding	IPR004910 (PFAM): PTHR13848:SF1	74,627	63,339	114,873	105,893	116,374									
Solyc03g082725	Protein IQ-DOMAIN 1 (AHRD V3.3 *-* W9RRW9_9ROSA)		F:GO:0005515	F:protein binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,639	1,739	2,311	1,752	2,160									
Solyc03g082730	Spc97 / Spc98 family of spindle pole body (SBP) component (AHRD V3.3 --* AT3G43610.3)					0,490	0,442	0,219	0,766	0,426									
Solyc03g082740	Protein yippee-like (AHRD V3.3 *** A0A0V0HBB0_SOLCH)		F:GO:0046872	F:metal ion binding	IPR004910 (PFAM): PTHR13848:SF3	6,366	5,609	5,740	5,670	6,052									
Solyc03g082820	Impaired sucrose induction protein, putative (AHRD V3.3 *** G7JST9_MEDTR)		P:GO:0006109	P:regulation of carbohydrate metabolic process	IPR012535 (PFAM): mobidb-lite (MOB	14,898	12,847	12,809	11,856	12,979									
Solyc03g082840	Dof zinc finger protein (AHRD V3.3 *** A0A068PXR9_TOBAC)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM Dof	1,680	1,540	0,613	0,903	0,800									
Solyc03g082850	3'-5' exonuclease domain-containing protein (AHRD V3.3 *** A0A061G214_THECC)		F:GO:0003676: P:G(	F:nucleic acid binding; P:nucleobase-containing compound meta	IPR002562 (SMART): IPR002562 (PF.	25,155	21,945	25,388	25,288	24,682									
Solyc03g082860	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9S1W1_9ROSA)		F:GO:0005515	F:protein binding	IPR001965 (SMART): IPR001214 (PF.	2,657	2,510	0,553	0,313	0,826									
Solyc03g082870	WD-repeat protein, putative (AHRD V3.3 *** B9T7W7_RICCO)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR001680 (SM	24,239	24,799	5,569	5,092	7,140									
Solyc03g082885	glutamate receptor 2 (AHRD V3.3 --* AT4G35290.5)				PTHR34061 (PANTHER)	22,538	19,995	34,811	34,821	29,631									
Solyc03g082890	Thylakoid lumenal 17.4 kDa protein (AHRD V3.3 *** B7FHD5_MEDTR)		C:GO:0016021	C:integral component of membrane	G3DSA:2.160.20.100 (GENE3D): IPR(	10,858	13,929	20,942	22,928	30,648			0,545	0,002				up	
Solyc03g082900	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SJT3_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D): IPR00(	0,369	0,158	0,316	0,392	0,495									
Solyc03g082910	Acyl-CoA-binding domain protein (AHRD V3.3 *** A0A072V293_MEDTR)		F:GO:0000062: F:G(	F:fatty-acyl-CoA binding; F:protein binding	IPR000582 (PRINTS): IPR002110 (PF	26,853	24,039	40,769	37,429	34,832									
Solyc03g082920	Heat shock protein 70 (AHRD V3.3 *** Q9M4E8_CUCSA)		F:GO:0005524: C:G(	F:ATP binding; C:er EC:1.3.1.74 2-alkenal reductase (	IPR013126 (PRINTS): G3DSA:3.90.64	288,157	313,877	323,644	308,685	303,073									
Solyc03g082940	Importin subunit beta-1 (AHRD V3.3 *** IMB1_ARATH)		P:GO:0006606: F:G(	P:protein import into nucleus; F:Ran GTPase binding; F:protein	IPR001494 (SMART): PF13513 (PFAM	132,848	95,732	123,022	139,622	142,439									
Solyc03g082950	BSD domain-containing protein (AHRD V3.3 --* AT2G10950.3)					0,000	0,019	0,025	0,000	0,047									
Solyc03g082970	Protein phosphatase 2C (AHRD V3.3 *** M9VDY5_9AQUA)		F:GO:0004722: P:G(	F:protein serine/thr EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	24,952	35,360	38,562	36,740	45,408									
Solyc03g082980	RNA-binding KH domain-containing protein (AHRD V3.3 *** A0A061G2I2_THECC)		F:GO:0003723	F:RNA binding	IPR004087 (SMART): IPR036612 (G3	69,878	62,650	110,154	108,171	104,814									
Solyc03g082990	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G53080.1)		F:GO:0005515	F:protein binding	IPR019734 (SMART): PF13424 (PFAM	8,081	7,783	4,693	4,115	5,955									
Solyc03g083000	transmembrane protein (AHRD V3.3 *** AT2G46550.3)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	11,777	10,916	12,338	9,761	10,885									
Solyc03g083005	RING/U-box superfamily protein (AHRD V3.3 --* AT5G10650.3)					0,040	0,041	0,022	0,000	0,000									
Solyc03g083010	Hydrolase, alpha/beta fold family protein (AHRD V3.3 *** D7MSC9_ARALL)		C:GO:0016021: F:G(	C:integral component of membrane; F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	22,848	47,228	16,902	12,864	16,213	1,071	0,025					up		
Solyc03g083030	ABL interactor-like protein 3 (AHRD V3.3 *** AT5G24310.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	6,144	10,540	63,538	77,685	62,754	0,805	0,023					up		
Solyc03g083060	Ribonuclease P protein subunit P38, related protein, putative (AHRD V3.3 *** G7J7F4_MEDTR)		F:GO:0005525: P:G(	F:GTP binding; P:signal transduction; C:membrane	mobidb-lite (MOBIDB_LITE): PTHR215	14,379	9,391	7,369	8,080	9,825									
Solyc03g083070	Vesicle-associated membrane family protein (AHRD V3.3 *** B9IDQ1_POPTR)		C:GO:0016021	C:integral component of membrane	G3DSA:3.30.450.50 (GENE3D): mobic	31,418	24,288	29,040	28,187	27,320									
Solyc03g083090	transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 --* AT1G6:	STS2				10,085	9,237	28,560	27,418	27,644									
Solyc03g083095	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *** K4BI85_SOLLC)		F:GO:0004373	F:glycogen (starch) EC:2.4.1.11 Glycogen(starch) syr	IPR013534 (PFAM): IPR001296 (PFA	176,217	172,637	522,964	473,277	475,469									
Solyc03g083100	SUN-like protein 10	SUN10	F:GO:0005515	F:protein binding	IPR000048 (SMART): IPR000048 (PF.	163,473	112,352	7,892	3,256	5,403					-1,276	0,002			down
Solyc03g083120	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 *-* AT5G24280.3)				PTHR33566:SF3 (PANTHER): PTHR3:	0,652	0,613	0,722	0,386	0,588									
Solyc03g083130	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 *** AT5G24280.3)				mobidb-lite (MOBIDB_LITE): PTHR335	9,211	8,594	7,849	7,019	8,212									
Solyc03g083140	Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain-containing protein (AHRD V3.3 --* AT3G44370.2)					7,883	6,123	7,401	7,747	6,844									
Solyc03g083147	Defective in meristem silencing 3 (AHRD V3.3 *** A0A061G2F1_THECC)				PTHR33566 (PANTHER)	3,631	4,146	4,726	4,137	4,783									
Solyc03g083160	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 *-* AT5G24280.3)				PTHR33566 (PANTHER): PTHR33566	1,701	1,848	1,076	0,432	0,712									
Solyc03g083170	Gamma-irradiation and mitomycin c induced 1, putative isoform 3 (AHRD V3.3 *-* A0A061G1V8_THECC)				mobidb-lite (MOBIDB_LITE): PTHR335	5,262	7,567	5,173	0,994	3,655					-2,376	0,000			down
Solyc03g083180	LOW QUALITY:gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 --* AT5G24280.3)				PTHR33566 (PANTHER)	1,169	1,542	1,399	0,167	1,020									
Solyc03g083190	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 *-* AT5G24280.3)				PTHR33566 (PANTHER): PTHR33566	3,210	1,896	2,026	2,517	1,587									
Solyc03g083195	defective in meristem silencing 3 (AHRD V3.3 *-* AT3G49250.1)				PTHR33566 (PANTHER): PTHR33566	2,677	1,897	1,998	2,211	1,740									
Solyc03g083200	En/Spm-like transposon (AHRD V3.3 --* AT5G24275.4)					4,009	3,473	4,043	3,524	2,971									
Solyc03g083210	Defective in meristem silencing 3 (AHRD V3.3 *** A0A061G2F1_THECC)				mobidb-lite (MOBIDB_LITE): PTHR335	28,511	27,689	19,793	16,717	19,480									
Solyc03g083240	Transcription factor jumonji domain-containing protein, putative isoform 2 (AHRD V3.3 --* A0A061G2X9_THE		F:GO:0003677	F:DNA binding	IPR017956 (SMART): mobidb-lite (MO	26,604	21,695	18,630	20,978	20,626									
Solyc03g083245	Transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 *** AT4G00990.1)		F:GO:0003677: F:G(	F:DNA binding; F:methyltransferase activity; P:methylation	IPR003347 (SMART): IPR003347 (PF.	28,598	27,983	24,182	26,633	26,243									
Solyc03g083250	ATP-dependent clp protease ATP-binding subunit clpx, putative (AHRD V3.3 *** B9RSF1_RICCO)		F:GO:0005524: P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding	IPR019489 (SMART): IPR003593 (SM	58,970	54,069	183,563	178,242	165,622									
Solyc03g083260	LOW QUALITY:Reticulocyte-binding protein 2 a (AHRD V3.3 *-* A0A1D1ZCA2_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	3,501	4,416	2,445	3,026	3,171									
Solyc03g083270	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4BIA3_SOLLC)		F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR018121 (PFAM): IPR008974 (G3D	8,627	9,424	10,295	8,298	9,275									
Solyc03g083280	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061G122_THECC)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	41,956	45,801	127,115	111,106	112,365									
Solyc03g083290	40S ribosomal protein S12 (AHRD V3.3 *** K4BIA5_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000530 (PRINTS): IPR029064 (G3	5,898	5,445	5,454	4,938	5,076									
Solyc03g083300	Mediator of RNA polymerase II transcription subunit 22 (AHRD V3.3 *** G7IT38_MEDTR)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription	IPR038427 (G3DSA:1.20.58.GENE3D	5,122	5,875	3,073	2,954	3,157									
Solyc03g083310	Zinc finger, C2H2 (AHRD V3.3 *-* A0A103YAQ2_CYNCS)		C:GO:0000790: F:G(	C:nuclear chromatin; F:RNA polymerase II proximal promoter se	PTHR14003:SF12 C2H2	20,018	20,082	31,182	30,843	30,771									
Solyc03g083320	calcium sensor calcineurin B	cbl	F:GO:0005509	F:calcium ion binding	PR00450 (PRINTS): IPR002048 (SMA	0,021	0,036	0,000	0,000	0,000									
Solyc03g083330	Dipeptidyl peptidase (AHRD V3.3 *** A0A0K9PD44_ZOSMR)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity	IPR002469 (PFAM): IPR001375 (PFA	34,443	36,184	60,618	61,057	55,630									
Solyc03g083350	phosphatidylinositol 4-kinase gamma-like protein (AHRD V3.3 *** AT5G24240.2)		F:GO:0005515	F:protein binding	IPR019956 (PRINTS): IPR000626 (SM	37,217	24,489	43,819	36,303	35,873									
Solyc03g083360	Pectinesterase (AHRD V3.3 *** K4BIB2_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR006501 (SMART): IPR012334 (G3	60,559	52,176	4,698	4,473	5,666									
Solyc03g083370	Lipase class 3 family protein (AHRD V3.3 *** B9GXJ5_POPTR)		P:GO:0006629	P:lipid metabolic process	IPR002921 (PFAM): IPR029058 (G3D	0,158	0,082	0,096	0,145	0,048									
Solyc03g083390	Nuclear migration nudC (AHRD V3.3 *** A0A0B0N407_GOSAR)		C:GO:0005737: P:G(	C:cytoplasm; P:protein folding; P:developmental process; F:unfc	IPR008978 (G3DSA:2.60.40.GENE3D	159,713	152,308	187,022	179,608	187,663									
Solyc03g083395	cytochrome P450, family 96, subfamily A, polypeptide 4 (AHRD V3.3 --* AT5G52320.2)					5,277	5,740	8,311	9,311	7,231									
Solyc03g083400	CCT motif family protein (AHRD V3.3 *** A0A061G1S7_THECC)		F:GO:0005515	F:protein binding	IPR010402 (PFAM): PTHR31717:SF2	31,985	31,283	3,396	3,267	4,285									
Solyc03g083410	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9PJE7_ZOSMR)		F:GO:0005515	F:protein binding	IPR003616 (SMART): IPR001965 (SM	23,260	20,864	21,008	23,123	20,497									
Solyc03g083420	OBP3-responsive protein 1 (AHRD V3.3 *** AT5G53450.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	51,087	55,041	126,094	130,993	122,741									
Solyc03g083430	Splicing factor 3A subunit 3 (AHRD V3.3 *** W9RDU1_9ROSA)		P:GO:0000398: F:G(	P:mRNA splicing, via spliceosome; F:RNA binding; C:spliceosor	IPR031774 (PFAM): PF13297 (PFAM)	160,892	134,820	125,395	115,092	118,786									
Solyc03g083440	Glutamate synthase, putative (AHRD V3.3 *** B9RII5_RICCO)		F:GO:0005506: P:G(	F:iron ion binding; F EC:1.4.1.14 Glutamate synthase (	PR00419 (PRINTS): IPR036188 (G3D	29,803	38,209	62,240	90,483	104,163			0,739	0,000	0,543	0,006		up	up
Solyc03g083450	UPF0369 protein C6orf57 (AHRD V3.3 *** A0A151S3J3_CAJCA)		C:GO:0005739: P:G(	C:mitochondrion; P:mitochondrial respiratory chain complex II a:	IPR012875 (PFAM): mobidb-lite (MOB	16,043	15,315	50,686	50,491	46,588									
Solyc03g083460	RING/U-box superfamily protein (AHRD V3.3 *** AT5G53110.1)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART): IPR001841 (PF.	0,972	2,286	1,678	1,755	1,621									
Solyc03g083470	Receptor-like kinase (AHRD V3.3 *** A0A072VF58_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	4,970	9,323	0,527	2,786	2,973			2,464	0,000	2,368	0,000		up	up
Solyc03g083480	Membrane receptor-like protein 1 (AHRD V3.3 *** B3TJG2_CAPAN)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR33138:SF7	1,966	4,643	0,308	0,578	0,633									
Solyc03g083490	DUF1442 family protein (AHRD V3.3 *** B7FH79_MEDTR)				IPR009902 (PFAM): G3DSA:3.40.50.1	0,000	0,018	0,000	0,000	0,000									
Solyc03g083500	DUF1442 family protein (AHRD V3.3 *** B7FH79_MEDTR)				IPR009902 (PFAM): G3DSA:3.40.50.1	0,000	0,019	0,000	0,000	0,000									
Solyc03g083510	Receptor-like kinase (AHRD V3.3 *** A0A191UPW4_CASSA)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001245 (PFAM): IPR001611 (PFA	0,061	0,081	0,000	0,000	0,000									
Solyc03g083520	Calmodulin family protein (AHRD V3.3 *** B9GVS4_POPTR)		F:GO:0005509	F:calcium ion binding	IPR002048 (SMART): G3DSA:1.10.23	42,186	45,414	46,027	41,852	41,944									
Solyc03g083530	40S ribosomal protein S13 (AHRD V3.3 *** RS13_SOYBN)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR012606 (SMART): IPR000589 (SM	941,039	886,161	462,273	432,787	412,919									
Solyc03g083540	Chloride conductance regulatory protein ICln (AHRD V3.3 *** W9RG94_9ROSA),Pfam:PF03517		P:GO:0000387: C:G(	P:spliceosomal snRNP assembly; C:cytosol; C:plasma membrar	IPR003521 (PRINTS): IPR039924 (PF	21,776	21,255	22,994	15,424	19,921					-0,573	0,001			down
Solyc03g083550	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE2-like	F:GO:0003824: F:G(	F:catalytic activity; F:coenzyme binding	PR01713 (PRINTS): G3DSA:3.40.50.7	1,482	1,198	2,177	2,908	3,048									
Solyc03g083560	Phosphate-responsive 1 family protein (AHRD V3.3 *** G7JP91_MEDTR)		C:GO:0009505: C:G(	C:plant-type cell wall; C:plasmodesma; C:integral component of	IPR006766 (PFAM): PTHR31279:SF7	104,998	97,147	21,286	24,888	22,336									
Solyc03g083570	low psii accumulation2 (AHRD V3.3 *** AT5G51545.1)		C:GO:0009534: C:G(	C:chloroplast thylakoid; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	6,317	9,288	14,309	14,030	16,250									
Solyc03g083580	Mitochondrial intermediate peptidase, putative (AHRD V3.3 *** B9R9Q2_RICCO)		F:GO:0004222: C:G(	F:metalloendopeptic EC:3.4.24 Acting on peptide bor	IPR001567 (PFAM): IPR024077 (G3D	8,269	7,873	9,273	8,513	7,676									
Solyc03g083590	Kinase, putative (AHRD V3.3 *** B9R9Q3_RICCO)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR000719 (SMART): G3DSA:3.30.20	1,963	2,673	2,789	4,511	2,869									
Solyc03g083610	UMP-CMP kinase (AHRD V3.3 *** A0A162A1U3_DAUCA)		F:GO:0004127: F:G(	F:cytidylate kinase EC:2.7.4.4; EC:2.7.4 Nucleoside-phosphat	IPR000850 (PRINTS): G3DSA:3.40.5(	23,595	16,495	30,907	29,880	27,467									
Solyc03g083615	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62350.1)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (PF.	18,915	25,477	125,129	136,380	105,662									
Solyc03g083640	LOW QUALITY:Late embryogenesis abundant protein, LEA-14 (AHRD V3.3 --* A0A103XCK5_CYNCS)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,607	0,515	0,332									
Solyc03g083650	Glycosyltransferase (AHRD V3.3 *** K4BIE1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	0,956	0,793	0,522	0,217	0,356									
Solyc03g083660	LOW QUALITY:Invertase/pectin methylesterase inhibitor family protein (AHRD V3.3 *** B9I4L9_POPTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (TIG	0,000	0,000	0,022	0,000	0,000									
Solyc03g083665	transmembrane protein (AHRD V3.3 *-* AT2G07674.1)		C:GO:0005739: C:G(	C:mitochondrion; C:membrane	PTHR35289 (PANTHER): PD020792 (	0,019	0,000	0,075	0,022	0,047									
Solyc03g083680	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,349	1,258	0,075	0,122	0,094									
Solyc03g083690	LOW QUALITY:RNA-dependent RNA polymerase (AHRD V3.3 --* A0A0D9UXX7_9ORYZ)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,063	0,436	0,000	0,025	0,000									
Solyc03g083700	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** A0A072UIY9_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (TIG	0,000	0,021	0,000	0,000	0,000									
Solyc03g083710	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** I3T947_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (PF.	0,019	0,255	0,025	0,000	0,000									
Solyc03g083720	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** I3T947_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (PF.	0,217	0,790	0,000	0,000	0,000									
Solyc03g083730	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62360.1)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (TIG	8,719	13,706	3,360	4,647	5,492									
Solyc03g083770	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62360.1)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (TIG	0,019	0,157	0,000	0,000	0,000									
Solyc03g083785	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SA73_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAN	0,019	0,000	0,000	0,000	0,024									
Solyc03g083800	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G48120.1)				IPR019557 (PFAM): mobidb-lite (MOB	0,019	0,080	0,025	0,000	0,047									
Solyc03g083810	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SA73_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAN	0,021	0,021	0,000	0,000	0,000									
Solyc03g083820	Endoglucanase (AHRD V3.3 *-* K4BIF7_SOLLC)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	0,040	0,000	0,047	0,025	0,000									
Solyc03g083880	NAC domain protein, (AHRD V3.3 *** A0A061G781_THECC)	NAC029	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,160	0,138	0,000	0,000	0,047									
Solyc03g083900	Monocopper oxidase-like protein SKU5 (AHRD V3.3 *** SKU5_ARATH)		F:GO:0005507: F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red	IPR008972 (G3DSA:2.60.40.GENE3D	22,294	26,004	40,383	68,350	53,893					0,761	0,000			up
Solyc03g083910	symbol=TIV1	TIV1/sucr	F:GO:0004575: P:G(	F:sucrose alpha-glu EC:3.2.1.2; EC:3.2.1 Alpha-glucosidase; S	IPR001362 (SMART): IPR023296 (G3	97,945	80,581	2240,490	482,651	648,618			-1,788	0,003	-2,208	0,000		down	down
Solyc03g083920	LOW QUALITY:Transposon-like element Lyt2-2 DNA (AHRD V3.3 *-* D5MNY6_SOLLC)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding	IPR007527 (PFAM): IPR031052 (PAN	0,000	0,000	0,963	0,073	0,264									
Solyc03g083960	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4BIH1_SOLLC)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	G3DSA:3.30.70.1020 (GENE3D): IPR(	9,374	8,374	0,982	1,209	1,221									
Solyc03g083970	BAG family molecular chaperone regulator 7 (AHRD V3.3 *** A0A0B0NKP0_GOSAR)		P:GO:0006457: C:G(	P:protein folding; C:plasmodesma; F:chaperone binding	mobidb-lite (MOBIDB_LITE): IPR0404(	94,576	100,863	80,781	90,500	88,274									
Solyc03g083990	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT2G45180.1)				IPR016140 (SMART): G3DSA:1.10.11	0,000	0,000	0,025	0,000	0,000									
Solyc03g093080	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4BII5_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	G3DSA:2.60.120.200 (GENE3D): IPR(	164,589	145,162	38,408	71,609	74,433									
Solyc03g093110	xyloglucan endotransglucosylase-hydrolase		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR008264 (PRINTS): IPR010713 (PF	44,083	14,228	7,680	20,429	17,316	-1,607	0,000	1,165	0,028	1,406	0,003	down	up	up
Solyc03g093120	xyloglucan endotransglucosylase-hydrolase		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR010713 (PFAM): G3DSA:2.60.120.	64,989	24,539	13,450	34,997	33,300	-1,384	0,002	1,302	0,004	1,376	0,004	down	up	up
Solyc03g093130	xyloglucan endotransglucosylase-hydrolase 3	xth3	F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR016455 (PIRSF): G3DSA:2.60.120	30,360	11,102	8,418	25,514	20,649	-1,429	0,014	1,286	0,004	1,595	0,000	down	up	up
Solyc03g093140	Glycerol-3-phosphate transporter, putative (AHRD V3.3 *** B9R9S6_RICCO)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D): IPR(	79,505	36,267	69,491	62,956	47,998	-1,103	0,000	-0,537	0,000			down	down	

Solyc03g093150	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SFW5_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	8,483	7,829	5,891	8,424	7,200									
Solyc03g093160	Luc7-like protein 3 (AHRD V3.3 *** A0A1D1Z0B4_9ARAE)		F:GO:0003729: C:G(	F:mRNA binding; C:U1 snRNP; P:mRNA splice site selection	IPR004882 (PFAM): mobidb-lite (MOB	87,989	78,481	85,168	77,059	81,668									
Solyc03g093170	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A118K6D3_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFAI	0,000	0,021	0,000	0,000	0,000									
Solyc03g093180	Peroxisomal membrane protein 11-4 (AHRD V3.3 *** A0A151TE35_CAJCA)		C:GO:0005779: P:G(	C:integral component of peroxisomal membrane; P:peroxisome	IPR008733 (PFAM): PTHR12652 (PAI	0,316	0,372	0,050	0,022	0,237									
Solyc03g093200	Cell number regulator 6 (AHRD V3.3 *** A0A0B0MIM9_GOSAR)		C:GO:0016021	C:integral component of membrane	IPR006461 (TIGRFAM): IPR006461 (I	52,998	56,076	42,299	36,721	38,873									
Solyc03g093210	DIS3-like exonuclease 2 (AHRD V3.3 *-* A0A0B0Q026_GOSAR)				G3DSA:2.40.50.140 (GENE3D): PTHR	6,240	4,539	2,941	2,868	3,078									
Solyc03g093220	transmembrane protein (AHRD V3.3 *** AT1G21930.1)		C:GO:0016021	C:integral component of membrane	PTHR35691 (PANTHER)	15,457	14,115	21,887	17,491	18,239									
Solyc03g093230	tonoplast intrinsic protein 5.1	TIP5.1	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR000425 (PF	0,324	0,333	0,049	0,022	0,000									
Solyc03g093240	nitric oxide synthase 1	nos1	F:GO:0005525	F:GTP binding	IPR006073 (PFAM): G3DSA:3.40.50.3	15,454	20,401	21,966	17,856	25,212									
Solyc03g093250	Structural maintenance of chromosomes protein (AHRD V3.3 *** A0A068V0V7_COFCA)		F:GO:0005515: F:G(	F:protein binding; F:ATP binding; C:chromosome; P:chromosom	IPR010935 (SMART): G3DSA:3.40.50	7,724	5,778	1,666	1,336	1,198									
Solyc03g093260	Structural maintenance of chromosomes protein (AHRD V3.3 *** A0A072TZX1_MEDTR)		F:GO:0005515: F:G(	F:protein binding; F:ATP binding; C:chromosome; P:chromosom	G3DSA:3.40.50.300 (GENE3D): IPR0(	7,221	6,597	1,516	1,151	1,151									
Solyc03g093270	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** A0A072UK59_MEDTR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020471 (PRINTS): IPR036812 (G3	0,000	0,018	0,000	0,000	0,000									
Solyc03g093300	2-phosphoglycerate kinase (AHRD V3.3 *** A0A151TLP9_CAJCA)				G3DSA:3.40.50.300 (GENE3D): mobic	16,550	13,216	16,036	18,589	17,580									
Solyc03g093310	F-box-like protein (AHRD V3.3 *** A0A072UUB0_MEDTR)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	1,364	0,818	0,864	3,736	0,706					2,101	0,000			up
Solyc03g093330	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C1J5_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	PR00019 (PRINTS): IPR000719 (SMA	9,242	8,481	0,196	0,075	0,046									
Solyc03g093335	tagatose-6-phosphate ketose/aldose isomerase, putative (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein) (AHRD V3.3 --* AT5G27390.2)					0,042	0,019	0,025	0,025	0,000									
Solyc03g093350	splicing factor-like protein (AHRD V3.3 *** AT5G51300.3)		F:GO:0003723: F:G(	F:RNA binding; F:zinc ion binding	IPR004087 (SMART): IPR001878 (SM	2,206	2,395	2,766	2,610	2,432									
Solyc03g093360	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)		F:GO:0005515	F:protein binding	IPR010417 (PFAM): G3DSA:2.60.60.2	283,875	219,899	13,436	7,566	9,061									
Solyc03g093370	Protein DYAD (AHRD V3.3 *** A0A0B2S174_GLYSO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,047									
Solyc03g093380	protein kinase family protein (AHRD V3.3 *** AT1G51870.2)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART): G3DSA:1.10.51	2,533	2,452	3,101	2,684	3,689									
Solyc03g093400	Sugar transporter protein 15	STP15	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): IPR005828 (PF	1,999	4,222	1,156	0,988	2,833	1,110	0,016	1,284	0,009			up	up	
Solyc03g093430	small G protein family protein / RhoGAP family protein (AHRD V3.3 *** AT5G61530.1)		P:GO:0007165	P:signal transduction	IPR000198 (SMART): IPR000198 (PF	23,372	19,693	40,201	36,582	34,010									
Solyc03g093440	Isoaspartyl peptidase/L-asparaginase (AHRD V3.3 *** G7IVL2_MEDTR)		F:GO:0016787	F:hydrolase activity	IPR000246 (PFAM): G3DSA:3.60.20.3	14,531	13,892	15,588	13,855	15,436									
Solyc03g093450	Kinase family protein (AHRD V3.3 *** D7MGJ0_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity	IPR003613 (SMART): IPR000719 (SM	8,069	12,139	7,795	8,713	10,669									
Solyc03g093460	Protein kinase (AHRD V3.3 *** Q6V5G5_ARAAE)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	1,004	1,111	0,115	0,243	0,116									
Solyc03g093470	LEAPSAA2 L.esculentum APS-AA2	apsaa2	F:GO:0003993	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR023214 (G3DSA:3.40.50.GENE3D	5,016	3,520	4,840	6,064	4,257									
Solyc03g093480	U3 small nucleolar RNA-associated protein 10 and NUC211 domain-containing protein, putative isoform 1 (A		P:GO:000462: C:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSI	IPR012954 (SMART): IPR012954 (PF	95,916	87,221	98,117	117,030	95,015									
Solyc03g093490	WD-repeat protein, putative (AHRD V3.3 *** B9R9Y2_RICCO)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR015943 (G3	1,616	1,788	0,462	0,777	0,564									
Solyc03g093500	WD-repeat protein, putative (AHRD V3.3 *-* B9R9Y2_RICCO)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	1,037	1,011	0,393	0,391	0,309									
Solyc03g093510	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G51180.2)		P:GO:0044255	P:cellular lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	35,415	77,420	25,296	20,128	22,423	1,154	0,000					up		
Solyc03g093520	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** A0A022PUV0_ERYGU)		F:GO:0003872: F:G(	F:6-phosphofructok EC:2.7.1.11 6-phosphofructokinas	IPR022953 (PRINTS): G3DSA:3.40.5(	12,729	14,194	15,127	18,952	18,789									
Solyc03g093535	Protein kinase superfamily protein (AHRD V3.3 --* AT5G03640.2)					4,630	2,859	0,143	0,428	0,488									
Solyc03g093540	Ethylene-responsive transcription factor 5 (AHRD V3.3 *** ERF5_TOBAC)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	63,151	32,969	2,093	6,925	7,434	-0,914	0,007	1,815	0,001	1,710	0,000	down	up	up
Solyc03g093550	Ethylene-responsive transcription factor (AHRD V3.3 *** M4WYH8_GOSHI)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	148,058	60,448	10,325	26,289	18,482	-1,268	0,000	0,838	0,048	1,349	0,000	down	up	up
Solyc03g093560	ethylene response factor C.6	ERF.B2	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	246,105	122,560	45,870	109,626	66,467	-0,981	0,002			1,261	0,000	down		up
Solyc03g093610	ethylene response factor A.2	ERF_A_2	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	30,175	23,580	2,841	2,788	2,566									
Solyc03g093620	Sulfotransferase (AHRD V3.3 *** K4BIN8_SOLLC)		F:GO:0008146	F:sulfotransferase activity	IPR000863 (PFAM): G3DSA:3.40.50.3	0,019	0,039	0,000	0,022	0,000									
Solyc03g093625	beta-galactosidase 10 (AHRD V3.3 --* AT5G63810.1)					0,683	0,572	0,625	0,704	0,782									
Solyc03g093630	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0K9PNP9_ZOSMR)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding	IPR002885 (PFAM): IPR011990 (G3D	1,521	1,875	1,858	1,493	1,789									
Solyc03g093640	embryonic flower 2	emf2	C:GO:0005634: F:G(	C:nucleus; F:chromatin DNA binding	IPR019135 (PFAM): PTHR22597 (PAI	8,293	7,674	9,669	9,497	10,054									
Solyc03g093643	Polycomb group protein VERNALIZATION 2 (AHRD V3.3 *** B9GK37_POPTR)		C:GO:0005634: F:G(	C:nucleus; F:chromatin DNA binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	35,264	32,279	38,766	39,772	40,415									
Solyc03g093650	ABC transporter B family protein (AHRD V3.3 *** A0A072UBK0_MEDTR)	ABCB6	F:GO:0005524: C:G(	F:ATP binding; C:int EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	0,057	0,019	0,000	0,000	0,000									
Solyc03g093680	Mago nashi protein (AHRD V3.3 *** K4BIP4_SOLLC)		P:GO:0008380: C:G(	P:RNA splicing; C:exon-exon junction complex	IPR036605 (G3DSA:3.30.1560.GENE	43,947	42,525	48,538	42,448	43,630									
Solyc03g093690	methionine sulfoxide reductase A4		F:GO:0008113: P:G(	F:peptide-methionin EC:1.8.4.11 Peptide-methionine (	IPR002569 (TIGRFAM): IPR036509 ((	99,146	149,424	206,189	233,867	300,740	0,619	0,015	0,542	0,004			up	up	
Solyc03g093700	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *-* W9S0E6_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C: EC:2.1.1.43 Histone-lysine N-met	IPR003105 (SMART): IPR007728 (SM	4,624	4,954	0,595	0,529	0,682									
Solyc03g093710	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *-* W9S0E6_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C: EC:2.1.1.43 Histone-lysine N-met	IPR001214 (SMART): IPR007728 (SM	1,694	2,332	1,878	2,011	3,040									
Solyc03g093740	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *-* W9S0E6_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C: EC:2.1.1.43 Histone-lysine N-met	IPR007728 (SMART): IPR001214 (SM	0,000	0,000	0,025	0,000	0,000									
Solyc03g093750	Beta-galactosidase (AHRD V3.3 *-* BGAL_SOLLC)		P:GO:0007034	P:vacuolar transport	PTHR22761 (PANTHER): PTHR22761	0,080	0,156	0,289	0,750	0,426									
Solyc03g093760	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *-* W9S0E6_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C: EC:2.1.1.43 Histone-lysine N-met	IPR001214 (SMART): IPR007728 (SM	0,732	0,802	7,609	10,564	6,548									
Solyc03g093780	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *-* A0A103XHT5_CYNCS)				PTHR44355 (PANTHER): PTHR44355	0,426	0,541	0,251	0,250	0,142									
Solyc03g093790	cyclinU4_2	CycU4_2	P:GO:0000079: F:G(	P:regulation of cyclin-dependent protein serine/threonine kinase	IPR012389 (PIRSF): IPR013922 (PFA	0,120	0,118	0,000	0,000	0,000									
Solyc03g093800	glycine-rich protein (AHRD V3.3 *-* AT5G61660.1)		C:GO:0016020	C:membrane	mobidb-lite (MOBIDB_LITE)	3,124	3,464	10,006	9,776	11,742									
Solyc03g093810	LOW QUALITY:multidrug resistance-associated protein 3 (AHRD V3.3 --* AT3G13080.5)					0,019	0,039	0,074	0,261	0,141									
Solyc03g093820	LOW QUALITY:Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein (AHRD V3.3 --* AT4G21750.4)				mobidb-lite (MOBIDB_LITE)	2,433	2,686	2,182	2,490	2,497									
Solyc03g093830	ORANGE protein-like	OR	C:GO:0005634: C:G(	C:nucleus; C:chloroplast; C:integral component of membrane; P	PTHR15852 (PANTHER): PTHR15852	28,129	33,004	70,192	75,492	68,588									
Solyc03g093840	ATP-dependent DNA helicase pcrA (AHRD V3.3 *** A0A0B0PSI4_GOSAR)		F:GO:0003677: F:G(	F:DNA binding; F:A' EC:3.6.1.3; EC:3.6.1 Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		1,048	0,643	0,441	0,565	0,355									
Solyc03g093850	ATP-dependent DNA helicase pcrA (AHRD V3.3 *** W9S1J2_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:A' EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR034739 (PFAM): IPR014017 (PFA	4,337	4,885	1,748	1,605	1,479									
Solyc03g093880	U6 snRNA phosphodiesterase (AHRD V3.3 *** K4BIR4_SOLLC)		F:GO:0004518: P:G(	F:nuclease activity; P:U6 snRNA 3'-end processing	IPR027521 (PFAM): G3DSA:3.90.114(	31,772	23,449	60,417	62,356	53,182									
Solyc03g093890	R2R3MYB transcription factor 52	R2R3MYB52	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,606	2,175	0,265	0,563	0,424									
Solyc03g093930	MYB family protein (AHRD V3.3 *-* A0A067JDM6_JATCU)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,042	0,039	0,000	0,000	0,000									
Solyc03g093970	Signal recognition particle subunit SRP68 (AHRD V3.3 *** K4BIS2_SOLLC)		F:GO:0005047: C:G(	F:signal recognition particle binding; C:signal recognition partick	IPR026258 (PIRSF): IPR026258 (PFA	20,308	25,736	24,229	26,054	24,413									
Solyc03g093980	multidrug resistance-associated protein 6 (AHRD V3.3 --* AT3G21250.5)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,759	0,817	4,081	1,827	2,006									
Solyc03g093990	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane	PF02466 (PFAM): IPR031926 (PFAM)	18,975	17,831	25,638	26,067	25,588									
Solyc03g094000	Light induced like protein (AHRD V3.3 *** C1E3F8_MICCC)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:integral component of men	mobidb-lite (MOBIDB_LITE): PTHR141	0,000	0,110	0,000	0,025	0,000									
Solyc03g094010	glutamate dehydrogenase		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:oxidoreductase activ	IPR006095 (PRINTS): IPR006096 (SM	8,900	9,570	8,424	6,452	7,042									
Solyc03g094020	Alpha-glucosidase-like (AHRD V3.3 *** Q5NBJ1_ORYSJ)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D): IPR00(	0,922	7,390	0,927	0,436	0,705	3,023	0,000					up		
Solyc03g094030	Mediator of RNA polymerase II transcription subunit 31 (AHRD V3.3 *** A0A0S2LKK3_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,	IPR008831 (PFAM): IPR038089 (G3D	7,672	7,496	16,044	16,813	13,503									
Solyc03g094040	Polyadenylate-binding protein, putative (AHRD V3.3 *** B9RA16_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	3,623	2,888	2,964	2,569	2,685									
Solyc03g094050	Phosphoenolpyruvate carboxylase (AHRD V3.3 --* CAPP_PEA)					0,433	0,488	0,490	0,535	0,662									
Solyc03g094060	RNA-binding family protein (AHRD V3.3 *-* A0A061FZR7_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	1,682	2,266	3,261	3,392	3,697									
Solyc03g094070	Mediator of RNA polymerase II transcription subunit 31 (AHRD V3.3 *-* A0A0S2LKK3_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,	IPR008831 (PANTHER)	1,009	0,927	1,833	2,544	2,052									
Solyc03g094080	RNA-binding family protein (AHRD V3.3 *** A0A061FZR7_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	54,582	49,362	71,715	63,322	67,102									
Solyc03g094090	Polyadenylate-binding 2 (AHRD V3.3 *-* A0A0B0NIR2_GOSAR)		F:GO:0003729: C:G(	F:mRNA binding; C:cytosol; F:poly(A) binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	52,603	47,201	66,797	55,123	63,636									
Solyc03g094100	LOW QUALITY:Nucleotide binding site-leucine rich repeat protein (AHRD V3.3 *** A0A0H5AGV4_SOLPI)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): G3DSA:1.10.8.43	0,303	0,956	0,022	0,022	0,071									
Solyc03g094110	Glycosyltransferase (AHRD V3.3 *** A0A164WZ41_DAUCA)		C:GO:0016021	C:integral component of membrane	IPR005069 (PFAM): PTHR24015 (PAI	0,021	0,036	0,025	0,246	0,187									
Solyc03g094120	Glycosyltransferase (AHRD V3.3 *** A0A164WZ41_DAUCA)		C:GO:0016021	C:integral component of membrane	IPR005069 (PFAM): PTHR24015 (PAI	0,099	0,560	0,521	0,807	1,361									
Solyc03g094145	Lysine--tRNA ligase (AHRD V3.3 --* SYK_SOLLC)					4,409	6,929	2,165	2,326	2,277									
Solyc03g094160	metacaspase 1 (AHRD V3.3 *** AT1G02170.1),Pfam:PF00656		F:GO:0004197: P:G(	F:cysteine-type enc EC:3.4.22 Acting on peptide bor	IPR005735 (TIGRFAM): PF00656 (PF	167,592	132,303	26,749	50,667	52,396			0,967	0,000	0,922	0,000		up	up
Solyc03g095180	Superoxide dismutase (AHRD V3.3 *** Q7YK44_SOLLC)		F:GO:0004784: P:G(	F:superoxide dismu EC:1.15.1.1 Superoxide dismutas	IPR001189 (PRINTS): IPR036324 (G3	1,456	2,211	2,250	2,000	2,221									
Solyc03g095190	ATP synthase epsilon chain (AHRD V3.3 *** A0A0K9P5X2_ZOSMR)		P:GO:0015986: C:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR036771 (G3DSA:2.60.15.GENE3D	0,042	0,098	0,075	0,048	0,094									
Solyc03g095210	Transducin/WD40 repeat protein (AHRD V3.3 *** G7JJ01_MEDTR)		F:GO:0005515: P:G(	F:protein binding; P:anaphase-promoting complex binding; F:ubi	IPR001680 (SMART): IPR001680 (PF	1,182	1,318	1,680	1,641	1,271									
Solyc03g095220	Translocase of chloroplast (AHRD V3.3 *** A0A0V0I1D8_SOLCH)		F:GO:0005525: P:G(	F:GTP binding; P:intracellular protein transport; C:chloroplast ou	IPR005688 (PIRSF): IPR006703 (PFA	65,428	73,838	69,163	64,168	65,168									
Solyc03g095240	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G33400.1)		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR011990 (G3	9,751	8,283	5,443	5,630	6,435									
Solyc03g095250	COP1-interacting-like protein, putative (AHRD V3.3 *** A0A072V1D3_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	27,113	21,853	8,426	6,715	7,300									
Solyc03g095260	Transducin/WD40 repeat protein (AHRD V3.3 *** G7J9R1_MEDTR)				PTHR31789 (PANTHER): SSF69322 (	32,366	33,376	37,701	40,448	36,685									
Solyc03g095290	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G10840.1)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	20,020	18,697	48,933	51,915	51,770									
Solyc03g095300	Calcium-dependent lipid-binding (CaLB domain) family protein, putative (AHRD V3.3 *** A0A072VBE8_MEDTR)				IPR000008 (SMART): IPR000008 (PF	0,665	1,004	0,168	0,435	0,400									
Solyc03g095310	Cytochrome P450 protein (AHRD V3.3 *** A0A0B0P3Q6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	2,560	4,169	5,914	8,873	6,892					0,590	0,042			up
Solyc03g095313	Oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 *** A0A0K9NVW2_ZOSMR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020843 (SMART): G3DSA:3.40.50	0,038	0,021	0,050	0,025	0,000									
Solyc03g095315	Quinone oxidoreductase-like protein 2 like (AHRD V3.3 *-* A0A0B2SCM2_GLYSO)		C:GO:0005777: C:G(	C:peroxisome; C:cytosol; F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process		0,019	0,000	0,022	0,000	0,000									
Solyc03g095317	Quinone oxidoreductase-like protein 2 (AHRD V3.3 *-* A0A1D1YS08_9ARAE)		C:GO:0005777: C:G(	C:peroxisome; C:cytosol; F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process		0,038	0,094	0,000	0,050	0,024									
Solyc03g095330	WD-40 repeat family protein / beige-like protein (AHRD V3.3 --* AT2G45540.6)					0,531	0,445	0,430	0,447	0,397									
Solyc03g095360	Oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 *** A0A0K9NVW2_ZOSMR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020843 (SMART): IPR013149 (PF	114,703	110,397	157,947	148,987	147,438									
Solyc03g095370	CLP protease regulatory subunit CLPX1, mitochondrial (AHRD V3.3 --* CLPX1_ARATH)					3,649	1,316	0,393	0,491	0,684	-1,439	0,001					down		
Solyc03g095377	syntaxin of plants 132 (AHRD V3.3 --* AT5G08080.5)					2,698	0,961	0,461	0,216	0,616	-1,445	0,019					down		
Solyc03g095410	exocyst complex component sec10 (AHRD V3.3 *** AT5G12370.2)		C:GO:000145: P:G(	C:exocyst; P:exocytosis; P:vesicle docking	IPR009976 (PFAM): G3DSA:1.20.58.1	74,443	68,525	99,036	98,536	97,742									
Solyc03g095420	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* POLX_TOBAC)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding	IPR013583 (PFAM): IPR013103 (PFA	0,019	0,018	0,000	0,000	0,000									
Solyc03g095440	LOW QUALITY:C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 --* A0A072ULK6_MEDTR)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane		0,000	0,000	0,022	0,025	0,023									
Solyc03g095450	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01960.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART): PF13920 (PFAI	8,995	8,726	10,204	10,346	9,959									
Solyc03g095470	import inner membrane translocase subunit (AHRD V3.3 *** AT2G40800.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	15,762	17,319	23,809	23,416	22,983									
Solyc03g095490	Receptor-like kinase (AHRD V3.3 *** G7K0V8_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR013210 (PFAM): IPR000719 (PFA	6,065	4,760	1,636	1,576	1,604									
Solyc03g095510	serine/threonine protein kinase 2 (AHRD V3.3 *** AT3G08720.4)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR000961 (SMART): IPR000719 (SM	5,343	4,851	15,112	14,883	15,536									
Solyc03g095550	Methyl esterase 17 (AHRD V3.3 *** A0A061FZJ0_THECC)		P:GO:0033473: P:G(	P:indoleacetic acid EC:3.1.1.1 Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	0,000	0,000	0,050	0,000	0,000									
Solyc03g095600	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** G7K0U4_MEDTR)		C:GO:0005774: F:G(	C:vacuolar membrane; F:actin filament binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	14,219	12,360	2,899	2,166	2,800									
Solyc03g095620	aarF domain-containing protein kinase		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation	IPR004147 (PFAM): PTHR43173 (PAI	25,946	30,552	80,157	79,567	95,385									
Solyc03g095650	MLO-like protein (AHRD V3.3 *** K4BIY8_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane	IPR004326 (PFAM): mobidb-lite (MOB	1,172	5,955	0,290	0,592	2,098	2,360	0,000					up		
Solyc03g095660	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103YCL0_CYNCS)		F:GO:0003743: P:G(	F:translation initiation factor activity; P:translational initiation	G3DSA:2.40.50.140 (GENE3D): mobic	0,098	0,244	0,097	0,198	0,117									
Solyc03g095680	SNF2 domain protein/helicase domain protein (AHRD V3.3 *** G7KD91_MEDTR)		F:GO:0005524	F:ATP binding	IPR014001 (SMART): IPR001965 (SM	17,115	13,550	19,283	19,770	21,876									
Solyc03g095690	SNF2 domain protein/helicase domain protein (AHRD V3.3 *-* G7KD91_MEDTR)		F:GO:0005524: F:G(	F:ATP binding; F:ligase activity; F:metal ion binding	IPR001650 (SMART): IPR001650 (PF	5,731	6,657	8,051	9,128	8,206									
Solyc03g095700	LOW QUALITY:Voltage-dependent T-type calcium channel subunit alpha-1I, putative (AHRD V3.3 *** A0A06'		C:GO:0009507	C:chloroplast	PTHR37758 (PANTHER)	0,252	0,178	2,589	3,758	2,126									
Solyc03g095710	Alpha-amylase (AHRD V3.3 *** K4BIZ4_SOLLC)		F:GO:0004556: F:G(	F:alpha-amylase ac EC:3.2.1.1 Alpha-amylase	IPR012850 (SMART): IPR006047 (SM	16,935	13,269	54,150	55,988	52,522									
Solyc03g095720	Transcription elongation factor TFIIS (AHRD V3.3 *** RDO2_ARATH)		F:GO:0003676: C:G(	F:nucleic acid binding; C:nucleus; P:regulation of transcription, I	IPR001222 (SMART): IPR003618 (SM	25,088	30,280	26,360	20,482	24,108									
Solyc03g095730	Ubiquinol-cytochrome c reductase complex 6.7 kDa protein (AHRD V3.3 *** UCR11_SOLTU)					30,613	36,218	37,085	32,663	34,847									
Solyc03g095750	Chlorophyllide A oxygenase (AHRD V3.3 *-* G7I8G8_MEDTR)	CAO	F:GO:0005506: F:G(	F:iron ion binding; F:chlorophyllide a oxygenase [overall] activity	PTHR21266 (PANTHER): PTHR21266	0,042	0,057	0,046	0,047	0,046									
Solyc03g095753	Glycerol-3-phosphate transporter (AHRD V3.3 *-* A0A0A0KL51_CUCSA)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:transmembrane transporter activity; P:transmembra		0,000	0,039	0,025	0,000	0,024									
Solyc03g095760	Rhodanese-like domain-containing protein (AHRD V3.3 *** A0A124SGQ2_CYNCS)				IPR001763 (SMART): IPR036873 (G3	12,568	14,066	6,143	3,795	6,743					-0,695	0,032			down
Solyc03g095770	WRKY transcription factor 80	WRKY80	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	48,202	57,171	3,913	11,283	10,568			1,430	0,000	1,527	0,000		up	up
Solyc03g095780	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)		F:GO:0004864: C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR023393 (G3DSA:3.30.530.GENE3	0,710	1,506	0,025	0,147	0,095									
Solyc03g095804	O-acyltransferase (WSD1-like) family protein (AHRD V3.3 --* AT5G16350.3)					0,000	0,160	0,022	0,050	0,000									
Solyc03g095810	Trichome birefringence-like protein (AHRD V3.3 *** G7K771_MEDTR)		C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR026057 (PFAM): IPR025846 (PFA	0,000	0,018	0,000	0,000	0,024									
Solyc03g095820	Trichome birefringence-like protein (AHRD V3.3 *** G7K771_MEDTR)		P:GO:0007166	P:cell surface receptor signaling pathway	IPR036537 (G3DSA:1.20.930.GENE3	9,277	8,586	0,935	0,339	0,634									
Solyc03g095830	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G16950.6)		F:GO:0016740	F:transferase activity	mobidb-lite (MOBIDB_LITE): PTHR346	0,079	0,037	0,047	0,000	0,000									
Solyc03g095840	eukaryotic translation initiation factor 2 alpha subunit family protein		F:GO:0003743	F:translation initiation factor activity	IPR022967 (SMART): IPR024054 (G3	64,055	72,442	78,863	74,670	74,869									
Solyc03g095845	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT2G40280.1)					0,057	0,062	0,068	0,122	0,095									
Solyc03g095850	LOW QUALITY:Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein (AHRD V3.3 *** AT5(		C:GO:0005773	C:vacuole	IPR021102 (PFAM): IPR021102 (PAN	10,314	8,977	20,988	19,919	19,528									
Solyc03g095860	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A103YIY1_CYNCS)		F:GO:0005515	F:protein binding	IPR002110 (PRINTS): IPR002110 (SM	9,711	9,763	47,430	46,102	44,103									
Solyc03g095870	Eukaryotic translation initiation factor 2 subunit alpha (AHRD V3.3 *-* A0A1C8FVJ5_TOBAC)		F:GO:0003676: C:G(	F:nucleic acid binding; C:protein-containing complex; C:cytoplas	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,799	0,809	14,783	12,652	12,419									
Solyc03g095880	LOW QUALITY:N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein (AHRD V3.3 --* AT3G27430.3)					0,000	0,000	11,782	21,176	8,641					0,850	0,003			up
Solyc03g095900	E8 protein homolog	e86	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3	10,742	6,324	5997,357	7223,777	5292,710									
Solyc03g095910	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06620.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR027443 (G3D	0,021	0,000	2,510	1,767	1,418									
Solyc03g095920	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061		P:GO:0009693: P:G(	P:ethylene biosynthetic process; P:fruit ripening; F:L-ascorbic a	IPR027443 (G3DSA:2.60.120.GENE3	0,000	0,021	0,025	0,069	0,187									
Solyc03g095950	Calcium-binding EF-hand family protein (AHRD V3.3 --* AT2G34020.2)					2,271	1,168	0,716	0,792	0,593									
Solyc03g095960	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RF13_RICCO)		F:GO:0005515	F:protein binding	IPR033443 (PFAM): IPR011990 (G3D	4,386	4,455	5,589	5,391	4,998									
Solyc03g095970	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G47140.1),Pfam:PF13561		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	2,169	2,514	0,050	0,073	0,023									
Solyc03g095980	bHLH transcription factor 021		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,738	0,596	0,097	0,224	0,186									
Solyc03g095985	Differentiation-associated protein 1, putative isoform 2 (AHRD V3.3 *** A0A061FKZ1_THECC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	17,450	21,386	27,008	38,330	31,300									
Solyc03g096000	Clathrin heavy chain (AHRD V3.3 *** K4BJ22_SOLLC)		F:GO:0005198: P:G(	F:structural molecule activity; P:intracellular protein transport; P	IPR000547 (SMART): IPR015348 (PF	94,227	90,152	137,135	160,211	145,025									
Solyc03g096030	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G55990.1)		P:GO:0050826	P:response to freezing	IPR025846 (PFAM): IPR026057 (PFA	1,202	0,906	0,050	0,098	0,188									
Solyc03g096040	1-Cys peroxiredoxin (AHRD V3.3 *** REHY_MEDTR)		P:GO:0045454: F:G(	P:cell redox homeo: EC:1.11.1.15 Peroxiredoxin	G3DSA:3.30.1020.10 (GENE3D): G3D	16,917	18,452	3,230	9,846	0,418									
Solyc03g096050	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G05600.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS): IPR005123 (PFA	0,269	2,798	4,438	4,972	3,805	3,374	0,001					up		
Solyc03g096055	DNA-directed RNA polymerase II protein (AHRD V3.3 --* AT1G77890.5)					0,019	0,037	0,050	0,025	0,071									

Solyc03g096070	Phosphoinositide phospholipase C (AHRD V3.3 *** K4BJ29_SOLLC)		F:GO:0004435: P:G(	F:phosphatidylinosit EC:3.1.4.11: EC:3.1. Phosphoinositide pho	IPR001192 (PRINTS): IPR001711 (SM	2,506	3,611	1,622	1,873	2,121									
Solyc03g096080	Protein yippee-like (AHRD V3.3 *** YIPL_SOLTU)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): IPR039058 (PAN	36,657	34,388	43,651	48,585	46,660									
Solyc03g096090	ATP binding protein, putative (AHRD V3.3 *** B9SLM8_RICCO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	9,762	7,690	6,117	4,920	5,713									
Solyc03g096097	Protein yippee-like (AHRD V3.3 *** K4BJ32_SOLLC)		F:GO:0046872	F:metal ion binding	IPR004910 (PFAM): PTHR13848:SF5	0,076	0,082	0,047	0,194	0,047									
Solyc03g096100	Protein yippee-like (AHRD V3.3 *** K4BJ32_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): IPR039058 (PAN	0,138	0,121	0,072	0,050	0,000									
Solyc03g096120	Protein yippee-like (AHRD V3.3 *** K4BJ34_SOLLC)		F:GO:0046872	F:metal ion binding	IPR004910 (PFAM): IPR039058 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc03g096130	Protein yippee-like (AHRD V3.3 *** YIPL_SOLTU)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	PTHR13848:SF5 (PANTHER): IPR039	0,182	0,119	0,050	0,099	0,024									
Solyc03g096135	phosphatidylserine decarboxylase 3 (AHRD V3.3 --* AT4G25970.1)					0,000	0,000	0,000	0,242	0,000									
Solyc03g096140	Protein yippee-like (AHRD V3.3 *** K4BJ36_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): mobidb-lite (MOB	0,235	0,158	0,476	0,421	0,593									
Solyc03g096160	Protein yippee-like (AHRD V3.3 *** K4BJ38_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): IPR039058 (PAN	1,575	0,393	0,748	1,309	0,786									
Solyc03g096180	ATP binding protein, putative (AHRD V3.3 *-* B9SLM8_RICCO)				mobidb-lite (MOBIDB_LITE): PTHR319	0,000	0,018	0,000	0,000	0,046									
Solyc03g096190	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR003591 (SMART): IPR000719 (SM	0,081	0,072	0,000	0,000	0,070									
Solyc03g096220	tRNA-splicing endonuclease subunit SEN54 (AHRD V3.3 *-* A0A1D1YH76_9ARAE)		F:GO:0004519: P:G(	F:endonuclease activity; P:nucleic acid phosphodiester bond hy	IPR024337 (PANTHER)	13,635	9,604	7,753	6,988	7,842									
Solyc03g096250	Protein yippee-like (AHRD V3.3 *** K4BJ47_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): PTHR13848:SF5	11,904	9,480	10,923	20,103	19,170					0,879	0,013			up
Solyc03g096260	Protein yippee-like (AHRD V3.3 *** K4BJ48_SOLLC)		C:GO:0000151: F:G(	C:ubiquitin ligase complex; F:metal ion binding	IPR004910 (PFAM): IPR039058 (PAN	0,438	0,607	0,050	0,117	0,000									
Solyc03g096290	plasma membrane intrinsic protein 1.7	PIP1.7	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR023271 (G3	12,062	25,797	3,731	2,848	3,367	1,121	0,000					up		
Solyc03g096350	Myb family transcription factor family protein (AHRD V3.3 *** B9HT09_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF_MYB	1,938	2,135	0,950	0,908	0,683									
Solyc03g096360	60S ribosomal protein L35a (AHRD V3.3 *** B6VC50_VERFO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001780 (PFAM): IPR038661 (G3D	165,527	182,120	172,201	153,242	157,685									
Solyc03g096380	proline transporter 2	prot2	P:GO:0003333: C:G(	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM): PTHR22950 (PAN	5,379	4,498	15,589	16,893	19,547									
Solyc03g096390	proline transporter 1	prot1	P:GO:0003333: C:G(	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM): PTHR22950:SF4	8,780	19,129	17,411	26,580	24,711	1,147	0,039	0,501	0,012	0,613	0,000	up	up	up
Solyc03g096410	LOW QUALITY:ARID/BRIGHT DNA-binding , ELM2 domain and myb-like DNA-binding domain-containing protein (AHRD V3.3 --* AT4G11400.2)					0,000	0,000	0,022	0,025	0,000									
Solyc03g096420	LOW QUALITY:CLIP-associating protein 1 (AHRD V3.3 --* A0A0B2NZ56_GLYSO)					0,000	0,000	0,000	0,048	0,000									
Solyc03g096430	LOW QUALITY:CLIP-associating protein 1 (AHRD V3.3 --* A0A0B2NZ56_GLYSO)					0,000	0,000	0,050	0,048	0,023									
Solyc03g096435	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *-* A0A072UYX1_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,018	0,047	0,000	0,000									
Solyc03g096450	Pentatricopeptide repeat-containing protein (AHRD V3.3 --* D7L220_ARALL)					3,330	3,629	1,828	2,173	2,182									
Solyc03g096460	wound/stress protein AY568721		F:GO:0004096: F:G(	F:catalase activity; EC:1.11.1.7; EC:1.1 Peroxidase; Catalase	IPR037060 (G3DSA:2.40.180.GENE3	5,074	5,389	0,269	0,146	0,093									
Solyc03g096530	LOW QUALITY:myosin-like protein XIF (AHRD V3.3 --* AT2G31900.5)					0,021	0,000	0,000	0,025	0,000									
Solyc03g096540	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)		F:GO:0005515	F:protein binding	IPR001024 (PFAM): G3DSA:2.60.60.2	0,000	0,000	0,928	0,800	0,636									
Solyc03g096550	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)		F:GO:0005515	F:protein binding	IPR001024 (PFAM): G3DSA:2.60.60.2	0,116	0,164	4,457	3,139	2,388									
Solyc03g096610	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G33350.2)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	3,290	2,546	2,658	3,344	3,370									
Solyc03g096615	F-box family protein (AHRD V3.3 *-* D7LS19_ARALL)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,719	0,749	0,669	0,803	1,110									
Solyc03g096620	F-box/LRR-repeat protein (AHRD V3.3 *** A0A0B2QK07_GLYSO)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,962	0,913	1,002	1,393	1,098									
Solyc03g096630	Ethylene insensitive 3 family protein (AHRD V3.3 *** AT5G10120.1),Pfam:PF04873		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus	IPR023278 (G3DS_EIL	0,178	0,043	0,025	0,169	0,047									
Solyc03g096650	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G29170.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	0,019	0,018	0,000	0,000	0,000									
Solyc03g096660	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		C:GO:0005829: F:G(	C:cytosol; F:oxidoreductase activity; P:oxidation-reduction proc	IPR002347 (PRINTS): IPR002347 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc03g096670	Protein phosphatase 2C (AHRD V3.3 *** Q8RVG0_TOBAC)		F:GO:0004722: P:G(	F:protein serine/thr EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	48,833	33,607	108,146	103,564	99,853									
Solyc03g096680	Eukaryotic translation initiation factor 3 subunit G (AHRD V3.3 *** K4BJ86_SOLLC)		F:GO:0003743: C:G(	F:translation initiation factor activity; C:eukaryotic translation in	IPR000504 (SMART): PIRSF037949 (	0,021	0,000	0,022	0,000	0,000									
Solyc03g096710	LOW QUALITY:Protein phosphatase 2C family protein (AHRD V3.3 --* AT1G79630.7)					0,019	0,039	0,000	0,000	0,000									
Solyc03g096720	LOW QUALITY:ABC-2 and Plant PDR ABC-type transporter family protein (AHRD V3.3 --* AT1G59870.1)					0,038	0,018	0,000	0,000	0,000									
Solyc03g096730	pollen-specific kinase partner protein	GMP	P:GO:0009058: F:G(	P:biosynthetic process; F:nucleotidyltransferase activity	IPR005835 (PFAM): IPR001451 (PFA	210,066	196,096	69,537	62,489	71,584									
Solyc03g096740	Unknown protein (AHRD V3.3)					4,391	3,428	4,353	4,795	4,306									
Solyc03g096760	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)		P:GO:0098869	P:cellular oxidant detoxification	IPR039282 (PANTHER): PTHR34283:	0,315	0,245	0,433	0,530	0,306									
Solyc03g096770	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)		P:GO:0098869	P:cellular oxidant detoxification	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,258	0,716	2,175	2,011	1,860									
Solyc03g096780	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)		P:GO:0098869	P:cellular oxidant detoxification	mobidb-lite (MOBIDB_LITE): IPR03928	2,699	3,313	11,493	12,320	10,540									
Solyc03g096790	autophagy-related protein 13		P:GO:0000045: C:G(	P:autophagosome assembly; C:Atg1/ULK1 kinase complex	IPR036570 (G3DSA:3.30.900.GENE3	15,064	14,729	28,916	30,659	28,094									
Solyc03g096800	Vacuolar iron transporter (VIT) family protein (AHRD V3.3 *-* A0A061G9Q5_THECC)		C:GO:0016020	C:membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	10,363	12,488	1,333	1,357	1,904									
Solyc03g096810	TMPIT-like protein (AHRD V3.3 *** AT4G10430.3)		C:GO:0016021	C:integral component of membrane	IPR012926 (PFAM): mobidb-lite (MOB	72,255	81,671	83,686	78,949	83,189									
Solyc03g096820	Aluminum-activated malate transporter-like (AHRD V3.3 *** K4BJA0_SOLLC)		P:GO:0015743	P:malate transport	IPR020966 (PFAM): PTHR31086:SF2	20,651	20,333	19,114	19,520	19,468									
Solyc03g096830	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S1X8_RICCO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	30,283	30,442	11,108	8,539	13,217									
Solyc03g096840	LOW QUALITY:Hydrogen peroxide-induced 1 (AHRD V3.3 *** B8Y3H9_TOBAC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	241,269	276,985	55,458	47,371	59,981									
Solyc03g096850	rubredoxin family protein (AHRD V3.3 *** AT5G17170.1)		F:GO:0005515	F:protein binding	G3DSA:2.30.42.10 (GENE3D): PTHR4	44,433	83,429	67,394	71,785	114,377	0,936	0,000	0,761	0,000			up	up	
Solyc03g096860	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT5G17210.1)		C:GO:0016021	C:integral component of membrane	IPR009606 (PFAM): PTHR31769 (PAN	39,056	35,393	47,812	51,680	43,120									
Solyc03g096870	cell division control 20-1		F:GO:0005515: F:G(	F:protein binding; F:anaphase-promoting complex binding; F:ubi	IPR001680 (SMART): IPR001680 (PF	0,537	0,850	0,047	0,097	0,023									
Solyc03g096880	Tudor/PWWP/MBT superfamily protein (AHRD V3.3 *** A0A0K9NN30_ZOSMR)		P:GO:0009791	P:post-embryonic development	G3DSA:2.30.30.140 (GENE3D): IPR0(	24,940	30,553	24,632	24,155	25,592									
Solyc03g096890	ATP binding protein, putative isoform 1 (AHRD V3.3 *** A0A061FVN5_THECC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR011989 (G3DSA:1.25.10.GENE3D	2,581	2,256	2,273	2,059	1,534									
Solyc03g096900	Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase isoform 3 (AHRD V3.3 *** A0A061F675_THECC		P:GO:0015969	P:guanosine tetraphosphate metabolic process	IPR007685 (SMART): IPR003607 (SM	10,160	9,856	4,392	4,859	6,385									
Solyc03g096910	ADP-ribosylation factor (AHRD V3.3 *** Q5FYS3_DAUCA)		F:GO:0005525	F:GTP binding	IPR006689 (PRINTS): SM00178 (SMA	22,888	21,737	38,395	35,214	34,110									
Solyc03g096920	Exportin-1 (AHRD V3.3 *** D1MAF2_SOLLC)		F:GO:0005049: P:G(	F:nuclear export signal receptor activity; P:intracellular protein t	IPR001494 (SMART): IPR014877 (SM	129,496	119,763	151,297	156,316	147,208									
Solyc03g096930	E3 ubiquitin-protein ligase synoviolin (AHRD V3.3 *-* A0A0B0NKN9_GOSAR)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity	mobidb-lite (MOBIDB_LITE)	10,600	11,656	17,341	18,588	16,689									
Solyc03g096935	RING/U-box superfamily protein (AHRD V3.3 *** AT3G16090.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART): IPR013083 (G3	23,219	19,401	33,234	35,487	31,954									
Solyc03g096940	peptidyl serine alpha-galactosyltransferase (AHRD V3.3 --* AT3G01720.1)					27,324	33,448	43,223	41,034	44,423									
Solyc03g096950	Vacuolar glucose transporter 2	VGT2	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): G3DSA:1.20.12	25,675	23,299	40,432	40,988	39,453									
Solyc03g096960	LOW QUALITY:D-serine dehydratase (AHRD V3.3 *** A0A1D1XH71_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	32,879	33,198	31,781	29,685	27,775									
Solyc03g096965	Cytochrome P450 (AHRD V3.3 *** Q1AGW1_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	1,718	1,402	2,212	2,128	2,189									
Solyc03g096980	Cytochrome P450 (AHRD V3.3 *** Q1AGW1_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	96,113	97,720	56,031	51,174	78,382			0,480	0,015				up	
Solyc03g096990	Cytochrome P450 (AHRD V3.3 *** Q1AGW1_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	70,371	67,110	168,116	153,895	159,398									
Solyc03g097000	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SAS7_CYNCS)		F:GO:0005515	F:protein binding	IPR033443 (PFAM): IPR002885 (TIGF	19,401	17,207	19,591	17,448	20,592									
Solyc03g097005	Zeta-carotene isomerase (AHRD V3.3 --* A0A164SUS7_DAUCA)					0,058	0,062	0,025	0,000	0,000									
Solyc03g097010	NADH-ubiquinone oxidoreductase-related protein		F:GO:0004129: C:G(	F:cytochrome-c oxi EC:1.9.3.1 Cytochrome-c oxidas	IPR019401 (PFAM): G3DSA:2.60.260	11,654	11,549	20,463	16,589	19,587									
Solyc03g097020	AAA-type ATPase family protein		F:GO:0005524: C:G(	F:ATP binding; C:mitochondrion; P:mitochondrion organization	IPR003593 (SMART): IPR021911 (PF	22,980	35,683	22,831	21,950	21,806									
Solyc03g097030	4-coumarate--CoA ligase	4CL	F:GO:0003824	F:catalytic activity	IPR000873 (PFAM): IPR025110 (PFA	53,116	42,313	40,623	35,774	40,224									
Solyc03g097040	Cysteine-rich protein (AHRD V3.3 -** AT2G22345.1)					0,000	0,000	0,000	0,000	0,023									
Solyc03g097050	Cellulose synthase-like protein (AHRD V3.3 *** L0ATQ4_POPTO)		C:GO:0016020: F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (U	PF14570 (PFAM): IPR005150 (PFAM)	405,286	193,345	175,063	524,390	603,981	-1,047	0,038	1,783	0,000	1,583	0,000	down	up	up
Solyc03g097060	Exostosin family protein (AHRD V3.3 *** AT5G16890.1)		P:GO:0006486: F:G(	P:protein glycosylation; F:transferase activity, transferring glyco	IPR004263 (PFAM): PTHR11062:SF1	32,120	31,705	22,880	19,918	21,630									
Solyc03g097070	Target of Myb protein 1 (AHRD V3.3 *** AT5G16880.4)		C:GO:0005622: P:G(	C:intracellular; P:intracellular protein transport	IPR002014 (SMART): IPR002014 (PF	113,720	188,551	178,925	171,892	175,611	0,754	0,033					up		
Solyc03g097080	Cystatin/monellin superfamily protein (AHRD V3.3 *** AT1G63205.1)				G3DSA:3.10.450.10 (GENE3D): PTHR	3,158	2,800	3,289	3,262	2,639									
Solyc03g097085	LOW QUALITY:Cysteine protease (AHRD V3.3 *-* Q40675_ORYSA)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (SMART): IPR000668 (PF	0,000	0,000	0,000	0,025	0,024									
Solyc03g097090	Lysine-specific demethylase (AHRD V3.3 *** A0A199VZ18_ANACO)		C:GO:0005634: F:G(	C:nucleus; F:methyltransferase activity; P:methylation	IPR003347 (SMART): IPR003349 (SM	0,375	0,399	1,394	1,452	1,231									
Solyc03g097100	Calmodulin, putative (AHRD V3.3 *** B9S227_RICCO)		F:GO:0005509	F:calcium ion binding	IPR002048 (SMART): G3DSA:1.10.23	10,624	9,897	11,818	13,711	12,847									
Solyc03g097110	RNA-binding family protein isoform 1 (AHRD V3.3 *** A0A061EZK4_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	34,065	41,753	63,411	72,207	61,085									
Solyc03g097120	SolycHsfA1b	HSF-04	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	38,094	40,288	70,361	73,896	72,364									
Solyc03g097130	Protein kinase family protein (AHRD V3.3 *** Q8GWD0_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): PTHR	10,590	11,557	12,160	13,361	13,955									
Solyc03g097140	N-acetyltransferase, putative (AHRD V3.3 *** B9S236_RICCO)		C:GO:0000139: F:G(	C:Golgi membrane; EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	G3DSA:3.40.630.30 (GENE3D): IPR0(	33,412	34,933	41,315	47,659	40,944									
Solyc03g097150	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4BJD2_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion bi EC:2.7.1.134; EC:2. Inositol-tetrakisphosp	PF17927 (PFAM): G3DSA:3.40.50.11	7,815	10,160	7,524	7,764	7,808									
Solyc03g097160	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A0K9NPY2_ZOSMR)		F:GO:0005515: P:G(	F:protein binding; P:rRNA processing; C:small-subunit processo	IPR020472 (PRINTS): IPR001680 (SM	32,997	33,220	29,806	30,301	27,737									
Solyc03g097170	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *** B9S247_RICCO)	CCR	F:GO:0003854: P:G(	F:3-beta-hydroxy-de EC:1.1.1.145 3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D): IPR0(	6,360	3,326	12,402	13,139	11,538	-0,911	0,035					down		
Solyc03g097180	Plasma membrane isoform 2 (AHRD V3.3 *** A0A061F6L3_THECC)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:plasma membrane	IPR011528 (PFAM): PTHR35287 (PAN	99,855	145,525	82,468	91,406	81,923									
Solyc03g097190	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT5G16730.1)		P:GO:0007131	P:reciprocal meiotic recombination	mobidb-lite (MOBIDB_LITE): mobidb-lit	197,691	171,425	48,952	43,704	48,902									
Solyc03g097200	F-box only protein (AHRD V3.3 *** AT1G65000.1)				PTHR35106 (PANTHER): PTHR35106	10,589	7,657	15,869	14,171	14,414									
Solyc03g097210	pfkB-like carbohydrate kinase family protein (AHRD V3.3 *** AT4G27600.1)		F:GO:0016301	F:kinase activity	IPR002139 (PRINTS): IPR011611 (PF	23,839	24,965	77,130	74,857	82,380									
Solyc03g097230	AIG2-like (avirulence induced gene) family protein (AHRD V3.3 *** AT3G02910.1)		F:GO:0061929	F:gamma-glutamyla EC:4.3.2.8 Gamma-glutamylamir	IPR009288 (PFAM): G3DSA:3.10.490	3,579	4,201	3,797	3,486	3,489									
Solyc03g097240	DnAJ-like protein (AHRD V3.3 *-* W9QKC5_9ROSA)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm	IPR001623 (SMART): IPR001623 (SM	3,743	3,493	3,276	4,210	3,482									
Solyc03g097250	Low-density receptor-like protein (AHRD V3.3 *** AT5G16660.1)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:chloroplast inner membran	mobidb-lite (MOBIDB_LITE): PTHR340	54,288	59,282	87,204	85,977	81,427									
Solyc03g097260	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *** G7K541_MEDTR)		F:GO:0046872	F:metal ion binding	IPR013083 (G3DSA:3.30.40.GENE3D	85,891	89,992	106,467	106,614	104,728									
Solyc03g097270	cystatin 9	cys9	F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity	IPR000010 (SMART): G3DSA:3.10.45	113,202	174,645	120,788	126,834	125,000									
Solyc03g097280	Alanine--tRNA ligase (AHRD V3.3 *-* K4BJE6_SOLLC)		F:GO:0003723: F:G(	F:RNA binding; F:al: EC:6.1.1.7 Alanine--tRNA ligase	IPR003891 (SMART): IPR003890 (SM	56,451	53,976	51,128	51,144	55,985									
Solyc03g097290	DB199		F:GO:0003676: F:G(	F:nucleic acid bindi EC:6.1.1.7 Alanine--tRNA ligase	IPR002318 (PRINTS): IPR012947 (SM	122,740	110,885	156,066	152,889	156,929									
Solyc03g097300	mediator of RNA polymerase II transcription subunit-like protein (AHRD V3.3 *** AT5G17510.2)				IPR015671 (PFAM): mobidb-lite (MOB	22,527	24,057	27,167	22,482	23,430									
Solyc03g097310	Major facilitator superfamily protein (AHRD V3.3 *** AT1G64890.1)		C:GO:0016021	C:integral component of membrane	IPR039309 (PFAM): G3DSA:1.20.125	16,190	16,217	25,528	30,026	22,212									
Solyc03g097320	Sigma factor (AHRD V3.3 *** Q9SLX4_TOBAC)	SIG1	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra	IPR000943 (PRINTS): IPR007627 (PF	4,323	6,008	1,838	2,768	4,991			1,424	0,000				up	
Solyc03g097330	Sigma factor (AHRD V3.3 *-* Q9SLX4_TOBAC)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra	PTHR30603 (PANTHER): PTHR30603	0,096	0,197	0,000	0,120	0,000									
Solyc03g097340	WD40 repeat protein (AHRD V3.3 *** L7T9S0_SOLTU)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR015943 (G3	24,698	32,489	30,001	30,346	27,841									
Solyc03g097350	Kinase family protein (AHRD V3.3 *** D7MHY5_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	mobidb-lite (MOBIDB_LITE): mobidb-lit	90,183	85,259	123,520	131,660	124,710									
Solyc03g097355	Protein kinase-like (AHRD V3.3 *-* Q9FGC1_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	29,785	23,339	37,028	44,172	38,733									
Solyc03g097360	BolA-like family protein (AHRD V3.3 *-* A0A061F070_THECC)				G3DSA:3.30.300.90 (GENE3D): IPR0(	32,471	36,370	40,651	37,414	42,080									
Solyc03g097370	DNA-binding SMUBP-2 (AHRD V3.3 *** A0A0B0N417_GOSAR)		F:GO:0003677: C:G(	F:DNA binding; C:chloroplast stroma; C:chloroplast envelope	IPR014001 (SMART): IPR003593 (SM	112,850	92,953	133,082	147,806	168,347									
Solyc03g097380	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G50740.5)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding	IPR006121 (PFAM): G3DSA:3.30.70.1	9,892	7,362	0,920	4,345	2,598			1,472	0,031	2,216	0,000		up	up
Solyc03g097390	Acyl-[acyl-carrier-protein] hydrolase (AHRD V3.3 *** K4BJF6_SOLLC)		P:GO:0006633: F:G(	P:fatty acid biosynthetic process; F:thiolester hydrolase activity	IPR002864 (PFAM): G3DSA:3.10.129	0,619	0,928	0,069	0,072	0,046									
Solyc03g097400	Mitotic-spindle organizing protein 1B (AHRD V3.3 *** MZT1B_ARATH)		C:GO:0008274: P:G(	C:gamma-tubulin ring complex; P:gamma-tubulin complex localiz	IPR022214 (PFAM): IPR022214 (PAN	3,299	2,144	2,041	1,869	1,532									
Solyc03g097410	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4BJF8_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion bi EC:2.7.1.134; EC:2. Inositol-tetrakisphosp	IPR040464 (PFAM): G3DSA:3.30.470	0,238	0,303	0,112	0,265	0,331									
Solyc03g097420	HVA22-like protein (AHRD V3.3 *** K4BJF9_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004345 (PFAM): PTHR12300:SF6	0,347	0,371	0,022	0,050	0,000									
Solyc03g097430	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072TUA2_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR025520 (PFAM): PTHR35762 (PAN	0,596	0,333	0,311	0,169	0,283									
Solyc03g097440	Dehydrogenase/reductase SDR family protein 7-like protein (AHRD V3.3 *** A0A0B0P5K8_GOSAR)		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; F	IPR002347 (PRINTS): IPR002347 (PF	9,599	8,520	77,698	182,650	102,794					1,239	0,000			up
Solyc03g097450	SWI/SNF complex subunit SWI3A (AHRD V3.3 *** W9QCB3_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:protein binding	IPR001005 (SMART): IPR032451 (PF	14,942	11,953	13,963	15,931	15,437									
Solyc03g097460	integrator complex subunit (AHRD V3.3 *** AT3G07530.3)		P:GO:0016180: C:G(	P:snRNA processing; C:integrator complex	IPR022712 (SMART): IPR022712 (PF	52,321	45,488	40,044	44,077	42,834									
Solyc03g097470	Ketoacyl-ACP synthase III (AHRD V3.3 *** M4QSR7_9ERIC)		F:GO:0004315: P:G(	F:3-oxoacyl-[acyl-c EC:2.3.1.41; EC:2.3. Beta-ketoacyl-[acyl-c	IPR016039 (G3DSA:3.40.47.GENE3D	44,954	56,243	295,779	338,588	236,879									
Solyc03g097490	Protein DEK (AHRD V3.3 *** A0A0B2QBX5_GLYSO)		C:GO:0005634: F:G(	C:nucleus; F:histone binding; P:regulation of double-strand brea	IPR014876 (PFAM): G3DSA:1.10.10.6	34,071	32,287	46,470	47,577	42,406									
Solyc03g097500	Feruloyl transferase (AHRD V3.3 *** D5FPG8_SOLTU)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3	2,419	1,494	1,195	1,124	2,118									
Solyc03g097510	Small auxin up-regulated RNA38	SAUR38	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): PTHR31374:SF1	0,000	0,000	0,100	0,025	0,070									
Solyc03g097520	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B2QAP3_GLYSO)		C:GO:0016021	C:integral component of membrane	PF13589 (PFAM): PF17942 (PFAM): I	39,832	33,359	51,457	52,222	47,425									
Solyc03g097530	Tapetum determinant 1 (AHRD V3.3 *** A0A061FZR9_THECC)		P:GO:0001709: C:G(	P:cell fate determination; C:integral component of membrane	IPR040361 (PANTHER): PTHR33184:	3,525	1,629	0,168	0,050	0,190									
Solyc03g097540	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)					0,738	0,451	0,025	0,025	0,023									
Solyc03g097550	Pseudouridine synthase (AHRD V3.3 *** K4BJH2_SOLLC)		P:GO:0001522: F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn	G3DSA:3.30.2350.10 (GENE3D): IPR(	34,529	33,905	36,938	36,481	37,811									
Solyc03g097560	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH3_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D): G3	0,117	0,178	0,025	0,098	0,118									
Solyc03g097570	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH4_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D): G3	0,000	0,000	0,165	0,385	0,397									
Solyc03g097580	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH5_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D): G3	56,623	65,896	17,913	20,122	25,875									
Solyc03g097600	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH7_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004316 (PFAM): G3DSA:1.20.128	0,199	0,136	0,810	1,745	1,617									
Solyc03g097630	S-acyltransferase (AHRD V3.3 *** K4BJI0_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic retic EC:2.3.1.225 Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	45,557	62,504	45,431	44,362	51,328									
Solyc03g097640	Mitochondrial import inner membrane translocase subunit (AHRD V3.3 *** S8CMW8_9LAMI)		C:GO:0005758: P:G(	C:mitochondrial intermembrane space; P:chaperone-mediated p	IPR035427 (G3DSA:1.10.287.GENE3	8,450	8,884	4,251	4,576	4,322									
Solyc03g097650	NAC domain protein (AHRD V3.3 *** B2ZGQ7_SOYBN)	NAC030	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM NAC	0,883	0,722	0,947	0,869	0,779									
Solyc03g097660	LOW QUALITY:nuclear polyadenylated RNA-binding protein (AHRD V3.3 --* AT5G50830.2)		F:GO:0004519: P:G(	F:endonuclease activity; P:nucleic acid phosphodiester bond hy	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc03g097670	ATP/DNA binding protein (AHRD V3.3 *** AT3G48770.2)				IPR036890 (G3DSA:3.30.565.GENE3	122,499	240,677	62,880	89,051	82,463	1,000	0,001			0,505	0,008	up		up
Solyc03g097675	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** B6TKX6_MAIZE)		F:GO:0004739: P:G(	F:pyruvate dehydro EC:1.2.4.1 Pyruvate dehydroger	IPR005475 (SMART): G3DSA:3.40.50	33,776	32,908	64,410	58,785	60,000									
Solyc03g097680	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *-* B6TKX6_MAIZE)		F:GO:0004739: P:G(	F:pyruvate dehydro EC:1.2.4.1 Pyruvate dehydroger	IPR009014 (G3DSA:3.40.50.GENE3D	0,863	0,952	1,361	1,380	1,245									
Solyc03g097690	Kinase family protein (AHRD V3.3 *** D7MQB8_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	2,578	3,248	3,681	3,654	3,182									
Solyc03g097695	tRNA (met) cytidine acetyltransferase, putative (DUF616) (AHRD V3.3 --* AT1G53040.6)					0,081	0,186	0,190	0,172	0,165									
Solyc03g097700	O-methyltransferase (AHRD V3.3 *** F6M2M1_VITPS)	ASMT05	F:GO:0008171: F:G(	F:O-methyltransferase activity; F:protein dimerization activity	G3DSA:3.40.50.150 (GENE3D): IPR0(	9,520	12,792	133,017	151,453	128,941									
Solyc03g097710	KH domain-containing protein (AHRD V3.3 --* M8CU99_AEGTA)					0,019	0,074	0,000	0,073	0,072									
Solyc03g097715	meiosis chromosome segregation family protein (AHRD V3.3 *** AT5G41110.2)				IPR025261 (SMART): IPR033473 (PF	33,302	34,462	57,136	63,991	63,084									
Solyc03g097720	CASP-like protein (AHRD V3.3 *** K4BJI9_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006459 (TIGRFAM): IPR006702 (F	0,000	0,019	0,000	0,000	0,000									
Solyc03g097730	CASP-like protein (AHRD V3.3 *** K4BJJ0_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM): IPR006459 (TIGF	0,137	0,057	0,000	0,000	0,000									

Solyc03g097740	Armadillo/beta-catenin repeat family protein (AHRD V3.3 *** B9IFI6_POPTR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR000225 (PF	40,109	25,462	31,515	38,771	32,746									
Solyc03g097750	Translocon-associated protein subunit beta (AHRD V3.3 *** A0A0D2RZS2_GOSRA),Pfam:PF05753		C:GO:0005774; C:GO	C:vacuolar membrane; C:endoplasmic reticulum; C:Golgi appara			PF05753 (PFAM); PTHR12861:SF5 (F	7,847	6,365	5,531	5,305	4,411									
Solyc03g097760	LOW QUALITY:Sterile alpha motif domain-containing protein (AHRD V3.3 *** A0A103XWE6_CYNCS)		F:GO:0016301; P:GO	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,528	1,250	0,661	0,413	0,707									
Solyc03g097770	LOW QUALITY:hydroxysteroid dehydrogenase 1 (AHRD V3.3 --* AT5G50700.1)							1,396	0,696	0,280	0,136	0,307									
Solyc03g097780	Sialyltransferase-like protein 2 (AHRD V3.3 *** SIA2_ARATH)		P:GO:0006486; F:GO	P:protein glycosylat	EC:2.4.99	Glycosyltransferases	IPR038578 (G3DSA:3.90.1480.GENE	43,494	45,390	39,677	42,441	40,154									
Solyc03g097800	V-type proton ATPase subunit C (AHRD V3.3 *** VATC_ARATH)		F:GO:0015078; P:GO	F:proton transmembrane transporter activity; P:ATP hydrolysis c			G3DSA:3.30.70.100 (GENE3D); IPR0	125,057	126,874	133,375	143,128	137,122									
Solyc03g097820	bHLH transcription factor 022		P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,970	1,979	0,481	0,764	0,516									
Solyc03g097830	Poly (A) polymerase (AHRD V3.3 *** A0A0B0NTQ5_GOSAR)		F:GO:0003723; P:GO	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti			IPR002646 (PFAM); G3DSA:1.10.309	7,004	6,601	7,748	8,453	8,388									
Solyc03g097840	Mitochondrial phosphate carrier protein, putative (AHRD V3.3 *** B9RH00_RICCO)		F:GO:0022857	F:transmembrane transporter activity			IPR018108 (PFAM); IPR023395 (G3D	0,418	0,752	0,685	1,534	1,389					1,141	0,040			up
Solyc03g097850	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UE17_ANACO)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR032867 (PFAM); IPR002885 (TIGF	2,631	3,001	3,311	3,290	3,264									
Solyc03g097860	Potassium transporter (AHRD V3.3 *** M1BRC1_SOLTU)		F:GO:0015079; C:GO	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM); IPR003855 (TIGF	0,077	0,158	0,075	0,222	0,165									
Solyc03g097870	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJK4_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004316 (PFAM); G3DSA:1.20.128	35,818	17,905	42,412	48,187	35,046									
Solyc03g097882	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,025	0,000	0,000									
Solyc03g097884	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,018	0,025	0,047	0,000									
Solyc03g097886	50S ribosomal protein L14, chloroplastic (AHRD V3.3 --* RK14_PHAVU)							0,060	0,037	0,096	0,069	0,047									
Solyc03g097900	40S ribosomal protein S3a (AHRD V3.3 *** RS3A_TOBAC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001593 (SMART); IPR001593 (PF	613,720	647,076	286,942	295,478	307,134									
Solyc03g097910	putative dehydrogenase	pyd1a	C:GO:0005737; F:GO	C:cytoplasm; F:oxidoreductase activity, acting on the CH-CH gr			IPR005720 (TIGRFAM); IPR005720 (F	85,972	76,797	104,410	99,867	104,576									
Solyc03g097920	MAP kinase kinase 4	MAPKK4	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS); IPR000719 (SM	53,648	30,411	20,670	25,324	17,602	-0,792	0,004					down		
Solyc03g097930	transcription regulator (AHRD V3.3 --* AT1G02080.3)							0,058	0,100	0,050	0,051	0,046									
Solyc03g097940	Potassium channel (AHRD V3.3 *** H2DPY4_9ROSA)		F:GO:0005216; F:GO	F:ion channel activity; F:protein binding; P:ion transport; C:mem			IPR002110 (SMART); IPR000595 (SM	7,731	9,900	6,864	9,402	7,214									
Solyc03g097950	50S ribosomal protein L29 (AHRD V3.3 *** F4YFA4_CAMSI)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001854 (PFAM); IPR001854 (TIGF	18,523	28,933	21,953	25,470	32,240	0,670	0,009	0,551	0,000			up	up	
Solyc03g097955	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT2G26200.2)							0,388	0,409	0,258	0,360	0,424									
Solyc03g097960	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein, putative (AHRD V3.3 *-* A0A061EBK4_THECC)						IPR004146 (PFAM); mobidb-lite (MOB	1,427	1,194	1,369	1,249	1,156									
Solyc03g097970	B-cell receptor-associated-like protein (AHRD V3.3 *** G7JZ88_MEDTR)		C:GO:0005783; P:GO	C:endoplasmic reticulum; P:intracellular protein transport; C:inte			IPR040463 (PFAM); PTHR12701:SF2	24,542	26,540	32,889	33,670	30,620									
Solyc03g097980	Guanine nucleotide-binding alpha-2 subunit (AHRD V3.3 *** A0A0B0N4X6_GOSAR)		F:GO:0003924; P:GO	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001019 (PRINTS); IPR001019 (SM	13,389	12,069	13,437	11,947	11,616									
Solyc03g097990	RNA polymerase II subunit A C-terminal domain phosphatase SSU72 (AHRD V3.3 *** A0A0B0NIE4_GOSAR		F:GO:0004721; C:GO	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threon	G3DSA:3.40.50.2300 (GENE3D); IPR(	44,083	55,632	18,307	17,371	25,260									
Solyc03g098000	alanine-tRNA ligase, putative (DUF760) (AHRD V3.3 *** AT1G48450.1)						IPR008479 (PFAM); mobidb-lite (MOB	97,826	133,109	248,482	228,710	278,613									
Solyc03g098010	phosphate starvation inducible gene TPSI1		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	0,272	0,229	0,112	0,089	0,000									
Solyc03g098020	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G73480.1)		C:GO:0016020	C:membrane			IPR022742 (PFAM); PTHR11614 (PAN	30,448	37,172	25,942	22,818	29,168									
Solyc03g098030	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** G7KHW0_MEDTR)		P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART); IPR036691 (G3	0,124	0,279	0,000	0,000	0,000									
Solyc03g098050	Calmodulin 6	CaM6	F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	172,840	246,460	97,215	106,006	106,545									
Solyc03g098070	Zinc finger family protein (AHRD V3.3 *** B9HJL4_POPTR)		P:GO:0009630	P:gravitropism			G3DSA:3.30.160.6 C2H2	2,416	2,264	1,173	1,059	1,341									
Solyc03g098090	CASP-like protein (AHRD V3.3 *** K4BJM4_SOLLC)		C:GO:0005886; C:GO	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM); PTHR33573:SF5	0,215	0,123	0,682	1,204	0,686									
Solyc03g098100	NAD(P)H-dependent oxidoreductase (AHRD V3.3 *** B6TLR8_MAIZE)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS); IPR036812 (G3	6,341	6,860	18,695	23,172	20,232									
Solyc03g098110	AT-rich interactive domain-containing protein 1A (AHRD V3.3 *-* A0A1D1ZJ01_9ARAE)						PTHR37203:SF2 (PANTHER); PTHR3	15,626	14,520	23,470	21,271	23,120									
Solyc03g098120	40S ribosomal protein (AHRD V3.3 *** AT1G57540.3)		C:GO:0016021	C:integral component of membrane			PTHR36331 (PANTHER)	11,165	11,967	9,206	9,351	9,071									
Solyc03g098125	Luminal-binding 5 (AHRD V3.3 --* A0A0B0N3E8_GOSAR)							3,335	2,685	3,042	2,205	2,737									
Solyc03g098130	Callose synthase 1 family protein (AHRD V3.3 *** B9HN92_POPTR)						PF06910 (PFAM); mobidb-lite (MOBID	40,322	40,831	42,161	40,718	39,702									
Solyc03g098140	Sugar isomerase domain-containing family protein (AHRD V3.3 *** B9H8N8_POPTR)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:isomerase activity; F:carb			IPR000644 (SMART); IPR001347 (PF	43,953	38,952	29,457	30,741	30,418									
Solyc03g098150	protein kinase 6	pk6	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	57,762	55,163	62,376	63,428	62,229									
Solyc03g098160	UPF0614 protein C14orf102 family (AHRD V3.3 *** A0A151S8I5_CAJCA)		F:GO:0005515; P:GO	F:protein binding; P:RNA processing			IPR003107 (SMART); IPR013633 (PF	27,386	21,316	22,253	23,488	22,558									
Solyc03g098170	tubulin folding cofactor B (AHRD V3.3 *** AT3G10220.1)		F:GO:0005515	F:protein binding			IPR000938 (SMART); IPR036859 (G3	44,549	38,933	51,734	46,380	46,226									
Solyc03g098180	DHHA1 domain protein (AHRD V3.3 *** AT1G53345.1)						G3DSA:3.10.310.30 (GENE3D); PTHF	11,861	11,727	15,621	16,705	15,849									
Solyc03g098200	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9N3B2_POPTR)		F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated; F:li			IPR001356 (SMAF HD-ZIP	1,649	1,445	0,920	1,792	0,986									
Solyc03g098210	Cyclic nucleotide gated channel CNGC15 (AHRD V3.3 *** A0A0B4U342_SOLLC)		F:GO:0005216; P:GO	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART); G3DSA:1.10.28	21,958	35,141	26,899	28,355	29,404	0,704	0,021					up		
Solyc03g098220	serine palmitoyltransferase		F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3	130,005	142,468	95,389	95,702	105,269									
Solyc03g098230	1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase (AHRD V3.3 *** A0A103YE80_CY		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.1100 (GENE3D); IPR(	64,578	73,591	179,572	179,701	178,923									
Solyc03g098240	glutamate decarboxylase	GAD	F:GO:0004351; P:GO	F:glutamate decarb	EC:4.1.1.15	Glutamate decarboxy	IPR015421 (G3DSA:3.40.640.GENE3	684,085	371,273	1522,164	1298,768	1434,039									
Solyc03g098250	DNA polymerase epsilon subunit (AHRD V3.3 *** K4BJP0_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA pc	G3DSA:1.10.8.60 (GENE3D); IPR024	4,354	3,364	4,494	4,097	3,686									
Solyc03g098260	Myb transcription factor (AHRD V3.3 *-* G7KJN3_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB_related	0,038	0,055	0,000	0,000	0,071									
Solyc03g098280	Argonaute 1b	AGO1b	F:GO:0003676; F:GO	F:nucleic acid binding; F:protein binding			IPR003165 (SMART); IPR003100 (SM	313,824	265,072	285,118	262,950	288,513									
Solyc03g098290	Sucrose synthase (AHRD V3.3 *** M5WCU1_PRUPE)	SUS6	P:GO:0005985; F:GO	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	G3DSA:3.40.50.2000 (GENE3D); IPR(	5,156	4,467	127,767	130,104	111,363									
Solyc03g098300	Ornithine decarboxylase 2 (AHRD V3.3 *** A0A060IIA7_ATRBE)		F:GO:0003824; P:GO	F:catalytic activity; P:polyamine biosynthetic process			IPR000183 (PRINTS); IPR002433 (PF	0,042	0,909	0,075	0,022	0,023									
Solyc03g098310	Ornithine decarboxylase 2 (AHRD V3.3 *** A0A060IIA7_ATRBE)		F:GO:0003824; P:GO	F:catalytic activity; P:polyamine biosynthetic process			IPR000183 (PRINTS); IPR002433 (PF	1,024	0,814	0,000	0,000	0,000									
Solyc03g098320	Myb transcription factor (AHRD V3.3 *** A0A072UBN0_MEDTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	31,650	16,905	9,697	10,471	10,829	-0,876	0,008					down		
Solyc03g098325	Coiled-coil domain-containing 84 (AHRD V3.3 *-* A0A0B0Q3P2_GOSAR)						IPR028015 (PFAM); IPR028015 (PAN	4,079	3,025	7,339	8,113	6,433									
Solyc03g098340	Coiled-coil domain-containing 84 (AHRD V3.3 *-* A0A0B0Q3P2_GOSAR)						IPR028015 (PFAM); mobidb-lite (MOB	3,152	3,677	4,478	4,746	4,716									
Solyc03g098345	nucleoporin protein Ndc1-Nup protein (AHRD V3.3 *** AT1G73240.1)		C:GO:0016021	C:integral component of membrane			IPR019049 (PFAM); IPR019049 (PAN	10,120	9,865	6,170	5,760	5,828									
Solyc03g098350	LOW QUALITY:F-box protein interaction domain containing protein (AHRD V3.3 *-* Q60D10_SOLDE)		F:GO:0016740	F:transferase activity			mobidb-lite (MOBIDB_LITE)	0,037	0,000	0,000	0,000	0,000									
Solyc03g098380	LOW QUALITY:F-box protein interaction domain containing protein (AHRD V3.3 *** Q60D10_SOLDE)		F:GO:0005515	F:protein binding			PTHR31790 (PANTHER); IPR036047 (	0,058	0,173	0,046	0,025	0,023									
Solyc03g098390	LOW QUALITY:F-box protein interaction domain containing protein (AHRD V3.3 *-* Q60D10_SOLDE)		F:GO:0005515	F:protein binding			IPR036047 (SUPERFAMILY)	0,415	0,135	0,075	0,000	0,048									
Solyc03g098400	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			SM00365 (SMART); IPR003591 (SMA	0,256	0,435	0,437	0,420	0,611									
Solyc03g098420	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y1J2_CYNCS)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM); IPR011990 ((	6,157	5,486	3,524	4,763	4,138									
Solyc03g098430	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4BJQ8_SOLLC)		F:GO:0004553; C:GO	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucc	IPR000757 (PFAM); IPR016455 (PIRS	4,424	3,885	3,480	3,416	3,775									
Solyc03g098440	tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *** AT3G17670.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART); G3DSA:3.40.30	5,164	6,661	6,432	7,101	9,460			0,554	0,042				up	
Solyc03g098450	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** A0A072UM28_MEDTR)		F:GO:0003779	F:actin binding			IPR011684 (PFAM); PTHR32258 (PAN	2,499	3,272	1,318	1,088	1,131									
Solyc03g098460	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G27760.1)						IPR002347 (PRINTS); IPR002347 (PF	23,454	19,934	36,907	36,947	32,021									
Solyc03g098470	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT4G30330.1)		P:GO:0000398; C:GO	P:mRNA splicing, via spliceosome; C:spliceosomal complex			IPR001163 (SMART); IPR001163 (PF	28,261	28,276	31,724	29,302	30,708									
Solyc03g098480	LOW QUALITY:cotton fiber (DUF761) (AHRD V3.3 --* AT1G61260.1)		C:GO:0016020	C:membrane			PTHR33098 (PANTHER); PTHR33098	2,199	1,186	28,161	21,564	20,496			-0,461	0,049				down	
Solyc03g098490	LOW QUALITY:Cotton fiber expressed protein (AHRD V3.3 *** A0A109XNG5_GOSHI)		C:GO:0016021	C:integral component of membrane			PTHR33098:SF11 (PANTHER); PTHR	0,260	0,277	0,194	0,072	0,214									
Solyc03g098560	zinc ion binding / nucleic acid binding protein (AHRD V3.3 --* AT3G43470.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,371	0,356	1,598	2,216	1,953									
Solyc03g098570	F-box protein (AHRD V3.3 *** W9QCJ9_9ROSA)						IPR017451 (TIGRFAM); PTHR31264:S	0,300	0,119	0,675	0,642	0,591									
Solyc03g098580	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2PX33_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,673	0,661	0,718	0,630	0,945									
Solyc03g098590	RING/U-box superfamily protein (AHRD V3.3 *** AT3G19950.3)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR001841 (SMART); IPR001841 (PF	26,007	22,691	38,340	32,936	32,909									
Solyc03g098600	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 (AHRD V3.3 *** A0A1D1YZP2		F:GO:0004576; P:GO	F:oligosaccharyl transferase activity; P:protein glycosylation; C			G3DSA:3.40.50.12610 (GENE3D); IPF	114,046	122,351	123,243	113,583	111,405									
Solyc03g098610	plastid division protein (AHRD V3.3 *** AT3G19180.1)		P:GO:0010020; C:GO	P:chloroplast fission; C:integral component of chloroplast inner			IPR025344 (PFAM); mobidb-lite (MOB	13,949	11,619	14,406	15,522	16,284									
Solyc03g098620	DNA-binding RHL1-like protein (AHRD V3.3 *** A0A0B0MTJ7_GOSAR)		F:GO:0003677; P:GO	F:DNA binding; P:DNA endoreduplication			mobidb-lite (MOBIDB_LITE); mobidb-lit	13,381	11,077	16,055	16,893	16,216									
Solyc03g098630	DUF789 family protein (AHRD V3.3 *-* G7KKC4_MEDTR)						IPR008507 (PFAM); mobidb-lite (MOB	11,438	10,175	10,943	14,001	12,639									
Solyc03g098635	MAP kinase kinase 9 (AHRD V3.3 --* AT1G73500.1)							0,040	0,062	0,051	0,070	0,048									
Solyc03g098640	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT5G19750.1)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM); mobidb-lite (MOB	9,805	9,437	9,393	8,340	8,527									
Solyc03g098650	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061EMU1_THECC)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); IPR0(	0,366	0,264	0,322	0,295	0,235									
Solyc03g098660	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** A0A072UCV9_MEDTR)						IPR004182 (SMART); IPR011993 (G3	19,313	16,776	2,957	3,749	7,121			1,256	0,004				up	
Solyc03g098680	Kunitz trypsin inhibitor (AHRD V3.3 *** Q4W181_POPTN)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (SMART); IPR002160 (PF	0,000	0,000	0,418	1,327	1,578									
Solyc03g098700	Kunitz-type protease inhibitor D (AHRD V3.3 *** M1LA62_SOLTU)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (SMART); G3DSA:2.80.10	1,418	1,797	0,000	0,022	0,000									
Solyc03g098710	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (SMART); IPR002160 (PF	0,618	0,576	0,000	0,000	0,000									
Solyc03g098720	Kunitz trypsin inhibitor (AHRD V3.3 *** Q4W188_POPTN)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (SMART); G3DSA:2.80.10	0,042	0,083	0,000	0,000	0,024									
Solyc03g098730	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS); IPR002160 (SM	5,796	12,559	4,733	13,896	9,956			1,069	0,031	1,556	0,000		up	up
Solyc03g098740	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS); IPR002160 (SM	1,144	2,175	61,649	101,454	68,653					0,723	0,000			up
Solyc03g098750	Transmembrane protein, putative (AHRD V3.3 -** A0A072U8W6_MEDTR)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane			PTHR33474 (PANTHER); PTHR33474	11,360	10,704	24,970	29,006	23,033									
Solyc03g098760	Kunitz-type protease inhibitor-like protein (AHRD V3.3 *** Q2XPY0_SOLTU)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS); IPR002160 (SM	0,186	0,082	1,920	0,025	0,093									
Solyc03g098780	Cathepsin D Inhibitor		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS); IPR002160 (SM	0,756	2,968	0,000	0,025	0,023									
Solyc03g098790	Cathepsin D Inhibitor		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (PRINTS); IPR002160 (SM	0,000	0,440	0,000	0,000	0,000									
Solyc03g104790	Protein kinase superfamily protein (AHRD V3.3 *-* AT1G74330.3)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc03g104810	WRKY transcription factor 5	WRKY5	F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF WRKY	87,903	69,829	100,578	95,904	94,786									
Solyc03g110850	Nuclear transcription factor Y subunit C-2 (AHRD V3.3 *** NFYC2_ARATH)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YC	0,000	0,019	0,000	0,000	0,000									
Solyc03g110860	Nuclear transcription factor Y subunit C-1 (AHRD V3.3 *** NFYC1_ARATH)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YC	18,204	17,563	16,233	18,861	19,434									
Solyc03g110870	RING/U-box superfamily protein (AHRD V3.3 --* AT4G35840.2)							10,040	11,424	14,645	17,485	13,816									
Solyc03g110875	Protein transport protein Sec61 subunit gamma (AHRD V3.3 *** SC61G_ORYSJ)		P:GO:0006605; F:GO	P:protein targeting; F:P-P-bond-hydrolysis-driven protein transm			IPR023391 (G3DSA:1.20.5.GENE3D):	46,375	47,726	59,832	67,237	59,203									
Solyc03g110880	RNA polymerase 4 second largest subunit (RPD2)	rpd2						0,019	0,037	0,044	0,025	0,047									
Solyc03g110885	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** K4BJV1_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007644 (PFAM); IPR007647 (PFA	79,511	68,984	83,489	71,327	74,412									
Solyc03g110890	LOW QUALITY:glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT4G24910.1)		P:GO:0045492	P:xylan biosynthetic process			IPR021148 (PFAM); IPR006514 (TIGF	0,160	0,101	0,072	0,073	0,046									
Solyc03g110900	P-loop nucleoside triphosphate hydrolase superfamily protein, putative (AHRD V3.3 *** A0A072UYW1_MED		F:GO:0005515; F:GO	F:protein binding; F:ATP binding			IPR003593 (SMART); G3DSA:3.40.50	233,446	190,793	327,220	325,757	319,063									
Solyc03g110905	Elongator complex protein 3 (AHRD V3.3 *-* ELP3_ORYSJ)		P:GO:0002926; F:GO	P:tRNA wobble bas	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR039661 (PANTHER); IPR034687 (I	11,077	10,712	14,547	13,176	12,854									
Solyc03g110910	HVA22-like protein (AHRD V3.3 *** K4BJV5_SOLLC)		C:GO:0016020	C:membrane			IPR004345 (PFAM); PTHR12300:SF6	9,350	8,368	12,204	12,288	11,045									
Solyc03g110930	Ribosomal protein S21 family protein (AHRD V3.3 *** AT3G27160.2)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001911 (PFAM); IPR038380 (G3D	4,791	4,742	11,273	10,043	11,029									
Solyc03g110940	Protein kinase superfamily protein (AHRD V3.3 *** AT5G50330.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR004147 (PF	11,701	11,069	6,458	7,699	8,321									
Solyc03g110950	LOW QUALITY:GRAS family transcription factor (AHRD V3.3 *** A0A061EZS1_THE GRAS		F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	0,000	0,000	0,000	0,022	0,000									
Solyc03g110960	Nucleoside diphosphate kinase (AHRD V3.3 *** K4BJV9_SOLLC)		F:GO:0004550; P:GO	F:nucleoside diphos	EC:2.7.4.6	Nucleoside-diphosph	IPR001564 (PRINTS); IPR034907 (SM	9,005	12,989	14,967	14,636	16,960									
Solyc03g110980	GDP-mannose transporter, putative (AHRD V3.3 *** B9RMI4_RICCO)		C:GO:0005794; P:GO	C:Golgi apparatus; P:nucleotide-sugar transmembrane transpor			IPR004853 (PFAM); mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc03g110983	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (AHRD V3.3 --* AT1G34040.1)							0,021	0,000	0,000	0,000	0,000									
Solyc03g110990	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G23540.3)						PTHR38398 (PANTHER)	0,019	0,039	0,000	0,000	0,000									
Solyc03g111000	Glyceraldehyde 3-phosphate dehydrogenase (AHRD V3.3 *** F4HQT1_ARATH)		F:GO:0016620; P:GO	F:oxidoreductase activity, acting on the aldehyde or oxo group c			IPR020828 (SMART); G3DSA:3.40.50	0,140	0,082	0,730	1,006	1,040									
Solyc03g111010	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K7WNY2_SOLTU)	GADPH	P:GO:0006006; F:GO	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS); IPR020828 (SM	277,266	255,754	1450,241	1211,101	1310,034									
Solyc03g111030	Nodulation receptor kinase (AHRD V3.3 *** A0A0B0NS62_GOSAR)		P:GO:0006979; C:GO	P:response to oxidative stress; C:integral component of membra			mobidb-lite (MOBIDB_LITE); mobidb-lit	6,753	7,383	5,035	5,268	5,404									
Solyc03g111040	Amino acid transporter, putative (AHRD V3.3 *** B9RAK8_RICCO)		P:GO:0003333; C:GO	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM); PTHR22950:SF2	0,000	0,000	0,000	0,000	0,047									
Solyc03g111050	CONSTANS interacting protein 5	CIP5	F:GO:0003676	F:nucleic acid binding			G3DSA:2.40.50.140 (GENE3D); mobic	23,006	31,857	48,323	48,059	49,587									
Solyc03g111060	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT1G24360.1)		F:GO:0004316; P:GO	F:3-oxoacyl-[acyl-ca	EC:2.3.1.85; EC:1.1.	Fatty-acid synthase;	G3DSA:3.40.50.720 (GENE3D); IPR0(	0,038	0,000	0,025	0,072	0,000									
Solyc03g111080	Ketoacyl ACP reductase (AHRD V3.3 *-* A0A0M4C341_JATCU)		F:GO:0004316; P:GO	F:3-oxoacyl-[acyl-ca	EC:2.3.1.85; EC:1.1.	Fatty-acid synthase;	G3DSA:3.40.50.720 (GENE3D); IPR0:	0,404	0,567	0,318	0,541	0,283									
Solyc03g111090	Transcription factor GTE10 (AHRD V3.3 *** W9SF96_9ROSA)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS); IPR001487 (SM	0,341	0,334	0,340	0,410	0,142									
Solyc03g111100	LOW QUALITY:AtIII18x5-like protein (AHRD V3.3 *** AT3G48510.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	3,828	2,268	29,998	30,263	21,701									
Solyc03g111110	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_VIGMU)							0,057	0,079	0,022	0,000	0,048									
Solyc03g111120	Malate synthase (AHRD V3.3 *** M1B824_SOLTU)		F:GO:0004474; P:GO	F:malate synthase a	EC:2.3.3.9	Malate synthase	IPR006252 (PIRSF); G3DSA:3.20.20.:	15,587	14,574	6,495	7,836	7,507									
Solyc03g111130	Malate synthase (AHRD V3.3 *** K4BJX6_SOLLC)		F:GO:0004474; P:GO	F:malate synthase a	EC:2.3.3.9	Malate synthase	IPR006252 (TIGRFAM); G3DSA:1.20.	0,000	0,115	0,046	0,097	0,023									
Solyc03g111140	Malate synthase (AHRD V3.3 *** K4BJX7_SOLLC)		F:GO:0004474; P:GO	F:malate synthase a	EC:2.3.3.9	Malate synthase	IPR001465 (PFAM); G3DSA:1.20.122	1,682	2,544	2,289	5,556	1,687									
Solyc03g111150	Extracellular ligand-gated ion channel protein (AHRD V3.3 *** A0A072U3Z3_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR021924 (PFAM); mobidb-lite (MOB	3,550	3,308	4,942	5,301	4,707									
Solyc03g111160	dual specificity protein phosphatase (DsPTP1) family protein (AHRD V3.3 *** AT3G52180.1)		P:GO:0005982; P:GO	P:starch metabolic	EC:3.1.3.16	Protein-serine/threon	IPR020422 (SMART); IPR029021 (G3	27,547	29,626	56,845	45,243	50,690									
Solyc03g111170	4-coumarate:CoA ligase-like protein (AHRD V3.3 *** G7J515_MEDTR)	4CL-like	F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D); IPF	16,183	32,740	43,274	41,253	45,082	1,043	0,000					up		
Solyc03g111180	Aspartyl aminopeptidase family protein (AHRD V3.3 *** B9IF79_POPTR)		F:GO:0004177; P:GO	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR001948 (PRINTS); IPR023358 (G3	49,362	50,126	117,728	118,500	115,462									
Solyc03g111190	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G63390.1)		P:GO:0006004; C:GO	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF); IPR019378 (PFA	0,098	0,018	0,025	0,025	0,000									
Solyc03g111200	Adenylate kinase family protein (AHRD V3.3 *** AT5G50370.1)		F:GO:0004017; F:GO	F:adenylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS); IPR007862 (PF	90,416	99,240	52,662	55,136	57,505									
Solyc03g111210	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GNH7_POPTR)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,835	4,094	6,336	6,017	5,926									
Solyc03g111215	U-box domain-containing protein 51 (AHRD V3.3 *-* A0A199VS34_ANACO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,237	0,159	0,337	0,220	0,518									
Solyc03g111230	Ribosomal protein (AHRD V3.3 *** Q947H2_PETHY)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005721 (TIGRFAM); IPR001063 (F	462,321	474,063	263,336	235,983	234,251									
Solyc03g111250	SWI/SNF complex component SNF12-like protein (AHRD V3.3 *** W9RMR8_9ROSA)		F:GO:0005515	F:protein binding			IPR019835 (SMART); IPR036885 (G3	22,585	26,859	67,083	64,831	62,329									
Solyc03g111260	Ribonuclease J (AHRD V3.3 *** A0A0B0P255_GOSAR)		F:GO:0004519; F:GO	F:endonuclease activity; F:5'-3' exonuclease activity; P:respons			IPR001279 (SMAF Trihelix	36,791	47,109	67,378	62,737	78,675									
Solyc03g111270	SAP domain-containing protein (AHRD V3.3 *** AT5G63460.2)						IPR003034 (SMART); IPR003034 (PF	52,674	45,629	64,239	54,297	54,732									
Solyc03g111275	RING/U-box superfamily protein (AHRD V3.3 --* AT4G28370.4)							0,019	0,043	0,072	0,025	0,000									
Solyc03g111280	Cytochrome P450, putative (AHRD V3.3 *** B9RAH1_RICCO)		F:GO:0004497; F:GO	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR001128 (PRINTS); IPR002403 (PF	0,167	3,996	1,015	0,150	0,562	4,571	0,000					up		
Solyc03g111290	Cytochrome P450, putative (AHRD V3.3 *** B9RAH1_RICCO)		F:GO:0004497; F:GO	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR001128 (PRINTS); IPR002403 (PF	0,247	6,057	1,183	0,251	0,844	4,616	0,000					up		
Solyc03g111300	Cytochrome P450, putative (AHRD V3.3 *** B9RAH1_RICCO)		F:GO:0004497; F:GO	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR002403 (PRINTS); IPR001128 (PF	0,181	4,512	1,239	0,277	0,752	4,598	0,000					up		
Solyc03g111310	SNF1-related protein kinase regulatory subunit gamma 1 (AHRD V3.3 *** A0A061G5Z8_THECC)		C:GO:0009505; F:GO	C:plant-type cell wall; F:kinase activity; F:protein kinase regulat			IPR000644 (SMART); IPR000644 (PF	159,743	156,584	245,125	207,803	244,576									

Solyc03g111320	Exocyst subunit exo70 family protein (AHRD V3.3 *** G7JLE3_MEDTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM); mobidb-lite (MOB	379,230	356,289	201,104	277,320	234,304					0,466	0,008			up
Solyc03g111330	UPF0235 protein At5g63440 (AHRD V3.3 *** Y6344_ARATH)						IPR003746 (SMART); IPR003746 (PF	12,788	10,742	15,028	13,602	14,570									
Solyc03g111340	Ubiquitin activating enzyme (AHRD V3.3 *** G3CKJ0_ORYSJ)		F:GO:0008641	F:ubiquitin-like modifier activating enzyme activity			G3DSA:3.40.50.720 (GENE3D); IPR0(	27,458	31,713	33,653	32,984	33,028									
Solyc03g111350	Deoxycytidylate deaminase (AHRD V3.3 *** A0A0B2RRI8_GLYSO)		F:GO:0003824	F:catalytic activity			IPR002125 (PFAM); G3DSA:3.40.140	2,849	2,084	0,871	0,667	0,823									
Solyc03g111360	Oxygen-independent coproporphyrinogen III oxidase, putative (AHRD V3.3 *** A0A0	HEMF/CPOX	F:GO:0004109; C:G(	F:coproporphyrinog	EC:1.3.3.3	Coproporphyrinogen	IPR006638 (SMART); IPR004559 (TIG	2,404	2,941	5,447	5,082	5,380									
Solyc03g111370	C2H2-like zinc finger protein (AHRD V3.3 *** AT5G63280.1)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	11,766	11,840	13,772	15,113	14,274									
Solyc03g111380	Tubulin gamma chain (AHRD V3.3 *** K4BK01_SOLLC)		C:GO:0000930; F:G(	C:gamma-tubulin co	EC:3.6.1.15	Nucleoside-triphosph	IPR000217 (PRINTS); IPR002454 (PF	16,818	16,158	5,190	5,000	4,860									
Solyc03g111385	Kelch repeat-containing family protein (AHRD V3.3 *-* A9PHX5_POPTR)		F:GO:0005515	F:protein binding			PF13418 (PFAM); PF13415 (PFAM); I	0,080	0,041	0,071	0,069	0,070									
Solyc03g111390	Kelch repeat protein, putative (AHRD V3.3 *** B9RAN1_RICCO)		F:GO:0005515	F:protein binding			PF13418 (PFAM); PF13415 (PFAM); F	21,860	23,278	14,954	13,034	14,091									
Solyc03g111410	B3 domain-containing protein (AHRD V3.3 *-* W9S5V1_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	9,549	9,493	14,559	14,983	13,173									
Solyc03g111420	DnAJ-like protein (AHRD V3.3 *-* A0A0B2QWH0_GLYSO)						IPR024593 (PFAM); mobidb-lite (MOB	3,290	2,700	3,742	4,995	4,335									
Solyc03g111425	DnaJ heat shock amino-terminal domain protein (AHRD V3.3 --* AT5G53150.6)							2,049	1,833	2,736	3,303	3,018									
Solyc03g111430	DnAJ-like protein (AHRD V3.3 --* A0A0B2QWH0_GLYSO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,669	0,503	0,944	1,305	0,992									
Solyc03g111440	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103YAX8_CYNCS)						PTHR44137 (PANTHER); PTHR44137	0,707	0,960	0,937	1,356	1,129									
Solyc03g111450	Nuclear transcription factor Y subunit C-1 (AHRD V3.3 *** NFYC1_ARATH)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YC	1,399	0,702	0,581	0,563	0,614									
Solyc03g111455	B3 domain-containing protein (AHRD V3.3 --* W9S5V1_9ROSA)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			PTHR31391 (PANTHER); PTHR31391	0,040	0,021	0,022	0,000	0,000									
Solyc03g111460	Nuclear transcription factor Y subunit C-1 (AHRD V3.3 *** NFYC1_ARATH)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YC	0,309	0,470	0,000	0,000	0,000									
Solyc03g111470	CONSTANS interacting protein 2a (AHRD V3.3 *-* Q2VY18_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; C:cytopla			mobidb-lite (MOBIL NF-YC	0,019	0,000	0,000	0,000	0,000									
Solyc03g111500	B3 domain-containing protein (AHRD V3.3 *-* W9S5V1_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	5,117	4,563	5,785	6,044	5,098									
Solyc03g111510	RING/U-box superfamily protein (AHRD V3.3 *** AT1G13195.1)		F:GO:0004386; C:G(	F:helicase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001841 (SMART); IPR013083 (G3	0,216	0,269	0,075	0,145	0,046									
Solyc03g111520	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 --* A0A072VF46_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR038408 (G3DSA:3.30.430.GENE3I	0,000	0,000	0,000	0,025	0,000									
Solyc03g111530	cysteine-rich RECEPTOR-like kinase (AHRD V3.3 *-* AT4G23230.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity			IPR038408 (G3DSA:3.30.430.GENE3I	0,019	0,000	0,000	0,000	0,000									
Solyc03g111540	cysteine-rich RECEPTOR-like kinase (AHRD V3.3 *** AT4G23160.1)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); G3DSA:1.10.51	0,000	0,156	0,025	0,000	0,000									
Solyc03g111550	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2PXL8_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	123,530	79,937	128,478	203,680	111,554					0,666	0,001			up
Solyc03g111570	glucan synthase-like 8 (AHRD V3.3 *** AT2G36850.1)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan syntl	IPR026899 (SMART); IPR026899 (PF	62,118	51,840	41,142	44,652	45,870									
Solyc03g111575	Callose synthase-like protein (AHRD V3.3 *-* A0A072V9X9_MEDTR)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan syntl	IPR003440 (PFAM); PTHR12741 (PAN	17,929	16,031	13,507	14,009	16,124									
Solyc03g111580	Zinc finger transcription factor 27	C3H27	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	13,418	13,336	18,792	18,442	16,327									
Solyc03g111590	Zinc finger protein (AHRD V3.3 *** A0A0K9NS69_ZOSMR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR013087 (SMAF C2H2	50,055	49,550	140,518	162,416	116,002									
Solyc03g111593	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *-* A0A0V0I3W2_SOLCH)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR036691 (G3DSA:3.60.10.GENE3D	2,501	2,460	4,031	3,113	2,614									
Solyc03g111595	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *-* K4BK23_SOLLC)		F:GO:0003906; F:G(	F:DNA-(apurinic or apyrimidinic site) endonuclease activity; F:nuclease activity; F:phosphodiesterase I				0,436	0,269	0,380	0,485	0,423									
Solyc03g111597	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *-* K4BK23_SOLLC)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR036691 (G3DSA:3.60.10.GENE3D	0,897	0,938	1,583	1,660	1,347									
Solyc03g111600	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *-* K4BK23_SOLLC)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR036691 (G3DSA:3.60.10.GENE3D	2,452	2,333	3,207	4,057	3,177									
Solyc03g111610	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** AT3G48420.1)		F:GO:0016787	F:hydrolase activity			IPR023214 (G3DSA:3.40.50.GENE3D	14,754	44,976	10,385	14,713	30,774	1,634	0,000	1,561	0,000			up	up	
Solyc03g111620	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM); G3DSA:3.40.50.1	3,791	1,737	4,285	5,326	5,521									
Solyc03g111630	Programmed cell death 4 (AHRD V3.3 *** A0A0B0N0N9_GOSAR)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR003891 (SMART); IPR016021 (G3	19,981	17,502	39,582	37,053	31,583									
Solyc03g111640	Programmed cell death 4 (AHRD V3.3 *** A0A0B0N0N9_GOSAR)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR003891 (SMART); IPR016021 (G3	104,613	116,700	144,048	132,775	135,353									
Solyc03g111650	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RT09_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	17,348	13,718	15,734	13,327	17,065									
Solyc03g111660	Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2 (AHRD V3.3 *** AT3G48380.1)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity			IPR012462 (PFAM); G3DSA:3.90.70.1	20,436	20,041	34,006	35,052	31,487									
Solyc03g111665	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT1G17890.3)							0,000	0,039	0,000	0,025	0,023									
Solyc03g111670	Protein kinase (AHRD V3.3 *** D6N3G3_MALDO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			G3DSA:3.30.200.20 (GENE3D); IPR0:	28,709	26,204	11,763	15,575	13,036									
Solyc03g111680	DNA polymerase III subunit gamma/tau (AHRD V3.3 *** A0A0B0NH82_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA pc	IPR003593 (SMART); G3DSA:1.10.8.6	2,744	3,868	0,025	0,022	0,000									
Solyc03g111690	Pectate lyase family protein (AHRD V3.3 *** AT1G67750.1)		F:GO:0030570; P:G(	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS); IPR002022 (SM	62,524	47,232	2592,468	2956,398	1802,761									
Solyc03g111700	Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 *** AT1G29700.2),Pfam:PF13483						IPR036866 (G3DSA:3.60.15.GENE3D	18,563	25,072	9,402	11,273	21,616			1,192	0,000				up	
Solyc03g111710	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)		F:GO:0003712; F:G(	F:transcription core	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR000210 (SMART); IPR000197 (SM	18,611	35,078	2,617	4,318	2,904	0,940	0,030					up		
Solyc03g111730	KDEL-tailed cysteine endopeptidase	CysEP	P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS); IPR000668 (SM	88,210	101,708	30,275	48,937	42,601									
Solyc03g111740	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G50230.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	10,599	10,788	17,505	16,908	16,669									
Solyc03g111750	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT5G50230.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	0,000	0,000	0,000	0,022	0,000									
Solyc03g111760	Argonaute15	AGO.15	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR003165 (SMART); IPR014811 (SM	0,102	0,472	0,100	0,101	0,023									
Solyc03g111770	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ED84_THECC)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	30,041	30,593	16,454	15,940	17,232									
Solyc03g111780	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G24530.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	0,000	0,000	0,000	0,025	0,000									
Solyc03g111785	centromere protein X (AHRD V3.3 *** AT1G78790.4)		P:GO:0006281; P:G(	P:DNA repair; P:kinetochore assembly			IPR018552 (PFAM); G3DSA:1.10.286	7,079	6,531	14,946	14,163	14,044									
Solyc03g111790	DNA-directed RNA polymerase 3B, chloroplastic (AHRD V3.3 --* RPO3B_TOBAC)							0,198	0,043	0,096	0,264	0,166									
Solyc03g111793	Receptor-like protein kinase (AHRD V3.3 *** Q8LP72_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART); G3DSA:3.30.20	2,324	12,583	2,532	3,003	4,636	2,458	0,000					up		
Solyc03g111797	Sieve element occlusion a (AHRD V3.3 *** E2FKJ8_9SOLN)		P:GO:0010088	P:phloem development			IPR027942 (PFAM); IPR027944 (PFA	11,680	17,117	1,154	1,581	2,116									
Solyc03g111820	Sieve element occlusion a (AHRD V3.3 *** E2FKJ8_9SOLN)		P:GO:0010088	P:phloem development			IPR027944 (PFAM); IPR027942 (PFA	0,815	1,174	0,000	0,120	0,046									
Solyc03g111830	Protein-L-isoaspartate O-methyltransferase (AHRD V3.3 *** K4BK44_SOLLC)		F:GO:0004719; P:G(	F:protein-L-isoaspa	EC:2.1.1.77	Protein-L-isoaspartat	PF01135 (PFAM); G3DSA:3.40.50.15(	0,177	0,211	0,100	0,047	0,070									
Solyc03g111840	RNA-binding protein (AHRD V3.3 *** A0A0K9NVY1_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR012677 (G3	33,301	50,078	64,746	61,628	72,342	0,616	0,009					up		
Solyc03g111850	Indole-3-glycerol phosphate synthase (AHRD V3.3 *** W8SVJ4_TOBAC)		F:GO:0004425	F:indole-3-glycerol-|	EC:4.1.1.48	Indole-3-glycerol-pho	IPR013798 (PFAM); IPR013785 (G3D	60,813	69,160	90,156	76,826	87,149									
Solyc03g111870	E3 ubiquitin-protein ligase RGLG2 (AHRD V3.3 *** A0A0B0PYM1_GOSAR)		F:GO:0016874	F:ligase activity			IPR002035 (SMART); IPR010734 (PF	93,526	131,459	157,880	175,891	165,473									
Solyc03g111880	Cytochrome P450, putative (AHRD V3.3 *** B9RAS2_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	0,198	0,096	0,195	0,264	0,235									
Solyc03g111887	Cytochrome P450 (AHRD V3.3 *-* A0A103XWG4_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,000	0,061	0,122	0,022	0,023									
Solyc03g111920	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,177	0,126	1,047	1,086	1,315									
Solyc03g111930	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	2,639	3,040	11,659	12,621	8,256									
Solyc03g111935	Cytochrome P450, putative (AHRD V3.3 *** B9RAS2_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	8,028	6,108	1,319	1,050	2,709									
Solyc03g111950	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,000	0,000	0,000	0,022	0,000									
Solyc03g111973	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	27,955	35,143	571,620	578,534	520,493									
Solyc03g111977	isocitrate dehydrogenase subunit 2 (AHRD V3.3 --* AT2G17130.2)							0,674	0,622	2,166	2,529	2,007									
Solyc03g111990	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,969	0,698	4,429	7,071	4,875									
Solyc03g111995	Cytochrome P450 (AHRD V3.3 *-* A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	0,134	0,170	1,326	0,947	0,779									
Solyc03g112010	Cytochrome P450 (AHRD V3.3 *** A0A103XWG4_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	2,110	1,524	7,934	8,304	6,918									
Solyc03g112030	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	1,626	7,408	4,956	5,313	7,960	2,202	0,038					up		
Solyc03g112040	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,104	0,472	56,534	35,870	22,368			-1,340	0,002				down	
Solyc03g112050	Kinase AFC1 (AHRD V3.3 *** A0A072URR8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	143,114	190,317	165,547	156,355	177,257									
Solyc03g112060	Quinolinate synthase A (AHRD V3.3 *** W9RJG8_9ROSA)		F:GO:0008987; P:G(	F:quinolinate synthetase A activity; P:NAD biosynthetic process			G3DSA:3.90.1010.10 (GENE3D); IPR(	34,328	71,171	3,427	1,926	4,144	1,076	0,003					up		
Solyc03g112075	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** K4BK61_SOLLC)		F:GO:0004617; P:G(	F:phosphoglycerate	EC:1.1.1.95	Phosphoglycerate de	IPR015878 (SMART); G3DSA:3.40.50	74,554	80,924	79,208	70,882	76,459									
Solyc03g112090	high-affinity nitrate transporter-like protein (AHRD V3.3 *-* AT4G24715.1)		P:GO:0010167; P:G(	P:response to nitrate; P:nitrate transport			IPR016605 (PFAM); IPR016605 (PAN	0,221	0,258	0,856	1,141	0,642									
Solyc03g112100	high-affinity nitrate transporter-like protein (AHRD V3.3 *** AT4G24715.1)		P:GO:0010167; P:G(	P:response to nitrate; P:nitrate transport			IPR016605 (PFAM); IPR016605 (PIRS	0,100	0,057	0,101	0,121	0,094									
Solyc03g112120	Protein prune (AHRD V3.3 *** A0A1D1YXQ3_9ARAE)						G3DSA:3.90.1640.10 (GENE3D); mob	1,252	0,850	0,022	0,047	0,069									
Solyc03g112140	MAP kinase kinase kinase 27	MAPKKK27	F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); G3DSA:3.30.20	18,256	16,435	10,221	11,012	10,558									
Solyc03g112150	Elongation factor Tu (AHRD V3.3 *** K4BK69_SOLLC)		F:GO:0003746; F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS); IPR004541 (TI(	48,608	83,683	92,501	86,410	111,966	0,810	0,000					up		
Solyc03g112160	Protein DEHYDRATION-INDUCED 19 (AHRD V3.3 *** A0A0K9PGN7_ZOSMR)						IPR008598 (PFAM); IPR027935 (PFA	25,476	23,029	43,245	45,962	39,757									
Solyc03g112170	Invertase/pectin methylesterase inhibitor family protein (AHRD V3.3 *** D7L6Q2_ARALL)		P:GO:0043086; F:G(	P:negative regulation of catalytic activity; F:pectinesterase inhil			IPR006501 (SMART); IPR006501 (PF	0,063	0,074	0,140	0,381	0,023									
Solyc03g112190	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RAT8_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,295	3,397	6,647	5,317	5,786									
Solyc03g112200	LOW QUALITY:Insulinase (Peptidase family M16) family protein isoform 3 (AHRD V3.3 --* A0A061GZ00_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	16,737	18,908	26,314	27,428	24,587									
Solyc03g112210	LOW QUALITY:Phloem specific protein (AHRD V3.3 -** G7J4R7_MEDTR)						PTHR38224 (PANTHER)	1,956	3,268	2,948	4,068	3,368									
Solyc03g112220	LOW QUALITY:Helicase/SANT-associated, DNA binding protein (AHRD V3.3 --* AT3G24880.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	22,116	21,676	17,134	16,417	17,346									
Solyc03g112230	Ubiquitin-associated/TS-N domain protein, putative (AHRD V3.3 *** A0A072V0X9_MEDTR)		F:GO:0008270; P:G(	F:zinc ion binding; P:macroautophagy; F:ubiquitin binding			IPR000433 (SMART); IPR000270 (SM	616,845	712,693	626,551	591,396	629,522									
Solyc03g112240	LOW QUALITY:pyrroline-5-carboxylate reductase (AHRD V3.3 *-* AT4G03600.1)		C:GO:0016021	C:integral component of membrane			PTHR34656:SF2 (PANTHER); PTHR3·	2,050	1,395	0,212	0,175	0,164									
Solyc03g112250	Protein DETOXIFICATION (AHRD V3.3 *** K4BK79_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM); IPR002528 (F	0,000	0,021	0,000	0,000	0,000									
Solyc03g112260	Protein DETOXIFICATION (AHRD V3.3 *** K4BK80_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); IPR002528 (TIGF	0,019	0,000	0,000	0,000	0,023									
Solyc03g112270	Leucine-rich repeat-containing protein, putative (AHRD V3.3 *** B9RAU9_RICCO)		F:GO:0005515	F:protein binding			SM00364 (SMART); IPR003591 (SMA	122,469	92,048	103,341	98,732	101,577									
Solyc03g112280	C2 and GRAM domain-containing protein (AHRD V3.3 *** A0A0B2RGK8_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR000008 (SMART); IPR004182 (SM	3,386	6,073	12,091	16,365	16,386									
Solyc03g112290	tonoplast monosaccharide transporter2 (AHRD V3.3 --* AT4G35300.9)		C:GO:0005680; P:G(	C:anaphase-promoting complex; P:regulation of mitotic cell cycl			IPR026182 (PFAM); mobidb-lite (MOB	30,076	27,787	43,310	37,925	37,724									
Solyc03g112293	LOW QUALITY:Ribonuclease H-like superfamily protein (AHRD V3.3 --* AT2G02650.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM); IPR036397 (G3D	1,142	0,798	1,460	0,916	1,411									
Solyc03g112297	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *-* A0A0K9NT10_ZOSMR)		F:GO:0005515	F:protein binding			IPR000270 (SMART); IPR000270 (PF	3,061	2,234	2,719	5,329	3,493					0,977	0,001			up
Solyc03g112300	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *-* A0A0K9NT10_ZOSMR)		F:GO:0005515	F:protein binding			IPR000270 (PFAM); PTHR31066:SF1	0,299	0,341	0,319	0,416	0,257									
Solyc03g112310	Clade X lectin receptor kinase (AHRD V3.3 *** K4BK85_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	41,982	32,161	28,353	52,416	34,403					0,890	0,000			up
Solyc03g112320	Ferric reduction oxidase 8 (AHRD V3.3 *** W9RI94_9ROSA)		C:GO:0016020; F:G(	C:membrane; F:oxidoreductase activity; P:oxidation-reduction p			IPR000778 (PRINTS); IPR013130 (PF	3,714	3,163	1,003	0,927	1,057									
Solyc03g112330	U-box domain-containing protein kinase family protein (AHRD V3.3 *-* AT2G19410.2)						IPR014729 (G3DSA:3.40.50.GENE3D	5,461	4,393	7,111	7,549	7,792									
Solyc03g112335	O-acyltransferase (WSD1-like) family protein (AHRD V3.3 --* AT2G38995.4)							0,040	0,018	0,000	0,000	0,023									
Solyc03g112340	RING/U-box superfamily protein (AHRD V3.3 *** AT3G05200.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART); IPR001841 (PF	72,335	23,667	119,331	149,588	101,411	-1,586	0,000					down		
Solyc03g112350	RNA helicase DEAD12	DEAD12	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART); G3DSA:3.40.50	26,466	23,000	26,785	25,175	29,076									
Solyc03g112353	DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 *-* A0A072UQ07_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (PFAM); G3DSA:3.40.50.3	10,814	9,846	11,479	9,837	10,571									
Solyc03g112357	DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 *-* A0A072URV4_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (PFAM); G3DSA:3.40.50.3	17,626	16,262	17,023	15,546	17,365									
Solyc03g112360	60S ribosomal protein L27A (AHRD V3.3 *** B6VC54_VERFO)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR021131 (PFAM); G3DSA:3.100.10	270,443	273,778	141,920	111,603	129,945									
Solyc03g112370	LOW QUALITY:trehalose-6-phosphate synthase (AHRD V3.3 --* AT1G78580.4)							8,771	7,886	14,345	15,298	12,234									
Solyc03g112380	LOW QUALITY:Armadillo repeat only 4 (AHRD V3.3 *-* A0A061G1B9_THECC)		P:GO:0007166	P:cell surface receptor signaling pathway			PTHR23315:SF222 (PANTHER); PTHI	6,386	6,084	12,239	12,560	10,216									
Solyc03g112390	R2R3MYB transcription factor 86	R2R3MYB86	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	10,279	14,816	0,190	0,122	0,166									
Solyc03g112410	Histone deacetylase (AHRD V3.3 *** K4BK95_SOLLC)		F:GO:0004407; P:G(	F:histone deacetyla	EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS); IPR003084 (PF	1,289	1,444	0,458	0,170	0,256									
Solyc03g112420	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XY30_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	2,828	3,010	2,139	2,053	2,511									
Solyc03g112430	LOB domain-containing protein, putative (AHRD V3.3 *** B9S640_RICCO)						IPR004883 (PFAM LBD	0,158	0,041	0,096	0,094	0,191									
Solyc03g112450	Signal recognition particle receptor subunit beta (AHRD V3.3 *** W9RN76_9ROSA)		F:GO:0005525	F:GTP binding			G3DSA:3.40.50.300 (GENE3D); IPR0(	36,503	34,616	47,240	45,554	44,608									
Solyc03g112460	Tryptophan aminotransferase related 2, putative (AHRD V3.3 *** A0A061FUE1_THECC)		F:GO:0016846	F:carbon-sulfur lyase activity			IPR015422 (G3DSA:3.90.1150.GENE	2,521	3,204	2,050	2,239	1,505									
Solyc03g112500	Raffinose synthase family protein (AHRD V3.3 *** A0A061FTV8_THECC)		F:GO:0003824	F:catalytic activity			IPR008811 (PFAM); IPR013785 (G3D	1,291	0,856	0,068	0,101	0,094									
Solyc03g112510	D111/G-patch domain-containing family protein (AHRD V3.3 *** B9GSH2_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000467 (SMART); PF17780 (PFAM	1,848	1,834	1,894	2,303	1,739									
Solyc03g112520	FKBP12-interacting of 37 kDa-like protein (AHRD V3.3 *** A0A0B0P0F0_GOSAR)		P:GO:0000381; C:G(	P:regulation of alternative mRNA splicing, via spliceosome; C:nu			IPR029732 (PFAM); mobidb-lite (MOB	31,943	32,216	30,238	28,047	29,998									
Solyc03g112530	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G49660.1)		F:GO:0005515	F:protein binding			IPR001632 (PRINTS); IPR020472 (PF	36,573	37,935	37,789	29,004	31,921									
Solyc03g112540	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G50130.1)		C:GO:0016021	C:integral component of membrane			IPR002347 (PRINTS); IPR002347 (PF	0,155	0,261	0,000	0,000	0,023									
Solyc03g112550	Kinetochore protein spc25, putative (AHRD V3.3 *** A0A061FUW7_THECC)		C:GO:0000777; P:G(	C:condensed chromosome kinetochore; P:chromosome segrega			IPR013255 (PFAM); G3DSA:3.30.457	5,597	4,677	4,525	3,399	4,496									
Solyc03g112560	Cyclin-like F-box (AHRD V3.3 --* A2Q5C7_MEDTR)							10,214	9,168	14,146	12,376	13,045									
Solyc03g112565	Ribonucleoside-diphosphate reductase subunit beta (AHRD V3.3 *** A0A0B0P1E0_GOSAR)							8,144	6,672	10,608	12,173	7,990									
Solyc03g112580	Receptor protein kinase, putative (AHRD V3.3 *** B9RAX9_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS); IPR000719 (SMA	17,145	9,350	5,599	3,404	4,106									
Solyc03g112590	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524; F:G(	F:ATP binding; F:hydrolase activity			IPR004201 (SMART); IPR003338 (SM	48,815	49,251	45,067	47,646	52,132									
Solyc03g112595	LOW QUALITY:F-box family protein (AHRD V3.3 *-* A0A061EN61_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); G3DSA:1.20.128	0,040	0,000	0,046	0,072	0,118									
Solyc03g112600	JmjC domain-containing protein (AHRD V3.3 *** A0A124SGF9_CYNCS)		F:GO:0000987; C:G(	F:proximal promoter sequence-specific DNA binding; C:nucleus;			IPR003347 (SMART); G3DSA:2.60.12	4,951	4,718	5,407	5,391	6,802									
Solyc03g112620	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)		C:GO:0016021	C:integral component of membrane			IPR025521 (PFAM); IPR004314 (PFA	6,602	5,672	2,998	3,551	2,987									
Solyc03g112630	FAS-associated factor 2-B (AHRD V3.3 *** W9RRH9_9ROSA)		F:GO:0005515	F:protein binding			IPR001012 (SMART); IPR006577 (SM	4,211	4,126	1,291	1,649	2,057									
Solyc03g112640	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT5G63060.1)		C:GO:0009507	C:chloroplast			IPR001251 (SMART); IPR001251 (PF	12,645	15,164	23,308	24,013	29,348									
Solyc03g112650	SOUL heme-binding family protein (AHRD V3.3 *** A0A061FUQ9_THECC)		F:GO:0020037	F:heme binding			IPR006917 (PFAM); IPR011256 (G3D	29,633	31,653	36,801	33,165	34,000									
Solyc03g112660	Protein MODIFIER OF SNC1 1 (AHRD V3.3 *** A0A0B2QEH1_GLYSO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	182,295	163,076	351,249	353,175	312,578									
Solyc03g112670	embryo defective 2759 (AHRD V3.3 *** AT5G63050.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	15,790	22,526	19,120	19,749	21,781									
Solyc03g112680	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PU50_ZOSMR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,000	0,018	0,000	0,000	0,000									
Solyc03g112690	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9PRX5_ZOSMR)		F:GO:0005515	F:protein binding			IPR001214 (SMART); IPR003616 (SM	0,019	0,000	0,000	0,051	0,000									
Solyc03g112700	calmodulin-binding protein (DUF1645) (AHRD V3.3 *** AT2G15760.1)		C:GO:0005886	C:plasma membrane			IPR012442 (PFAM); mobidb-lite (MOB	7,655	4,968	5,372	9,745	6,231					0,862	0,001			up
Solyc03g112720	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** A9PAA6_POPTR)		F:GO:0019789	F:SUMO transferase activity			SM00212 (SMART); IPR000608 (PFAI	2,946	2,999	1,520	1,259	1,460									
Solyc03g112730	Cysteine-rich receptor-like protein kinase 1		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	0,199	0,134	0,194	0,145	0,142									
Solyc03g112740	Homeobox protein knotted-1, putative (AHRD V3.3 *-* B9RAZ8_RICCO)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR005541 (SMART); IPR005540 (SM	0,000	0,000	0,025	0,000	0,000									
Solyc03g112750	Tornado 1 (AHRD V3.3 *** A0A061F576_THECC)		F:GO:0005515	F:protein binding			SM00368 (SMART); G3DSA:3.40.50.3	0,516	0,410	0,196	0,261	0,238									
Solyc03g112755	Tornado 1 (AHRD V3.3 *-* A0A061F576_THECC)						PTHR24106 (PANTHER); PTHR24106	0,214	0,159	0,097	0,170	0,072									
Solyc03g112760	transmembrane protein (AHRD V3.3 *** AT3G48200.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	108,081	98,930	4,999	4,137	14,205			1,498	0,000				up	
Solyc03g112770	Glutaredoxin (AHRD V3.3 *** I2FJT7_SOLTU)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR014025 (PRINTS); IPR002109 (PF	33,758	29,259	39,668	36,270	37,209									

Solyc03g112790	Wall-associated receptor kinase 3-like protein (AHRD V3.3 *** A0A0B0PX41_GOSAR)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR33355:SF3	0,560	0,988	0,747	0,477	0,591									
Solyc03g112810	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane	PF02466 (PFAM): PTHR13002 (PANT	0,118	0,199	0,225	0,099	0,119									
Solyc03g112820	U3 small nucleolar ribonucleoprotein protein MPP10 (AHRD V3.3 *** K4BKD5_SOLLC)		C:GO:0005732; P:G(	C:small nucleolar ribonucleoprotein complex; P:rRNA processing	IPR012173 (PIRSF): IPR012173 (PFA	10,595	10,244	8,959	8,788	8,524									
Solyc03g112830	Phox domain-containing family protein (AHRD V3.3 *** B9I3B8_POPTR)		F:GO:0035091	F:phosphatidylinositol binding	IPR025258 (SMART): IPR025258 (PF	19,612	21,321	38,591	44,928	33,921									
Solyc03g112840	Transmembrane protein, putative (AHRD V3.3 *** G7J5E4_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:integral component of membrane	PTHR12242:SF10 (PANTHER): PTHR	0,176	0,158	0,141	0,237	0,284									
Solyc03g112850	60S ribosomal protein L44 (AHRD V3.3 *** RL44_GOSHI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000552 (PFAM): G3DSA:3.10.450	268,294	253,165	241,106	198,909	217,276									
Solyc03g112860	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT1G10650.1)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:ligase activity	IPR017066 (PIRSF): IPR017066 (PAN	20,440	16,544	17,188	22,032	18,181									
Solyc03g112870	Phosphate/phosphoenolpyruvate translocator (AHRD V3.3 *** P93390_TOBAC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR004853 (PFAM): IPR004696 (TIGF	53,941	61,729	101,184	108,449	103,480									
Solyc03g112880	Fasciclin-like arabinogalactan family protein (AHRD V3.3 *** A0A061GX88_THECC)		P:GO:0009738; P:G(	P:abscisic acid-activated signaling pathway; P:multidimensional	IPR000782 (SMART): IPR036378 (G3	6,238	6,599	0,259	0,237	0,377									
Solyc03g112890	LOW QUALITY:R2R3MYB transcription factor	R2R3MYB118	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,121	0,037	0,000	0,000	0,000									
Solyc03g112900	Iron-sulfur cluster assembly protein (AHRD V3.3 *** K4BKE3_SOLLC)		F:GO:0005506; P:G(	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl	G3DSA:3.90.1010.10 (GENE3D): IPR(	132,192	143,348	158,037	151,569	153,534									
Solyc03g112910	pantothenate kinase 2 (AHRD V3.3 *** AT4G32180.1)		F:GO:0004594; F:G(	F:pantothenate kina EC:2.7.1.33 Pantothenate kinase	IPR002791 (PFAM): G3DSA:3.30.420	67,039	69,526	71,624	74,546	72,994									
Solyc03g112920	Zinc finger family protein (AHRD V3.3 *-* B9HJL4_POPTR)		P:GO:0009630	P:gravitropism	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,080	0,036	0,000	0,050	0,048									
Solyc03g112930	Dof zinc finger protein (AHRD V3.3 *** A0A0B6VJP1_TOBAC)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM Dof	0,242	0,415	0,000	0,022	0,000									
Solyc03g112950	Serine/Threonine-kinase ATM-like protein (AHRD V3.3 *** AT3G48190.2)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR003152 (SMART): IPR000403 (SM	51,743	40,469	18,516	17,308	24,456									
Solyc03g112960	LOW QUALITY:Pectinesterase (AHRD V3.3 *-* A0A068TR01_COFCA)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (PF	2,774	4,883	1,523	1,431	1,480									
Solyc03g112970	Pectinesterase (AHRD V3.3 *-* B9GXZ7_POPTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR035513 (G3	1,241	2,592	0,942	0,970	1,080									
Solyc03g112980	translation initiation factor 3 subunit I (AHRD V3.3 --* AT1G54680.4)					0,550	3,066	0,381	0,984	0,778	2,495	0,000					up		
Solyc03g112990	LOW QUALITY:Pectinesterase inhibitor (AHRD V3.3 *** A0A103XZ28_CYNCS)		F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (SMART): IPR006501 (PF	23,191	27,550	15,131	16,553	16,787									
Solyc03g112995	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0H3YBT8_SALMI)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR036638 (G3DSA:4.10.280.GENE3	0,120	0,077	0,000	0,000	0,000									
Solyc03g113000	RINT-1/TIP-1-like protein (AHRD V3.3 *** A0A103XXR6_CYNCS)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:Golgi vesicle transport	IPR007528 (PFAM): PTHR13520:SF1	35,540	30,931	55,471	54,832	49,753									
Solyc03g113010	F-box/kelch-repeat protein family (AHRD V3.3 *** A0A151RZC6_CAJCA)		F:GO:0005515	F:protein binding	IPR006652 (SMART): IPR015915 (G3	48,603	37,369	22,483	24,325	31,010			0,461	0,015				up	
Solyc03g113020	Vacuolar protein sorting-associated protein 29 (AHRD V3.3 *** K4BKF5_SOLLC)		C:GO:0030904; P:G(	C:retromer complex; P:retrograde transport, endosome to Golgi	IPR024654 (PFAM): IPR029052 (G3D	35,720	48,920	91,743	90,130	92,727									
Solyc03g113030	Aldose 1-epimerase (AHRD V3.3 *** K4BKF6_SOLLC)		F:GO:0016853; P:G(	F:isomerase activity; P:hexose metabolic process; F:carbohydr	IPR008183 (PFAM): IPR015443 (PIRS	15,758	12,831	62,032	62,293	53,771									
Solyc03g113040	ABC transporter A family protein (AHRD V3.3 *** A0A072UUA7_MEDTR)	ABCA2	F:GO:0005524; C:G(	F:ATP binding; C:inl EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	2,532	5,118	2,907	3,959	3,668									
Solyc03g113060	ABC transporter A family protein (AHRD V3.3 *** A0A072UUA7_MEDTR)	ABCA3	F:GO:0005524; C:G(	F:ATP binding; C:inl EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): PF12698 (PFAM	57,456	50,324	25,095	20,078	23,114									
Solyc03g113070	ABC transporter A family protein (AHRD V3.3 *** A0A072UVK2_MEDTR)	ABCA9	F:GO:0005319; F:G(	F:lipid transporter a EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	PF12698 (PFAM): PTHR45592 (PANT	7,791	9,059	6,444	8,254	8,415									
Solyc03g113080	ABC transporter family protein (AHRD V3.3 *-* A0A097P9Q6_HEVBR)	ABCA8	F:GO:0005524; C:G(	F:ATP binding; C:inl EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR(	9,585	12,730	9,190	9,720	10,930									
Solyc03g113090	Serine/threonine-protein kinase atr (AHRD V3.3 *** A0A0B0N9L0_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,791	1,979	0,379	0,273	0,166									
Solyc03g113100	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A072TRF9_MEDTR)		P:GO:0000209; F:G(	P:protein polyubiquitination; F:ATP binding; P:DNA repair; F:liga	SM00212 (SMART): IPR000608 (PFAI	139,591	102,526	271,039	328,860	264,541									
Solyc03g113120	WRKY transcription factor 73	WRKY73	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	0,000	0,000	0,000	0,025	0,000									
Solyc03g113130	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B0PVN9_GOSAR)		F:GO:0016702; P:G(	F:oxidoreductase a EC:1.13.11 Acting on single donc	IPR012864 (PFAM): IPR014710 (G3D	6,472	4,446	3,304	2,745	2,916									
Solyc03g113140	Nuclear ribonuclease Z (AHRD V3.3 *** A0A0B0P2G1_GOSAR)		P:GO:0034414; F:G(	P:tRNA 3'-trailer cle EC:3.1.3; EC:3.1.26 Acting on ester bonds	IPR001279 (PFAM): IPR036866 (G3D	8,169	7,191	9,405	9,298	8,860									
Solyc03g113150	Pectate lyase (AHRD V3.3 *** K4BKG8_SOLLC)		F:GO:0030570	F:pectate lyase act EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	0,040	0,323	0,051	0,050	0,024									
Solyc03g113160	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9H429_POPTR)				IPR005174 (PFAM): PTHR44259 (PAI	0,080	0,041	0,000	0,000	0,000									
Solyc03g113170	16.6 kDa heat shock protein (AHRD V3.3 *** A0A0B2SUX8_GLYSO)		C:GO:0016020	C:membrane	IPR002068 (PFAM): IPR008978 (G3D	0,000	0,039	0,000	0,000	0,000									
Solyc03g113180	16.6 kDa heat shock protein (AHRD V3.3 *** A0A0B2SUX8_GLYSO)	Hsp23.7	C:GO:0016020	C:membrane	IPR002068 (PFAM): IPR008978 (G3D	0,353	0,298	0,315	0,293	0,236									
Solyc03g113190	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT1G74720.1)		C:GO:0016021	C:integral component of membrane	IPR000008 (SMART): IPR035892 (G3	16,735	16,874	7,144	7,710	7,880									
Solyc03g113200	LOW QUALITY:nucleolar-like protein (AHRD V3.3 --* AT3G57780.5)				mobidb-lite (MOBIDB_LITE): PTHR368	0,000	0,021	0,000	0,000	0,000									
Solyc03g113210	Mitochondrial outer membrane porin (AHRD V3.3 *** VDAC1_WHEAT)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe	IPR023614 (G3DSA:2.40.160.GENE3	0,082	0,074	0,000	0,000	0,047									
Solyc03g113220	Hypersensitive-induced response protein (AHRD V3.3 *** A6YGE4_CARPA)				IPR001107 (SMART): IPR001107 (PF	52,334	80,992	44,403	55,844	52,201									
Solyc03g113230	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G23460.2)	PG69	F:GO:0004650; P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	0,021	0,000	0,000	0,050	0,023									
Solyc03g113240	transmembrane protein, putative (DUF1118) (AHRD V3.3 *** AT1G74730.1)		C:GO:0009515; C:G(	C:granal stacked thylakoid; C:chloroplast thylakoid membrane; F	IPR009500 (PFAM): PTHR31425 (PAI	28,272	47,852	23,031	32,365	50,171	0,786	0,006	1,121	0,000	0,495	0,009	up	up	up
Solyc03g113250	nitrate transporter 1:2 (AHRD V3.3 *** AT1G69850.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): mobidb-lite (MOB	0,264	0,139	0,000	0,076	0,024									
Solyc03g113255	Tyrosyl-DNA phosphodiesterase 1 (AHRD V3.3 --* A0A1D1Z6W5_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,021	0,075	0,047	0,024									
Solyc03g113270	LEVAHOX1G L.esculentum homeobox	vahox1	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR000047 (PRIN HD-ZIP	286,498	214,659	862,167	915,179	683,952									
Solyc03g113280	Integral membrane HPP family protein (AHRD V3.3 *** AT3G47980.1)		C:GO:0016021	C:integral component of membrane	IPR007065 (PFAM): PTHR33741 (PAI	3,223	2,885	2,947	5,431	2,760					0,880	0,041			up
Solyc03g113290	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 --* AT1G59960.1)					0,000	0,000	0,000	0,025	0,000									
Solyc03g113300	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061G3Y5_THECC),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	1,549	1,359	0,951	0,976	0,867									
Solyc03g113320	LOW QUALITY:Tuliposide A-converting enzyme 1, chloroplastic (AHRD V3.3 --* TCEA1_TULGE)					0,000	0,043	0,025	0,098	0,023									
Solyc03g113330	Nodulin / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A061FXW3_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM): G3DSA:1.20.125(	18,934	17,300	33,567	33,634	34,790									
Solyc03g113340	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** AT1G74780.1)		C:GO:0016021	C:integral component of membrane	IPR010658 (PFAM): PTHR21576 (PAI	13,116	6,944	23,227	26,374	22,319	-0,892	0,011					down		
Solyc03g113350	Zinc finger protein, putative (AHRD V3.3 *** B9R926_RICCO)		F:GO:0008270	F:zinc ion binding	IPR001841 (SMART): G3DSA:2.20.28	46,491	36,085	0,926	1,188	1,341									
Solyc03g113370	Ubiquitin carboxyl-terminal hydrolase-related protein (AHRD V3.3 *** AT3G47890.2)		F:GO:0005515; P:G(	F:protein binding; P EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR0(	30,082	29,305	30,395	41,196	30,736					0,440	0,046			up
Solyc03g113380	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9R930_RICCO)		F:GO:0005515	F:protein binding	IPR002625 (SMART): IPR002885 (PF	78,342	87,195	61,832	91,007	94,730			0,613	0,000	0,559	0,001		up	up
Solyc03g113390	Calcium-dependent protein kinase (AHRD V3.3 *** B9I317_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR000719 (SMART): IPR002048 (SM	102,650	140,901	140,686	144,100	139,701									
Solyc03g113400	TOMLHA1 H+-ATPase	lha1	C:GO:0016021	C:integral component of membrane	IPR004014 (SMART): G3DSA:2.60.12	30,923	29,245	20,805	18,528	20,542									
Solyc03g113405	Plasma membrane ATPase (AHRD V3.3 *** A0A067KG17_JATCU)		F:GO:0000166; C:G(	F:nucleotide binding; C:integral component of membrane	PR00119 (PRINTS): IPR001757 (PRII	122,967	124,433	81,113	68,953	81,447									
Solyc03g113410	Auxin response factor (AHRD V3.3 *-* M0ZGK3_SOLTU)		F:GO:0005515	F:protein binding	IPR033389 (PFAM): G3DSA:3.10.20.9	0,021	0,018	0,000	0,070	0,069									
Solyc03g113420	Major facilitator superfamily protein (AHRD V3.3 *** AT5G62680.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): PTHR11654:SF5	3,874	9,167	12,897	15,879	19,057									
Solyc03g113430	Nitrate transporter NRT1-2 (AHRD V3.3 *** Q9FRU5_SOYBN)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): IPR000109 (PAN	13,046	59,463	49,684	52,287	72,936	2,214	0,000	0,549	0,005			up	up	
Solyc03g113440	Major facilitator superfamily protein (AHRD V3.3 *** AT5G28470.2)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): IPR000109 (PAN	0,508	0,924	0,208	0,227	0,116									
Solyc03g113450	Receptor-like protein kinase (AHRD V3.3 *** Q9FM23_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	5,522	5,687	1,881	1,822	2,679									
Solyc03g113460	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G47130.1),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	16,630	13,739	6,818	4,006	6,187					-0,764	0,040			down
Solyc03g113470	Hedgehog-interacting-like protein (AHRD V3.3 *** C3TX91_BRASY)		F:GO:0003824	F:catalytic activity	IPR012938 (PFAM): IPR011042 (G3D	0,000	0,000	0,122	0,150	0,071									
Solyc03g113480	LOW QUALITY:arginine N-methyltransferase, putative (DUF688) (AHRD V3.3 --* AT2G30990.5)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,562	2,469	35,381	59,474	49,586					0,754	0,003			up
Solyc03g113490	HIPL1-like protein (AHRD V3.3 *** A0A0B0MLG6_GOSAR)		F:GO:0003824	F:catalytic activity	IPR011042 (G3DSA:2.120.10.GENE3	1,627	2,484	0,437	0,701	0,447									
Solyc03g113500	Aminoacyl-tRNA synthetase (AHRD V3.3 *** Q2PF39_TRIPR)				IPR028942 (PFAM): IPR018501 (PFA	52,432	50,285	54,301	52,077	49,672									
Solyc03g113510	F17F16.3 protein (AHRD V3.3 *** Q9FWR1_ARATH)				mobidb-lite (MOBIDB_LITE): mobidb-lit	2,858	3,461	1,704	2,624	1,811									
Solyc03g113520	Galactosyltransferase family protein (AHRD V3.3 *** AT5G62620.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR001079 (SMART): G3DSA:2.60.12	31,709	30,768	12,381	12,730	16,297									
Solyc03g113540	Dynein light chain (AHRD V3.3 *** Q4W5W8_VICFA)		P:GO:0007017; C:G(	P:microtubule-based process; C:dynein complex	IPR001372 (SMART): IPR001372 (PF	1,557	2,198	1,025	0,908	1,103									
Solyc03g113560	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT5G62610.2)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	3,280	2,696	3,176	2,699	2,354									
Solyc03g113570	Germin-like protein		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS): IPR006045 (SM	0,021	0,000	0,000	0,000	0,000									
Solyc03g113580	Germin-like protein (AHRD V3.3 *** Q8H2A6_ANACO)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS): IPR006045 (SM	0,037	0,064	0,022	0,050	0,023									
Solyc03g113590	5-formyltetrahydrofolate cycloligase		F:GO:0005524; C:G(	F:ATP binding; C:mi EC:6.3.3.2 5-formyltetrahydrofol	IPR002698 (PFAM): IPR024185 (G3D	60,463	56,396	67,006	64,575	70,922									
Solyc03g113610	Protein CLP1 homolog (AHRD V3.3 *-* W1PAU8_AMBTC)		P:GO:0000448; F:G(	P:cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricist	IPR032319 (PFAM): G3DSA:3.40.50.3	17,455	19,200	13,330	12,374	12,243									
Solyc03g113620	MYB transcription factor (AHRD V3.3 *** B2CZJ3_CAPAN)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	131,693	96,952	16,381	15,807	20,470									
Solyc03g113630	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K3S7_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFA	27,192	28,226	53,006	53,266	56,084									
Solyc03g113640	Serine esterase family protein, putative (AHRD V3.3 *** A0A072VDP9_MEDTR)		P:GO:0044255	P:cellular lipid metabolic process	IPR022122 (PFAM): mobidb-lite (MOB	43,816	52,507	43,041	42,979	44,024									
Solyc03g113650	LOW QUALITY:Receptor homology region, transmembrane domain- and RING domain-containing protein 1 (AHRD V3.3 --* RMR1_ARATH)					0,040	0,018	0,000	0,000	0,000									
Solyc03g113660	Nuclear mitotic apparatus 1 (AHRD V3.3 *-* A0A0B0NXR3_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	29,751	24,943	29,605	28,067	28,591									
Solyc03g113670	AT3g47831/T23J7 (AHRD V3.3 *** Q94F43_ARATH)		C:GO:0016021	C:integral component of membrane	PTHR38525 (PANTHER)	0,079	0,158	0,118	0,101	0,189									
Solyc03g113680	Microtubule-associated protein TORTIFOLIA1 (AHRD V3.3 *** A0A151R900_CAJCA)		C:GO:0005874; F:G(	C:microtubule; F:microtubule binding	IPR011989 (G3DSA:1.25.10.GENE3D	49,627	47,419	3,968	3,722	6,219									
Solyc03g113690	Abc transporter family protein (AHRD V3.3 *** D7LZ77_ARALL)	ABCG6	F:GO:0005524; C:G(	F:ATP binding; C:mi EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF	1,526	0,939	0,521	0,678	0,847									
Solyc03g113700	RING/U-box superfamily protein (AHRD V3.3 *** AT5G62910.2)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;	IPR013083 (SMART): G3DSA:3.30.40.GENE3D	71,427	58,379	82,156	75,286	78,135									
Solyc03g113710	Formin-like protein (AHRD V3.3 *** K4BKM3_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR015425 (SMART): G3DSA:1.20.58	0,078	0,000	0,025	0,073	0,048									
Solyc03g113720	Two-component response regulator (AHRD V3.3 *** W9S9I1_9ROSA)	TRR 75	P:GO:0000160	P:phosphorelay signal transduction system	IPR001789 (SMART): G3DSA:3.40.50	2,742	4,668	0,498	0,319	0,589									
Solyc03g113740	anaphase-promoting complex subunit 8 (AHRD V3.3 *** AT3G48150.2)		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR011990 (G3	5,152	5,170	5,515	5,428	5,312									
Solyc03g113750	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9R8Z2_RICCO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	9,550	8,085	9,258	6,789	8,323									
Solyc03g113760	E2F transcription factor-like E2FE (AHRD V3.3 *** W9SXR3_9ROSA)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:transcription facto	IPR003316 (SMAF E2F/DP	1,049	1,388	0,247	0,291	0,235									
Solyc03g113770	Pyridoxamine 5-phosphate oxidase, putative (AHRD V3.3 *** B9RJT5_RICCO)		F:GO:0004733; P:G(	F:pyridoxamine-pho EC:1.4.3.5 Pyridoxal 5'-phospha	IPR012349 (G3DSA:2.30.110.GENE3	22,567	21,554	35,783	35,529	34,575									
Solyc03g113780	Pyridoxamine 5-phosphate oxidase, putative (AHRD V3.3 *** B9RJT5_RICCO)		F:GO:0004733; P:G(	F:pyridoxamine-pho EC:1.4.3.5 Pyridoxal 5'-phospha	IPR012349 (G3DSA:2.30.110.GENE3	49,156	51,697	43,646	38,529	48,723									
Solyc03g113790	Mannose-1-phosphate guanyltransferase, putative (AHRD V3.3 *** B9R8Y9_RICCO)		P:GO:0009058; F:G(	P:biosynthetic process; F:nucleotidyltransferase activity	IPR001451 (PFAM): IPR005835 (PFA	50,035	54,811	21,244	21,103	25,011									
Solyc03g113800	Betaine aldehyde dehydrogenase (AHRD V3.3 *** A0A0B5EBW5_SOLTU)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR016162 (G3DSA:3.40.605.GENE3	435,467	421,518	368,836	289,107	338,623					-0,348	0,037			down
Solyc03g113810	LOW QUALITY:CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 *** A0A061FTS5_THECC)				PTHR33386:SF4 (PANTHER): PTHR3	0,000	0,021	0,000	0,000	0,000									
Solyc03g113820	Alpha-n-acetylglucosaminidase, putative (AHRD V3.3 *-* B9R8Y6_RICCO)				IPR024732 (PFAM): G3DSA:1.20.120	0,000	0,000	0,022	0,000	0,000									
Solyc03g113830	Riboflavin biosynthesis protein ribD (AHRD V3.3 *-* A0A151TAT0_CAJCA)		F:GO:0008703; F:G(	F:5-amino-6-(5-pho EC:3.5.4.26; EC:1.1. Diaminohydroxypho	mobidb-lite (MOBIDB_LITE)	0,019	0,021	0,022	0,050	0,000									
Solyc03g113840	Bax inhibitor 1 (AHRD V3.3 *-* A0A0B2RP92_GLYSO)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	IPR024732 (PFAM): G3DSA:1.20.120	0,021	0,000	0,000	0,000	0,024									
Solyc03g113845	Alpha-N-acetylglucosaminidase family protein (AHRD V3.3 *-* A0A072UZT3_MEDTR)				G3DSA:3.20.20.80 (GENE3D): IPR02	0,000	0,018	0,000	0,000	0,000									
Solyc03g113860	Ribosomal RNA small subunit methyltransferase G (AHRD V3.3 *** W9SLG2_9ROSA)		C:GO:0005737; P:G(	C:cytoplasm; P:rRNA processing; F:rRNA methyltransferase act	IPR003682 (TIGRFAM): G3DSA:3.40.	0,696	0,850	0,617	0,574	0,639									
Solyc03g113870	U-box domain-containing protein 38 (AHRD V3.3 *** W9QMF7_9ROSA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR003613 (SMART): IPR000225 (SM	8,507	8,983	2,495	2,293	2,938									
Solyc03g113880	DNA glycosylase (AHRD V3.3 *** A0A103YC06_CYNCS)		F:GO:0003824; P:G(	F:catalytic activity; P:base-excision repair	IPR003265 (SMART): IPR023170 (G3	2,702	2,816	1,526	1,562	1,292									
Solyc03g113890	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *-* B9HJ48_POPTR)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.60 (GENE3D): PTHR	0,159	0,246	0,118	0,069	0,141									
Solyc03g113900	alpha-1,2-Mannosidase (AHRD V3.3 *** K4BKP2_SOLLC)		F:GO:0004571; F:G(	F:mannosyl-oligosa EC:3.2.1.113; EC:3.2 Mannosyl-oligosacch	IPR001382 (PRINTS): IPR012341 (G3	6,706	6,857	8,381	9,723	7,715									
Solyc03g113910	Snakin-2-like protein (AHRD V3.3 *** I3VFF2_TOBAC)				IPR003854 (PFAM): PTHR23201 (PAI	0,436	1,386	0,071	0,177	0,023	1,666	0,008					up		
Solyc03g113920	Calmodulin binding protein-like protein (AHRD V3.3 *** AT5G62570.4)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): mobidb-lite (MOB	15,485	20,106	12,437	16,731	20,705			0,733	0,010				up	
Solyc03g113930	Heat-shock protein, putative (AHRD V3.3 *** B9S5K5_RICCO)	Hsp21.5A	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;	IPR008978 (G3DSA:2.60.40.GENE3D	26,406	16,312	427,119	436,234	431,951									
Solyc03g113940	Calmodulin binding protein-like protein (AHRD V3.3 *** AT5G62570.1)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): IPR012416 (PAN	0,021	0,043	0,000	0,000	0,000									
Solyc03g113950	Calmodulin-binding protein (AHRD V3.3 *-* AT5G57580.1)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): PTHR31713:SF1	0,166	0,502	0,050	0,139	0,116									
Solyc03g113960	Calmodulin binding protein-like protein (AHRD V3.3 *-* AT5G62570.2)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): PTHR31713:SF1	0,000	0,021	0,000	0,000	0,000									
Solyc03g113970	Calmodulin-binding protein (AHRD V3.3 *-* AT5G57580.1)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): mobidb-lite (MOB	1,374	4,148	0,168	0,507	0,542	1,614	0,001					up		
Solyc03g113980	Calmodulin binding protein-like protein (AHRD V3.3 *** AT5G62570.2)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): IPR012416 (PAN	0,380	0,561	0,025	0,299	0,304									
Solyc03g113990	Thiol-disulfide oxidoreductase DCC (AHRD V3.3 *** A0A072UZ36_MEDTR)		C:GO:0005739; F:G(	C:mitochondrion; F:protein disulfide oxidoreductase activity; P:t	IPR007263 (PFAM): PTHR34290 (PAI	4,084	5,080	17,863	19,715	20,314									
Solyc03g114000	Pollen-specific protein SF3, putative (AHRD V3.3 *** Q53J16_SOLLC)		F:GO:0046872	F:metal ion binding	IPR001781 (SMART): IPR001781 (PF	28,939	38,241	24,059	19,463	24,335									
Solyc03g114010	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YC17_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	3,451	2,901	2,038	2,167	1,994									
Solyc03g114020	D-ribose-binding periplasmic protein (AHRD V3.3 *** AT1G60010.1)				IPR025322 (PFAM): mobidb-lite (MOB	32,878	24,635	10,640	11,322	14,930			0,485	0,045				up	
Solyc03g114030	Permeasel-like protein	perm	C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR006043 (PFAM): PTHR11119 (PAI	176,152	152,068	38,416	39,375	34,345									
Solyc03g114040	Protein PRD1 (AHRD V3.3 *** A0A0B2SCJ2_GLYSO)				mobidb-lite (MOBIDB_LITE): PTHR363	5,897	4,679	4,535	4,155	4,988									
Solyc03g114050	ribosomal protein L29 family protein (AHRD V3.3 *** AT1G07830.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:mitochondrial ribosome;	IPR001854 (TIGRFAM): IPR038340 ((	14,253	15,049	14,765	13,851	14,760									
Solyc03g114060	BAH domain-containing protein, putative (AHRD V3.3 *** Q53J12_SOLLC)		F:GO:0003682; C:G(	F:chromatin binding; C:nucleus	IPR003617 (SMART): IPR001025 (SM	190,213	227,625	211,643	210,336	221,114									
Solyc03g114070	Rac-like small GTP-binding protein (AHRD V3.3 *** B5U2V7_SCODU)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	1,756	2,305	3,303	3,319	2,381									
Solyc03g114080	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** A0A061G0X7_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,000	0,000	0,000	0,023									
Solyc03g114090	RING/U-box superfamily protein (AHRD V3.3 *** AT5G40250.1)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART): IPR001841 (PF	0,329	0,476	0,164	0,290	0,280									
Solyc03g114100	4-coumarate:CoA ligase 1 (AHRD V3.3 --* AT1G51680.3)	4CL			mobidb-lite (MOBIDB_LITE): PTHR341	6,963	10,568	3,360	3,746	4,156									
Solyc03g114110	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9RB50_RICCO)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmen	IPR000595 (SMART): IPR005821 (PF	27,988	26,154	23,359	22,894	20,897									
Solyc03g114120	Ribonuclease 3 (AHRD V3.3 *** A0A0B2QFA7_GLYSO)		F:GO:0004525; P:G(	F:ribonuclease III a EC:3.1.3; EC:3.1.26; Acting on ester bonds	IPR000999 (SMART): IPR036389 (G3	38,891	37,400	25,171	20,673	24,038									
Solyc03g114130	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 *-* A0A061EBN2_THECC)				PTHR13833:SF41 (PANTHER): PTHR	5,308	3,710	7,801	7,039	7,893									
Solyc03g114140	RNA-dependent RNA polymerase2	RDR2	F:GO:0003676; F:G(	F:nucleic acid bindi EC:2.7.7.48 RNA-directed RNA pc	IPR007855 (PFAM): IPR012677 (G3D	61,198	43,426	82,151	76,461	77,132									
Solyc03g114150	aldehyde dehydrogenase family 2 member B7a		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR016163 (G3DSA:3.40.309.GENE3	58,575	80,780	14,765	13,706	23,399			0,659	0,004				up	
Solyc03g114160	U-box domain-containing protein 19, putative (AHRD V3.3 *** A0A061G0Z4_THECC)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR000225 (SMART): IPR003613 (SM	17,710	4,116	4,441	17,558	7,922	-2,081	0,000			1,976	0,000	down		up
Solyc03g114165	Deleted in split hand/splt foot protein 1 (AHRD V3.3 --* D2XQ35_IPOBA)					0,140	0,118	0,051	0,198	0,023									
Solyc03g114180	Glycosyltransferase (AHRD V3.3 *** K4BKS0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	3,412	10,945	1,234	1,639	1,639	1,704	0,006					up		
Solyc03g114190	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FV20_THECC)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART): IPR001841 (PF	0,019	0,000	0,000	0,000	0,024									
Solyc03g114200	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BKS2_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D): IPI	0,040	0,061	0,000	0,000	0,071									
Solyc03g114210	Protein kinase (AHRD V3.3 *** Q9FGB1_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PRINTS): IPR000719 (SM	4,323	7,111	2,623	2,500	3,681									
Solyc03g114230	bHLH transcription factor 082		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase	PTHR13935:SF59 bHLH	0,000	0,060	0,000	0,000	0,000									
Solyc03g114240	Polygalacturonase non-catalytic protein (AHRD V3.3 *** G7K1D9_MEDTR)				IPR004873 (SMART): IPR004873 (PF	1,286	1,235	0,022	0,022	0,071									
Solyc03g114250	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT5G62840.1)				IPR029033 (G3DSA:3.40.50.GENE3D	8,361	12,302	6,023	5,686	10,773			0,833	0,000				up	
Solyc03g114270	LOW QUALITY:DNA binding protein (AHRD V3.3 *** E5GC39_CUCME)				PTHR34451:SF2 (PANTHER): PTHR3	0,000	0,000	0,000	0,022	0,000									
Solyc03g114280	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G61180.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART): IPR001841 (PF	9,595	9,460	10,856	10,202	11,214									
Solyc03g114290	CASP-like protein (AHRD V3.3 *** K4BKT1_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM): mobidb-lite (MOB	5,613	6,151	5,177	4,732	5,444									

Solyc03g114300	4-hydroxybenzoate polyprenyltransferase, mitochondrial (AHRD V3.3 *-* K4BKT2_S	PPT	C:GO:0016021; F:GC	C:integral component of membrane; F:transferase activity, trans			G3DSA:1.10.357.140 (GENE3D); G3D	12,071	11,189	14,551	16,160	15,409									
Solyc03g114310	MAP kinase kinase kinase 28	MAPKKK28	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS); IPR000719 (SM	0,790	1,030	0,171	0,147	0,139									
Solyc03g114320	Protein KINESIN LIGHT CHAIN-RELATED 3 (AHRD V3.3 *** KLCR3_ARATH)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	53,170	38,600	41,543	60,121	50,520					0,535	0,000			up
Solyc03g114330	Peroxisomal membrane protein PEX14 (AHRD V3.3 *** W9RQB1_9ROSA)		F:GO:0005515; C:GC	F:protein binding; C:peroxisomal membrane; P:protein import int			IPR006785 (PFAM); IPR036388 (G3D	43,304	34,759	26,730	26,466	24,524									
Solyc03g114340	1-deoxy-D-xylulose-5-phosphate reductoisomerase	DXR	F:GO:0005515; P:GC	F:protein binding; P	EC:1.1.1.267	1-deoxy-D-xylulose-5	IPR013644 (PFAM); G3DSA:3.40.50.7	71,166	88,997	87,209	85,661	103,812									
Solyc03g114350	LOW QUALITY:DUF1645 family protein (AHRD V3.3 *** G7J5G5_MEDTR)						IPR012442 (PFAM); mobidb-lite (MOB	2,363	4,589	0,924	0,828	1,383									
Solyc03g114360	Poly [ADP-ribose] polymerase (AHRD V3.3 *** A0A067K7U4_JATCU)		F:GO:0003950	F:NAD+ ADP-ribosv	EC:2.4.2.3	NAD(+) ADP-ribosvltr	IPR022003 (PFAM); G3DSA:3.90.228	14,657	16,488	13,022	19,247	19,434			0,575	0,031	0,564	0,047		up	up
Solyc03g114370	RNA helicase DEAD13	DEAD13	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding			IPR025313 (SMART); IPR014001 (SM	39,819	46,889	39,207	35,098	35,089									
Solyc03g114380	Kinesin-like protein (AHRD V3.3 *** M1C9W2_SOLTU)		F:GO:0003777; F:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	0,751	0,454	0,000	0,000	0,000									
Solyc03g114390	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G23100.1)						IPR006460 (PFAM); IPR006460 (TIGF	2,443	2,543	2,083	2,082	1,837									
Solyc03g114400	Nuclear transcription factor Y protein (AHRD V3.3 *** G7JT12_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YB	13,483	13,424	15,647	14,942	15,148									
Solyc03g114410	G patch domain-containing protein 1 (AHRD V3.3 *** A0A0B2Q5S1_GLYSO)		F:GO:0003723; P:GC	F:RNA binding; P:mRNA processing			IPR000061 (SMART); IPR035967 (G3	80,675	67,133	83,514	78,052	79,639									
Solyc03g114420	Calmodulin, putative (AHRD V3.3 *** B9RLA1_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,157	0,216	0,025	0,000	0,047									
Solyc03g114430	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072VIN4_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR334	0,391	0,296	0,238	0,390	0,305									
Solyc03g114440	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9SE25_9ROSA)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,323	0,185	0,158	0,022	0,048									
Solyc03g114450	Calcium-sensing receptor (AHRD V3.3 *** K7ZLE1_NICBE)		C:GO:0005739; C:GC	C:mitochondrion; C:chloroplast thylakoid membrane; P:de-etiola			IPR036873 (G3DSA:3.40.250.GENE3	40,848	73,045	56,298	61,052	84,574	0,866	0,003	0,584	0,000			up	up	
Solyc03g114460	Acetyl-coenzyme A synthetase (AHRD V3.3 *** A0A151TDT7_CAJCA)		F:GO:0003824	F:catalytic activity			G3DSA:3.30.300.30 (GENE3D); G3DS	72,601	66,023	153,599	134,353	145,098									
Solyc03g114465	LOW QUALITY:Stem-specific protein tsjt1, putative (AHRD V3.3 *-* D6BRF0_JATCU)						IPR024286 (PFAM)	1,574	1,761	2,691	3,103	2,825									
Solyc03g114470	Cell growth defect factor-like (AHRD V3.3 *** Q307Y4_SOLTU)		C:GO:0005739; P:GC	C:mitochondrion; P:protein folding; P:cell death; C:chloroplast th			IPR021788 (PFAM); PTHR33372:SF3	57,863	70,359	107,342	114,671	112,305									
Solyc03g114480	Tetraspanin family protein (AHRD V3.3 *** A0A072V357_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR018499 (PFAM); PTHR32191:SF2	3,552	3,099	10,697	11,854	10,874									
Solyc03g114490	Tetraspanin family protein (AHRD V3.3 --* G7JT30_MEDTR)		C:GO:0016021	C:integral component of membrane				0,000	0,000	0,000	0,000	0,024									
Solyc03g114500	Enolase, putative (AHRD V3.3 *** B9RE72_RICCO)	ENO	C:GO:0000015; F:GC	C:phosphopyruvate	EC:4.2.1.11	Phosphopyruvate hy	IPR000941 (PRINTS); IPR020810 (SM	0,341	0,233	0,247	0,239	0,283									
Solyc03g114510	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B0NKG5_GOSAR)		F:GO:0016702; P:GC	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR014710 (G3DSA:2.60.120.GENE3	0,450	0,245	0,044	0,145	0,117									
Solyc03g114520	Kinetochore protein (AHRD V3.3 *** D0FYH3_NICTO)		P:GO:0000278; C:GC	P:mitotic cell cycle; C:chromosome, centromeric region; C:nucle			IPR008685 (PFAM); IPR008685 (PAN	9,092	7,070	3,618	2,868	3,607									
Solyc03g114540	Strictosidine synthase-like protein, putative (AHRD V3.3 *** G7JT39_MEDTR)		P:GO:0009058; F:GC	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR011042 (G3DSA:2.120.10.GENE3	4,487	4,205	1,113	0,882	1,481									
Solyc03g114550	Strictosidine synthase-like protein, putative (AHRD V3.3 *** G7JT39_MEDTR)		P:GO:0009058; F:GC	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR011042 (G3DSA:2.120.10.GENE3	0,096	0,181	0,000	0,025	0,000									
Solyc03g114560	Strictosidine synthase-like protein, putative (AHRD V3.3 *** G7JT39_MEDTR)		P:GO:0009058; F:GC	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR018119 (PFAM); IPR011042 (G3D	0,238	0,143	0,047	0,025	0,140									
Solyc03g114565	H/ACA ribonucleoprotein complex subunit 2-like protein (AHRD V3.3 *-* A0A0B2QAW4_GLYSO)		F:GO:0003723; C:GC	F:RNA binding; C:nucleolus			IPR029064 (G3DSA:3.30.1330.GENE	0,258	0,349	0,200	0,200	0,143									
Solyc03g114580	Uridine kinase (AHRD V3.3 *** A0A0K9NRI5_ZOSMR)		F:GO:0005524; F:GC	F:ATP binding; F:kinase activity			PR00988 (PRINTS); IPR023577 (PFA	71,853	60,567	76,884	84,294	77,198									
Solyc03g114585	H/ACA ribonucleoprotein complex subunit 2-like protein (AHRD V3.3 *** A0A199UMB2_ANACO)		P:GO:0000469; P:GC	P:cleavage involved in rRNA processing; P:maturation of LSU-r			IPR029064 (G3DSA:3.30.1330.GENE	0,707	0,595	1,055	0,788	1,015									
Solyc03g114590	serine/threonine protein kinase 3 (AHRD V3.3 *** AT5G08160.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	3,744	4,627	2,687	2,626	2,351									
Solyc03g114600	Alternaria stem canker resistance	asc	C:GO:0016021	C:integral component of membrane			IPR006634 (SMART); IPR016439 (PIF	0,553	0,499	0,075	0,264	0,141									
Solyc03g114610	LOW QUALITY:glutamine dumper 1 (AHRD V3.3 -** AT4G31730.1)							0,019	0,104	0,000	0,025	0,000									
Solyc03g114625	Carbohydrate-binding-like fold (AHRD V3.3 --* AT5G01260.2)							0,037	0,018	0,025	0,048	0,047									
Solyc03g114640	signal peptide peptidase (AHRD V3.3 *** AT1G73990.1)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity			IPR002142 (PFAM); G3DSA:3.90.226	18,141	24,363	30,143	28,330	30,919									
Solyc03g114650	T3.1 protein (AHRD V3.3 *** I7JQ52_9ROSA)						PTHR34741 (PANTHER)	0,097	0,154	0,218	0,096	0,116									
Solyc03g114660	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XYK3_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	7,900	12,676	11,855	11,941	13,107	0,708	0,042					up		
Solyc03g114670	40S ribosomal protein S13 (AHRD V3.3 --* RS13_PEA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	4,119	3,675	4,873	4,628	4,097									
Solyc03g114680	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G08139.1)		F:GO:0016874	F:ligase activity			IPR001841 (SMART); IPR013083 (G3	0,433	0,534	0,296	0,242	0,424									
Solyc03g114690	WD-repeat protein, putative (AHRD V3.3 *** B9RVD7_RICCO)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR024977 (PF	6,007	5,130	1,572	0,759	1,175									
Solyc03g114700	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT5G57300.4)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,061	0,000	0,190	0,197	0,234									
Solyc03g114705	DELLA protein (AHRD V3.3 --* Q0HA73_MALDO)						mobidb-lite (MOBIDB_LITE)	0,218	0,598	0,659	0,588	0,934									
Solyc03g114710	Glycosyltransferase (AHRD V3.3 *** M1CAF1_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); G3D	26,331	60,774	69,796	91,305	77,170	1,229	0,014					up		
Solyc03g114720	bHLH transcription factor 023	bHLH023	P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	158,650	109,882	39,885	39,457	49,313									
Solyc03g114730	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G15740.1)		P:GO:0006004; C:GC	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF); IPR019378 (PFA	113,717	99,950	13,797	9,269	14,602									
Solyc03g114740	BSD domain containing protein (AHRD V3.3 *** B4FWY5_MAIZE)						IPR005607 (SMART); IPR035925 (G3	16,701	20,414	10,490	9,349	10,366									
Solyc03g114750	18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *-* AT2G03810.7)		P:GO:0009786	P:regulation of asymmetric cell division			IPR040378 (PANTHER); PTHR33914:	8,386	5,897	74,379	73,063	61,678									
Solyc03g114760	movement protein binding protein 2C (AHRD V3.3 *** AT5G08120.1)		F:GO:0008017; P:GC	F:microtubule binding; P:plasmodesmata-mediated intercellular t			mobidb-lite (MOBIDB_LITE); mobidb-lit	4,173	4,534	8,156	8,150	8,064									
Solyc03g114770	breaking of asymmetry in the stomatal lineage (AHRD V3.3 *** AT5G60880.1)		P:GO:0009786	P:regulation of asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,000	0,025	0,000									
Solyc03g114780	RNA helicase DEAH-box9	DEAH9	F:GO:0003676; F:GC	F:nucleic acid binding; F:protein binding; F:ATP binding			IPR001650 (SMART); IPR014001 (SM	17,517	14,098	11,811	10,419	12,306									
Solyc03g114790	Isoaspartyl peptidase/L-asparaginase (AHRD V3.3 *** ASPG_LUPLU)		F:GO:0016787	F:hydrolase activity			IPR000246 (PFAM); G3DSA:3.60.20.3	16,998	14,808	18,210	17,361	18,084									
Solyc03g114800	Sulfotransferase (AHRD V3.3 *** K4BKY2_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM); G3DSA:3.40.50.3	7,085	7,138	0,785	0,609	0,613									
Solyc03g114810	Hexosyltransferase (AHRD V3.3 *** K4BKY3_SOLLC)	GAUT11	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR029044 (G3DSA:3.90.550.GENE3	38,998	48,893	33,440	47,246	31,608					0,503	0,001			up
Solyc03g114820	Adenine nucleotide alpha hydrolases-like superfamily protein, putative (AHRD V3.3 *** A0A061FX93_THECC)						IPR014729 (G3DSA:3.40.50.GENE3D	0,369	0,291	0,022	0,173	0,118									
Solyc03g114830	FRUITFULL-like MADS-box 2	FUL2	F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	175,604	170,150	123,952	211,618	98,593					0,775	0,000			up
Solyc03g114840	MADS-box protein 1	MADS1	F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	45,883	46,376	13,466	18,401	13,115									
Solyc03g114850	Squamosa promoter binding protein 6a		F:GO:0003677; C:GC	F:DNA binding; C:nucleus			IPR004333 (PFAM SBP	27,324	21,906	4,715	7,989	7,948					0,755	0,013			up
Solyc03g114860	UDP-arabinose mutase-like protein		F:GO:0016866; P:GC	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR004901 (PIRSF); IPR037595 (PFA	16,256	40,825	10,352	7,661	5,755	1,353	0,000	-0,847	0,031			up	down	
Solyc03g114870	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); PTHR23272:SF5	0,000	0,021	0,025	0,000	0,000									
Solyc03g114875	COBRA-like protein (AHRD V3.3 *-* B6E8Y8_EUCNI)		P:GO:0010215; P:GC	P:cellulose microfibril organization; P:cell growth; C:anchored cc			IPR006918 (PFAM); PTHR31673:SF2	0,000	0,021	0,000	0,000	0,000									
Solyc03g114880	Protein COBRA (AHRD V3.3 *** COBRA_ARATH)		P:GO:0010215; P:GC	P:cellulose microfibril organization; P:cell growth; C:anchored cc			IPR006918 (PIRSF); IPR006918 (PFA	0,042	0,080	0,000	0,000	0,000									
Solyc03g114910	Protein COBRA (AHRD V3.3 *** COBRA_ARATH)		P:GO:0010215; P:GC	P:cellulose microfibril organization; P:cell growth; C:anchored cc			IPR006918 (PIRSF); IPR006918 (PFA	0,021	0,021	0,022	0,000	0,000									
Solyc03g114920	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT5G60960.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	32,757	32,678	44,510	40,209	41,899									
Solyc03g114930	photosystem II reaction center PsbP family protein		F:GO:0005509; C:GC	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR002683 (PFAM); IPR016123 (G3D	8,547	20,963	2,855	3,380	7,428	1,322	0,000	1,366	0,000			up	up	
Solyc03g114940	Cytochrome P450 (AHRD V3.3 *** A0A103Y3J6_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	3,371	4,418	0,047	0,025	0,024									
Solyc03g114960	ABC transporter B family protein (AHRD V3.3 *** A0A072URQ8_MEDTR)		F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR036640 (G3	54,999	40,201	52,321	58,155	44,299									
Solyc03g114965	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 *** AT1G18610.2)		F:GO:0005515	F:protein binding			IPR006652 (SMART); IPR011498 (PF	32,019	33,353	39,567	42,345	37,758									
Solyc03g114970	SPIRAL1-like1 (AHRD V3.3 *** AT1G26355.1)		P:GO:0043622	P:cortical microtubule organization			mobidb-lite (MOBIDB_LITE); mobidb-lit	100,505	107,631	40,912	33,319	39,767									
Solyc03g114980	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *-* AT3G29760.5)		F:GO:0004721; P:GC	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threor	IPR004274 (SMART); IPR023214 (G3	12,228	12,583	14,982	18,788	15,312									
Solyc03g115000	Longifolia protein (AHRD V3.3 *** A0A072UUU5_MEDTR)		P:GO:0051513	P:regulation of monopolar cell growth			IPR032795 (PFAM); IPR025486 (PFA	27,833	21,475	2,462	2,176	6,519			1,389	0,000				up	
Solyc03g115005	Oxygen-evolving enhancer protein 3 (AHRD V3.3 *** B6SQ77_MAIZE)		F:GO:0005509; C:GC	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR008797 (PFAM); G3DSA:1.20.120	0,019	0,073	0,025	0,000	0,000									
Solyc03g115010	TCP transcription factor 4	TCP4	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	0,021	0,000	0,000	0,000	0,000									
Solyc03g115020	wiskott-aldrich syndrome family protein, putative (DUF1118) (AHRD V3.3 *** AT5G08050.1)		C:GO:0009515; C:GC	C:granal stacked thylakoid; C:chloroplast thylakoid membrane; F			IPR009500 (PFAM); mobidb-lite (MOB	106,031	152,437	68,765	77,460	98,797			0,520	0,001				up	
Solyc03g115025	Mitochondrial import receptor subunit TOM5 (AHRD V3.3 *-* A0A061G4X4_THECC)		C:GO:0005742	C:mitochondrial outer membrane translocase complex			IPR034553 (PANTHER)	0,061	0,136	0,025	0,075	0,116									
Solyc03g115030	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061ELJ0_THECC)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,489	0,719	1,578	1,200	1,247									
Solyc03g115050	Replication A 70 kDa DNA-binding subunit (AHRD V3.3 *** A0A0B0N129_GOSAR)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D			IPR013955 (PFAM); IPR007199 (PFA	8,198	6,574	0,863	0,263	0,636									
Solyc03g115060	Assimilatory nitrate reductase catalytic subunit (AHRD V3.3 *** A0A0B0NYS4_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	4,874	4,911	2,884	3,579	4,154									
Solyc03g115070	LOW QUALITY:Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9IK79_POPTR)		C:GO:0000145; P:GC	C:exocyst; P:exocytosis			IPR004140 (PFAM); PTHR12542:SF4	23,684	17,758	10,087	21,150	13,407					1,067	0,000			up
Solyc03g115075	Presenilin (AHRD V3.3 *** M1CAI2_SOLTU)		F:GO:0004190; C:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001108 (PRINTS); IPR006639 (SM	5,802	6,268	7,934	6,085	6,413									
Solyc03g115100	Formate hydrogenlyase subunit 5 (AHRD V3.3 *** A0A0B0NQY9_GOSAR)		P:GO:0008356	P:asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	15,891	17,110	13,215	11,358	14,583									
Solyc03g115110	ATP synthase subunit gamma (AHRD V3.3 *** A0A061FYD0_THECC)		P:GO:0015986; C:GC	P:ATP synthesis co	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR000131 (PRINTS); G3DSA:3.40.13	177,532	185,566	217,432	197,837	210,505									
Solyc03g115120	DnaJ domain-containing protein (AHRD V3.3 *** A0A103YCB1_CYNCS)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001623 (PRIN C2H2	0,516	0,448	0,143	0,047	0,046									
Solyc03g115140	DnaJ domain-containing protein (AHRD V3.3 *** A0A103YCB1_CYNCS)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001623 (PRINTS); IPR001623 (SM	9,731	7,869	7,550	7,330	6,411									
Solyc03g115150	histone deacetylase 5 (AHRD V3.3 *** AT5G61060.1)		C:GO:0005634; F:GC	C:nucleus; F:NAD-d	EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS); G3DSA:3.10.45	17,560	12,719	18,301	16,759	17,337									
Solyc03g115160	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	6,841	5,748	0,339	0,098	0,351									
Solyc03g115163	Pectin lyase-like superfamily protein (AHRD V3.3 --* AT1G04680.1)							17,414	12,873	2,285	1,629	1,905									
Solyc03g115167	Reticulon-like protein (AHRD V3.3 *-* Q2PYX0_SOLTU)		C:GO:0005789; C:GC	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM); PTHR10994:SF7	2,991	2,373	2,165	2,405	2,217									
Solyc03g115170	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 --* AT3G66654.5)							0,203	0,160	0,150	0,048	0,165									
Solyc03g115180	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)		F:GO:0046872	F:metal ion binding			PTHR33304:SF2 (PANTHER); PTHR3	5,403	4,235	4,135	2,921	4,270									
Solyc03g115190	Phosphoglycerate mutase family protein (AHRD V3.3 --* AT5G64460.5)							0,101	0,101	0,025	0,076	0,093									
Solyc03g115200	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** K8DWB8_CUCSA)		P:GO:0009733; C:GC	P:response to auxin; C:integral component of membrane			IPR012946 (SMART); IPR012946 (PF	0,239	0,438	0,025	0,025	0,072									
Solyc03g115220	Flavonoid 3'-hydroxylase (AHRD V3.3 *** A0A0N6XG41_LYCBA)	F3'H	F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	40,817	33,323	141,039	138,081	128,115									
Solyc03g115230	Solanum lycopersicum heat shock protein	tfhs1	F:GO:0005524; P:GC	F:ATP binding; P:protein metabolic process			IPR001270 (PRINTS); IPR019489 (SM	390,500	213,340	739,964	704,672	727,996	-0,846	0,002					down		
Solyc03g115235	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* A0A0S2GM58_DENCH)							0,847	0,578	0,611	0,369	0,777									
Solyc03g115240	RNA polymerase-associated protein LEO1 (AHRD V3.3 *-* A0A151SLW2_CAJCA)		P:GO:0006368; P:GC	P:transcription elongation from RNA polymerase II promoter; P:I			mobidb-lite (MOBIDB_LITE); mobidb-lit	22,968	30,103	25,305	23,158	21,844									
Solyc03g115243	leo1-like family protein (AHRD V3.3 *-* AT5G61150.2)		P:GO:0006368; P:GC	P:transcription elongation from RNA polymerase II promoter; P:I			IPR007149 (PFAM); IPR007149 (PAN	5,197	6,057	5,650	5,126	4,803									
Solyc03g115247	Leo1-like protein (AHRD V3.3 *** A0A103XYL9_CYNCS)		P:GO:0006368; P:GC	P:transcription elongation from RNA polymerase II promoter; P:I			mobidb-lite (MOBIDB_LITE); mobidb-lit	54,259	59,891	47,669	41,958	46,354									
Solyc03g115250	Dentin sialophosphoprotein-related, putative (AHRD V3.3 *** A0A061FY91_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	74,346	58,628	80,235	86,427	84,781									
Solyc03g115255	Nodule-inception protein (AHRD V3.3 -** A0A1B1XWN4_ARAHY)		C:GO:0016021	C:integral component of membrane				0,902	0,754	0,949	0,730	0,921									
Solyc03g115270	Expansin (AHRD V3.3 *** Q76HY8_MALDO)	EXPA19	C:GO:0005576; P:GC	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS); IPR002963 (PF	0,021	0,000	0,022	0,000	0,000									
Solyc03g115275	Protein Ycf2 (AHRD V3.3 --* YCF2_COFAR)							0,334	0,217	0,377	0,314	0,285									
Solyc03g115280	Dentin sialophosphoprotein-related, putative (AHRD V3.3 *-* A0A061FY91_THECC)						PTHR31267 (PANTHER); PTHR31267	0,136	0,239	0,093	0,218	0,236									
Solyc03g115290	Agenet and bromo-adjacent homology (BAH) domain-containing protein (AHRD V3.3 --* AT5G55600.3)		C:GO:0016021	C:integral component of membrane				0,202	0,159	0,022	0,097	0,118									
Solyc03g115300	Expansin (AHRD V3.3 *** Q9ZTG7_SOLLC)	EXPA7	C:GO:0005576; P:GC	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS); IPR002963 (PF	0,254	0,498	0,065	0,097	0,166									
Solyc03g115310	Expansin (AHRD V3.3 *** Q84L76_PYRCO)	EXPA20	C:GO:0005576; P:GC	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS); IPR007118 (PF	0,593	0,819	0,170	0,122	0,119									
Solyc03g115320	Expansin (AHRD V3.3 *** Q7X9Q3_SAMNI)	EXPA22	C:GO:0005576; P:GC	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS); IPR007118 (PF	0,182	0,136	0,074	0,000	0,141									
Solyc03g115330	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT1G19470.1)		C:GO:0016021	C:integral component of membrane				10,495	8,553	4,724	5,250	5,257									
Solyc03g115340	Expansin (AHRD V3.3 *** Q7FWM1_9ROSA)	EXPA23	C:GO:0005576; P:GC	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS); IPR007118 (PF	0,037	0,041	0,025	0,025	0,047									
Solyc03g115360	40S ribosomal protein S19-like (AHRD V3.3 *** Q2VCJ6_SOLTU)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001266 (SMART); IPR038111 (G3	317,975	314,367	182,903	166,611	169,506									
Solyc03g115365	Protein TIC 214 (AHRD V3.3 --* TI214_NICTO)							2,398	2,240	1,556	1,298	1,206									
Solyc03g115370	Diacylglycerol kinase (AHRD V3.3 *** K4BL39_SOLLC)		F:GO:0003951; F:GC	F:NAD+ kinase acti	EC:2.7.1.23; EC:2.7.	NAD(+) kinase; Diacy	IPR000756 (SMART); IPR002219 (SM	53,762	70,119	90,774	86,105	84,854									
Solyc03g115380	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT3G29360.2)		F:GO:0003979; F:GC	F:UDP-glucose 6-de	EC:1.1.1.22	UDP-glucose 6-dehy	IPR014027 (SMART); IPR001732 (PF	0,000	0,039	0,000	0,000	0,000									
Solyc03g115390	RNA helicase DEAH-box10	DEAH10	F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR007502 (SMART); IPR001650 (SM	30,985	31,094	29,646	27,421	30,036									
Solyc03g115400	Pre-mrna-splicing factor atp-dependent rna helicase dhx16 (AHRD V3.3 *-* A0A0M8KRL3_NICAT)		P:GO:0006397	P:mRNA processing			IPR002483 (PFAM); mobidb-lite (MOB	4,192	2,992	3,169	3,730	3,416									
Solyc03g115410	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT5G07910.1)		F:GO:0005515	F:protein binding			SM00364 (SMART); IPR003591 (SMA	11,837	15,299	8,889	8,481	8,969									
Solyc03g115415	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT3G59130.1)							0,559	0,804	0,121	0,433	0,448									
Solyc03g115440	AT-rich interactive domain-containing protein 2 (AHRD V3.3 *** A0A0B2QRH4_GLYSO)						mobidb-lite (MOBIL MYB_related	24,521	21,344	22,882	23,127	22,470									
Solyc03g115450	LOW QUALITY:Zinc finger protein 1 (AHRD V3.3 *** A0A151SLY5_CAJCA)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	1,339	0,915	0,187	0,146	0,095									
Solyc03g115460	Transmembrane protein, putative (AHRD V3.3 *-* G7LDL9_MEDTR)		C:GO:0005739; C:GC	C:mitochondrion; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	3,836	6,493	5,739	7,837	6,233									
Solyc03g115470	Soluble N-ethylmaleimide-sensitive factor adaptor protein (AHRD V3.3 *** A0A072UQP3_MEDTR)		C:GO:0005886	C:plasma membrane			IPR000727 (SMART); G3DSA:1.20.5.1	31,844	26,059	24,325	24,537	23,336									
Solyc03g115490	Complex 1 LYR protein (AHRD V3.3 *** A0A118JYZ0_CYNCS)						IPR008011 (PFAM); PTHR13166 (PAN	16,827	18,135	29,732	31,623	28,718									
Solyc03g115500	Heparanase 1-like protein (AHRD V3.3 *** T2D261_TOBAC)		C:GO:0016020; F:GC	C:membrane; F:hydrolase activity, acting on glycosyl bonds			G3DSA:3.20.20.80 (GENE3D); IPR00	1,808	3,039	10,883	15,387	9,660									
Solyc03g115510	S phase cyclin A-associated in the endoplasmic reticulum (AHRD V3.3 *** A0A0B0NPR6_GOSAR)						IPR032446 (PFAM); mobidb-lite (MOB	28,725	25,302	46,856	51,101	48,653									
Solyc03g115520	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT4G10740.1)							0,116	0,036	0,044	0,070	0,117									
Solyc03g115530	SNF2 domain-containing protein (AHRD V3.3 *** D7M0M5_ARALL)		F:GO:0003676; F:GC	F:nucleic acid binding; F:endonuclease activity; F:ATP binding			IPR003615 (SMART); IPR014001 (SM	32,351	45,413	18,734	16,123	16,920									
Solyc03g115540	bHLH transcription factor 024	PIF7a	P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,000	0,000	0,050	0,022	0,000									
Solyc03g115550	Phytochrome C (AHRD V3.3 --* Q8LRY1_9ROSI)							32,314	22,709	26,093	25,287	25,394									
Solyc03g115560	Flavin-containing monooxygenase (AHRD V3.3 *** K4BL58_SOLLC)		F:GO:0004499; F:GC	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.	Flavin-containing mo	IPR000960 (PRINTS); IPR020946 (PF	10,028	8,315	8,765	6,510	6,417									
Solyc03g115580	DNA excision repair protein ERCC-1 (AHRD V3.3 *-* ERCC1_ARATH)		F:GO:0003684; F:GC	F:damaged DNA binding; F:endonuclease activity; C:nucleus; P			G3DSA:1.10.150.20 (GENE3D); IPR0	2,112	2,181	2,737	2,247	2,923									
Solyc03g115590	T-box transcription factor, putative (DUF863) (AHRD V3.3 *-* AT1G26620.1)						IPR008581 (PFAM); mobidb-lite (MOB	15,729	15,237	18,923	21,523	18,797									
Solyc03g115600	Zinc finger protein (AHRD V3.3 *-* A0A0B0MNI3_GOSAR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			IPR013087 (SMART); IPR003604 (SM	0,175	0,444	0,025	0,000	0,000									
Solyc03g115610	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072USD7_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS); IPR000719 (SMA	14,574	26,647	10,884	18,815	15,039					0,792	0,001			up
Solyc03g115620	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *-* AT1G12150.2)		C:GO:0005829; P:GC	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			IPR008545 (PFAM); PTHR32054 (PAN	0,075	0,059	0,000	0,000	0,047									
Solyc03g115630	Carbamoyl-phosphate synthase small chain (AHRD V3.3 *** A0A0B0PDS6_GOSAR)		F:GO:0004088; P:GC	F:carbamoyl-phospl	EC:6.3.5.5	Carbamoyl-phosphat	PR00099 (PRINTS); PR00097 (PRINT	156,305	155,754	135,697	130,408	140,226									
Solyc03g115640	DUF538 family protein (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT2G03350.1)						IPR036758 (G3DSA:2.30.240.GENE3	10,792	11,531	1,983	1,985	2,824									
Solyc03g115650	eukaryotic translation initiation factor 5A-1	tif5a-1	F:GO:0003746; P:GC	F:translation elongation factor activity; P:translational frameshif			IPR020189 (SMART); IPR014722 (G3	613,997	516,077	490,431	484,326	426,204									
Solyc03g115660	Protein kinase superfamily protein (AHRD V3.3 *** AT1G18670.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	0,986	1,478	0,328	0,246	0,515									
Solyc03g115680	Protein kinase superfamily protein (AHRD V3.3 *-* AT1G18670.3)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PR01217 (PRINTS); IPR000719 (SMA	92,935	63,273	127,086	135,999	125,132									
Solyc03g115690	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072UQ71_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33133 (PANTHER); PTHR33133	1,980	1,761	0,140	0,432	0,448									
Solyc03g115700	SNF1-related protein kinase		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR015940 (SM	80,476	66,068	105,947	102,632	98,250									
Solyc03g115720	zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 *** AT1G18660.3)		F:GO:0005515	F:protein binding			IPR003111 (SMART); IPR019734 (SM	20,597	17,752	25,912	26,989	29,384									

Solyc03g115730	transmembrane protein (AHRD V3.3 *-* AT5G07730.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); PTHR372	8,666	10,454	12,992	11,156	11,276									
Solyc03g115740	Xyloglucan alpha-1,6-xylosyltransferase (AHRD V3.3 *** X5MPI5_PINTA)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans	IPR029044 (G3DSA:3.90.550.GENE3I	153,552	159,821	88,235	119,011	110,066					0,433	0,041			up
Solyc03g115760	Vesicle transport v-SNARE protein (AHRD V3.3 *** A0A0K0XR76_TOBAC)		F:GO:0005484; C:G(	F:SNAP receptor activity; C:Golgi apparatus; P:intracellular prot	IPR007705 (PFAM); IPR038407 (G3D	111,089	99,338	132,663	129,711	126,206									
Solyc03g115770	Timing of cab expression 1/pseudo-response regulator 1 (AHRD V3.3 *** J9PWT0_NICAT)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:protein binding	IPR001789 (SMART); IPR001789 (PF	8,008	7,285	12,851	12,688	15,001									
Solyc03g115780	APOLLO (AHRD V3.3 *** U5U5R8_9BRAS)		F:GO:0003676	F:nucleic acid binding	IPR013520 (SMART); IPR013520 (PF	3,736	3,722	0,803	0,486	1,194									
Solyc03g115790	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2QFK0_GLYSO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR002885 (PFA	1,567	1,406	1,219	1,052	1,177									
Solyc03g115800	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XX58_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR002885 (I	0,504	0,540	0,433	0,335	0,401									
Solyc03g115810	Mon1 superfamily protein		C:GO:0005768; P:G(	C:endosome; P:intracellular protein transport; P:vacuole organiz	IPR004353 (PRINTS); IPR004353 (PF	43,689	40,133	38,464	40,939	40,790									
Solyc03g115820	Ribulose-phosphate 3-epimerase (AHRD V3.3 *** A0A072V1G6_MEDTR)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:racemase and epimerase	IPR000056 (TIGRFAM); IPR000056 (I	50,553	109,547	66,026	74,445	102,993	1,143	0,000	0,639	0,000			up	up	
Solyc03g115830	Galactoside 2-alpha-L-fucosyltransferase (AHRD V3.3 *** W9QNS6_9ROSA)		F:GO:0008107; C:G(	F:galactoside 2-alpl EC:2.4.1.69 Type 1 galactoside a	IPR004938 (PFAM); G3DSA:3.40.50.1	1,096	0,500	0,112	0,119	0,140									
Solyc03g115840	DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061FXW0_THECC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	15,250	17,060	13,731	12,130	13,192									
Solyc03g115843	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *-* AT1G18700.5)		C:GO:0016021	C:integral component of membrane		2,199	1,738	1,895	1,349	1,889									
Solyc03g115845	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *-* AT1G18700.5)		C:GO:0016020	C:membrane		2,627	2,640	2,505	2,474	2,002									
Solyc03g115847	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *-* AT1G18700.5)		C:GO:0016021	C:integral component of membrane		3,391	2,722	2,749	3,153	3,044									
Solyc03g115850	NAC domain-containing protein	NAM2/ORE1S03	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAN NAC	1,069	1,252	0,261	0,805	0,515									
Solyc03g115860	ER membrane protein, putative (DUF962) (AHRD V3.3 *** AT1G18720.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:sphingoid catabolic proce	IPR009305 (PFAM); IPR009305 (PAN	7,351	9,299	18,901	26,098	19,699					0,466	0,022			up
Solyc03g115870	Thioredoxin (AHRD V3.3 *** A0A072UTZ5_MEDTR)		P:GO:0045454	P:cell redox homeostasis	IPR013766 (PFAM); G3DSA:3.40.30.1	11,984	14,284	2,162	2,712	2,208									
Solyc03g115880	LOW QUALITY:NADH-ubiquinone oxidoreductase chain 1 (AHRD V3.3 --* NU1M_CITLA)				mobidb-lite (MOBIDB_LITE)	1,509	1,600	0,610	0,442	0,428									
Solyc03g115890	expansin 10	EXPA10	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization	IPR007118 (PRINTS); IPR002963 (PF	0,667	0,624	0,222	0,149	0,119									
Solyc03g115900	chlorophyll a-b binding protein CAB11		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane	IPR023329 (G3DSA:1.10.3460.GENE	122,804	376,151	68,197	89,996	178,891	1,643	0,001	1,387	0,000			up	up	
Solyc03g115910	Transcription factor, MADS-box (AHRD V3.3 *** A0A118JYM5_CYNCS)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR002100 (PRIN' M-type_MADS	0,098	0,137	0,025	0,050	0,070									
Solyc03g115920	RING/U-box superfamily protein (AHRD V3.3 *** AT3G14250.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART); IPR013083 (G3	11,922	8,868	7,632	26,715	15,648			1,026	0,001	1,802	0,000		up	up
Solyc03g115930	Calcium-binding EF-hand family protein (AHRD V3.3 *-* AT5G39670.1)		F:GO:0005509	F:calcium ion binding	IPR002048 (SMART); G3DSA:1.10.23	2,006	3,838	3,238	6,929	3,115					1,098	0,000			up
Solyc03g115940	Dof zinc finger protein (AHRD V3.3 *** C4B6D7_IPOBA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAN Dof	11,891	18,444	10,823	5,986	10,633					-0,853	0,001			down
Solyc03g115950	transmembrane protein (AHRD V3.3 -** AT3G47510.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE); PTHR334	4,383	5,330	0,195	0,098	0,260									
Solyc03g115960	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2P2I1_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,040	0,098	0,235	0,196	0,374									
Solyc03g115970	Protein yippee-like (AHRD V3.3 *** K4C9V4_SOLLC)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,022	0,023									
Solyc03g115980	Geranylgeranyl reductase (AHRD V3.3 *** A0A097P6G1_SOLHA)	GGDR	P:GO:0015979; P:G(	P:photosynthesis; P:chlorophyll biosynthetic process; F:oxidore	PR00420 (PRINTS); IPR036188 (G3D	135,215	246,278	192,584	151,576	289,871	0,893	0,026	0,586	0,002			up	up	
Solyc03g115990	Malate dehydrogenase (AHRD V3.3 *** A0A061G4A3_THECC)		P:GO:0005975; P:G(	P:carbohydrate met EC:1.1.1.37 Malate dehydrogenas	IPR010097 (TIGRFAM); IPR022383 (I	50,346	57,270	112,268	96,878	96,392									
Solyc03g116000	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2SV07_GLYSO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (PFAM); IPR011990 (G3D	1,748	2,446	2,111	1,909	1,860									
Solyc03g116020	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0K9PPT9_ZOSMR)		C:GO:0005634; P:G(	C:nucleus; P:nucleologenesis	G3DSA:3.10.450.40 (GENE3D); PF11	40,497	39,552	19,998	18,416	19,735									
Solyc03g116030	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT3G47550.6)		F:GO:0008270	F:zinc ion binding	IPR011016 (SMART); IPR022143 (PF	9,295	16,925	7,019	5,950	7,654	0,890	0,030					up		
Solyc03g116060	Exostosin family protein (AHRD V3.3 *** AT1G74680.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco	IPR004263 (PFAM); PTHR11062:SF9	14,606	11,665	10,807	10,598	9,512									
Solyc03g116070	Zinc finger family protein (AHRD V3.3 *** B9H0F7_POPTR)		C:GO:0005634; P:G(	C:nucleus; P:floral meristem determinacy; P:plant-type ovary de	IPR006456 (PFAN ZF-HD	0,000	0,043	0,000	0,025	0,000									
Solyc03g116085	LOW QUALITY:DVA-1 polyprotein (AHRD V3.3 *-* A0A0B0N1N3_GOSAR)				IPR027921 (PFAM); IPR027921 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc03g116100	R2R3MYB transcription factor 31	R2R3MYB31	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	1,727	3,706	3,464	5,067	4,378									
Solyc03g116110	Alpha/beta hydrolase family protein (AHRD V3.3 *** A0A072TEB1_MEDTR)		C:GO:0009507	C:chloroplast	IPR000073 (PFAM); IPR029058 (G3D	40,704	47,814	148,240	149,354	131,748									
Solyc03g116120	Glutathione s-transferase, putative (AHRD V3.3 *** B9R999_RICCO)	GSTU8	F:GO:0005515	F:protein binding	G3DSA:1.20.1050.10 (GENE3D); IPR(	0,000	0,000	0,000	0,022	0,000									
Solyc03g116140	Activating signal cointegrator 1 (AHRD V3.3 *** A0A0B0MCE7_GOSAR)		C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated; F:zinc i	IPR009349 (PFAM); mobidb-lite (MOB	17,892	18,583	29,501	27,654	28,961									
Solyc03g116150	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G26850.2)		F:GO:0008168	F:methyltransferase activity	IPR004159 (PFAM); G3DSA:3.40.50.1	23,682	16,605	32,477	30,815	29,595									
Solyc03g116170	Nucleosome assembly protein family (AHRD V3.3 *** A9RDJ7_PHYPA)		C:GO:0005634; P:G(	C:nucleus; P:nucleosome assembly	G3DSA:3.30.1120.90 (GENE3D); IPR(	18,182	22,056	12,823	11,134	10,998									
Solyc03g116190	LOW QUALITY:Chitinase (AHRD V3.3 *-* P93327_MEDTR)		F:GO:0008061	F:chitin binding	IPR001002 (SMART); IPR001002 (PF	0,195	0,327	16,444	29,351	15,550					0,842	0,013			up
Solyc03g116200	LOW QUALITY:glutamate synthase 1 (AHRD V3.3 --* AT5G04140.2)				mobidb-lite (MOBIDB_LITE)	49,858	76,329	104,366	137,235	105,708									
Solyc03g116225	42kDa chitin-binding protein (AHRD V3.3 *** D0VX39_SOLLC)		F:GO:0008061	F:chitin binding	IPR001002 (SMART); IPR036861 (G3	831,881	1060,507	654,200	163,976	425,897					-1,992	0,000			down
Solyc03g116230	42kDa chitin-binding protein (AHRD V3.3 *** D0VX39_SOLLC)		F:GO:0008061	F:chitin binding	IPR001002 (PRINTS); IPR001002 (SN	12,303	16,874	16,936	15,039	18,728									
Solyc03g116240	LOW QUALITY:Chitinase (AHRD V3.3 *-* E2J9M1_MORAL)		F:GO:0008061	F:chitin binding	IPR036861 (G3DSA:3.30.60.GENE3D	0,021	0,060	0,230	0,118	0,187									
Solyc03g116243	Kinase, putative (AHRD V3.3 --* B9S8F7_RICCO)					0,335	0,422	0,457	0,241	0,214									
Solyc03g116245	Cathepsin B-like cysteine protease (AHRD V3.3 *-* Q2HV10_MEDTR)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	G3DSA:3.90.70.10 (GENE3D); IPR00(	0,747	0,547	0,311	0,320	0,327									
Solyc03g116247	Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 *-* Q2MGS1_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR007652 (PFAM); PTHR12042:SF3	3,988	4,069	2,653	3,186	3,602									
Solyc03g116250	Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 --* Q2MGS1_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		0,690	0,375	0,478	0,664	0,637									
Solyc03g116260	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3I	0,240	0,059	0,050	0,025	0,094									
Solyc03g116270	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM); IPR026992 (PFA	0,077	0,061	0,025	0,000	0,000									
Solyc03g116280	1-aminocyclopropane-1-carboxylate oxidase 2 (AHRD V3.3 *-* M7YEU7_TRIUA)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3I	8,694	7,580	0,000	0,000	0,000									
Solyc03g116290	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM); IPR005123 (PFA	0,158	0,078	0,000	0,025	0,000									
Solyc03g116320	TCP transcription factor 16	TCP16	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR017887 (PFAN TCP	3,900	4,432	3,056	4,052	3,160									
Solyc03g116330	transmembrane protein (AHRD V3.3 *** AT1G74530.3)		C:GO:0016021	C:integral component of membrane	PTHR37204 (PANTHER)	22,319	17,960	14,201	14,463	16,266									
Solyc03g116335	Fructose-1,6-bisphosphatase, cytosolic (AHRD V3.3 --* F16P2_ORYSI)					2,127	1,078	1,979	3,674	2,778					0,889	0,022			up
Solyc03g116340	bHLH transcription factor 025	bHLH025	F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DSA:4.10.280.GENE3I	126,602	60,034	112,615	177,009	144,463	-1,051	0,000			0,655	0,000	down		up
Solyc03g116350	HVA22-like protein (AHRD V3.3 *** K4BLD7_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004345 (PFAM); IPR004345 (PAN	38,204	28,249	42,972	36,112	39,532									
Solyc03g116360	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** G7K368_MEDTR)		F:GO:0046872	F:metal ion binding	IPR000408 (PRINTS); IPR000306 (SN	35,290	31,519	32,780	38,649	35,777									
Solyc03g116370	RP/EB family microtubule-associated protein (AHRD V3.3 *** A0A072TJV8_MEDTR)		F:GO:0008017	F:microtubule binding	IPR004953 (PFAM); G3DSA:1.20.5.11	0,862	0,855	0,000	0,000	0,070									
Solyc03g116380	WD repeat-containing protein 43 (AHRD V3.3 *** A0A0B2P182_GLYSO)		F:GO:0005515	F:protein binding	IPR007148 (PFAM); IPR015943 (G3D	42,454	48,448	37,947	35,292	34,372									
Solyc03g116390	Late embryogenesis abundant protein (AHRD V3.3 *** E1AZA3_SOLLC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	G3DSA:1.20.120.20 (GENE3D); mobic	26,728	35,962	10,761	20,381	7,920									
Solyc03g116410	Zinc finger transcription factor 28	C3H28	F:GO:0046872	F:metal ion binding	IPR000571 (SMAF C3H	0,102	0,180	0,000	0,000	0,047									
Solyc03g116430	LOW QUALITY:ethylene-dependent gravitropism-deficient and yellow-green-like 2 (AHRD V3.3 --* AT5G05740.1)					0,460	0,368	0,359	0,373	0,400									
Solyc03g116440	PHD finger protein family (AHRD V3.3 *-* A0A151RBP6_CAJCA)		F:GO:0046872	F:metal ion binding	IPR001965 (SMART); IPR013083 (G3	0,415	0,663	0,419	0,171	0,214									
Solyc03g116450	Stigma-specific protein Stig1 (AHRD V3.3 *-* A0A103Y1F6_CYNCS)				IPR006969 (PFAM); mobidb-lite (MOB	0,615	0,245	0,000	0,000	0,024									
Solyc03g116460	Aspartate racemase (AHRD V3.3 *** A0A0B2QLV5_GLYSO)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:racemase activity, a	IPR015942 (PFAM); G3DSA:3.40.50.1	20,991	25,291	54,017	59,267	56,145									
Solyc03g116465	heavy metal atpase 4 (AHRD V3.3 --* AT2G19110.3)				mobidb-lite (MOBIDB_LITE); mobidb-lit	3,093	3,179	6,545	7,985	6,743									
Solyc03g116470	transmembrane protein (AHRD V3.3 *** AT1G80200.3)		C:GO:0016021	C:integral component of membrane	PTHR35288 (PANTHER); PTHR35288	0,220	0,190	0,903	1,152	0,984									
Solyc03g116480	LOW QUALITY:F-box only protein 6 (AHRD V3.3 *** A0A0B2SU90_GLYSO)		F:GO:0005515	F:protein binding	IPR001810 (SMART); G3DSA:1.20.12	2,892	2,314	17,694	26,942	21,925					0,612	0,011			up
Solyc03g116490	plant/protein (AHRD V3.3 *** AT5G20100.1)				IPR031421 (PFAM); mobidb-lite (MOB	17,381	16,356	27,293	23,094	21,955									
Solyc03g116500	polygalacturonase (XOPG1)	PG17-1 (XPG1)	F:GO:0004650; P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR006626 (SMART); IPR000743 (PF	5,456	5,954	0,343	0,314	0,612	3,121	0,003	0,588	0,026			up	up	
Solyc03g116510	cotton fiber protein (AHRD V3.3 *** AT1G15385.1)				IPR008480 (PFAM); mobidb-lite (MOB	0,975	8,417	8,332	10,684	12,517									
Solyc03g116520	LOW QUALITY:cotton fiber protein (AHRD V3.3 --* AT1G15385.1)				IPR008480 (PFAM); mobidb-lite (MOB	0,000	0,118	0,097	0,047	0,024									
Solyc03g116530	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)		F:GO:0016740; F:G(	F:transferase activity; F:lyase activity	IPR004360 (PFAM); IPR029068 (G3D	15,125	10,472	28,987	33,499	31,737									
Solyc03g116540	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SY25_RICCO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	2,317	1,648	1,504	1,440	1,129									
Solyc03g116550	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G52630.1)		C:GO:0005737; P:G(	C:cytoplasm; P:fucose metabolic process; F:transferase activit	IPR024709 (PIRSF); IPR019378 (PFA	20,330	28,998	17,899	15,380	17,314	0,539	0,048					up		
Solyc03g116570	Thiol-disulfide oxidoreductase DCC (AHRD V3.3 *** A0A0K9PRB5_ZOSMR)		C:GO:0010287	C:plastoglobule	IPR007263 (PFAM); PTHR33639 (PAN	12,750	18,860	49,986	50,254	63,339									
Solyc03g116580	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G80170.1)	PG68	F:GO:0004650; F:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR006626 (SMART); IPR012334 (G3	0,291	0,138	0,262	0,098	0,165									
Solyc03g116590	Embryo-specific 3 (AHRD V3.3 *** A0A118K3J4_CYNCS)		F:GO:0005515	F:protein binding	IPR010417 (PFAM); PTHR31718:SF8	2,044	2,201	3,781	3,298	3,156									
Solyc03g116600	Coatomer subunit zeta-3 (AHRD V3.3 *** A0A1D1YYD5_9ARAE)		P:GO:0006890; C:G(	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r	G3DSA:3.30.450.60 (GENE3D); PTHF	9,222	9,557	13,525	15,041	14,174									
Solyc03g116610	Ethylene-responsive transcription factor WIN1 (AHRD V3.3 *** A0A199V560_ANACO)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN' ERF	0,000	0,000	0,022	0,000	0,000									
Solyc03g116620	Phospholipase D (AHRD V3.3 *** M0ZIV2_SOLTU)		F:GO:0004630; F:G(	F:phospholipase D EC:3.1.4.4 Phospholipase D	IPR000008 (SMART); IPR001736 (SN	0,040	0,019	0,240	0,511	0,261									
Solyc03g116630	cytochrome P450 family protein (AHRD V3.3 *** AT1G52565.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE); PTHR335	3,949	4,775	81,608	61,314	63,221									
Solyc03g116640	DUF4050 family protein (AHRD V3.3 *-* G7JGZ5_MEDTR)				IPR025124 (PFAM); PTHR33373:SF4	2,084	2,135	2,923	2,421	2,405									
Solyc03g116660	ALBINO OR PALE-GREEN 13 (AHRD V3.3 --* AT1G63680.3)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	3,438	3,609	14,762	13,099	13,209									
Solyc03g116670	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G80130.1)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	436,979	480,410	218,235	168,746	249,918									
Solyc03g116680	Methyl-CpG-binding domain protein (AHRD V3.3 *-* G7JE44_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus	G3DSA:3.30.890.10 (GENE3D); IPR(	105,582	80,833	130,743	153,897	136,746									
Solyc03g116690	Blue copper protein, putative (AHRD V3.3 *** B9RV67_RICCO)		F:GO:0009055	F:electron transfer activity	IPR003245 (PFAM); IPR008972 (G3D	0,422	0,721	0,000	0,047	0,047									
Solyc03g116700	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)		F:GO:0009055	F:electron transfer activity	IPR003245 (PFAM); IPR008972 (G3D	3,853	15,750	1,657	1,591	2,253	2,050	0,009					up		
Solyc03g116710	LURP-one-like protein (AHRD V3.3 *** G7II68_MEDTR)				IPR007612 (PFAM); IPR038595 (G3D	13,376	15,449	7,955	6,047	6,753									
Solyc03g116720	Histidine-containing phosphotransfer protein, putative (AHRD V3.3 *** B9RV70_RICCO)		P:GO:0000160	P:phosphorelay signal transduction system	IPR008207 (PFAM); IPR036641 (G3D	0,619	0,575	0,068	0,152	0,257									
Solyc03g116730	fatty acid desaturase 5 (AHRD V3.3 *** AT3G15850.1)		P:GO:0006629; F:G(	P:lipid metabolic prc EC:1.14.19 Acting on paired donc	IPR015876 (PRINTS); IPR005804 (PF	5,579	17,749	1,394	1,545	1,431	1,697	0,001					up		
Solyc03g116740	phosphatidic acid phosphatase-related / PAP2-like protein (AHRD V3.3 *** AT3G15820.1)		F:GO:0004142; P:G(	F:diacylglycerol chc EC:2.7.8.2 Diacylglycerol choline	mobidb-lite (MOBIDB_LITE); mobidb-lit	27,864	37,372	59,654	57,505	59,716									
Solyc03g116750	WD-repeat protein, putative (AHRD V3.3 *** B9SMF9_RICCO)	TPL4	F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated	IPR006595 (SMART); IPR001680 (SN	273,073	271,418	281,289	243,718	258,402									
Solyc03g116760	Pti1-like kinase (AHRD V3.3 *** G7II77_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	78,893	71,251	68,022	65,583	59,307									
Solyc03g116770	seed dormancy control protein (AHRD V3.3 *** AT1G15320.2)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir	IPR025422 (PFAM); PTHR22952 (PAN	5,133	3,802	0,234	0,000	0,071									
Solyc03g116780	Ubiquitin system component CUE protein (AHRD V3.3 *** G7JGX3_MEDTR)		F:GO:0005515	F:protein binding	IPR003892 (PFAM); G3DSA:1.10.8.1(	3,529	3,400	3,382	3,199	3,628									
Solyc03g116790	Chaperone protein dnaJ (AHRD V3.3 *** A0A151SPS5_CAJCA)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc	IPR001623 (PRINTS); IPR001623 (SN	32,940	70,075	47,813	41,589	53,412	1,113	0,009					up		
Solyc03g116795	Heat shock 70 kDa protein (AHRD V3.3 --* C1E762_MICCC)					0,939	0,596	0,267	0,300	0,660									
Solyc03g116810	Signal recognition particle 54 kDa protein (AHRD V3.3 *** G7JGX1_MEDTR)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR013822 (SMART); IPR000897 (SN	42,414	42,967	62,252	61,789	59,740									
Solyc03g116815	Subtilisin-chymotrypsin inhibitor-2A (AHRD V3.3 --* ICI2_HORVU)					0,124	0,144	0,075	0,069	0,023									
Solyc03g116820	Phox domain-containing family protein (AHRD V3.3 *-* B9N177_POPTR)		C:GO:0010008; P:G(	C:endosome membrane; P:protein transport; F:phosphatidylinos	mobidb-lite (MOBIDB_LITE)	7,924	7,464	10,901	11,150	10,841									
Solyc03g116830	Phox domain-containing family protein (AHRD V3.3 *** B9N177_POPTR)		F:GO:0035091	F:phosphatidylinositol binding	IPR001683 (SMART); IPR036871 (G3	21,685	17,830	29,619	29,517	27,773									
Solyc03g116840	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061G8Z6_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR003656 (SMART); IPR003656 (PF	5,198	6,058	2,761	2,790	2,616									
Solyc03g116843	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061GFS6_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (TIGRFAM); IPR032867 (I	0,759	0,712	0,376	0,390	0,445									
Solyc03g116847	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein (AHRD V3.3 --* AT5G12440.8)					0,075	0,078	0,000	0,000	0,000									
Solyc03g116850	cyclic nucleotide gated channel 8 (AHRD V3.3 *** AT1G19780.1)		F:GO:0005249; P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra	IPR003938 (PRINTS); IPR000595 (SN	0,000	0,018	0,000	0,000	0,000									
Solyc03g116860	Acyl-CoA N-acyltransferases superfamily protein (AHRD V3.3 *** A0A061G857_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR000182 (PFAM); G3DSA:3.40.630	0,000	0,000	0,051	0,123	0,095									
Solyc03g116870	NAD(P)H dehydrogenase subunit 48 (AHRD V3.3 *** A0A0F7GZU3_9ROSI)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:photosynthetic electron tra	G3DSA:3.40.50.2000 (GENE3D); mob	14,340	24,286	14,486	16,354	36,283	0,788	0,011	1,318	0,000			up	up	
Solyc03g116880	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9STQ9_RICCO)		P:GO:0006284; F:G(	P:base-excision rep EC:3.2.2.21; EC:3.2. DNA-3-methyladenine	G3DSA:1.10.340.30 (GENE3D); IPR0(	10,907	9,635	9,045	8,041	7,488									
Solyc03g116890	WRKY transcription factor 39	WRKY39	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc	IPR003657 (SMAF WRKY	18,189	40,814	6,515	9,206	6,962									
Solyc03g116900	Metal transporter (AHRD V3.3 *** C4TNX3_TOBAC)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane	IPR001046 (PRINTS); IPR001046 (TI(	64,449	56,591	33,866	29,421	35,261									
Solyc03g116910	cinnamoyl-CoA reductase 2	ccr2	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding	IPR001509 (PFAM); G3DSA:3.40.50.7	8,018	7,698	13,884	15,754	14,909									
Solyc03g116920	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2PCJ8_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion	G3DSA:2.30.30.140 (GENE3D); mobic	18,949	11,593	4,895	7,307	5,805									
Solyc03g116930	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2PCJ8_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion	IPR007942 (PFAM); mobidb-lite (MOB	16,716	13,996	24,084	25,225	22,215									
Solyc03g116935	Ferredoxin--NADP reductase, leaf isozyme, chloroplastic (AHRD V3.3 --* FENR1_PEA)					0,119	0,144	0,191	0,318	0,307									
Solyc03g116940	Sister chromatid cohesion PDS5 B (AHRD V3.3 *-* A0A0B0PRG3_GOSAR)		P:GO:0007064	P:mitotic sister chromatid cohesion	IPR007942 (PFAM); mobidb-lite (MOB	0,078	0,081	0,025	0,099	0,000									
Solyc03g116950	phospholipase-like protein (PEARLI 4) family protein (AHRD V3.3 *-* AT4G35110.6)		P:GO:0007064	P:mitotic sister chromatid cohesion	IPR007942 (PFAM); mobidb-lite (MOB	0,232	0,121	0,121	0,243	0,046									
Solyc03g116960	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G18975.4)					0,197	0,184	0,144	0,300	0,211									
Solyc03g116970	Sister chromatid cohesion PDS5 B-B (AHRD V3.3 *-* A0A0B0PPN5_GOSAR)		P:GO:0007064	P:mitotic sister chromatid cohesion	IPR007942 (PFAM); IPR039776 (PAN	1,635	1,912	0,508	0,792	0,540									
Solyc03g116975	SNARE-interacting KEULE-like protein (AHRD V3.3 --* A0A0B0MFS4_GOSAR)		P:GO:0007064	P:mitotic sister chromatid cohesion		0,650	0,382	0,101	0,239	0,093									
Solyc03g116990	Protein transport protein Sec61 subunit beta, putative (AHRD V3.3 *** B9SK56_RICCO)		C:GO:0005784; P:G(	C:Sec61 translocon complex; P:intracellular protein transport	IPR016482 (PFAM); IPR030671 (PIRS	2,682	3,964	4,428	3,554	4,488									
Solyc03g117000	Vesicle transport protein, Got1/SFT2-like protein (AHRD V3.3 *** A0A118K470_CYNCS)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo	IPR007305 (PFAM); PTHR23137:SF1	5,404	4,108	5,803	7,353	4,921									
Solyc03g117010	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2PCJ8_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion	G3DSA:2.30.30.140 (GENE3D); IPR0(	46,335	39,276	38,781	39,130	39,367									
Solyc03g117020	Stromal cell-derived factor 2-like protein (AHRD V3.3 *** SDF2_ARATH)		C:GO:0016020	C:membrane	IPR016093 (SMART); G3DSA:2.80.10	63,800	65,856	105,898	109,878	94,899									
Solyc03g117030	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT2G32070.1)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.13; EC:3.1.1! Acting on ester bonds	IPR006941 (PFAM); IPR006941 (PFA	15,275	16,063	27,981	26,037	26,286									
Solyc03g117040	XH/XS domain-containing protein (AHRD V3.3 *** A0A061GG53_THECC)		P:GO:0031047	P:gene silencing by RNA	IPR038588 (G3DSA:3.30.70.GENE3D	245,434	224,345	181,630	164,773	168,943									
Solyc03g117050	NOD26-like intrinsic protein 6.1	NIP6.1	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS); IPR000425 (PF	1,868	1,526	1,003	0,858	1,558									
Solyc03g117060	60S ribosomal protein L7 (AHRD V3.3 *** B9GMC3_POPTR)		P:GO:0000463; F:G(	P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU	IPR012988 (PFAM); IPR036919 (G3D	93,845	81,625	57,757	52,224	55,051									
Solyc03g117070	Zinc finger protein, putative (AHRD V3.3 *** B9SMU5_RICCO)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.6 C2H2	0,254	0,078	0,025	0,025	0,047									
Solyc03g117080	Mitochondrial glycoprotein family protein (AHRD V3.3 *** AT1G15870.1)		C:GO:0005759	C:mitochondrial matrix	IPR003428 (PFAM); IPR036561 (G3D	2,900	2,757	2,842	3,120	2,023									
Solyc03g117090	stress response NST1-like protein (AHRD V3.3 *** AT1G80700.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	10,823	10,690	10,367	10,921	9,758									
Solyc03g117100	PPPDE putative thiol peptidase family protein (AHRD V3.3 *** AT1G80690.1)				IPR008580 (SMART); G3DSA:3.90.17	2,866	2,980	0,662	0,399	0,680									
Solyc03g117110	Defective in cullin neddylation protein (AHRD V3.3 *** K4BLL3_SOLLC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:ubiquitin conjugating enzyme bindir	G3DSA:1.10.238.10 (GENE3D); G3DS	25,252	31,754	30,687	34,900	31,789									
Solyc03g117120	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *** A0A0B0P3R7_GOSAR)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural con:	IPR007230 (PFAM); IPR036903 (G3D	38,400	33,921	38,466	38,486	37,433									
Solyc03g117130	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RS58_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN' ERF	0,019	0,043	0,072	0,025	0,023									
Solyc03g117150	Plasma membrane ATPase (AHRD V3.3 *** A0A0V0IWA6_SOLCH)		F:GO:0000166; F:G(	F:nucleotide bindinc EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	PR00119 (PRINTS); IPR001757 (PRII	0,337	0,327	1,448	1,302	1,768									
Solyc03g117180	Protein kinase family protein (AHRD V3.3 *** F4IRL6_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); IPR000719 (PF	15,558	12,045	6,216	7,293	9,687			0,631	0,030				up	
Solyc03g117190	LOW QUALITY:Vegetative cell wall protein gp1, putative (AHRD V3.3 --* B9SMV7_RICCO)				PR01217 (PRINTS); mobidb-lite (MOB	12,772	11,029	12,078	10,900	11,925									

Solyc03g117200	F-box/LRR protein, putative (AHRD V3.3 *-* A0A072UPD5_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001810 (PF	12,114	12,999	21,017	21,172	18,806									
Solyc03g117210	abscisic acid responsive elements-binding factor 3 (AHRD V3.3 --* AT4G34000.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	44,123	27,914	9,311	10,872	15,354									
Solyc03g117230	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RS64_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,019	0,000	0,000	0,000	0,000									
Solyc03g117260	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G02645.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): PTHR31549:SF2	0,042	0,669	0,097	0,000	0,071									
Solyc03g117270	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** A0A061F027_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART): G3DSA:1.20.12	4,340	3,273	1,194	1,280	1,033									
Solyc03g117280	transmembrane protein (AHRD V3.3 *** AT2G25270.1)		C:GO:0005886; C:G(	C:plasma membrane; C:plasmodesma; C:integral component of			IPR040283 (PANTHER): PTHR31414:	64,545	70,770	123,669	153,589	137,191									
Solyc03g117300	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9Q4D1_ZOSMR)		C:GO:0005634; C:G(	C:nucleus; C:integral component of membrane; P:response to k			G3DSA:1.20.1250.20 (GENE3D): IPR(	21,278	18,531	11,865	8,695	11,582									
Solyc03g117310	LOW QUALITY:Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT1G80520.1)						G3DSA:1.10.150.50 (GENE3D): mobic	2,147	5,680	18,368	23,539	16,872	1,422	0,008					up		
Solyc03g117320	Ribosomal protein L3 (AHRD V3.3 *** A0A103XT80_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR019927 (TIGRFAM): IPR000597 (F	48,086	42,896	59,862	56,025	56,893									
Solyc03g117330	tRNA synthetase-related family protein (AHRD V3.3 *** B9GTA1_POPTR)		F:GO:0004827; F:G(	F:proline-tRNA ligas	EC:6.1.1.15	Proline--tRNA ligase	IPR002316 (PRINTS): IPR016061 (SM	2,249	6,476	3,479	3,042	2,958	1,548	0,003					up		
Solyc03g117350	LOW QUALITY:Amino acid transporter, putative (AHRD V3.3 *** B9SWV0_RICCO)		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): PTHR22950 (PAN	13,945	12,738	8,169	9,001	9,028									
Solyc03g117360	TOPLESS1	TPL1	F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated			IPR001680 (SMART): IPR006595 (SM	123,645	117,637	38,112	37,453	41,113									
Solyc03g117365	14-3-3-like protein (AHRD V3.3 --* 1433_OENEH)						mobidb-lite (MOBIDB_LITE)	3,542	3,095	1,340	1,407	1,578									
Solyc03g117370	TOPLESS-related 1 (AHRD V3.3 *-* AT1G80490.3)		F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated			IPR001680 (SMART): IPR001680 (PF	10,787	8,567	6,327	5,868	5,718									
Solyc03g117380	Protein TOPLESS (AHRD V3.3 *-* TPL_ARATH)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR027728 (PANTHER): PTHR44083:	2,080	2,911	2,307	2,456	2,498									
Solyc03g117390	TOPLESS-related 1 (AHRD V3.3 *-* AT1G80490.3)		P:GO:0006355	P:regulation of transcription, DNA-templated				0,442	0,592	0,597	0,532	0,685									
Solyc03g117420	F-box/LRR-repeat protein (AHRD V3.3 *** A0A0K9PK37_ZOSMR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR032675 (G3	366,368	226,769	761,529	739,355	703,960	-0,665	0,010					down		
Solyc03g117425	Protein TOPLESS (AHRD V3.3 *-* A0A0B2P1H0_GLYSO)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR027728 (PANTHER): PTHR44083:	0,261	0,257	0,169	0,222	0,116									
Solyc03g117430	COBW domain-containing protein 1 (AHRD V3.3 *** A0A0B2RY32_GLYSO)						IPR011629 (SMART): IPR011629 (PF	74,495	96,395	229,629	234,065	225,031									
Solyc03g117440	RNA helicase DEAD14	DEAD14	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding; F:zinc ion binding			IPR001878 (SMART): IPR014001 (SM	17,260	16,998	14,180	11,651	14,574									
Solyc03g117450	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (PF	0,000	0,000	0,000	0,022	0,024									
Solyc03g117470	Calcium-binding EF-hand family protein (AHRD V3.3 *** AT3G18430.3)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	0,799	0,541	1,068	0,871	0,968									
Solyc03g117480	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)		F:GO:0004427; F:G(	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (TIGRFAM): IPR002048 (F	187,216	204,349	339,243	394,296	341,769									
Solyc03g117490	Glycerol kinase (AHRD V3.3 *** GLPK_ARATH)		F:GO:0004370; P:G(	F:glycerol kinase ac	EC:2.7.1.3	Glycerol kinase	IPR018484 (PFAM): G3DSA:3.30.420	26,206	24,863	9,360	10,492	13,135									
Solyc03g117500	VQ motif-containing protein (AHRD V3.3 *** AT1G80450.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR008889 (PFAM): mobidb-lite (MOB	2,210	2,234	11,401	15,215	12,480									
Solyc03g117510	Formamidopyrimidine-DNA glycosylase, putative (AHRD V3.3 *** B9RVA4_RICCO)		F:GO:0003684; F:G(	F:damaged DNA bir	EC:3.2.2.23	DNA-formamidopyrim	IPR015886 (SMART): IPR012319 (SM	20,364	17,329	10,470	9,127	9,849									
Solyc03g117520	Protein FAR1-RELATED SEQUENCE 6 (AHRD V3.3 *** W9R3Q8_9ROSA)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	19,805	21,193	22,728	16,956	21,100					-0,420	0,040			down
Solyc03g117530	Hus1-like protein (AHRD V3.3 *** A0A097PQI1_SOLLC)		P:GO:0000077; C:G(	P:DNA damage checkpoint; C:nucleolus; C:checkpoint clamp co			G3DSA:3.70.10.10 (GENE3D): IPR00	7,152	6,772	6,331	5,898	6,675									
Solyc03g117540	ABC transporter family protein (AHRD V3.3 *-* A0A097P9P6_HEVBR)	ABCC3	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR011527 (PFAM): IPR036640 (G3D	4,895	3,240	1,642	2,699	2,339									
Solyc03g117543	ABC transporter family protein (AHRD V3.3 *-* A0A097P9P6_HEVBR)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): PTHR24223 (PAN	1,581	1,152	0,523	0,485	0,497									
Solyc03g117547	ABC transporter family protein (AHRD V3.3 *** A0A097P9P6_HEVBR)		F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR036640 (G3	8,874	7,019	3,383	4,404	4,827									
Solyc03g117550	Kinase family protein (AHRD V3.3 *** B9GVL5_POPTR)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR024171 (PIF	2,011	1,881	0,262	0,261	0,449									
Solyc03g117570	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RGM1_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,078	0,142	0,193	0,097	0,046									
Solyc03g117580	GAG1At protein (AHRD V3.3 *** AT1G16000.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR359	0,796	0,845	0,418	0,346	0,353									
Solyc03g117590	Heat shock protein binding protein (AHRD V3.3 *** E2DDU6_SOLLC)		C:GO:0005737; C:G(	C:cytoplasm; C:integral component of membrane			IPR001623 (PRINTS): IPR001623 (SM	0,300	0,181	0,197	0,163	0,118									
Solyc03g117600	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase (AHRD V3.:	HCT	F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	11,466	19,366	53,666	62,606	54,805	0,781	0,012					up		
Solyc03g117640	MAP kinase kinase kinase 29	MAPKKK29	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	4,010	1,939	2,272	4,350	2,540					0,939	0,003			up
Solyc03g117650	Phosphatidylinositol-glycan biosynthesis class F protein (AHRD V3.3 --* A0A199W8X3_ANACO)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:GPI anchor biosynthetic process; C:integral component of memb				10,612	8,858	10,063	11,317	9,477									
Solyc03g117660	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G21500.2)						IPR001841 (SMART): IPR013083 (G3	9,620	10,451	12,126	12,647	13,647									
Solyc03g117670	Snf1-related kinase interactor 1, putative (AHRD V3.3 *-* A0A072UGK4_MEDTR)		P:GO:0009909	P:regulation of flower development			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,421	2,469	3,514	4,652	4,405									
Solyc03g117675	ATP-dependent DNA helicase (AHRD V3.3 *** AT2G24100.1)						mobidb-lite (MOBIDB_LITE): PTHR334	37,505	21,799	68,001	86,386	72,620									
Solyc03g117680	Nascent polypeptide-associated complex subunit beta (AHRD V3.3 --* A0A059PZU4_9POAL)							1,536	1,702	2,619	3,059	3,137									
Solyc03g117690	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061GAK7_THECC)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR021109 (G3D	0,079	0,060	0,000	0,000	0,024									
Solyc03g117700	Major facilitator superfamily protein (AHRD V3.3 *-* A0A061G9T3_THECC)		C:GO:0016021	C:integral component of membrane			IPR039309 (PFAM): PTHR31585:SF1	0,060	0,094	0,025	0,025	0,070									
Solyc03g117710	Major facilitator superfamily protein (AHRD V3.3 *-* AT1G79710.2)		C:GO:0016020	C:membrane			IPR039309 (PFAM): IPR039309 (PAN	0,058	0,000	0,000	0,025	0,000									
Solyc03g117720	AP2-like ethylene-responsive transcription factor family (AHRD V3.3 *** A0A151UF47_CAJCA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN AP2	7,826	6,099	3,804	6,162	4,485					0,704	0,025			up
Solyc03g117730	Tubby protein, putative (AHRD V3.3 *** B9RGP8_RICCO)		F:GO:0035091	F:phosphatidylinositol binding			IPR000007 (PRINTS): IPR025659 (G3	0,255	0,250	0,022	0,000	0,024									
Solyc03g117740	nuclear protein (AHRD V3.3 *** AT1G16080.1)		C:GO:0009570; C:G(	C:chloroplast stroma; C:chloroplast envelope; C:apoplast			PTHR34044 (PANTHER)	22,692	33,357	21,814	21,066	25,542	0,584	0,027					up		
Solyc03g117750	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G19170.1)	PG57	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	4,188	2,717	3,409	3,840	3,555									
Solyc03g117760	Ephrin-A3 (AHRD V3.3 *** A0A0B0PTB6_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	70,412	63,671	47,322	51,315	46,000									
Solyc03g117770	Serine-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 *** AT1G16180.2)		C:GO:0016020	C:membrane			IPR005016 (PFAM): mobidb-lite (MOB	230,957	217,320	344,126	371,232	354,430									
Solyc03g117780	Rad23 UV excision repair protein family (AHRD V3.3 *** AT1G79650.1)		F:GO:0003684; F:G(	F:damaged DNA binding; F:protein binding; C:nucleus; P:nucleot			IPR004806 (PRINTS): IPR006636 (SM	33,209	36,280	58,343	55,915	52,821									
Solyc03g117790	Kinase (AHRD V3.3 *** D7KWK7_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,505	0,519	0,000	0,101	0,024									
Solyc03g117800	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT5G57800.1)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR021940 (PFAM): IPR006694 (PFA	2,558	1,327	1,189	0,897	0,513									
Solyc03g117810	ABC transporter family protein (AHRD V3.3 *** A0A097P9R8_HEVBR)	ABCI4	F:GO:0005315; F:G(	F:inorganic phosph	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	23,201	15,028	5,684	5,074	5,453	-0,598	0,047					down		
Solyc03g117820	Transcriptional adapter 1 (AHRD V3.3 *** A0A0B0NYM8_GOSAR)		C:GO:0070461	C:SAGA-type complex			IPR024738 (PFAM): mobidb-lite (MOB	4,870	4,493	4,028	3,833	3,742									
Solyc03g117830	LOW QUALITY:Signal anchor, putative (AHRD V3.3 --* A0A072UJ16_MEDTR)							0,040	0,019	0,000	0,050	0,000									
Solyc03g117840	Negative regulator of sporulation MDS3 (AHRD V3.3 *** A0A0B0N6H6_GOSAR)						PTHR33181 (PANTHER): PTHR33181	10,068	14,642	2,616	1,527	1,445									
Solyc03g117850	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *** A0A072VDJ3_MEDTR)		F:GO:0005524	F:ATP binding			G3DSA:1.10.8.1070 (GENE3D): G3DS	24,051	39,039	24,057	23,162	29,763	0,724	0,027					up		
Solyc03g117860	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G14250.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR002867 (SMART): IPR002867 (PF	5,676	21,458	2,110	3,754	3,134	1,943	0,000					up		
Solyc03g117870	4-coumarate--CoA ligase	4CL	F:GO:0003824	F:catalytic activity			G3DSA:3.30.300.30 (GENE3D): IPR0(	210,959	257,224	418,628	490,060	425,799									
Solyc03g117880	LOW QUALITY:Senescence-specific cysteine protease SAG39 (AHRD V3.3 --* SAG39_ORYSI)							0,000	0,000	0,000	0,000	0,237									
Solyc03g117890	ACT domain-containing protein (AHRD V3.3 *** A0A0K9PHE5_ZOSMR)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast stroma			G3DSA:3.30.70.260 (GENE3D): PTHF	79,595	92,505	223,171	261,668	290,813			0,379	0,030				up	
Solyc03g117900	Cytochrome c oxidase assembly protein (AHRD V3.3 *** A0A0K9NUD4_ZOSMR)		C:GO:0005739; P:G(	C:mitochondrion; P:mitochondrial respiratory chain complex IV a			IPR018793 (PFAM): IPR018793 (PAN	8,607	8,310	15,597	13,930	13,583									
Solyc03g117910	FRIGIDA-like protein, putative (AHRD V3.3 *-* A0A061G6R8_THECC)		P:GO:0032502	P:developmental process			IPR012474 (PFAM): mobidb-lite (MOB	0,201	0,121	0,071	0,119	0,118									
Solyc03g117920	Protein FRIGIDA, putative (AHRD V3.3 *** B9RA29_RICCO)		P:GO:0007275	P:multicellular organism development			IPR012474 (PFAM): mobidb-lite (MOB	0,059	0,100	0,118	0,025	0,211									
Solyc03g117930	Protein FRIGIDA (AHRD V3.3 *** FRIGI_ARATH)		P:GO:0007275	P:multicellular organism development			IPR012474 (PFAM): mobidb-lite (MOB	12,229	12,889	19,193	15,398	16,269									
Solyc03g117940	U2 small nuclear ribonucleoprotein A (AHRD V3.3 *** AT1G09760.1),Pfam:PF14580		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:nucleolus; C:cytosol; P:re:			PF14580 (PFAM): IPR032675 (G3DS/	37,785	39,318	62,633	60,469	56,532									
Solyc03g117950	ATP-dependent Clp protease (AHRD V3.3 *** A0A059Q1P9_9POAL)		F:GO:0005524; P:G(	F:ATP binding; P:protein metabolic process			IPR001270 (PRINTS): IPR003593 (SM	51,036	67,346	198,825	215,619	200,724									
Solyc03g117960	forkhead-associated domain-containing protein / FHA domain-containing protein (AHRD V3.3 *** AT5G0740(		F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; C:nucleus; P:DNA repa			IPR000253 (SMART): IPR010347 (PF	2,264	3,037	9,435	6,153	9,628									
Solyc03g117970	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4BLU8_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:N/	EC:2.4.2.3	NAD(+) ADP-ribosylt	IPR012982 (SMART): IPR001357 (SM	33,810	31,377	19,451	16,754	17,612									
Solyc03g117980	whitefly-induced gp91-phox	wfi1	F:GO:0004601; F:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000778 (PRINTS): IPR013623 (PF	436,084	523,729	46,799	38,102	74,627									
Solyc03g117990	LOW QUALITY:BnaC09g48580D protein (AHRD V3.3 *** A0A078ED39_BRANA)						mobidb-lite (MOBIDB_LITE): PTHR383	1,437	1,349	0,582	0,384	0,586									
Solyc03g118000	Inositol polyphosphate multikinase (AHRD V3.3 *** K4BLV1_SOLLC)		F:GO:0016301; P:G(	F:kinase activity; P:inositol phosphate biosynthetic process			IPR005522 (PFAM): IPR038286 (G3D	1,122	1,700	3,594	3,849	3,294									
Solyc03g118010	Nuclease domain-containing protein 1 (AHRD V3.3 *** A0A0B2PPT4_GLYSO)		C:GO:0016442; P:G(	C:RISC complex; P:gene silencing by RNA			IPR002999 (SMART): IPR016071 (SM	78,327	71,923	78,256	65,028	72,931									
Solyc03g118020	Nuclease domain-containing protein 1 (AHRD V3.3 *** A0A0B2RH39_GLYSO)		C:GO:0016442; P:G(	C:RISC complex; P:gene silencing by RNA			IPR002999 (SMART): IPR016071 (SM	316,529	332,953	401,121	346,193	343,763									
Solyc03g118030	Glutamyl-tRNA(Gln) amidotransferase subunit A (AHRD V3.3 *** A0A151S2E8_CAJCA)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR036928 (G3DSA:3.90.1300.GENE	59,262	51,592	52,242	50,715	50,827									
Solyc03g118040	calnexin	cnx	F:GO:0005509; C:G(	F:calcium ion binding; C:endoplasmic reticulum; P:protein foldinc			IPR001580 (PRINTS): IPR001580 (PF	560,419	607,622	701,721	719,724	679,060									
Solyc03g118050	NADH-ubiquinone reductase complex 1 MLRQ subunit (AHRD V3.3 *** G7K3Q0_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33919 (PANTHER): PTHR33919	2,185	4,773	2,937	4,123	2,119									
Solyc03g118060	NADH-ubiquinone reductase complex 1 MLRQ subunit (AHRD V3.3 *** G7K3Q0_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33919:SF2 (PANTHER): PTHR3	0,819	0,230	42,078	41,438	35,597									
Solyc03g118070	Sucrose nonfermenting 4-like protein (AHRD V3.3 *** SNF4_ARATH)						IPR000644 (SMART): G3DSA:3.10.58	18,315	16,709	5,651	3,817	5,362									
Solyc03g118090	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G51050.1)		F:GO:0005509; F:G(	F:calcium ion binding; F:transmembrane transporter activity; P:t			IPR002067 (PRINTS): IPR002048 (SM	7,948	19,359	7,135	6,258	6,875	1,309	0,001					up		
Solyc03g118100	(+)-neomenthol dehydrogenase (AHRD V3.3 *** A0A0B2R9Q6_GLYSO)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.40.50.720 (GENE3D): PTHF	0,099	0,153	0,668	1,523	0,983									
Solyc03g118110	Ankyrin repeat family protein (AHRD V3.3 *** A0A0G4AMZ0_9ROSI)		C:GO:0005739; P:G(	C:mitochondrion; P:tricarboxylic acid cycle; P:mitochondrial elec			IPR036714 (G3DSA:1.10.150.GENE3	58,497	57,184	257,432	245,711	245,001									
Solyc03g118120	Transferase, transferring glycosyl groups, putative (AHRD V3.3 *** B9RG20_RICCO)						IPR038941 (PANTHER): PTHR33880:	16,739	13,283	1,079	1,094	1,453									
Solyc03g118130	Rubredoxin (AHRD V3.3 *** A0A0K9Q129_ZOSMR)		F:GO:0005506	F:iron ion binding			IPR024935 (PFAM): G3DSA:2.20.28.1	55,808	74,198	29,203	34,403	44,183			0,595	0,001				up	
Solyc03g118140	Protein kish (AHRD V3.3 *** K4BLW5_SOLLC)		C:GO:0005623; P:G(	C:cell; P:protein secretion; C:integral component of membrane;			IPR009653 (PFAM): PTHR13229:SF1	3,229	2,835	4,981	3,801	3,877									
Solyc03g118150	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G01630.1)						IPR011074 (SMART): IPR001251 (SM	11,167	10,933	8,399	8,748	8,068									
Solyc03g118160	falsiflora	fa	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR035079 (PFAM LFY	0,224	0,200	0,349	0,220	0,167									
Solyc03g118170	Glycyl-tRNA synthetase family protein (AHRD V3.3 *** B9GMU1_POPTR)		F:GO:0004820; F:G(	F:glycine-tRNA ligas	EC:6.1.1.14	Glycine--tRNA ligase	IPR002315 (PRINTS): IPR002315 (TI(	63,636	59,312	66,493	56,170	59,883									
Solyc03g118175	E3 ubiquitin-protein ligase ORTHRUS 2 (AHRD V3.3 *-* A0A0B0PT11_GOSAR)		C:GO:0005634; F:G(	C:nucleus; F:ligase activity; F:metal ion binding				0,019	0,036	0,143	0,048	0,143									
Solyc03g118180	RING-finger E3 ubiquitin ligase, putative (AHRD V3.3 --* A0A072VDM7_MEDTR)		C:GO:0005634; F:G(	C:nucleus; F:ligase activity; F:metal ion binding			IPR036987 (G3DSA:2.30.280.GENE3	5,545	6,599	8,560	7,064	6,873									
Solyc03g118190	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9S0J2_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,205	0,335	0,603	1,094	0,472									
Solyc03g118200	Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 *** AT5G61900.3)		F:GO:0005544; P:G(	F:calcium-dependent phospholipid binding; P:negative regulation			IPR002035 (SMART): IPR000008 (SM	58,437	94,135	37,089	40,270	43,745	0,713	0,030					up		
Solyc03g118220	Transducin/WD40 repeat protein (AHRD V3.3 *** G7J399_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:positive regulation of TOR signaling			IPR001680 (SMART): IPR001680 (PF	0,897	2,369	0,094	0,145	0,046									
Solyc03g118230	Homeodomain-like protein (AHRD V3.3 *** A0A103XY92_CYNCS)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 Trihelix	0,000	0,039	0,000	0,000	0,000									
Solyc03g118240	Magnesium-protoporphyrin O-methyltransferase (AHRD V3.3 *** A0A0B0NE87_GO!	CHLM	P:GO:0015995; F:G(	P:chlorophyll biosyr	EC:2.1.1.11	Magnesium protopor	IPR010251 (TIGRFAM): IPR010940 (F	25,712	57,346	26,249	30,505	53,577	1,185	0,000	1,026	0,000			up	up	
Solyc03g118250	mRNA cap guanine-N7 methyltransferase (AHRD V3.3 *** K4BLX6_SOLLC)		F:GO:0004482; C:G(	F:mRNA (guanine-N	EC:2.1.1.56	mRNA (guanine-N(7)-	IPR004971 (PFAM): G3DSA:3.40.50.1	7,655	6,915	8,391	8,330	8,528									
Solyc03g118260	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *** G5DWI4_SILLA)		F:GO:0005096; F:G(	F:GTPase activator activity; F:protein binding; C:cytoplasm			IPR001164 (PRINTS): IPR001849 (SM	8,609	7,424	5,049	4,521	4,388									
Solyc03g118270	GDP-mannose 4,6 dehydratase 1 (AHRD V3.3 *** GMD1_ARATH)		F:GO:0008446; P:G(	F:GDP-mannose 4,(	EC:4.2.1.47	GDP-mannose 4,6-d	IPR016040 (PFAM): G3DSA:3.90.25.1	56,494	68,414	88,976	77,598	72,560									
Solyc03g118280	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RA74_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	9,188	9,891	7,924	8,998	8,364									
Solyc03g118290	auxin response factor 2A	ARF2a	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF ARF	249,792	198,480	445,839	488,155	395,599									
Solyc03g118300	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (AHRD V3.3 --* AT3G17720.1)							5,287	4,589	9,495	11,833	8,058									
Solyc03g118310	bHLH transcription factor 083		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	5,222	3,257	0,199	0,123	0,118									
Solyc03g118320	AAA family ATPase (AHRD V3.3 *** G7KFD2_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding; F:ATP binding; P:DNA replicati			IPR015940 (SMART): IPR003593 (SM	1,499	1,035	0,981	0,944	0,871									
Solyc03g118325	LRR receptor-like kinase family protein (AHRD V3.3 *-* A0A072UEN8_MEDTR)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,139	0,083	0,118	0,050	0,141									
Solyc03g118330	Receptor-kinase, putative (AHRD V3.3 *-* B9RVA8_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	0,214	0,163	0,144	0,119	0,236									
Solyc03g118333	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGP3_ARATH)		F:GO:0016740	F:transferase activity			IPR032675 (G3DSA:3.80.10.GENE3D	0,416	0,293	0,172	0,192	0,378									
Solyc03g118337	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT5G06940.1)		F:GO:0000166; F:G(	F:nucleotide binding; F:protein kinase activity; C:membrane; P:phosphorylation				0,196	0,156	0,143	0,145	0,071									
Solyc03g118340	Chloroplast ATP-dependent Clp protease chaperone protein (AHRD V3.3 *** A0A088FCE7_NICBE)		F:GO:0005515; F:G(	F:protein binding; F:ATP binding; P:protein metabolic process			IPR001270 (PRINTS): IPR003593 (SM	72,029	78,417	346,877	387,579	333,565									
Solyc03g118350	dual specificity protein phosphatase family protein (AHRD V3.3 *** AT5G23720.2)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR000340 (PF	25,703	27,377	27,537	26,438	26,964									
Solyc03g118355	dual specificity protein phosphatase family protein (AHRD V3.3 *-* AT5G23720.1)		F:GO:0004725; C:G(	F:protein tyrosine p	EC:3.1.3.16; EC:3.1.	Protein-serine/threor	IPR015275 (PFAM): mobidb-lite (MOB	11,551	9,937	9,742	10,550	10,075									
Solyc03g118360	LOW QUALITY:ATP-dependent Clp protease ATP-binding subunit (AHRD V3.3 *-* A0A072V2V0_MEDTR)		P:GO:0019538	P:protein metabolic process			IPR004176 (PFAM): IPR036628 (G3D	0,000	0,000	0,025	0,000	0,000									
Solyc03g118370	Carboxypeptidase (AHRD V3.3 *** K4BLY8_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): G3DSA:3.40.5(	2,055	2,338	0,115	0,000	0,024									
Solyc03g118380	DNA-directed RNA polymerase II subunit RPB7 (AHRD V3.3 *** A0A0B0PUV3_GOSAR)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA p(	G3DSA:2.40.50.140 (GENE3D): IPR0(	29,684	24,499	41,001	32,651	35,864									
Solyc03g118390	coiled-coil protein (AHRD V3.3 *** AT3G48860.2)		P:GO:0000911	P:cytokinesis by cell plate formation			mobidb-lite (MOBIDB_LITE): mobidb-lit	72,729	93,662	92,909	86,824	97,674									
Solyc03g118410	Acyl carrier protein (AHRD V3.3 *** Q672Q9_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR036736 (G3DSA:1.10.1200.GENE	17,787	29,864	10,518	15,583	26,282	0,776	0,014	1,317	0,000			up	up	
Solyc03g118425	NF-X1-type zinc finger protein NFXL1 (AHRD V3.3 *** W9QPA3_9ROSA)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000967 (SMART): IPR000967 (PF	55,329	70,913	76,678	60,429	67,996									
Solyc03g118430	Insulinase (Peptidase family M16) family protein (AHRD V3.3 *** AT5G42390.1)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			IPR011765 (PFAM): G3DSA:3.30.830	111,172	109,773	205,321	227,197	235,498									
Solyc03g118440	knotted 1-binding protein (AHRD V3.3 *** AT5G03050.2)						mobidb-lite (MOBIDB_LITE): PTHR355	0,101	0,135	0,096	0,025	0,000									
Solyc03g118450	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)						PTHR34780 (PANTHER): PTHR34780	0,921	0,772	0,819	1,006	0,779									
Solyc03g118455	defective in meristem silencing 3 (AHRD V3.3 --* AT3G49250.1)							0,021	0,000	0,000	0,000	0,024									
Solyc03g118470	Nudix hydrolase (AHRD V3.3 *** A0A061E9N4_THECC)		F:GO:0016787	F:hydrolase activity			IPR000086 (PFAM): G3DSA:3.90.79.1	83,459	28,532	33,852	125,327	44,657	-1,524	0,000			1,891	0,000	down		up
Solyc03g118480	Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 *-* AT2G23530.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018866 (PFAM): mobidb-lite (MOB	0,813	2,161	0,477	0,172	0,327	1,439	0,017					up		
Solyc03g118490	Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 *-* AT2G23530.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018866 (PFAM): mobidb-lite (MOB	0,495	0,638	0,319	0,072	0,328									
Solyc03g118500	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SU82_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS): IPR001623 (SM	17,945	19,218	20,359	17,714	19,180									
Solyc03g118510	Ovary receptor kinase 27 (AHRD V3.3 *** S4WIQ7_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM): IPR000719 (PFA	62,670	34,585	8,301	5,596	7,155									
Solyc03g118520	ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 *-* AT3G51610.1)		C:GO:0005886; P:G(	C:plasma membrane; P:response to oxidative stress; P:pollen d			PTHR36768 (PANTHER)	20,641	22,835	26,470	26,064	25,842									
Solyc03g118523	ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 *-* AT3G51610.1)		C:GO:0005886; P:G(	C:plasma membrane; P:response to oxidative stress; P:pollen d			PTHR36768 (PANTHER)	9,350	8,837	9,758	11,089	10,290									
Solyc03g118525	ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 *-* A0A0B0NSV6_GOSAR)		C:GO:0016020	C:membrane				9,178	10,149	11,295	10,722	9,853									
Solyc03g118530	Kinase, putative (AHRD V3.3 *** B9T5A7_RICCO)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR000719 (PF	51,957	50,212	81,264	103,588	87,393					0,353	0,049			up
Solyc03g118540	Jasmonate ZIM-domain protein 7b (AHRD V3.3 *** T1WMB9_TOBAC)		C:GO:0005634; P:G(	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (SMART): IPR018467 (PF	4,662	5,765	9,958	11,314	10,459									
Solyc03g118550	Tetratricoredoxin (AHRD V3.3 *** Q8VZH4_TOBAC)		P:GO:0045454; F:G(	P:cell redox homeostasis; F:protein dimerization activity			IPR019734 (SMART): IPR011990 (G3	39,343	36,829	38,191	37,509	38,526									
Solyc03g118570	RAB geranylgeranyl transferase beta subunit 2 (AHRD V3.3 *** AT3G12070.3)		F:GO:0004663; P:G(	F:Rab geranylgerar	EC:2.5.1.6	Protein geranylgeran	IPR001330 (PFAM): G3DSA:1.50.10.2	15,705	14,007	27,475	26,253	24,227									
Solyc03g118580	Lipid transfer protein, putative (AHRD V3.3 *** Q8LA57_ARATH)		C:GO:0031225	C:anchored component of membrane			IPR016140 (SMART): G3DSA:1.10.11	0,000	0,021	0,000	0,000	0,000									
Solyc03g118610	SURF1-like protein (AHRD V3.3 *** K4BM10_SOLLC)		C:GO:0016020	C:membrane			IPR002994 (PFAM): mobidb-lite (MOB	10,132	9,934	12,073	12,017	11,446									
Solyc03g118620	Outer arm dynein light chain 1 (AHRD V3.3 *** G7LE75_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	64,778	66,545	48,382	58,178	57,907									
Solyc03g118630	transmembrane protein (AHRD V3.3 *** AT3G17950.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,607	2,979	2,281	1,744	2,683									
Solyc03g118640	ketose-bisphosphate aldolase class-II family protein (AHRD V3.3 *** AT1G18270.1)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:zinc ion binding; F:oxidore			IPR000771 (TIGRFAM): IPR000771 (F	109,363	97,235	79,430	75,366	80,607									
Solyc03g118650	Aldose 1-epimerase (AHRD V3.3 *** K4BM14_SOLLC)		F:GO:0016853; P:G(	F:isomerase activity; P:hexose metabolic process; F:carbohydr			IPR015443 (PIRSF): IPR014718 (G3D	38,795	36,799	79,055	81,099	74,556									
Solyc03g118660	Vacuolar protein sorting-associated protein 26 (AHRD V3.3 *** AT1G48550.1)		C:GO:0005829; C:G(	C:cytosol; C:retromer complex; P:retrograde transport, endosor			IPR028934 (PFAM): IPR014752 (G3D	22,605	19,769	26,465	28,651	24,976									

Solyc03g118670	Protein sel-1 (AHRD V3.3 *** A0A0B0MWE3_GOSAR)		F:GO:0005515	F:protein binding			IPR006597 (SMART): IPR011990 (G3	57,482	61,279	68,048	65,109	64,681									
Solyc03g118680	Zinc finger protein (AHRD V3.3 *** W9RJ16_9ROSA)		F:GO:0046872	F:metal ion binding			IPR001876 (SMART): IPR001876 (PF	20,001	19,479	22,428	19,497	24,189									
Solyc03g118690	Translocon at the outer membrane of chloroplasts 64 (AHRD V3.3 *** TOC64_PEA)		F:GO:0004040; F:G(	F:amidase activity;	EC:3.5.1.4	Amidase	IPR019734 (SMART): IPR023631 (PF	25,661	32,505	44,959	45,339	43,607									
Solyc03g118700	Nuclear localized protein 1 (AHRD V3.3 *** E1AWW8_NICBE)						IPR028045 (PFAM): mobidb-lite (MOB	1,982	1,801	1,984	1,906	2,162									
Solyc03g118710	C2-domain ABA-related family protein						IPR000008 (SMART): IPR035892 (G3	12,306	12,854	10,541	14,344	12,445									
Solyc03g118720	C2-domain ABA-related family protein						IPR000008 (SMART): IPR000008 (PF	11,961	15,808	22,581	22,381	19,612									
Solyc03g118740	SIPIN1	PIN1	C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): IPR014024 (TIGF	4,705	4,092	1,167	0,683	0,659									
Solyc03g118750	phosphoethanolamine N-methyltransferase		F:GO:0000234; P:G(	F:phosphoethanolai	EC:2.1.1.13	Phosphoethanolamin	G3DSA:3.40.50.150 (GENE3D): PF13	12,592	11,110	14,822	12,271	12,588									
Solyc03g118755	Phosphoethanolamine N-methyltransferase (AHRD V3.3 *** Q9AXH3_SOLLC),Pfam:PF13489		F:GO:0000234; P:G(	F:phosphoethanolai	EC:2.1.1.13	Phosphoethanolamin	G3DSA:3.40.50.150 (GENE3D): PF13	9,890	10,363	13,283	10,350	10,503									
Solyc03g118760	Tubulin beta chain (AHRD V3.3 *** TBB_HORVU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	0,258	0,335	0,934	0,409	0,523									
Solyc03g118770	WUSCHEL-related homeobox 1-like protein (AHRD V3.3 *** A0A0B0P6I0_GOSAR)		F:GO:0003677	F:DNA binding			IPR001356 (SMAF WOX	1,135	1,929	0,000	0,050	0,023									
Solyc03g118780	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7LDC8_MEDTR)						IPR001938 (PRINTS): IPR001938 (SM	2,348	3,866	0,025	0,148	0,023									
Solyc03g118790	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SU85_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	5,342	4,906	3,948	4,145	4,326									
Solyc03g118800	Spliceosome associated protein, putative (AHRD V3.3 *** B9RRM5_RICCO)		F:GO:0003676	F:nucleic acid binding			PR01217 (PRINTS): IPR000504 (SMA	66,379	70,663	83,006	78,942	78,372									
Solyc03g118810	Calcium binding protein (AHRD V3.3 *** Q93YA8_SESRO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	113,155	155,574	43,986	70,699	56,520					0,686	0,028			up
Solyc03g118820	RAB GTPase A6A (AHRD V3.3 *** A0A061FW42_THECC)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00177 (SMAR	0,916	0,798	1,784	2,490	2,020									
Solyc03g118830	3-oxo-5-alpha-steroid 4-dehydrogenase (AHRD V3.3 *** G7LDB8_MEDTR)		P:GO:0006629; F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t			IPR010721 (PFAM): G3DSA:1.20.120	8,704	12,362	13,480	12,588	14,071									
Solyc03g118840	RING/U-box superfamily protein (AHRD V3.3 *** AT1G73760.1)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga:			IPR001841 (SMART): IPR001841 (PF	26,980	28,937	25,461	28,468	28,630									
Solyc03g118850	Catalytic, putative (AHRD V3.3 *** B9SFW5_RICCO)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR029058 (G3DSA:3.40.50.GENE3D	17,061	16,147	27,304	25,476	28,247									
Solyc03g118860	UDP-N-acetylglucosamine--N-acetylmuramyl-(Pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosan		P:GO:0005975; P:G(	P:carbohydrate met	EC:2.4.1.227	Undecaprenyldiphosr	G3DSA:3.40.50.2000 (GENE3D): IPR(	23,795	20,103	20,571	17,823	18,652									
Solyc03g118870	Octicosapeptide/Phox/Bem1p family protein, putative (AHRD V3.3 *** A0A061FV54_THECC)		F:GO:0005515	F:protein binding			IPR000270 (SMART): G3DSA:3.10.20	0,218	0,236	0,318	0,346	0,189									
Solyc03g118880	F-box protein (AHRD V3.3 --* AT1G57906.1)							0,077	0,152	0,075	0,098	0,094									
Solyc03g118890	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G18030.1)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	27,179	26,505	33,860	33,556	34,494									
Solyc03g118900	WAT1-related protein (AHRD V3.3 *** K4BM39_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF6:	0,021	0,018	0,000	0,000	0,000									
Solyc03g118905	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 --* CLPP_ADICA)							0,180	0,094	0,143	0,073	0,094									
Solyc03g118910	T-complex protein 1 subunit delta (AHRD V3.3 *** K4BM40_SOLLC)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR002423 (PF	37,057	33,363	34,139	33,285	31,714									
Solyc03g118920	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9S355_RICCO)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR014720 (SMART): IPR001650 (SM	64,684	61,681	82,131	87,198	83,530									
Solyc03g118930	LOW QUALITY:Glycosyltransferase, putative (AHRD V3.3 *** B9S2Z4_RICCO)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM): IPR007657 (PAN	0,132	0,289	0,000	0,025	0,000									
Solyc03g118940	Glycosyltransferase, putative (AHRD V3.3 *** B9S2Z4_RICCO)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM): PTHR20961:SF5	0,042	0,058	0,025	0,000	0,000									
Solyc03g118945	Protein DETOXIFICATION (AHRD V3.3 *-* K7WNX8_SOLTU)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			PTHR11206:SF198 (PANTHER): PTHI	0,056	0,410	0,000	0,025	0,000									
Solyc03g118947	Protein DETOXIFICATION (AHRD V3.3 *-* M5VPE8_PRUPE)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			PTHR11206:SF198 (PANTHER): PTHI	0,021	0,018	0,000	0,000	0,000									
Solyc03g118960	Protein DETOXIFICATION (AHRD V3.3 *** K4BM46_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): PTHR11206 (PAI	0,134	0,269	0,000	0,000	0,047									
Solyc03g118970	Protein DETOXIFICATION (AHRD V3.3 *** K4BM46_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	46,042	62,308	12,069	8,676	12,319									
Solyc03g118990	Elongation factor 1 alpha (AHRD V3.3 *-* A0A1B2LUN9_9CARY)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): G3DS	0,178	0,224	0,511	0,358	0,470									
Solyc03g118995	Elongation factor 1 alpha (AHRD V3.3 *-* A0A1B2LUN9_9CARY),Pfam:PF00009		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0(	2,397	1,943	3,086	3,377	3,180									
Solyc03g119010	Pre-mRNA-splicing factor SPF27 (AHRD V3.3 *** A0A151TKA6_CAJCA)		P:GO:0006397	P:mRNA processing			IPR008409 (PFAM): IPR008409 (PAN	75,579	66,439	60,000	58,941	52,292									
Solyc03g119020	regulatory protein (NPR1) (AHRD V3.3 --* AT1G64280.1)							0,061	0,000	0,047	0,000	0,000									
Solyc03g119030	Peroxin-3 (AHRD V3.3 *-* A0A103Y8T9_CYNCS)		C:GO:0016021	C:integral component of membrane				8,258	9,370	10,774	11,822	10,712									
Solyc03g119035	peroxin 3 (AHRD V3.3 *-* AT1G48635.2)		C:GO:0005779; P:G(	C:integral component of peroxisomal membrane; P:peroxisome			IPR006966 (PFAM): IPR006966 (PAN	12,615	12,720	14,538	15,151	16,222									
Solyc03g119040	LeArcA2 protein containing 7 WD40 repeats	arca2	F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	131,626	148,410	119,656	98,404	105,648									
Solyc03g119050	MYB family protein (AHRD V3.3 *-* A0A067L078_JATCU)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	16,688	16,894	13,353	11,354	12,172									
Solyc03g119060	divaricata	div	F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR019791 (PFAM): IPR037120 (G3D	158,058	160,399	56,869	45,509	66,702									
Solyc03g119070	LOW QUALITY:Flap endonuclease 1 (AHRD V3.3 *** A0A0K9P479_ZOSMR)		F:GO:0003677; F:G(	F:DNA binding; F:nuclease activity; P:DNA repair			IPR006084 (PRINTS): IPR008918 (SM	0,760	0,549	0,071	0,069	0,093									
Solyc03g119080	beta-mannosidase enzyme		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS): G3DSA:3.20.2(	122,311	138,332	210,982	208,514	209,908									
Solyc03g119090	WD repeat-containing protein 1 (AHRD V1 ***- B5X1Z0_SALSA)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	84,059	80,564	121,375	122,757	108,267									
Solyc03g119100	FLOWERING LOCUS T/ TERMINAL FLOWER 1-like protein (AHRD V3.3 *** Q6L5N9_POPNI)		C:GO:0005634; P:G(	C:nucleus; P:response to abscisic acid; P:positive regulation of			IPR008914 (PFAM): IPR036610 (G3D	3,562	2,427	0,049	0,126	0,000									
Solyc03g119110	Transmembrane protein, putative (AHRD V3.3 *** Q1SN14_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR34056:SF1 (PANTHER): IPR040	8,412	8,052	1,986	3,043	3,360									
Solyc03g119120	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2QPN9_GLYSO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (TIGF	3,983	4,572	3,532	3,410	3,930									
Solyc03g119130	Histone H1 (AHRD V3.3 *-* A0A151TEL4_CAJCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assen			IPR017956 (PRINTS): IPR017956 (SM	136,507	163,254	179,027	165,959	162,768									
Solyc03g119140	MAP kinase kinase kinase 30	MAPKKK30	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): PF14381 (PFAM	47,938	45,720	23,216	25,898	25,593									
Solyc03g119150	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 *** AT1G18170.1)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer:	G3DSA:3.10.50.40 (GENE3D): IPR00'	1,925	3,671	0,998	1,033	3,382			1,736	0,000				up	
Solyc03g119160	Ribosomal protein S24/S35, mitochondrial (AHRD V3.3 *-* A0A061F6N1_THECC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:mitochondrion; P:mitoch			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,096	7,916	7,923	8,145	6,944									
Solyc03g119170	Ribosomal protein S24/S35, mitochondrial (AHRD V3.3 *** A0A061F6N1_THECC)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:mitochondrial translation			IPR019349 (PFAM): G3DSA:3.30.160	37,198	40,092	44,736	41,666	40,647									
Solyc03g119180	LOW QUALITY:Lysine--tRNA ligase (AHRD V3.3 --* V7B2W1_PHAVU)						PTHR37199:SF2 (PANTHER): PTHR3'	0,363	0,308	0,022	0,000	0,000									
Solyc03g119190	Reticulon-like protein (AHRD V3.3 *** K4BM68_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994 (PAI	0,220	0,211	0,025	0,047	0,024									
Solyc03g119200	L-Ala-D/L-Glu epimerase (AHRD V3.3 *** A0A061FV22_THECC)		F:GO:0016855	F:racemase and epimerase activity, acting on amino acids and			IPR013342 (SMART): IPR029017 (G3	20,820	29,823	10,714	11,217	19,333			0,848	0,000				up	
Solyc03g119210	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)		P:GO:0006869	P:lipid transport			IPR016140 (SMART): G3DSA:1.10.11	3,208	10,046	0,583	0,713	2,476	1,671	0,000	2,069	0,000			up	up	
Solyc03g119220	Kinesin-like protein (AHRD V3.3 *** K4BM71_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,768	0,816	0,093	0,174	0,281									
Solyc03g119230	Kinase superfamily protein (AHRD V3.3 *** A0A061G213_THECC)		F:GO:0030247	F:polysaccharide binding			IPR025287 (PFAM): IPR032872 (PFA	0,664	1,084	0,883	1,348	1,221									
Solyc03g119240	Protein kinase family protein (AHRD V3.3 *** AT5G38210.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR032872 (PF	2,293	4,450	4,162	5,138	4,731									
Solyc03g119250	Calmodulin binding protein-like, putative (AHRD V3.3 *** A0A061G202_THECC)		F:GO:0005516	F:calmodulin binding			IPR012416 (PFAM): mobidb-lite (MOB	372,776	343,226	50,161	96,886	111,012			1,143	0,006	0,949	0,003		up	up
Solyc03g119260	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *-* AT1G68390.1)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR31042:SF7	0,056	0,019	0,097	0,097	0,047									
Solyc03g119270	AP-3 complex subunit delta (AHRD V3.3 *** K4BM76_SOLLC)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR002553 (PFAM): IPR011989 (G3D	27,652	27,082	38,826	37,894	36,982									
Solyc03g119280	Histidyl-tRNA synthetase, putative (AHRD V3.3 *** B9S0H3_RICCO)		F:GO:0004821; F:G(	F:histidine-tRNA lig:	EC:6.1.1.21	Histidine--tRNA ligas	IPR004516 (PIRSF): IPR015807 (TIGI	15,706	18,779	34,482	37,296	37,876									
Solyc03g119290	Elongation factor 1-alpha, putative (AHRD V3.3 *** B9SPP6_RICCO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004160 (PF	52,343	50,765	59,835	58,221	58,156									
Solyc03g119300	Zinc finger protein, putative (AHRD V3.3 *-* B9SLY6_RICCO)		F:GO:0005506; C:G(	F:iron ion binding; C:nucleus; F:zinc ion binding; P:cellular respo			IPR012312 (PFAM): G3DSA:1.20.120	1,497	1,161	1,134	1,442	1,458									
Solyc03g119305	zinc finger protein-like protein (AHRD V3.3 *** AT3G18290.1)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	11,278	8,846	8,996	10,790	13,162			0,544	0,029				up	
Solyc03g119310	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 --* RBL_ANTLU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	23,829	23,619	9,409	8,162	9,358									
Solyc03g119320	LOW QUALITY:membrane-associated kinase regulator (AHRD V3.3 *** AT1G67050.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,774	3,500	0,838	0,899	1,152									
Solyc03g119330	AMSH-like ubiquitin thioesterase 1 (AHRD V3.3 *** A0A0B2QJP6_GLYSO)		F:GO:0005515	F:protein binding			IPR000555 (SMART): IPR015063 (PF	30,660	29,211	43,836	46,358	42,119									
Solyc03g119340	Cysteine-rich RLK 29 isoform 1 (AHRD V3.3 *** A0A061FUX1_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	9,696	7,177	4,643	5,363	5,300									
Solyc03g119350	peptidase M50B-like protein (AHRD V3.3 *-* AT1G67060.1)		C:GO:0016021	C:integral component of membrane			PF13398 (PFAM): PTHR33979:SF3 (F	0,248	0,162	0,000	0,000	0,000									
Solyc03g119360	40S ribosomal protein S7-like protein (AHRD V3.3 *** Q3HRX6_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000554 (PFAM): IPR000554 (PAN	174,865	201,319	171,484	150,483	157,187									
Solyc03g119370	R2R3MYB transcription factor 62	R2R3MYB62	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,178	0,293	0,294	0,169	0,327									
Solyc03g119380	50S ribosomal protein L14 (AHRD V3.3 *** A0A1D1Y377_9ARAE)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR000218 (SMART): IPR000218 (PF	37,883	44,232	38,255	33,739	35,909									
Solyc03g119390	bHLH transcription factor 026		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,195	0,525	0,267	0,199	0,210									
Solyc03g119400	heat-inducible transcription repressor (DUF639) (AHRD V3.3 *** AT1G48840.1)		C:GO:0016021	C:integral component of membrane			IPR006927 (PFAM): PTHR31860:SF6	59,455	42,808	54,002	57,212	53,934									
Solyc03g119410	LOW QUALITY:VQ motif-containing family protein (AHRD V3.3 *** B9I2L4_POPTR)		P:GO:0006952	P:defense response			IPR008889 (PFAM): IPR039607 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc03g119420	Anamorsin homolog (AHRD V3.3 *** K4BM91_SOLLC)		C:GO:0005737; P:G(	C:cytoplasm; P:iron-sulfur cluster assembly; F:iron-sulfur cluster			G3DSA:3.40.50.150 (GENE3D): IPR0(	15,029	18,350	23,456	23,725	21,346									
Solyc03g119430	Zinc finger transcription factor 30	C3H30	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000571 (SMART): IPR000504 (SM	6,367	5,863	8,021	7,743	8,309									
Solyc03g119440	C2 domain-containing family protein (AHRD V3.3 *** B9IE39_POPTR)		F:GO:0008289	F:lipid binding			IPR000008 (SMART): IPR000008 (PF	23,973	26,783	27,907	29,569	32,513									
Solyc03g119450	Chloroplastic group IIA intron splicing facilitator CRS1 (AHRD V3.3 *** W9QX15_9ROSA)		F:GO:0003723	F:RNA binding			IPR001890 (SMART): IPR035920 (G3	32,110	34,253	55,135	55,312	60,439									
Solyc03g119460	Cleavage stimulation factor subunit 2 (AHRD V3.3 *** A0A0B0MYT9_GOSAR)		P:GO:0031124	P:mRNA 3'-end processing			IPR025742 (PFAM): IPR038192 (G3D	113,129	84,423	84,894	73,898	83,245									
Solyc03g119470	DUF1666 family protein (AHRD V3.3 *** G7KN40_MEDTR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM): mobidb-lite (MOB	0,042	0,099	0,000	0,025	0,000									
Solyc03g119475	Cysteine-rich receptor-like protein kinase 28 (AHRD V3.3 --* CRK28_ARATH)							0,079	0,153	0,000	0,000	0,094									
Solyc03g119480	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)						PTHR33384:SF1 (PANTHER): PTHR3:	16,360	11,732	9,367	8,395	8,863									
Solyc03g119490	MAP kinase kinase 3	MAPKK3	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	3,600	5,672	1,271	0,678	1,434									
Solyc03g119500	LOW QUALITY:F-box/LRR protein, putative (AHRD V3.3 --* G7JVM8_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR032675 (G3	0,000	0,000	0,025	0,000	0,000									
Solyc03g119510	ATP synthase subunit B (AHRD V3.3 --* AT5G10320.6)							0,580	0,432	0,438	0,394	0,567									
Solyc03g119520	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)						PTHR33384:SF1 (PANTHER): PTHR3:	51,580	43,623	35,667	30,821	35,642									
Solyc03g119530	LOB domain protein 40 (AHRD V3.3 *** K7VSW9_SOLTU)						IPR004883 (PFAM LBD	211,939	190,928	255,191	169,591	163,928			-0,641	0,000	-0,587	0,000		down	down
Solyc03g119540	CONSTANS-like zinc finger protein (AHRD V3.3 *** I1LEW9_SOYBN)	BBX14	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR000315 (SMAF CO-like	16,710	18,230	3,176	1,552	3,709									
Solyc03g119550	LysM domain GPI-anchored protein 1, putative (AHRD V3.3 *** B9T592_RICCO)						IPR018392 (SMART): IPR018392 (PF	0,000	0,000	0,022	0,000	0,000									
Solyc03g119570	Carbon catabolite repressor-like protein (AHRD V3.3 *** A0A072UBP6_MEDTR)						IPR005135 (PFAM): mobidb-lite (MOB	6,733	6,553	3,797	4,277	4,269									
Solyc03g119590	LOW QUALITY:NIMIN2c protein (AHRD V3.3 *** A0FJY4_TOBAC)		P:GO:0010112	P:regulation of systemic acquired resistance			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,094	0,632	0,000	0,225	0,186									
Solyc03g119600	LOW QUALITY:NIMIN2b protein (AHRD V3.3 *** Q0MR95_TOBAC)		P:GO:0010112	P:regulation of systemic acquired resistance			mobidb-lite (MOBIDB_LITE): mobidb-lit	47,954	37,472	14,659	14,571	16,393									
Solyc03g119610	LOW QUALITY:ATP synthase subunit alpha, chloroplastic (AHRD V3.3 --* ATPA_SOLTU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	85,640	127,075	23,477	26,712	18,672	0,597	0,029					up		
Solyc03g119620	LOW QUALITY:Lipid transfer protein (AHRD V3.3 *-* A0A072VQ00_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	0,040	0,000	0,000	0,000	0,000									
Solyc03g119630	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 --* AT5G24580.4)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): PTHF	0,328	0,374	0,435	0,481	0,400									
Solyc03g119640	Aluminum-activated malate transporter-like (AHRD V3.3 *** K4BMB3_SOLLC)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): mobidb-lite (MOB	50,621	33,647	14,184	19,862	19,732									
Solyc03g119650	stomatal cytokinesis defective / SCD1 protein (SCD1) (AHRD V3.3 *** AT1G49040.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001194 (SM	205,798	160,733	176,639	163,246	186,144									
Solyc03g119660	Plant cadmium resistance 2 (AHRD V3.3 *-* A0A0K9PLA8_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR006461 (TIGRFAM): IPR006461 (F	0,122	1,770	0,147	0,050	0,142	3,794	0,000					up		
Solyc03g119670	Protein CASP (AHRD V3.3 *-* CASP_ARATH)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; P:intra-Golgi vesicle-media			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,386	2,017	1,964	1,986	2,137									
Solyc03g119700	ATP-dependent Clp protease adaptor protein ClpS (AHRD V3.3 *** G7JYE1_MEDTR)		P:GO:0030163	P:protein catabolic process			IPR014719 (G3DSA:3.30.1390.GENE	46,589	48,637	44,803	40,158	53,739									
Solyc03g119710	Carbon catabolite repressor-like protein (AHRD V3.3 *** G7L904_MEDTR)						IPR005135 (PFAM): PTHR12121:SF4	18,652	20,349	16,237	15,882	19,448									
Solyc03g119720	Lipase family protein (AHRD V3.3 *** B9I2Q8_POPTR)		P:GO:0006629	P:lipid metabolic process			IPR006693 (PFAM): IPR029058 (G3D	42,012	42,713	57,757	60,501	51,459									
Solyc03g119725	ATP-dependent helicase/nuclease subunit A isoform 1 (AHRD V3.3 *-* A0A061G1N6_THECC)		C:GO:0016021	C:integral component of membrane				11,199	9,050	15,209	12,094	12,278									
Solyc03g119730	Histone deacetylase (AHRD V3.3 *** A0A023IUN7_ARAHY)		C:GO:0005634; P:G(	C:nucleus; P:DNA n	EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS): IPR037138 (G3	20,172	20,255	18,269	17,627	16,390									
Solyc03g119740	MYB-like transcription factor family protein (AHRD V3.3 *** A0A072USM0_MEDTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	15,616	18,339	31,388	29,391	27,481									
Solyc03g119750	TESMIN/TSO1-like CXC 2 (AHRD V3.3 --* AT4G14770.3)		F:GO:0017112	F:Rab guanyl-nucleotide exchange factor activity				4,042	4,476	3,212	2,920	3,558									
Solyc03g119755	Protein FAM116A (AHRD V3.3 *** A0A0B2PMT6_GLYSO)		F:GO:0017112	F:Rab guanyl-nucleotide exchange factor activity			PF08616 (PFAM): IPR024224 (PANTH	20,736	17,220	9,404	8,758	9,500									
Solyc03g119760	Transmembrane Fragile-X-F-associated protein (AHRD V3.3 *** AT1G18470.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	21,093	17,209	19,719	20,836	20,866									
Solyc03g119780	Transcription initiation factor TFIID subunit 2 (AHRD V3.3 *** W9SEB8_9ROSA)		C:GO:0005669; F:G(	C:transcription factor TFIID complex; F:metallopeptidase activit			G3DSA:1.10.390.60 (GENE3D): IPR0'	78,269	66,615	65,860	68,375	70,194									
Solyc03g119790	Transcription initiation factor IIE alpha subunit family protein (AHRD V3.3 *** B9N8Y4_POPTR)		P:GO:0006367; F:G(	P:transcription initiation from RNA polymerase II promoter; F:se			IPR002853 (SMART): IPR013083 (G3	60,964	57,654	59,945	53,617	56,194									
Solyc03g119800	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9R099_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,019	0,000	0,025	0,000	0,000									
Solyc03g119810	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7JT03_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR332	1,870	3,239	0,498	0,535	0,658									
Solyc03g119820	Oleosin family protein (AHRD V3.3 *** A0A061FVM3_THECC)		C:GO:0012511; C:G(	C:monolayer-surrounded lipid storage body; C:integral compone			IPR000136 (PFAM): mobidb-lite (MOB	1,269	1,598	0,170	0,700	0,093									
Solyc03g119830	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061G1J7_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR019050 (SMART): IPR003656 (SM	4,262	3,608	5,975	5,770	5,056									
Solyc03g119840	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G48960.1)						IPR006016 (PFAM): IPR014729 (G3D	0,078	0,140	0,050	0,124	0,094									
Solyc03g119850	Decapping 5-like, putative isoform 5 (AHRD V3.3 *-* A0A061GEA8_THECC)						IPR019050 (SMART): IPR025609 (SM	0,115	0,018	0,000	0,000	0,046									
Solyc03g119860	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** G7JRX9_MEDTR)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PFAM): mobidb-lite (MOB	0,080	0,039	0,087	0,098	0,071									
Solyc03g119870	C3HC zinc finger-like protein (AHRD V3.3 *** AT1G48950.1)		C:GO:0005634; F:G(	C:nucleus; F:zinc ion binding			IPR012935 (PFAM): mobidb-lite (MOB	5,532	4,778	6,963	7,274	6,377									
Solyc03g119880	Early nodulin-like protein (AHRD V3.3 *** G7JR03_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	0,094	0,215	0,022	0,025	0,000									
Solyc03g119890	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** G7IHX4_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR032675 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc03g119900	neurogenic locus notch-like protein (AHRD V3.3 *-* AT4G14746.1)						PTHR33881:SF2 (PANTHER): PTHR3:	0,568	0,304	0,000	0,000	0,000									
Solyc03g119910	Le3OH-23b-hydroxylase	3oh2	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	0,059	0,236	0,000	0,025	0,000									
Solyc03g119920	LOW QUALITY:Cytochrome b559 subunit alpha (AHRD V3.3 --* PSBE_ADICA)		C:GO:0016021	C:integral component of membrane			IPR021319 (PFAM): PTHR33389:SF4	21,432	17,205	15,080	13,589	14,899									
Solyc03g119930	Sulfate transporter, putative (AHRD V3.3 *** B9RUY1_RICCO)		F:GO:0015098; P:G(	F:molybdate ion transmembrane transporter activity; P:molybda			IPR031563 (PFAM): IPR031563 (PAN	36,684	28,769	7,630	5,942	8,426									
Solyc03g119940	MJK13.21 protein (AHRD V3.3 *** G7IMF6_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,910	1,060	0,570	0,591	0,896									
Solyc03g119970	ATP/ADP transporter (AHRD V3.3 *** A0A0X9Q301_MENSP)		F:GO:0005471; P:G(	F:ATP:ADP antiporter activity; P:nucleotide transport; C:integral			IPR004667 (TIGRFAM): IPR004667 (I	6,878	6,644	11,332	10,024	10,585									
Solyc03g119980	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G11090.1)		F:GO:0003846; F:G(	F:2-acylglycerol O-:	EC:3.1.1.5; EC:2.3.1	Lysophospholipase;	IPR022742 (PFAM): IPR029058 (G3D	17,859	14,316	26,272	24,384	24,679									
Solyc03g119990	Alpha/beta hydrolase-like (AHRD V3.3 *** A0A0K9P0U5_ZOSMR)		F:GO:0003824; C:G(	F:catalytic activity; C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	1,570	1,214	0,269	0,444	0,899									
Solyc03g120000	RING/U-box superfamily protein (AHRD V3.3 --* AT1G72220.1)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:ubiquitin-protein transferase activi			IPR001607 (SMART): IPR001841 (SM	0,218	0,237	0,485	0,522	0,282									
Solyc03g120010	Eukaryotic translation initiation factor 3 subunit I (AHRD V3.3 *** A0A0K9NVH2_ZOSMR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR001680 (SMART): IPR013083 (G3	198,042	200,203	191,360	165,841	167,970									
Solyc03g120020	Boron transporter, putative (AHRD V3.3 *** A0A061G9M0_THECC)		F:GO:0005452; P:G(	F:inorganic anion exchanger activity; P:anion transport; C:integ			IPR011531 (PFAM): PTHR11453:SF4	0,000	0,341	0,121	0,153	0,000									
Solyc03g120040	transmembrane protein, putative (Protein of unknown function, DUF642) (AHRD V3.3 *** AT5G11420.1)						IPR006946 (PFAM): PTHR31265 (PAI	0,141	0,244	0,223	0,215	0,117									
Solyc03g120050	Elongation factor Tu, chloroplastic (AHRD V3.3 --* EFTU_CHLAT)							0,675	0,584	0,584	0,644	0,588									
Solyc03g120060	castasterone 26-hydroxylase	CYP734A7	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	1,984	1,994	0,481	1,472	0,988									
Solyc03g120070	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5FID5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:protein binding; F:oxidoreductase activity, a			IPR011990 (G3DSA:1.25.40.GENE3D	3,882	2,417	1,986	2,674	2,844									
Solyc03g120080	WD40 repeat-like protein (AHRD V3.3 *** I0YM64_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	18,983	21,243	13,190	12,944	13,335									
Solyc03g120090	Pyridoxin biosynthesis protein PDX1, putative (AHRD V3.3 *** B9RQN9_RICCO)		F:GO:0003824; P:G(	F:catalytic activity; P:pyridoxal phosphate biosynthetic process			IPR001852 (PIRSF): IPR013785 (G3D	59,724	60,415	60,283	61,589	58,936									

Solyc03g120100	Mitochondrial carrier protein (AHRD V3.3 *** A0A0K9PC13_ZOSMR)		F:GO:0022857: P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR018108 (PF	1,153	1,131	1,199	1,026	1,178									
Solyc03g120110	Serine/threonine-protein kinase (AHRD V3.3 *** A0A178VFP7_ARATH)		F:GO:0004674: F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	0,379	1,504	1,895	1,991	4,159			1,131	0,036				up	
Solyc03g120120	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061GBK3_THECC)		P:GO:0015031	P:protein transport			G3DSA:1.20.1260.60 (GENE3D): IPR(	10,481	6,187	5,593	7,478	6,814									
Solyc03g120130	Methyltransferase family protein, putative (AHRD V3.3 *** A0A061GCA1_THECC)		P:GO:0006479: F:G(	P:protein methylation; F:protein methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	10,973	9,817	10,915	10,508	9,577									
Solyc03g120140	BZIP protein (AHRD V3.3 *** G7II39_MEDTR)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM): IPR006868 (PFA	42,919	46,907	85,427	86,903	74,274									
Solyc03g120150	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT4G13270.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	19,485	11,664	44,751	49,120	41,086	-0,710	0,010					down		
Solyc03g120160	serine-rich protein-like protein (AHRD V3.3 --* AT5G55980.1)		P:GO:0008150	P:biological_process			PTHR33132:SF10 (PANTHER): PTHR	2,365	1,335	0,336	1,012	0,583									
Solyc03g120170	NHL domain-containing protein, putative (AHRD V3.3 --* A0A061EBN2_THECC)						PTHR33168:SF6 (PANTHER): PTHR3	1,220	1,359	0,473	0,581	0,495									
Solyc03g120175	serine-rich protein-like protein (AHRD V3.3 --* AT5G55980.1)						PTHR33132 (PANTHER): PTHR33132	0,555	0,378	0,094	0,150	0,188									
Solyc03g120180	Transmembrane protein, putative (AHRD V3.3 *** G7JJB2_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35469:SF3 (PANTHER): PTHR3	0,084	0,258	0,049	0,000	0,024									
Solyc03g120190	ovate family protein 7	OFP7	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (PFAM): IPR006458 (TIGF	0,401	0,303	0,049	0,025	0,093									
Solyc03g120200	RNA helicase DEAH-box11	DEAH11	F:GO:0003677: F:G(	F:DNA binding; F:A	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR006554 (SMART): IPR006555 (SM	16,710	15,142	16,270	17,172	18,039									
Solyc03g120210	LOW QUALITY:Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 --* A0A061GBF7_THECC)						IPR007650 (PFAM): mobidb-lite (MOB	0,975	0,310	0,000	0,075	0,000									
Solyc03g120230	MAR-binding filament-like protein 1 (AHRD V3.3 *** MFP1_SOLLC)		F:GO:0003677: C:G(	F:DNA binding; C:nuclear matrix			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,038	14,533	13,448	13,201	15,368									
Solyc03g120240	Protein SYS1 (AHRD V3.3 *** B4FDL6_MAIZE)		C:GO:0000139	C:Golgi membrane			IPR019185 (PFAM): IPR016973 (PIRS	22,239	20,752	28,532	28,729	25,865									
Solyc03g120250	Sulfate transporter, putative (AHRD V3.3 *** B9SQC2_RICCO)		F:GO:0008271: P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR001902 (TIGRFAM): IPR036513 ((	0,021	0,021	0,025	0,000	0,000									
Solyc03g120260	Coatomer beta subunit, putative (AHRD V3.3 *-* B9SQC0_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	2,338	20,024	4,274	12,418	10,148	3,114	0,000	1,236	0,044	1,529	0,000	up	up	up
Solyc03g120270	Coatomer beta subunit, putative (AHRD V3.3 *** B9SQC0_RICCO)		F:GO:0005198: F:G(	F:structural molecule activity; F:protein binding; P:intracellular p			IPR020472 (PRINTS): IPR001680 (SM	202,323	197,587	200,321	185,730	186,532									
Solyc03g120280	Ran-binding protein 1 domain-containing (AHRD V3.3 *** B9GEK5_POPTR)		C:GO:0005643: P:G(	C:nuclear pore; P:intracellular transport			IPR000156 (SMART): IPR015007 (PF	88,446	92,125	91,445	81,774	82,294									
Solyc03g120290	thionin-like protein (AHRD V3.3 *** AT1G12663.1)		C:GO:0016021	C:integral component of membrane			PTHR36312:SF1 (PANTHER): IPR038	1,451	1,593	0,137	0,101	0,047									
Solyc03g120300	CASC3/barentsz eIF4AIII-binding protein (AHRD V3.3 *** A0A072UG99_MEDTR)						IPR018545 (SMART): IPR018545 (PF	75,274	73,508	94,288	81,509	82,025									
Solyc03g120310	Glycosyltransferase, putative (AHRD V3.3 *** B9SQA7_RICCO)		C:GO:0016021	C:integral component of membrane			IPR001296 (PFAM): PF16994 (PFAM)	69,682	47,622	63,445	55,941	50,603									
Solyc03g120320	F box kelch like protein (AHRD V3.3 *** A0A0B7NXR4_SOLLC)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR006652 (PF	0,000	0,000	0,000	0,025	0,023									
Solyc03g120330	F-box/kelch-repeat protein (AHRD V3.3 *** W9S4X9_9ROSA)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR006652 (PF	0,733	0,977	0,577	0,265	0,330									
Solyc03g120340	centromere protein C1	cenpc1	C:GO:0000776: F:G(	C:kinetochore; F:centromeric DNA binding; P:kinetochore asser			mobidb-lite (MOBIDB_LITE): mobidb-lit	20,057	17,066	11,575	11,456	12,394									
Solyc03g120350	N-alpha-acetyltransferase 16, NatA auxiliary subunit (AHRD V3.3 *** A0A0B2P106_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): G3DSA:1.25.40	103,803	98,186	113,840	114,157	107,195									
Solyc03g120360	LOW QUALITY:phospholipase-like protein (PEARLI 4) family protein (AHRD V3.3 *-* AT2G16900.6)						IPR007942 (PFAM): mobidb-lite (MOB	0,077	0,076	0,507	0,980	0,426									
Solyc03g120370	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524: C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc03g120380	auxin-regulated IAA19	IAA19	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	18,199	25,818	0,025	0,000	0,000									
Solyc03g120390	Auxin responsive protein_IPR003311_AUX_IAA protein	IAA15	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	209,064	174,250	88,655	61,516	67,969			-0,386	0,015	-0,524	0,000		down	down
Solyc03g120410	Hypothetical conserved protein						PTHR35105:SF2 (PANTHER): PTHR3	8,888	10,526	1,287	1,110	1,338									
Solyc03g120420	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein (AHRD V3.3 --* AT3G14920.1)							0,528	0,408	1,051	0,702	0,751									
Solyc03g120430	D-glycerate 3-kinase (AHRD V3.3 *** G7IME0_MEDTR)		F:GO:0008887: C:G(	F:glycerate kinase a	EC:2.7.1.31	Glycerate 3-kinase	G3DSA:3.40.50.300 (GENE3D): PTHR	1,788	2,896	2,540	1,808	3,016									
Solyc03g120440	cyclin A2_1	CycA2_1	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	48,095	39,228	78,183	63,950	61,422									
Solyc03g120450	Aspartate aminotransferase (AHRD V3.3 *** W9S4V9_9ROSA)		F:GO:0003824: P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3	26,338	28,660	11,442	10,144	12,082									
Solyc03g120460	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151T2K6_CAJCA)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,016	7,788	6,537	6,754	7,069									
Solyc03g120470	tonoplast intrinsic protein 2.2	TIP2.2	P:GO:0008033	P:tRNA processing			IPR027794 (PFAM): IPR036866 (G3D	21,446	22,536	30,023	30,014	31,813									
Solyc03g120475	Tonoplast intrinsic protein, putative (AHRD V3.3 *** B9RQI0_RICCO)		F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	3,235	7,072	1,985	0,972	1,153	1,150	0,002					up		
Solyc03g120480	Activating signal cointegrator 1 complex subunit 1 (AHRD V3.3 *** A0A0B2NTB9_GLYSO)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR036612 (G3	15,439	16,231	15,403	17,029	16,445									
Solyc03g120490	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** AT3G16200.1)		C:GO:0005768: C:G(	C:endosome; C:trans-Golgi network; C:integral component of m			G3DSA:3.40.50.150 (GENE3D): mobic	37,843	30,254	47,335	40,134	38,952									
Solyc03g120495	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT1G02840.5)							0,000	0,000	0,050	0,025	0,000									
Solyc03g120500	auxin-regulated IAA27	IAA27	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	49,409	48,090	21,226	16,662	18,537									
Solyc03g120520	Peroxisome biogenesis protein 2 (AHRD V3.3 *** A0A0B0MVT3_GOSAR)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	3,210	1,987	0,728	0,340	0,540									
Solyc03g120530	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT4G29100.1)		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	6,805	5,158	2,179	1,942	2,211									
Solyc03g120540	Isochorismatase hydrolase family protein (AHRD V3.3 *** F4YFC0_CAMSI)		F:GO:0003824	F:catalytic activity			IPR036380 (G3DSA:3.40.50.GENE3D	9,104	9,271	10,937	12,376	11,590									
Solyc03g120550	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	279,370	378,655	352,208	480,619	488,211									
Solyc03g120560	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	31,262	25,730	49,968	56,520	45,966									
Solyc03g120570	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,652	0,453	317,754	492,637	163,260			-0,964	0,011				down	
Solyc03g120580	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT4G20270.1)							2,411	1,642	2,203	2,380	1,606									
Solyc03g120590	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	0,121	0,021	0,075	0,047	0,023									
Solyc03g120600	Plant cadmium resistance 2 (AHRD V3.3 *** A0A0K9NVT8_ZOSMR)						IPR006461 (PFAM): IPR006461 (TIGF	0,000	0,079	0,000	0,000	0,071									
Solyc03g120610	Cytochrome c-type biogenesis CcmH (AHRD V3.3 *** A0A0B0PL66_GOSAR)		C:GO:0005743: P:G(	C:mitochondrial inner membrane; P:embryo development ending			IPR038297 (G3DSA:1.10.8.GENE3D):	9,040	7,584	13,104	11,104	11,046									
Solyc03g120620	Homeobox leucine zipper protein (AHRD V3.3 *** G7IUR3_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (SMAF HD-ZIP	32,112	36,054	9,167	9,069	11,222									
Solyc03g120630	ribosomal protein S17 (AHRD V3.3 *** AT1G79850.1)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000266 (PRINTS): G3DSA:2.40.50	51,917	89,323	42,686	49,650	68,621	0,810	0,004	0,683	0,000			up	up	
Solyc03g120640	Photosystem I reaction center subunit VI (AHRD V3.3 *** B7FN63_MEDTR)		C:GO:0009538: P:G(	C:photosystem I reaction center; P:photosynthesis			IPR004928 (PFAM): IPR023833 (TIGF	83,951	203,841	86,212	102,497	158,215	1,308	0,000	0,873	0,000			up	up	
Solyc03g120650	GDP-mannose pyrophosphorylase	GMP (VTC1)	F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.1310 (GENE3D): IPR(	0,098	0,138	0,072	0,217	0,333									
Solyc03g120660	Glyoxylate reductase (AHRD V3.3 *** A0A0B0MTB0_GOSAR)		F:GO:0016616: F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0(	0,912	1,089	0,125	0,050	0,119									
Solyc03g120670	Glyoxylate reductase (AHRD V3.3 *** A0A0B2P9G3_GLYSO)	HPPR1	F:GO:0016616: F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): G3DS	50,266	56,853	78,969	70,878	85,809									
Solyc03g120680	Glyoxylate reductase (AHRD V3.3 *** A0A1D1YDH1_9ARAE)		F:GO:0016616: F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0(	5,739	6,404	5,085	4,901	5,708									
Solyc03g120690	Dynein light chain family protein (AHRD V3.3 *** B9GXB1_POPTR)		P:GO:0007017: C:G(	P:microtubule-based process; C:dynein complex			IPR001372 (SMART): IPR037177 (G3	0,369	0,296	1,770	2,055	1,676									
Solyc03g120700	Vps51/Vps67 family (components of vesicular transport) protein (AHRD V3.3 *** AT5G16300.1)		P:GO:0006891: C:G(	P:intra-Golgi vesicle-mediated transport; C:Golgi transport com			PF08700 (PFAM): mobidb-lite (MOBID	53,881	51,124	88,612	91,685	81,189									
Solyc03g120710	Late embryogenesis abundant protein (AHRD V3.3 *** G7II20_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	225,353	151,328	112,121	80,941	99,470					-0,467	0,003			down
Solyc03g120720	Protein disulfide isomerase like protein (AHRD V3.3 *** C4T847_SOYBN)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	52,860	54,285	156,411	165,138	147,609									
Solyc03g120730	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM): PTHR14255:SF6	28,378	29,659	49,351	62,584	45,016									
Solyc03g120740	LOW QUALITY:At1g15230/F9L1_18 (AHRD V3.3 *** Q9XI45_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,198	12,486	12,889	12,313	9,407									
Solyc03g120750	Rab family GTPase (AHRD V3.3 *** D8RRT7_SELML)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	25,081	24,808	45,597	45,556	42,904									
Solyc03g120760	Receptor-like kinase (AHRD V3.3 *** G7KPX0_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	17,037	14,508	11,772	11,304	12,565									
Solyc03g120770	Phox-associated domain,Phox-like,Sorting nexin isoform 1 (AHRD V3.3 *** A0A061GBL5_THECC)		F:GO:0035091	F:phosphatidylinositol binding			IPR001683 (SMART): IPR003114 (SM	35,874	47,311	23,414	21,673	25,209									
Solyc03g120780	Ribosomal protein L37 (AHRD V3.3 *** K4BMM7_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001569 (PFAM): IPR011331 (G3D	38,938	46,851	44,118	38,851	39,042									
Solyc03g120790	LOW QUALITY:ovate family protein 8	OFP8					PTHR35461 (PANTHER): PTHR35461	1,522	1,359	0,075	0,049	0,047									
Solyc03g120800	Peroxidase (AHRD V3.3 *-* K4BMM9_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PFAM): G3DSA:1.10.420	0,451	0,936	0,000	0,022	0,000									
Solyc03g120805	Peroxidase (AHRD V3.3 *** K4BMM9_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,121	0,287	0,000	0,000	0,023									
Solyc03g120810	Kinesin-like protein (AHRD V3.3 *** K4BMN0_SOLLC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	21,113	28,995	14,149	12,973	13,812									
Solyc03g120820	Cytochrome c oxidase assembly protein COX19, putative (AHRD V3.3 *-* B9RQH5_RICCO)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,984	7,634	9,032	7,240	7,051									
Solyc03g120830	transmembrane protein (AHRD V3.3 *** AT1G52155.1)		C:GO:0016021	C:integral component of membrane			PTHR21229:SF51 (PANTHER): IPR00	0,118	0,041	0,125	0,073	0,165									
Solyc03g120840	ethylene-responsive transcription factor (AHRD V3.3 *-* AT5G07580.1)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRINT ERF	1,831	2,488	2,725	1,796	2,359									
Solyc03g120850	Chaperonin-60 beta subunit (AHRD V3.3 *** P93570_SOLTU)		F:GO:0005524: C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR002423 (PF	126,458	192,055	153,923	123,343	200,875	0,630	0,021	0,381	0,027			up	up	
Solyc03g120860	LOW QUALITY:Early nodulin-like protein (AHRD V3.3 *** A0A072U7R7_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	1,388	0,691	0,000	0,000	0,000									
Solyc03g120870	CASP-like protein (AHRD V3.3 *** K4BMN6_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 in			IPR006702 (PFAM): IPR006459 (TIGF	0,278	0,273	0,394	0,047	0,048									
Solyc03g120880	Nuclear pore complex protein NUP35 (AHRD V3.3 *** A0A0V0I4U8_SOLCH)		F:GO:0003676: P:G(	F:nucleic acid binding; P:nucleocytoplasmic transport; C:nuclear			IPR007846 (PFAM): IPR017389 (PIRS	117,079	87,181	85,810	71,939	74,876									
Solyc03g120885	Coiled-coil domain-containing protein 18, putative isoform 1 (AHRD V3.3 --* A0A061DKF7_THECC)						mobidb-lite (MOBIDB_LITE): PTHR348	0,192	0,076	0,000	0,000	0,000									
Solyc03g120890	GATA transcription factor (AHRD V3.3 *** K4BMN8_SOLLC)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ior			IPR000679 (SMAF GATA	15,030	11,022	3,126	3,042	3,875									
Solyc03g120900	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G01340.2)		F:GO:0005198: F:G(	F:structural molecule activity; F:protein binding; C:COPII vesicle			IPR001680 (SMART): IPR001680 (PF	4,982	4,218	15,139	20,639	16,455									
Solyc03g120910	Homeobox leucine-zipper protein (AHRD V3.3 *** Q76CL1_ZINVI)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (SMAF HD-ZIP	44,430	29,104	7,881	7,052	9,192									
Solyc03g120930	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)						IPR008480 (PFAM): mobidb-lite (MOB	2,446	1,919	5,667	6,691	6,499									
Solyc03g120940	Sequence-specific DNA-binding transcription factor (AHRD V3.3 *** A0A072TMY2_MEDTR)		F:GO:0003682	F:chromatin binding			G3DSA:2.40.50.40 (GENE3D): G3DS	81,744	71,130	80,373	76,960	78,341									
Solyc03g120950	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G44970.3)						PTHR36355 (PANTHER)	0,058	0,144	0,000	0,022	0,000									
Solyc03g120955	Protein STIG1 (AHRD V3.3 *-* STIG1_SOLLC)		C:GO:0048046	C:apoplast				0,021	0,021	0,000	0,000	0,000									
Solyc03g120980	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TSU1_ACAMN)	ABCG35	F:GO:0005524: C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013581 (PF	8,872	13,239	318,848	423,872	423,631									
Solyc03g120990	Malic enzyme (AHRD V3.3 *** M0ZRW2_SOLTU)		F:GO:0004471: F:G(	F:malate dehydroge	EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS): IPR012301 (SM	382,592	533,934	46,387	33,125	63,931									
Solyc03g121000	RNA polymerase II-associated factor 1 (AHRD V3.3 --* A0A0B0MF48_GOSAR)		F:GO:0005488: C:G(	F:binding; C:nucleus; P:nitrogen compound metabolic process; F			PR01217 (PRINTS): mobidb-lite (MOB	18,921	26,250	24,618	23,093	32,397									
Solyc03g121010	RNA polymerase II-associated factor 1 like (AHRD V3.3 *** A0A0B2S4P2_GLYSO)		P:GO:0006368: P:G(	P:transcription elongation from RNA polymerase II promoter; P:I			IPR007133 (PFAM): mobidb-lite (MOB	124,874	90,534	177,075	145,587	141,061									
Solyc03g121020	RNA polymerase II-associated factor 1 like (AHRD V3.3 *** A0A0B2S4P2_GLYSO)		P:GO:0006368: P:G(	P:transcription elongation from RNA polymerase II promoter; P:I			IPR007133 (PFAM): mobidb-lite (MOB	5,983	5,218	6,855	5,991	6,001									
Solyc03g121030	MMS19 nucleotide excision repair (AHRD V3.3 *** A0A0B0MQY6_GOSAR)		P:GO:0097428	P:protein maturation by iron-sulfur cluster transfer			IPR029240 (PFAM): IPR011989 (G3D	24,911	28,133	17,536	15,043	15,391									
Solyc03g121040	Clavaminate synthase-like protein (AHRD V3.3 *** W9REK5_9ROSA)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			G3DSA:3.60.130.10 (GENE3D): IPR0(	7,271	7,710	31,033	34,862	31,242									
Solyc03g121050	Lyk3 (AHRD V3.3 *** G3KGB0_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR018392 (SM	84,956	52,394	68,718	60,878	65,964	-0,669	0,009					down		
Solyc03g121060	auxin-regulated IAA26	IAA26	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	0,000	0,021	0,000	0,000	0,000									
Solyc03g121070	hexokinase	hxk1	P:GO:0001678: F:G(	P:cellular glucose h	EC:2.7.1.1	Hexokinase	PR00475 (PRINTS): IPR022673 (PFA	27,971	32,506	10,974	8,562	10,575									
Solyc03g121080	Syntaxin-124 protein (AHRD V3.3 *-* A0A0B0PZL0_GOSAR)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,155	0,215	0,000	0,050	0,047									
Solyc03g121100	Acid phosphatase-like protein 1 (AHRD V3.3 *** V9MHL3_9ROSA)		F:GO:0003993: P:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR005519 (PFAM): IPR023214 (G3D	0,077	0,178	0,093	0,000	0,069									
Solyc03g121110	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5FXJ6_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	15,410	13,428	15,149	14,084	13,719									
Solyc03g121120	DNA repair protein RadA-like protein (AHRD V3.3 *** AT5G50340.3)		F:GO:0003677: F:G(	F:DNA binding; F:A	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR01874 (PRINTS): IPR003593 (SMA	19,258	17,348	17,401	14,928	16,478									
Solyc03g121130	rRNA-processing FCF1 (AHRD V3.3 *** A0A0B0NCB3_GOSAR)		C:GO:0032040	C:small-subunit processome			IPR002716 (SMART): G3DSA:3.40.50	1,581	1,603	1,309	1,213	1,345									
Solyc03g121140	Protein CHUP1, chloroplastic (AHRD V3.3 *** A0A0B2P7K8_GLYSO)		C:GO:0032040	C:small-subunit processome			IPR002716 (SMART): G3DSA:3.40.50	0,218	0,424	1,468	3,519	1,865					1,264	0,014			up
Solyc03g121160	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** A0A061G0Z9_THECC)		F:GO:0005515	F:protein binding			IPR040338 (PANTHER): IPR001810 (I	0,000	0,000	0,000	0,025	0,024									
Solyc03g121170	GDSL esterase/lipase family (AHRD V3.3 *** A0A151TNI3_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,040	0,000	0,000	0,000	0,000									
Solyc03g121180	GDSL esterase/lipase family (AHRD V3.3 *** A0A151U1D5_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR001087 (PFA	83,057	69,571	1,713	2,562	0,745									
Solyc03g121190	transmembrane protein (AHRD V3.3 -** AT1G51920.1)		F:GO:0003674: P:G(	F:molecular_function; P:biological_process; C:integral compone			PTHR36328 (PANTHER)	0,058	0,575	0,025	0,000	0,000									
Solyc03g121200	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 --* A0A151QNQ1_CAJCA)							0,056	0,000	0,000	0,025	0,000									
Solyc03g121210	Mediator of RNA polymerase II transcription subunit 6 (AHRD V3.3 *** A0A0S2LKL8_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR038566 (G3DSA:3.10.450.GENE3	8,925	9,477	16,176	18,032	14,168									
Solyc03g121230	protein kinase family protein (AHRD V3.3 *** AT1G51870.2)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR024788 (PF	0,984	0,469	2,097	1,793	2,829									
Solyc03g121250	3'-5' exonuclease domain-containing family protein (AHRD V3.3 *** B9ING4_POPTR)		F:GO:0003723: P:G(	F:RNA binding; P:nucleobase-containing compound metabolic pr			IPR004087 (SMART): IPR002562 (SM	7,412	7,122	7,673	6,824	6,727									
Solyc03g121260	RNA methyltransferase family protein (AHRD V3.3 *** AT3G21300.1)		P:GO:0006396: F:G(	P:RNA processing; F:RNA methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): TIGR(	8,407	10,554	10,459	9,754	13,266									
Solyc03g121270	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9RQ74_RICCO)		F:GO:0016787	F:hydrolase activity			IPR011650 (PFAM): IPR002933 (PFA	105,052	56,753	78,067	66,547	69,068	-0,859	0,001					down		
Solyc03g121280	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT3G21310.3)		F:GO:0008375: C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR31042 (PAN	18,198	9,730	9,505	7,943	9,276	-0,873	0,001					down		
Solyc03g121290	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** G7IHX4_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	29,637	30,779	41,279	45,081	37,305									
Solyc03g121295	Mannose-binding lectin superfamily protein (AHRD V3.3 *** AT1G73040.1)		F:GO:0030246	F:carbohydrate binding			IPR001229 (SMART): IPR001229 (PF	22,954	26,680	29,930	39,576	38,160					0,408	0,033			up
Solyc03g121310	RWD domain-containing protein (AHRD V3.3 *** Q38HU0_SOLTU)		F:GO:0005515	F:protein binding			IPR006575 (SMART): IPR006575 (PF	172,501	164,504	165,337	131,283	139,583									
Solyc03g121320	Tudor/PWWP/MBT superfamily protein (AHRD V3.3 *** A0A072TXL6_MEDTR)						G3DSA:2.30.30.140 (GENE3D): IPR0(	21,819	19,188	19,667	18,642	18,586									
Solyc03g121330	60S ribosomal protein L28, putative (AHRD V3.3 *** B9RKC5_RICCO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.390.110 (GENE3D): IPR(	253,014	266,368	156,034	142,686	143,902									
Solyc03g121340	LOW QUALITY:isopentenyltransferase 5 (AHRD V3.3 --* AT5G19040.3)						PTHR36484 (PANTHER): PTHR36484	0,610	0,612	0,411	0,843	0,685									
Solyc03g121350	anoctamin-like protein (AHRD V3.3 *** AT1G73020.3)		C:GO:0016021	C:integral component of membrane			IPR007632 (PFAM): PTHR12308:SF7	7,341	5,241	0,363	1,504	0,678									
Solyc03g121360	Charged multivesicular body 1 (AHRD V3.3 *** A0A0B0N0L1_GOSAR)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): PTHR10476 (PAN	195,149	143,176	117,103	160,128	124,900									
Solyc03g121370	Ribosomal protein S8 (AHRD V3.3 *** A0A124SDM5_CYNCS)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.1490.10 (GENE3D): G3D	21,013	20,746	25,743	25,282	24,222									
Solyc03g121380	Dentin sialophosphoprotein-related, putative isoform 1 (AHRD V3.3 *** A0A061GCA0_THECC)						IPR010844 (PFAM): mobidb-lite (MOB	51,448	58,996	50,108	48,938	51,489									
Solyc03g121400	Dof zinc finger protein14	Dof14	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	20,375	11,482	15,287	41,649	28,190			0,878	0,000	1,445	0,000		up	up
Solyc03g121410	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B (AHRD V3.3 *** K4BMU0_SOLLC)		C:GO:0000159: F:G(	C:protein phosphatase type 2A complex; F:protein binding; F:pro			IPR000009 (PRINTS): IPR001680 (SM	27,731	26,357	38,284	39,582	36,622									
Solyc03g121420	Inorganic pyrophosphatase 2 (AHRD V3.3 *** A0A0B2S4R2_GLYSO)		F:GO:0016791	F:phosphatase activity			IPR023214 (G3DSA:3.40.50.GENE3D	1,251	0,993	2,836	2,474	2,555									
Solyc03g121430	Inorganic pyrophosphatase 2 (AHRD V3.3 *-* PPSP2_ARATH)		F:GO:0016791	F:phosphatase activity			IPR023214 (G3DSA:3.40.50.GENE3D	0,038	0,080	0,000	0,000	0,023									
Solyc03g121440	Kinase family protein (AHRD V3.3 *** U5GQI1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	18,244	11,752	7,645	6,330	7,422									
Solyc03g121450	RNA-binding family protein (AHRD V3.3 *** B9MWQ9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	22,341	22,526	23,519	20,814	21,018									
Solyc03g121470	Phospholipase D (AHRD V3.3 *** B9MWR1_POPTR)		F:GO:0004630: F:G(	F:phospholipase D a	EC:3.1.4.4	Phospholipase D	IPR001736 (SMART): IPR024632 (PF	1,447	1,420	1,794	1,359	1,533									
Solyc03g121480	Thioredoxin, putative (AHRD V3.3 *** B9RK57_RICCO)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D): IPR01	3,859	3,928	3,925	6,131	4,657									
Solyc03g121490	tubby like protein 6 (AHRD V3.3 --* AT1G47270.3)							6,072	6,820	8,778	7,055	6,924									
Solyc03g121500	Myosin-like protein (AHRD V3.3 *** G7ZWG9_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	17,492	19,897	26,584	23,964	23,167									
Solyc03g121505	SKU5 similar 1 (AHRD V3.3 --* AT4G25240.2)						mobidb-lite (MOBIDB_LITE)	0,603	0,519	1,070	0,565	0,591									
Solyc03g121520	WAS/WASL-interacting family protein (AHRD V3.3 *** AT1G55160.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR343	4,434	4,688	5,259	4,997	4,226									
Solyc03g121530	Ribonuclease III		F:GO:0004525: P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR000999 (PFAM): IPR036389 (G3D	8,579	14,797	17,260	17,207	19,588	0,812	0,024					up		
Solyc03g121540	beta-galactosidase 3	TBG3	F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): IPR008979 (G3	59,863	39,418	839,765	916,156	766,167									
Solyc03g121550	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G18750.1)							0,272	0,198	0,168	0,243	0,119									
Solyc03g121560	AT1G17665-like protein (AHRD V3.3 *** A0A0G4AP21_9ROSI)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,731	3,484	2,638	3,577	3,070									

Solyc03g121570	Transmembrane 9 superfamily member (AHRD V3.3 *** M0ZRA0_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): PTHR10766:SF8	0,740	0,515	0,735	0,841	0,825									
Solyc03g121580	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G19520.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	21,591	22,412	21,673	15,550	17,535					-0,475	0,023			down
Solyc03g121590	Protein ROOT HAIR DEFECTIVE 3 homolog (AHRD V3.3 *** K4BMV8_SOLLC)		F:GO:0005525	F:GTP binding			IPR008803 (PFAM): G3DSA:3.40.50.3	277,271	279,375	298,801	292,985	292,184									
Solyc03g121600	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G72970.1)		F:GO:0016614; F:GC	F:oxidoreductase activity, acting on CH-OH group of donors; F:			IPR000172 (PFAM): G3DSA:3.30.410	77,039	55,343	0,044	0,199	0,094									
Solyc03g121610	Protein kinase (AHRD V3.3 *** E5GCB1_CUCME)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0	36,599	23,593	10,757	8,028	10,432									
Solyc03g121630	Protein FAR1-RELATED SEQUENCE 4 (AHRD V3.3 *** W9QKD5_9ROSA)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	26,573	19,473	28,127	26,363	26,687									
Solyc03g121640	Chaperonin Cpn60 (AHRD V3.3 *** A0A124SDT3_CYNCS)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR001844 (TI	54,874	51,697	49,296	41,326	44,674									
Solyc03g121650	Agenet-like domain-containing protein (AHRD V3.3 *-* A0A103YNT6_CYNCS)						IPR014002 (SMART): IPR008395 (PF	14,161	11,538	12,898	11,668	13,097									
Solyc03g121660	Zinc finger family protein (AHRD V3.3 *** D7MN23_ARALL)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	73,464	87,411	89,317	110,407	105,353									
Solyc03g121670	Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 *** AT3G13800.4)		F:GO:0016787	F:hydrolase activity			IPR001279 (PFAM): PTHR42663:SF3	5,731	6,484	14,254	15,577	13,578									
Solyc03g121680	Cell wall invertase (AHRD V3.3 *** K4HUT0_MALDO)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001362 (SMART): IPR023296 (G3	0,076	0,116	0,000	0,025	0,000									
Solyc03g121700	Nucleosome assembly protein 1-like 1 (AHRD V3.3 *** A0A0B2RCF4_GLYSO)		C:GO:0005634; P:GC	C:nucleus; P:nucleosome assembly			G3DSA:3.30.1120.90 (GENE3D): IPR	85,181	85,951	86,816	71,317	72,248									
Solyc03g121710	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G17640.3)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	39,188	40,168	52,731	47,878	48,095									
Solyc03g121720	3-hydroxyisobutyrate dehydrogenase, putative (AHRD V3.3 *** B9S5X5_RICCO)		F:GO:0016491; F:GC	F:oxidoreductase activity; F:NADP binding; F:NAD binding; P:ox			G3DSA:3.40.50.720 (GENE3D): IPR0	17,490	31,300	11,294	11,561	16,210	0,867	0,012	0,521	0,043			up	up	
Solyc03g121730	5'-nucleotidase surE (AHRD V3.3 *** A0A0B0MS13_GOSAR)		F:GO:0008252	F:nucleotidase acti	EC:3.1.3.31	Nucleotidase	IPR002828 (PFAM): IPR036523 (G3D	45,426	43,385	47,099	47,373	49,499									
Solyc03g121760	SUN-like protein 11	SUN11	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR000048 (PF	0,079	0,246	0,000	0,000	0,000									
Solyc03g121770	calmodulin-binding family protein (AHRD V3.3 *** AT3G58480.1)						PTHR31250 (PANTHER): PTHR31250	0,060	0,039	0,047	0,022	0,024									
Solyc03g121780	LOW QUALITY:Kinase family protein (AHRD V3.3 *** B9IJN5_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	0,140	0,059	0,025	0,117	0,071									
Solyc03g121790	Epidermal patterning factor-like protein (AHRD V3.3 *** G7LI49_MEDTR)		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): IPR039455 (PANTH	0,863	0,703	0,824	0,631	0,779									
Solyc03g121800	copz1 nonclathrin coat protein zeta1-COP	copz1	P:GO:0006890; C:GC	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			G3DSA:3.30.450.60 (GENE3D): IPR0	12,017	13,334	12,240	11,790	10,733									
Solyc03g121810	Phospholipid-transporting ATPase (AHRD V3.3 *** M0ZRQ8_SOLTU)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): PF13246 (PFAM)	0,624	0,383	0,000	0,025	0,024									
Solyc03g121820	Casein kinase, putative (AHRD V3.3 *** B9S5V9_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	144,885	122,433	132,492	128,640	121,205									
Solyc03g121830	Glycylpeptide N-tetradecanoyltransferase (AHRD V3.3 *** K4BMY2_SOLLC)		F:GO:0004379; P:GC	F:glycylpeptide N-te	EC:2.3.1.97	Glycylpeptide N-tetra	IPR000903 (PIRSF): G3DSA:3.40.630	39,812	43,575	46,381	42,724	41,378									
Solyc03g121840	MYB transcription factor (AHRD V3.3 *** E5GB88_CUCME)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR001005 (SMAF MYB_related	19,776	14,825	61,477	59,644	54,080									
Solyc03g121850	DNA gyrase subunit B (AHRD V3.3 *-* A0A1D1ZIS3_9ARAE)						PTHR33913 (PANTHER): SSF54768 (	29,183	26,714	27,453	25,799	27,712									
Solyc03g121860	Mitochondrial import inner membrane translocase subunit tim23 (AHRD V3.3 *** A0A0K9Q5U7_ZOSMR)		C:GO:0005744; F:GC	C:TIM23 mitochondrial import inner membrane translocase com			PF02466 (PFAM): mobidb-lite (MOBID	127,445	121,432	107,823	95,135	91,048									
Solyc03g121870	Methyltransferase-like protein (AHRD V3.3 *** A0A103XXH9_CYNCS)		F:GO:0008168; P:GC	F:methyltransferase activity; P:methylation			IPR026113 (PIRSF): PF13489 (PFAM	0,610	1,088	0,262	0,117	0,235									
Solyc03g121880	Protein phosphatase 2c, putative (AHRD V3.3 *** B9S5U9_RICCO)		F:GO:0004722; P:GC	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART): IPR036457 (G3	99,581	95,773	166,554	160,788	156,039									
Solyc03g121890	LOW QUALITY:Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *** A0A061GCS5_THE		C:GO:0005634; C:GC	C:nucleus; C:cytosol; C:plasma membrane; C:integral componen			IPR008480 (PFAM): mobidb-lite (MOB	54,848	29,635	43,382	118,295	78,894	-0,864	0,007	0,859	0,000	1,450	0,000	down	up	up
Solyc03g121900	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT5G		F:GO:0005504; P:GC	F:fatty acid binding; P:systemic acquired resistance			IPR016140 (SMART): G3DSA:1.10.11	1,373	6,014	0,221	0,073	0,142	2,156	0,002					up		
Solyc03g121910	Threonine synthase, putative (AHRD V3.3 *** B9RK44_RICCO)		F:GO:0004795; P:GC	F:threonine synthas	EC:4.2.3.1	Threonine synthase	IPR004450 (TIGRFAM): G3DSA:3.40.5	61,670	66,447	13,456	19,186	23,617			0,805	0,008				up	
Solyc03g121920	Mitochondrial carrier protein (AHRD V3.3 *** F8WLA3_CITUN)		F:GO:0022857; P:GC	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR023395 (G3	36,164	31,502	19,748	19,049	18,105									
Solyc03g121930	PHD finger alfin-like protein (AHRD V3.3 *** A0A072VES1_MEDTR)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:histone binding			IPR001965 (SMART): IPR021998 (PF	3,399	4,764	3,582	4,045	3,857									
Solyc03g121940	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRIN' NF-YA	2,764	4,194	3,527	4,812	4,519									
Solyc03g121950	Ataxin-2 related protein (AHRD V3.3 *** A2PZE4_IPONI)		C:GO:0010494; P:GC	C:cytoplasmic stress granule; P:regulation of cytoplasmic mRN			IPR009604 (SMART): IPR009604 (PF	98,607	85,455	128,447	131,837	125,408									
Solyc03g121960	phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** AT5G13640.1)		P:GO:0006629; F:GC	P:lipid metabolic process; F:O-acyltransferase activity			IPR003386 (PFAM): IPR029058 (G3D	53,659	56,828	134,057	127,107	129,642									
Solyc03g121970	Protein BIG GRAIN 1-like A (AHRD V3.3 *** BIG1A_ARATH)		P:GO:0009734	P:auxin-activated signaling pathway			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,744	3,821	1,476	0,862	1,114									
Solyc03g121980	Developmentally regulated GTP binding family protein (AHRD V3.3 *** B9GWB7_POPTR)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR031662 (PF	118,393	114,062	111,482	98,633	104,451									
Solyc03g121990	Telomere repeat-binding factor like-protein (AHRD V3.3 *** A0A0K1SBL3_REHGL)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	77,119	79,069	94,364	89,381	85,647									
Solyc03g122000	Cytochrome b6-f complex subunit 4 (AHRD V3.3 *** PETD_POPAL)		P:GO:0009767; C:GC	P:photosynthetic electron transport chain; C:thylakoid membran			G3DSA:1.10.287.980 (GENE3D): IPR	0,000	0,169	0,075	0,150	0,140									
Solyc03g122010	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_PHYPA)		C:GO:0005739; C:GC	C:mitochondrion; C:	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM): PTHR22773 (PAN	0,021	0,021	0,025	0,022	0,000									
Solyc03g122020	Transcription initiation factor TFIID subunit 12 (AHRD V3.3 *-* W9RRR4_9ROSA)		C:GO:0000124; C:GC	C:SAGA complex; C:transcription factor TFIID complex; P:DNA-			IPR003228 (PFAM): IPR009072 (G3D	27,285	23,621	37,678	36,352	35,633									
Solyc03g122030	Transcription factor (AHRD V3.3 *** G7L8C7_MEDTR)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			PF13837 (PFAM): Trihelix	26,031	31,304	30,703	31,419	27,570									
Solyc03g122040	Erect panicle 2 protein (AHRD V3.3 *-* I2AW42_9POAL)						mobidb-lite (MOBIDB_LITE): mobidb-lit	115,986	115,134	23,948	20,036	26,217									
Solyc03g122050	ABC transporter B family-like protein (AHRD V3.3 *-* G7L8C5_MEDTR)	ABCB22	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	0,101	0,078	0,118	0,000	0,070									
Solyc03g122070	ABC transporter B family-like protein (AHRD V3.3 *** G7L8C5_MEDTR)	ABCB23	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR011527 (PF	0,323	0,233	0,044	0,000	0,142									
Solyc03g122080	DUF936 family protein (AHRD V3.3 *** A0A072THZ7_MEDTR)						IPR010341 (PFAM): PTHR31928:SF2	0,177	0,660	0,075	0,100	0,070									
Solyc03g122090	25, vesicle transport protein (AHRD V3.3 *** A0A1D1XNZ8_9ARAE)		C:GO:0016021; P:GC	C:integral component of membrane; P:vesicle-mediated transpo			IPR010908 (SMART): G3DSA:3.30.45	24,752	23,877	40,251	46,553	36,886									
Solyc03g122100	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *-* A0A072V6B8_MEDTR)		F:GO:0003824; F:GC	F:catalytic activity; F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	1,545	1,937	3,578	3,457	3,156									
Solyc03g122110	LOW QUALITY:Pre-mRNA-splicing factor CWC22 (AHRD V3.3 *** A0A0B0NK35_GOSAR)		F:GO:0003723; F:GC	F:RNA binding; F:protein binding			IPR003890 (SMART): IPR003891 (SM	3,462	1,496	3,679	6,419	4,018	-1,176	0,025			0,799	0,029	down		up
Solyc03g122120	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** A0A067G2G2_CITSI)		F:GO:0003824	F:catalytic activity			IPR020841 (SMART): IPR014030 (PF	47,934	59,017	128,337	136,076	119,979									
Solyc03g122130	Peroxisomal (S)-2-hydroxy-acid oxidase (AHRD V3.3 *** GOX_SPIOL)		F:GO:0010181; F:GC	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR012133 (PIRSF): IPR000262 (PFA	4,457	5,470	11,555	10,429	14,358									
Solyc03g122140	Peroxisomal (S)-2-hydroxy-acid oxidase (AHRD V3.3 *** GOX_SPIOL)		F:GO:0010181; F:GC	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			SM01240 (SMART): IPR013785 (G3D	0,019	0,021	0,050	0,095	0,118									
Solyc03g122150	Peroxisomal (S)-2-hydroxy-acid oxidase (AHRD V3.3 *-* GOX_SPIOL)		F:GO:0016491	F:oxidoreductase activity			IPR013785 (G3DSA:3.20.20.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc03g122170	Peroxisomal (S)-2-hydroxy-acid oxidase (AHRD V3.3 *** GOX_SPIOL)		F:GO:0010181; F:GC	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR012133 (PIRSF): IPR000262 (PFA	2,766	2,988	3,298	2,561	3,440									
Solyc03g122180	RNA-binding family protein (AHRD V3.3 *** A0A061GD25_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	8,935	7,780	9,323	8,416	8,519									
Solyc03g122190	Jasmonate zim-domain protein (AHRD V3.3 *** G7IIQ4_MEDTR)		C:GO:0005634; P:GC	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (SMART): IPR018467 (PF	33,073	106,852	16,247	12,993	16,391	1,716	0,000					up		
Solyc03g122230	Receptor-like kinase, putative (AHRD V3.3 *** A0A072TMR8_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR032675 (G3	0,021	0,018	0,000	0,000	0,000									
Solyc03g122240	Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9N7F2_POPTR)		C:GO:0000145; P:GC	C:exocyst; P:exocytosis			IPR004140 (PFAM): IPR004140 (PAN	27,299	27,477	33,853	32,373	29,458									
Solyc03g122250	Lung seven transmembrane receptor family protein (AHRD V3.3 *** AT1G72480.1)		C:GO:0016021	C:integral component of membrane			IPR009637 (PFAM): mobidb-lite (MOB	52,387	54,494	3,996	3,975	4,142									
Solyc03g122260	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT3G14080.2)		P:GO:0000956	P:nuclear-transcribed mRNA catabolic process			IPR001163 (SMART): G3DSA:2.30.30	7,175	5,845	6,489	5,136	5,017									
Solyc03g122270	Inter-alpha-trypsin inhibitor heavy chain-related, putative (AHRD V3.3 *** A0A061GD07_THECC)		P:GO:0000956	P:nuclear-transcribed mRNA catabolic process			IPR001163 (SMART): IPR002035 (SM	195,613	190,934	438,246	473,860	398,056									
Solyc03g122280	Sn1-specific diacylglycerol lipase alpha (AHRD V3.3 *** A0A0B0PYL4_GOSAR)		P:GO:0016042	P:lipid catabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	16,696	20,541	29,115	26,142	26,939									
Solyc03g122300	DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)						IPR012876 (PFAM): IPR012876 (PAN	7,510	5,666	8,174	9,874	7,954									
Solyc03g122310	Aldehyde dehydrogenase (AHRD V3.3 *** Q9FPK6_ORYSA)		F:GO:0016620; P:GC	F:oxidoreductase activity, acting on the aldehyde or oxo group			IPR015590 (PFAM): IPR016162 (G3D	55,603	57,024	97,174	87,260	101,159									
Solyc03g122340	lipoxygenase D	LOX4	F:GO:0005515; F:GC	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	323,159	478,534	76,927	116,031	137,290									
Solyc03g122350	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	247,581	410,117	430,570	720,484	494,196					0,745	0,000			up
Solyc03g122360	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	9,626	5,021	52,775	51,969	35,797									
Solyc03g122370	ARM repeat superfamily protein (AHRD V3.3 *** AT1G72560.7)		F:GO:0000049; F:GC	F:tRNA binding; F:Ran GTPase binding; P:tRNA re-export from r			IPR011989 (G3DSA:1.25.10.GENE3D	22,413	21,788	22,892	25,186	22,117									
Solyc03g123370	RelA/SpoT-like protein (AHRD V3.3 *** A8DD65_IPONI)		P:GO:0015969	P:guanosine tetraphosphate metabolic process			IPR003607 (SMART): IPR007685 (SM	101,188	94,508	104,187	144,476	113,956					0,475	0,009			up
Solyc03g123380	LOW QUALITY:Serine rich protein (AHRD V3.3 *** Q4VYD0_MEDTR)		C:GO:0016020	C:membrane			PTHR35758:SF1 (PANTHER): PTHR3	0,188	0,080	0,000	0,048	0,000									
Solyc03g123390	Alpha/beta-Hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061GDN4_THECC)		C:GO:0016021; F:GC	C:integral component of membrane; F:hydrolase activity			IPR000073 (PRINTS): IPR029058 (G3	2,614	1,954	0,484	0,730	0,234									
Solyc03g123400	GRAS16	GRAS16	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAN GRAS	4,421	3,517	0,941	0,979	0,732									
Solyc03g123410	Germin-like protein (AHRD V3.3 *** Q0PWM4_CAPCH)		F:GO:0030145; F:GC	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SM	0,040	0,329	0,000	0,000	0,000									
Solyc03g123420	Proline-rich family protein (AHRD V3.3 *** B9GW18_POPTR)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): mobidb-lite (MOB	8,216	7,623	6,887	5,919	5,079									
Solyc03g123430	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A0K9NMH9_ZOSMR)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' AP2	10,799	6,811	0,625	0,526	0,490									
Solyc03g123440	DNA demethylase 4		F:GO:0003824; P:GC	F:catalytic activity; P:base-excision repair; F:4 iron, 4 sulfur clu			IPR003651 (SMART): IPR003265 (SM	28,596	21,663	17,061	17,335	18,493									
Solyc03g123460	DUF581 family protein (AHRD V3.3 *-* G7L953_MEDTR)						IPR007650 (PFAM): PTHR33059:SF7	16,437	9,064	5,427	7,285	6,198	-0,826	0,022					down		
Solyc03g123490	Subtilisin-like protease (AHRD V3.3 *** W9R4Z9_9ROSA)		F:GO:0004252; P:GC	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.30	120,641	93,183	85,547	72,975	81,693									
Solyc03g123500	GCC box binding protein C.4	ERF_C_4	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' ERF	77,958	98,068	152,686	147,094	137,639									
Solyc03g123510	Harpin-induced protein (AHRD V1 *--- B4FP99_MAIZE)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): PTHR31852:SF3	0,057	0,142	0,075	0,022	0,023									
Solyc03g123520	Polyphosphoinositide phosphatase (AHRD V1 ***- C1H752_PARBA)		P:GO:0007033; P:GC	P:vacuole organization; P:phosphatidylinositol-3-phosphate bios			IPR002013 (PFAM): mobidb-lite (MOB	65,903	68,515	43,807	46,117	55,504									
Solyc03g123530	CCAAT/enhancer-binding zeta (AHRD V3.3 *** A0A0B0MUY0_GOSAR)		P:GO:0042254	P:ribosome biogenesis			IPR005612 (PFAM): mobidb-lite (MOB	32,699	30,049	24,755	24,312	25,758									
Solyc03g123540	Heat-shock protein, putative (AHRD V3.3 *** B9ST51_RICCO)	Hsp16.1A	P:GO:0006457; P:GC	P:protein folding; P:response to heat; P:response to high light ir			IPR002068 (PFAM): IPR008978 (G3D	3,438	2,862	15,319	12,379	16,730									
Solyc03g123550	Small auxin up-regulated RNA39	SAUR39	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	0,451	0,561	8,134	7,321	7,122									
Solyc03g123560	DnaJ domain-containing protein (AHRD V3.3 *** A0A118K3E9_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	72,291	50,838	76,379	82,770	72,398									
Solyc03g123580	LL-diaminopimelate aminotransferase (AHRD V3.3 *** A0A0B0NUF6_GOSAR)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			PTHR34206 (PANTHER)	2,272	2,235	1,620	1,857	2,805									
Solyc03g123590	Remorin family protein (AHRD V3.3 *** B9N7I2_POPTR)						IPR005516 (PFAM): mobidb-lite (MOB	1,604	1,756	0,365	0,417	0,826									
Solyc03g123600	alanine aminotransferase 2 (AHRD V3.3 *** AT1G72330.3)		F:GO:0003824; P:GC	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR004839 (PFAM): IPR015421 (G3D	28,636	29,932	99,431	112,005	100,412									
Solyc03g123610	alanine aminotransferase 2 (AHRD V3.3 *** AT1G72330.1)		F:GO:0003824; P:GC	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3	99,615	112,250	167,582	169,014	166,197									
Solyc03g123620	Pectinesterase (AHRD V1 ***- B9GXZ7_POPTR)		F:GO:0004857; F:GC	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (PF	182,543	157,387	29,018	48,965	59,965			1,044	0,033				up	
Solyc03g123630	pectin methylesterase	pmeu1	F:GO:0004857; F:GC	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR012334 (G3	1177,953	796,763	41,077	14,576	30,646					-1,495	0,002			down
Solyc03g123640	pumilio 23 (AHRD V3.3 *** AT1G72320.4)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR011989 (G3	27,476	25,766	26,089	26,034	25,520									
Solyc03g123650	Outer arm dynein light chain 1 protein (AHRD V3.3 --* AT4G03260.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,058	0,000	0,022	0,023									
Solyc03g123660	ubiquitin conjugating enzyme 2		P:GO:0000209; C:GC	P:protein polyubiquitination; C:endoplasmic reticulum; C:integral			SM00212 (SMART): IPR000608 (PFAI	53,410	60,851	37,694	34,195	39,228									
Solyc03g123670	Rhizopuspepsin-4 (AHRD V3.3 *** A0A1D1XDZ3_9ARAE)						mobidb-lite (MOBIDB_LITE): PTHR354	0,256	0,353	0,096	0,201	0,165									
Solyc03g123680	RING/U-box superfamily protein (AHRD V3.3 *** AT1G72310.1)		C:GO:0016021; P:GC	C:integral component of membrane; P:protein ubiquitination			IPR001841 (SMART): IPR001841 (PF	0,383	0,668	0,227	0,238	0,352									
Solyc03g123700	muscle M-line assembly protein (AHRD V3.3 *** AT1G53800.1)		F:GO:0003677	F:DNA binding			IPR003611 (PFAM): mobidb-lite (MOB	6,731	8,414	5,397	5,631	6,458									
Solyc03g123710	purple acid phosphatase 17 (AHRD V3.3 --* AT3G17790.1)							13,598	11,282	24,674	17,712	25,404									
Solyc03g123720	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G50420.1)		P:GO:0006004; C:GC	P:fucose metabolic process; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	94,722	85,868	56,533	52,827	53,156									
Solyc03g123730	26S protease regulatory subunit (AHRD V3.3 *** T2DN87_PHAVU)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata			IPR003593 (SMART): PF17862 (PFAM	16,216	20,001	43,301	46,864	40,790									
Solyc03g123740	Ovule receptor-like kinase 28 (AHRD V3.3 *** A4GWX5_SOLCH)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PFAM): IPR032675 (G3D	104,794	123,345	11,526	11,005	13,573									
Solyc03g123750	Lipase (AHRD V3.3 *** Q5S8F1_RICCO)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	20,949	17,743	24,634	26,638	29,004									
Solyc03g123760	phytoene desaturase	PDS	P:GO:0016117; F:GC	P:carotenoid biosynthetic process; F:phytoene dehydrogenase			IPR014102 (TIGRFAM): IPR036188 ((	85,031	101,505	255,172	303,801	320,712									
Solyc03g123770	LOW QUALITY:Disease resistance protein (AHRD V3.3 --* Q19HX1_ARATH)							0,358	0,118	0,243	0,022	0,236									
Solyc03g123780	Receptor kinase (AHRD V3.3 *** B8XA57_GOSBA)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR000719 (SMA	38,428	29,545	19,018	29,935	24,466					0,655	0,000			up
Solyc03g123790	vacuolar cation/proton exchanger (AHRD V3.3 *** AT1G55720.2)		P:GO:0006816; F:GC	P:calcium ion transport; F:calcium:proton antiporter activity; C:ir			G3DSA:1.20.1420.30 (GENE3D): IPR	48,350	41,878	22,257	22,452	25,379									
Solyc03g123800	MAP kinase kinase 2	MAPKK2	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	116,746	132,080	121,579	124,610	119,976									
Solyc03g123820	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G73050.1)		F:GO:0016614; F:GC	F:oxidoreductase activity, acting on CH-OH group of donors; F:			IPR007867 (PFAM): IPR036188 (G3D	0,551	0,080	0,398	0,000	0,304									
Solyc03g123830	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** K4BN81_SOLLC)		F:GO:0004617; P:GC	F:phosphoglycerate	EC:1.1.1.95	Phosphoglycerate de	G3DSA:3.40.50.720 (GENE3D): G3DS	443,677	315,432	113,081	47,092	100,740					-1,261	0,001			down
Solyc03g123840	RNA-binding family protein (AHRD V3.3 *** A0A061GFC4_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	88,379	79,882	78,152	74,761	78,573									
Solyc03g123860	Receptor-like protein kinase INRPK1c	INRPK1c	F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): SM00365 (SMA	5,299	19,952	2,731	1,539	2,263	1,936	0,000					up		
Solyc03g123870	Exocyst complex component 8 (AHRD V3.3 *** A0A0B2RY33_GLYSO)		C:GO:0000145; P:GC	C:exocyst; P:exocytosis			IPR032403 (PFAM): PF08700 (PFAM)	61,182	62,758	81,340	92,598	78,094									
Solyc03g123880	Glutamyl-tRNA reductase binding protein (AHRD V3.3 *** E9N732_TOBAC)		F:GO:0048037	F:cofactor binding			IPR019595 (PFAM): IPR037119 (G3D	32,779	49,088	68,990	75,205	78,528	0,609	0,016					up		
Solyc03g123890	Calcium-transporting ATPase (AHRD V3.3 *** A0A022PY01_ERYGU)		F:GO:0005388; F:GC	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR004014 (SMA	32,017	24,115	26,668	24,751	25,097									
Solyc03g123900	alpha-1,2-Mannosidase (AHRD V3.3 *** K4BN88_SOLLC)		F:GO:0004571; F:GC	F:mannosyl-oligosa	EC:3.2.1.113; EC:3.2	Mannosyl-oligosacch	IPR001382 (PRINTS): IPR012341 (G3	99,591	91,048	108,662	103,768	104,782									
Solyc03g123910	Kelch repeat-containing protein family (AHRD V3.3 *** A0A151RPA1_CAJCA)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	196,015	165,670	129,732	111,254	121,774									
Solyc03g123920	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *** A0A061G9T7_THECC)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity; C:integral component of mer			mobidb-lite (MOBIDB_LITE): mobidb-lit	52,491	40,967	36,742	34,277	33,280									
Solyc03g123930	Zinc finger family protein (AHRD V3.3 *-* D7KFZ7_ARALL)		F:GO:0008270; C:GC	F:zinc ion binding; C:integral component of membrane; F:ligase			IPR033275 (PANTHER): PTHR23012:	5,633	5,628	8,356	8,088	6,975									
Solyc03g123940	60S ribosomal protein L44 (AHRD V3.3 *** RL44_GOSHI)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000552 (PFAM): G3DSA:3.10.450	0,142	0,111	0,050	0,235	0,165									
Solyc03g123950	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *-* AT1G50440.5)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	15,280	14,822	20,166	21,923	18,682									
Solyc03g123960	Mediator of RNA polymerase II transcription subunit 8, putative (AHRD V3.3 *** G7JYQ3_MEDTR)		C:GO:0016592	C:mediator complex			mobidb-lite (MOBIDB_LITE): mobidb-lit	26,458	23,478	30,047	27,624	26,164									
Solyc03g123970	LOW QUALITY:Lipid-binding serum glycoprotein family protein isoform 2 (AHRD V3.3 *-* A0A061GA66_THECC)						PTHR10504:SF90 (PANTHER): IPR03	0,138	0,060	0,000	0,000	0,000									
Solyc03g123980	Pumilio-like protein (AHRD V3.3 *** A0A0B0PV05_GOSAR)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR011989 (G3	100,938	88,186	162,532	167,213	150,712									
Solyc03g123990	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT3G20240.1)		F:GO:0022857; P:GC	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR018108 (PF	6,488	6,649	5,482	5,243	6,201									
Solyc03g124010	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061C		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): PF13	68,784	57,068	60,872	65,393	60,117									
Solyc03g124030	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G78915.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	30,633	38,715	29,751	34,302	35,295									
Solyc03g124040	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT1G78930.1)		F:GO:0003690; P:GC	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART): IPR038538 (G3	22,389	24,883	13,349	14,813	15,617									
Solyc03g124050	Receptor protein kinase, putative (AHRD V3.3 *** B9RHT1_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	0,075	0,076	0,025	0,000	0,023									
Solyc03g124060	StAR-related lipid transfer protein 7, mitochondrial (AHRD V3.3 *** A0A1D1Z6M2_9ARAE)		F:GO:0008289	F:lipid binding			IPR002913 (PFAM): IPR023393 (G3D	34,199	34,624	41,139	39,763	40,817									
Solyc03g124110	CBF		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' ERF	16,009	2,539	7,410	30,216	15,180	-2,624	0,000	1,032	0,015	2,029	0,000	down	up	up
Solyc04g005010	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond	IPR036397 (G3DSA:3.30.420.GENE3	3,861	5,452	7,130	9,682	7,451									
Solyc04g005020	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061FTT2_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,353	0,399	4,177	4,317	2,862									
Solyc04g005030	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT1G24130.1)		F:GO:0005515; P:GC	F:protein binding; P:carbohydrate metabolic process; F:intramol			IPR005841 (PRINTS): IPR001680 (SM	63,343	75,602	87,468	82,080	85,560									
Solyc04g005035	Phosphoglucomutase/phosphomannomutase family protein (AHRD V3.3 *-* G7I385_MEDTR)		P:GO:0005975; F:GC	P:carbohydrate metabolic process; F:intramolecular transferase			IPR005844 (PFAM): G3DSA:3.40.120	13,736	17,058	19,469	17,043	20,878									
Solyc04g005040	Matrix metalloproteinase (AHRD V3.3 *** I7KJ40_SOLLC)		F:GO:0004222; P:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR021190 (PRINTS): IPR006026 (SM	130,308	188,128	21,965	12,133	22,120									
Solyc04g005050	matrix metalloproteinase		F:GO:0004222; P:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR021190 (PRINTS): IPR006026 (SM	76,161	67,946	9,127	10,479	12,494									
Solyc04g005060	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *** G7K5M5_MEDTR)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	28,726	22,642	4,510	2,240	3,196									
Solyc04g005070	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	3,596	3,786	0,706	0,248	0,401									
Solyc04g005080	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** K4BNB4_SOLLC)		F:GO:0004739; P:GC	F:pyruvate dehydro	EC:1.2.4.1	Pyruvate dehydroger	IPR017597 (TIGRFAM): IPR001017 (F	60,587	64,908	89,638	76,925	79,244									
Solyc04g005090	cofactor assembly of complex C (AHRD V3.3 *** AT1G59840.2)		C:GO:0009507; P:GC	C:chloroplast; P:cytochrome b6f complex assembly			IPR021325 (PFAM): PTHR34943 (PAN	7,425	7,892	6,894	6,588	8,465									

Solyc04g005100	Myb-like transcription factor family protein (AHRD V3.3 *** A0A061E7E9_THECC)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	222,210	120,499	112,035	108,683	117,957	-0,858	0,003					down		
Solyc04g005120	short hypocotyl in white light1 (AHRD V3.3 *-* AT1G69935.1)		P:GO:0009787; P:GC	P:regulation of abscisic acid-activated signaling pathway; P:nec			IPR039324 (PANTHER): PTHR35474:	7,757	9,317	15,422	14,193	14,838									
Solyc04g005130	bHLH transcription factor 027		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	7,212	5,636	3,296	4,092	3,587									
Solyc04g005140	LOW QUALITY:Phosphoribulokinase / Uridine kinase family (AHRD V3.3 *** AT1G26190.5)		P:GO:0002237; F:GC	P:response to molecule of bacterial origin; F:ATP binding; C:mit			PTHR10285:SF76 (PANTHER): PTHR	1,153	0,743	1,243	1,114	1,178									
Solyc04g005150	Uridine kinase (AHRD V3.3 *-* A0A0K9NRI5_ZOSMR)		F:GO:0005524; F:GC	F:ATP binding; F:kinase activity			PR00988 (PRINTS): IPR006083 (PFA	0,260	0,161	0,364	0,340	0,186									
Solyc04g005160	6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *** A0A0K1P904_6PGD1		F:GO:0004616; P:GC	F:phosphogluconat	EC:1.1.1.44	Phosphogluconate de	IPR006183 (PRINTS): IPR006114 (SM	129,216	190,097	137,578	154,387	145,267									
Solyc04g005170	BZip transcription factor (AHRD V3.3 *** Q9AT29_PHAVU)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	0,000	0,021	0,000	0,000	0,000									
Solyc04g005180	Isochorismate synthase, chloroplastic (AHRD V3.3 *-* ICS_CATRO)		P:GO:0009063; P:GC	P:cellular amino aci	EC:4.2.99.2; EC:2.2.	2-succinyl-6-hydroxy	PTHR11236:SF24 (PANTHER): PTHR	1,641	1,714	0,488	0,692	0,918									
Solyc04g005200	2-oxoglutarate decarboxylase/hydro-lyase/magnesium ion-binding protein (AHRD V3.3 *** AT1G68890.1)		P:GO:0009234; F:GC	P:menaquinone bios	EC:2.2.1.9	2-succinyl-5-enolpyru	IPR013342 (SMART): IPR011766 (PF	8,200	10,005	3,292	4,346	7,264			1,128	0,002				up	
Solyc04g005210	ascorbate peroxidase 1 (AHRD V3.3 --* AT1G07890.6)							0,038	0,018	0,050	0,022	0,000									
Solyc04g005220	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G68920.4)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulation of transcription, I bHLH				0,019	0,000	0,000	0,000	0,000									
Solyc04g005223	Basic helix-loop-helix DNA-binding superfamily protein, putative isoform 2 (AHRD V3.3 *-* A0A061E965_THE		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,037	0,000	0,000	0,000	0,000									
Solyc04g005230	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	0,019	0,043	0,000	0,000	0,000									
Solyc04g005255	Phosphatidylinositol 4-kinase (AHRD V3.3 *** J3R305_GOSBA)		F:GO:0016301; P:GC	F:kinase activity; P:phosphorylation			IPR000403 (PFAM): PTHR15245 (PAN	148,778	107,471	206,560	162,100	184,956									
Solyc04g005260	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9RLG1_RICCO)		P:GO:0006284; F:GC	P:base-excision rep	EC:3.2.2.21; EC:3.2.	DNA-3-methyladenine	IPR005019 (PFAM): G3DSA:1.10.340	0,040	0,057	0,025	0,000	0,023									
Solyc04g005280	bHLH transcription factor 028		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBII bHLH	19,079	17,584	24,478	26,427	23,687									
Solyc04g005290	18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *-* AT2G03810.7)		P:GO:0009786	P:regulation of asymmetric cell division			mobidb-lite (MOBIDB_LITE): mobidb-lit	10,074	10,173	11,474	14,345	12,414									
Solyc04g005300	D-aminoacyl-tRNA deacylase (AHRD V3.3 *-* AT2G03800.2)		F:GO:0051499	F:D-aminoacyl-tRNA	EC:3.1.1.96; EC:3.1.	D-aminoacyl-tRNA de	IPR007508 (PFAM): G3DSA:3.40.50.1	6,134	6,643	17,380	18,123	14,234									
Solyc04g005310	translin-associated factor X		F:GO:0043565	F:sequence-specific DNA binding			IPR002848 (PFAM): IPR016068 (G3D	8,294	8,449	13,189	12,198	13,492									
Solyc04g005320	MADS-box transcription factor (AHRD V3.3 *** Q8SL4_SOLLC)		F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	0,815	1,992	0,314	0,050	0,142									
Solyc04g005330	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061DJK9_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	133,404	114,283	133,465	119,245	123,128									
Solyc04g005340	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (AHRD V3.3 *** UPTG1_SOLTU)		F:GO:0016866; P:GC	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR037595 (PFAM): IPR004901 (PIRS	324,515	322,357	205,358	193,399	187,293									
Solyc04g005350	RNA binding (AHRD V3.3 *** A0A0K9NXI0_ZOSMR)		F:GO:0003723; F:GC	F:RNA binding; F:pe	EC:5.2.1.8	Peptidylprolyl isomer	IPR000504 (SMART): IPR000504 (PF	23,946	21,181	27,674	21,112	23,751									
Solyc04g005380	Ninja-family protein AFP1-like protein (AHRD V3.3 *** V5KZR9_SOLNI)		P:GO:0007165	P:signal transduction			IPR012463 (PFAM): IPR032308 (PFA	4,846	4,143	2,208	1,709	3,245									
Solyc04g005410	Ureide permease (AHRD V3.3 *** A0A124SG70_CYNCS)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR009834 (PFAM): PTHR31081:SF5	0,019	0,060	0,075	0,147	0,142									
Solyc04g005420	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *-* A0A0B2SF50_GLYSO)		C:GO:0016020	C:membrane			IPR012946 (SMART): IPR012946 (PF	15,183	18,028	62,251	62,831	53,235									
Solyc04g005425	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** A0A061EBH5_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,787	3,769	5,153	5,307	5,224									
Solyc04g005430	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G78240.2)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	34,588	30,724	31,335	34,239	31,458									
Solyc04g005440	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HID5_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMART): PF13912 (PFAM	1,336	1,860	0,488	0,382	0,330									
Solyc04g005450	Purple acid phosphatase (AHRD V3.3 *** K4BNF1_SOLLC)		F:GO:0003993; F:GC	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR008963 (G3DSA:2.60.40.GENE3D	163,290	128,306	118,228	114,373	113,848									
Solyc04g005460	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061E9T8_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	1,010	1,081	0,807	0,713	0,988									
Solyc04g005470	Remorin family protein (AHRD V3.3 *-* AT1G13920.4)		F:GO:0003677; F:GC	F:DNA binding; F:helicase activity			IPR005516 (PFAM): mobidb-lite (MOB	0,060	0,059	0,312	0,566	0,165									
Solyc04g005480	LOW QUALITY:Nodulin-related protein 1, putative (AHRD V3.3 *** A0A061EHK7_THECC)		P:GO:0009408; P:GC	P:response to heat; P:regulation of abscisic acid biosynthetic p			mobidb-lite (MOBIDB_LITE): mobidb-lit	79,583	119,982	48,510	79,704	67,809									
Solyc04g005490	appr-1-p processing enzyme family protein (AHRD V3.3 *** AT1G69340.2)						IPR001251 (SMART): IPR002589 (SM	42,754	59,001	40,476	46,274	46,876									
Solyc04g005500	T-box transcription factor, putative (DUF863) (AHRD V3.3 *** AT1G69360.1)						IPR008581 (PFAM): mobidb-lite (MOB	35,077	34,704	76,513	74,848	68,534									
Solyc04g005510	Eukaryotic translation initiation factor 5A (AHRD V3.3 *** K4BNF7_SOLLC)		F:GO:0003746; P:GC	F:translation elongation factor activity; P:translational frameshif			IPR020189 (SMART): G3DSA:2.40.50	38,286	41,631	21,327	21,286	21,614									
Solyc04g005520	Delta-1-pyrroline-5-carboxylate synthetase (AHRD V3.3 --* A0A072UIU3_MEDTR)		F:GO:0016301	F:kinase activity			IPR024192 (PIRSF): IPR001048 (PFA	2,494	3,852	0,663	1,232	1,316									
Solyc04g005530	transmembrane protein (AHRD V3.3 *** AT3G11810.1)		C:GO:0016021	C:integral component of membrane			PTHR33133:SF7 (PANTHER): PTHR3	61,895	46,681	53,022	47,916	46,843									
Solyc04g005540	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	72,674	65,109	27,949	31,737	31,539									
Solyc04g005550	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G40060.1)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	7,641	15,921	2,389	4,174	7,745			1,686	0,000	0,802	0,045		up	up
Solyc04g005560	Pattern formation EMB30-like protein (AHRD V3.3 *** A0A0B0NVB0_GOSAR)		F:GO:0005086; P:GC	F:ARF guanyl-nucleotide exchange factor activity; P:regulation			IPR000904 (SMART): IPR023394 (G3	9,062	7,411	3,519	2,100	3,054									
Solyc04g005570	Transmembrane emp24 domain-containing protein 10 (AHRD V3.3 *** W9SPK8_9ROSA)		C:GO:0005789; C:GC	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR009038 (SMART): IPR009038 (PF	0,314	0,259	0,214	0,126	0,164									
Solyc04g005580	LOW QUALITY:GCK domain-containing protein (AHRD V3.3 *-* AT1G14060.1)						SM01227 (SMART): IPR012891 (PFAM	0,493	0,639	0,508	0,453	0,449									
Solyc04g005590	Ribosomal protein L32 (AHRD V3.3 *** K7VPA9_SOLTU)		F:GO:0003735; P:GC	F:structural constituent of ribosome; P:translation; C:large ribos			IPR002677 (TIGRFAM): IPR002677 (F	32,607	27,198	39,584	30,930	32,617									
Solyc04g005600	MYB-related transcription factor (AHRD V3.3 *-* A0A059PRK4_SALMI)	R2R3MYB23	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,000	0,019	0,000	0,000	0,000									
Solyc04g005610	NAC domain protein NAC2	SNAC035	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,358	1,026	2,313	5,085	4,815			1,053	0,003	1,141	0,000		up	up
Solyc04g005620	CASP-like protein (AHRD V3.3 *** K4BNG8_SOLLC)		C:GO:0005886; P:GC	C:plasma membrane; P:cell-cell junction assembly; C:integral cc			IPR006702 (PFAM): IPR006459 (TIGF	0,021	0,058	0,025	0,050	0,023									
Solyc04g005630	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT4G02990.2)		F:GO:0003690; P:GC	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR003690 (PF	11,329	13,006	84,790	86,219	81,424									
Solyc04g005650	Mitochondrial substrate carrier family protein (AHRD V3.3 *** A0A061FTE7_THECC)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	69,307	70,122	131,684	132,108	125,385									
Solyc04g005670	Kelch repeat-containing F-box family protein, putative (AHRD V3.3 *** Q6L3I4_SOLDE)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR015915 (G3	88,637	69,618	104,852	190,589	135,142					0,864	0,000			up
Solyc04g005680	Ribosomal protein (AHRD V3.3 *** B3TM27_ELAGV)		F:GO:0003723; F:GC	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR002942 (SMART): IPR036986 (G3	343,744	379,048	306,850	267,375	289,625									
Solyc04g005685	Guanine nucleotide-binding protein alpha-1 subunit (AHRD V3.3 --* GPA1_LUPLU)						mobidb-lite (MOBIDB_LITE)	0,479	0,473	0,550	0,506	0,374									
Solyc04g005690	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein (AHRD V3.3 *'		F:GO:0003723; F:GC	F:RNA binding; F:protein binding; P:RNA processing			PR01217 (PRINTS): IPR000626 (SMA	64,588	64,857	64,554	63,551	65,682									
Solyc04g005720	Caleosin-related family protein (AHRD V3.3 *** AT1G70680.1)		F:GO:0004497; F:GC	F:monooxygenase activity; F:calcium ion binding; C:membrane;			IPR007736 (PFAM): IPR007736 (PAN	0,037	0,039	0,000	0,000	0,000									
Solyc04g005730	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q7G3C6_ORYSJ)						IPR029480 (PFAM): IPR004252 (PFA	11,975	10,985	8,229	8,966	8,998									
Solyc04g005740	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART): IPR011016 (SM	0,063	0,000	0,000	0,025	0,023									
Solyc04g005760	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR001841 (SM	0,141	0,043	0,050	0,149	0,141									
Solyc04g005770	Pentatricopeptide repeat (PPR) superfamily protein, putative (AHRD V3.3 *** A0A061EAL4_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,659	0,999	0,479	0,604	0,518									
Solyc04g005780	LOW QUALITY:glyoxal oxidase-related protein (AHRD V3.3 *** AT1G14430.1)						IPR009880 (PFAM): IPR037293 (G3D	0,749	0,750	0,753	0,502	0,591									
Solyc04g005790	nitrate transporter 1:2 (AHRD V3.3 *** AT1G69850.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): PTHR11654:SF9	0,665	0,750	0,575	0,934	0,657									
Solyc04g005800	Homeobox leucine zipper family protein (AHRD V3.3 *** G7K9R5_MEDTR)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN HD-ZIP	0,489	0,368	0,112	0,119	0,046									
Solyc04g005820	DnaJ-like protein (AHRD V3.3 *** Q9SP09_TOBAC)		P:GO:0006457; F:GC	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS): IPR001623 (SM	8,720	9,532	8,359	7,830	6,971									
Solyc04g005830	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G33290.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): PF13604 (PFAM	5,388	6,048	2,907	3,562	3,714									
Solyc04g005840	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7IDH7_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART): IPR002123 (PF	0,021	0,000	0,000	0,000	0,023									
Solyc04g005850	exocyst complex component 84B (AHRD V3.3 *** AT5G49830.1)		C:GO:0000145; P:GC	C:exocyst; P:exocytosis			IPR032403 (PFAM): PF08700 (PFAM)	0,021	0,000	0,000	0,000	0,000									
Solyc04g005860	CW14 protein (DUF1336) (AHRD V3.3 *** AT1G59650.1)						IPR009769 (PFAM): mobidb-lite (MOB	83,863	119,551	66,794	65,131	83,001									
Solyc04g005900	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR006566 (SMART): IPR032675 (G3	5,733	5,303	3,607	4,844	3,132									
Solyc04g005910	NSP-interacting kinase 2 (AHRD V3.3 *** AT3G25560.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR000719 (PF	13,639	9,689	10,633	10,650	10,681									
Solyc04g005920	LOW QUALITY:micronuclear linker histone polyprotein-like protein (AHRD V3.3 *** AT3G25590.1)						PTHR34197:SF3 (PANTHER): PTHR3	1,944	1,090	0,861	0,771	0,804									
Solyc04g006930	Kinase family protein (AHRD V3.3 *-* B9HIU4_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (SMART): IPR000719 (SM	20,830	16,012	8,468	8,275	8,980									
Solyc04g006940	Phospholipid-transporting ATPase (AHRD V3.3 *** M1CCQ9_SOLTU)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): PF13246 (PFAM)	0,772	1,124	0,256	0,192	0,214									
Solyc04g006960	ABC transporter family protein (AHRD V3.3 *** A0A097P9T3_HEVBR)	ABCG7	F:GO:0005524; C:GC	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	3,445	2,536	3,256	3,268	3,392									
Solyc04g006970	Phosphoenolpyruvate carboxylase (AHRD V3.3 *** A6YM33_RICCO)		P:GO:0006099; F:GC	P:tricarboxylic acid	EC:4.1.1.31; EC:4.1.	Phosphoenolpyruvate	IPR021135 (PRINTS): IPR021135 (PF	1199,721	1015,133	324,544	162,702	331,587					-0,994	0,002			down
Solyc04g006980	TCP transcription factor 22	TCP22	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	0,000	0,076	0,000	0,000	0,000									
Solyc04g006983	low-molecular-weight cysteine-rich 56 (AHRD V3.3 -** AT3G20993.1)						IPR010851 (PFAM)	0,311	0,968	0,000	0,000	0,000									
Solyc04g006990	bHLH transcription factor 029		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,789	1,014	0,688	1,028	0,778									
Solyc04g007000	AP2/B3 transcription factor family protein (AHRD V3.3 *** AT1G25560.1)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (SMAF RAV	0,161	0,668	0,454	1,487	0,822									
Solyc04g007010	Sn-2 protein (AHRD V3.3 *** Q39467_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR000916 (PF	0,019	0,039	0,000	0,000	0,000									
Solyc04g007020	BRO1 domain-containing protein (AHRD V3.3 *** A0A103XVG7_CYNCS)						IPR004328 (SMART): IPR038499 (G3	97,147	111,041	57,350	55,003	54,338									
Solyc04g007030	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,080	0,099	0,025	0,196	0,071									
Solyc04g007050	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,019	0,000	0,044	0,025	0,024									
Solyc04g007060	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	17,131	28,218	4,826	6,211	7,347	0,748	0,009					up		
Solyc04g007070	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *** AT5G38350.1)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	28,773	105,309	5,382	6,819	10,989	1,896	0,000	1,023	0,003			up	up	
Solyc04g007075	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G69550.1)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,365	0,431	0,000	0,025	0,024									
Solyc04g007090	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G69550.1)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,084	0,160	0,000	0,025	0,000									
Solyc04g007100	Serine/threonine protein phosphatase 2a regulatory subunit A, putative (AHRD V3.3 *** B9ST19_RICCO)		F:GO:0005515	F:protein binding			IPR011989 (G3DSA:1.25.10.GENE3D	20,954	20,671	18,392	17,770	19,397									
Solyc04g007110	Transmembrane protein, putative (AHRD V3.3 *** G7JZC5_MEDTR)		C:GO:0016020	C:membrane			PTHR36367 (PANTHER)	7,319	6,520	9,212	8,809	9,912									
Solyc04g007120	Rad23 UV excision repair protein family (AHRD V3.3 *** AT3G02540.3)		F:GO:0003684; F:GC	F:damaged DNA binding; F:protein binding; C:nucleus; P:nucleot			IPR004806 (PRINTS): IPR006636 (SM	159,260	154,717	283,070	268,705	262,893									
Solyc04g007140	LOW QUALITY:zinc knuckle (CCHC-type) family protein (AHRD V3.3 --* AT5G20220.4)		P:GO:0010112	P:regulation of systemic acquired resistance			IPR031425 (PFAM): PTHR35735:SF1	0,134	1,497	0,115	0,722	0,280									
Solyc04g007150	Alpha-glucosidase (AHRD V3.3 *** Q9LEC9_SOLTU)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:2.60.40.1760 (GENE3D): IPR	40,844	41,538	16,762	16,799	18,693									
Solyc04g007160	Alpha-glucosidase (AHRD V3.3 *-* Q9LEC9_SOLTU)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000322 (PFAM): IPR013780 (G3D	33,734	41,111	13,274	14,866	17,509									
Solyc04g007170	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A0B0PZB9_GOSAR)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINTS): IPR001471 (SM	8,042	9,662	4,832	6,661	6,704									
Solyc04g007200	methylketone synthase IIb						G3DSA:3.10.129.10 (GENE3D): IPR0	0,059	0,019	0,025	0,000	0,000									
Solyc04g007210	CONSTANS-like zinc finger protein (AHRD V3.3 *** I1LEW9_SOYBN)	BBX13	F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR000315 (SMAF CO-like	17,844	17,750	4,447	5,325	4,849									
Solyc04g007220	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)						mobidb-lite (MOBIDB_LITE): PTHR333	20,018	25,110	24,490	15,020	18,844					-0,702	0,000			down
Solyc04g007230	Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *** A0A061ED43_THECC)		P:GO:0015031	P:protein transport			IPR005061 (PFAM): G3DSA:1.20.126	19,772	19,260	24,306	25,215	24,813									
Solyc04g007240	Adenylate isopentenyltransferase (AHRD V3.3 *** I0IUP7_SOLLC)		P:GO:0008033	P:tRNA processing			IPR018022 (PFAM): G3DSA:3.40.50.3	1,164	0,482	0,219	0,240	0,141									
Solyc04g007250	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7K1J5_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR36715 (PANTHER)	0,667	0,427	0,701	1,407	0,781									
Solyc04g007260	Thioesterase-like protein (AHRD V3.3 *** B5B3P5_SOLLC)						IPR006683 (PFAM): G3DSA:3.10.129	6,212	8,770	9,226	9,550	9,573									
Solyc04g007270	PHD finger protein family (AHRD V3.3 *** A0A151U5J9_CAJCA)		F:GO:0046872	F:metal ion binding			IPR001965 (SMART): IPR019787 (PF	62,740	57,633	60,030	57,302	56,069									
Solyc04g007280	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *** A0A0B0NW09_GOSAR)		C:GO:0005643; P:GC	C:nuclear pore; P:nucleocytoplasmic transport; F:structural cons			IPR036903 (G3DSA:3.30.1610.GENE	118,227	99,938	149,736	144,643	140,377									
Solyc04g007290	DUF639 family protein (AHRD V3.3 *** G7L0J4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR006927 (PFAM): PTHR31860 (PAN	0,098	0,082	0,000	0,050	0,023									
Solyc04g007300	bHLH transcription factor 030		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR036638 (G3DS bHLH	0,019	0,000	0,075	0,047	0,046									
Solyc04g007310	Thaumatin (AHRD V3.3 *** A0A103YF64_CYNCS)						IPR001938 (PRINTS): IPR001938 (SM	0,158	0,477	0,000	0,000	0,000									
Solyc04g007320	Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 *** Q2HUD1_MEDTR)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR003593 (SMA	0,146	0,361	0,047	0,295	0,119									
Solyc04g007330	HORMA domain-containing 1 (AHRD V3.3 *** A0A0B0NC02_GOSAR)						IPR003511 (PFAM): IPR036570 (G3D	9,593	6,961	3,044	2,437	2,798									
Solyc04g007340	DUF1639 family protein (AHRD V3.3 *** G7IC98_MEDTR)						IPR012438 (PFAM): mobidb-lite (MOE	13,171	18,512	14,268	11,327	11,874									
Solyc04g007350	DUF1639 family protein (AHRD V3.3 *** G7KMZ9_MEDTR)						IPR012438 (PFAM): PTHR33130:SF1	6,852	11,661	17,272	13,330	13,297									
Solyc04g007360	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 -** A0A072TJU3_MEDTR)						IPR008480 (PFAM): PTHR33265 (PAN	0,000	0,039	0,000	0,000	0,024									
Solyc04g007370	Chaperone protein dnaJ 15 (AHRD V3.3 *** DNJ15_ARATH)						IPR001623 (PRINTS): IPR001623 (SM	39,262	43,460	50,918	51,810	49,151									
Solyc04g007390	Protein kinase family protein (AHRD V3.3 *** AT5G38210.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000615 (	0,040	0,251	0,000	0,095	0,142									
Solyc04g007400	Protein kinase family protein (AHRD V3.3 *-* AT5G38210.2)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR002347 (PRINTS): IPR002347 (PF	6,416	4,980	1,463	1,482	1,579									
Solyc04g007410	transmembrane protein (AHRD V3.3 *** AT3G45050.4)						PTHR37230 (PANTHER)	2,330	3,081	0,985	1,024	1,856									
Solyc04g007420	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT4G28800.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMART): IPR007175 (PF	4,908	3,999	3,326	3,440	3,811									
Solyc04g007450	alpha/beta hydrolase family protein (AHRD V3.3 *** AT1G15060.3)		F:GO:0016298; P:GC	F:lipase activity; P:cellular lipid metabolic process			IPR000073 (PFAM): IPR016969 (PIRS	12,583	10,491	25,388	25,980	22,823									
Solyc04g007460	Octicosapeptide/Phox/Bem1p family protein, putative (AHRD V3.3 *** A0A061E4Y6_THECC)		F:GO:0005515	F:protein binding			IPR000270 (SMART): IPR000270 (PF	78,462	55,616	60,464	58,779	58,561									
Solyc04g007470	Drought responsive Zinc finger protein	BBX27	F:GO:0008270	F:zinc ion binding			IPR000315 (SMART): mobidb-lite (MO	1,070	1,404	6,310	7,383	7,791									
Solyc04g007480	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G31050.8)							0,241	0,300	0,191	0,025	0,210									
Solyc04g007490	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	44,346	33,373	26,912	25,473	26,306									
Solyc04g007500	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G04240.2)		C:GO:0016021; F:GC	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR013083 (G3	98,675	98,095	36,448	35,873	35,160									
Solyc04g007510	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9SJY8_RICCO)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR014001 (SMART): IPR001650 (SM	14,348	12,069	17,769	19,605	17,543									
Solyc04g007520	Phosphatidylserine synthase 2 (AHRD V3.3 *** W8TFN0_TOBAC)		P:GO:0006659	P:phosphatidylserine biosynthetic process			IPR004277 (PFAM): PTHR15362:SF2	15,683	12,440	16,175	16,865	15,761									
Solyc04g007530	Protein DETOXIFICATION (AHRD V3.3 *** K4BNR0_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): IPR002528 (TIGF	3,543	5,591	7,604	8,663	8,123									
Solyc04g007540	Protein DETOXIFICATION (AHRD V3.3 *** K4BNR1_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	26,375	20,249	10,491	10,074	9,645									
Solyc04g007550	ATP synthase subunit beta (AHRD V3.3 *** W8SRJ3_TOBAC)		C:GO:0000275; F:GC	C:mitochondrial pro	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): PIRSF039072 (	258,753	273,299	273,707	242,124	241,587									
Solyc04g007560	ALG-2 interacting protein X (AHRD V3.3 *** A0A0B2PBQ1_GLYSO)		F:GO:0005515	F:protein binding			IPR004328 (SMART): G3DSA:1.20.12	89,531	74,537	124,934	123,157	116,992									
Solyc04g007570	GDSL esterase/lipase 6 (AHRD V3.3 *** W9RD56_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	2,611	1,457	0,025	0,126	0,000									
Solyc04g007580	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IAV0_MEDTR)						IPR025322 (PFAM): PTHR33052:SF2	23,727	11,383	11,326	24,439	16,358					1,112	0,001			up
Solyc04g007590	WAT1-related protein (AHRD V3.3 *** K4BNR6_SOLLC)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	0,663	0,633	0,296	0,000	0,000									
Solyc04g007600	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EGA0_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	13,094	12,513	22,123	19,550	20,496									
Solyc04g007610	Sulfhydryl oxidase (AHRD V3.3 *** K4BNR8_SOLLC)		F:GO:0016971; P:GC	F:flavin-linked sulfh	EC:1.8.3.2	Thiol oxidase	IPR013766 (PFAM): IPR017905 (PFA	44,762	48,108	59,645	56,700	59,205									
Solyc04g007620	LOW QUALITY:mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT2G01300.1)		C:GO:0016021	C:integral component of membrane			PTHR33782:SF5 (PANTHER): PTHR3	7,965	3,951	2,720	8,156	4,812	-0,988	0,035			1,581	0,000	down		up
Solyc04g007630	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT1G71050.1)		P:GO:0030001; F:GC	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0	0,061	0,021	0,137	0,234	0,117									
Solyc04g007640	U-box domain-containing protein 10 (AHRD V3.3 *** A0A061E7I3_THECC)		F:GO:0004842; F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR000225 (SMART): IPR003613 (SM	31,281	20,810	32,744	37,907	32,654									
Solyc04g007650	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** W9S0D4_9ROSA)		F:GO:0005524; F:GC	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;			IPR002498 (SMART): G3DSA:1.20.58	56,713	38,085	16,372	15,597	19,333									
Solyc04g007660	LOW QUALITY:Six-bladed beta-propeller, TolB-like protein (AHRD V3.3 *** A0A103XVG9_CYNCS)		C:GO:0005774; C:GC	C:vacuolar membrane; C:endoplasmic reticulum; C:plasma mem			IPR011042 (G3DSA:2.120.10.GENE3I	12,481	14,991	12,079	11,002	9,981									
Solyc04g007670	LOW QUALITY:CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,060	0,022	0,000	0,000									
Solyc04g007685	Hydroxyproline-rich glycoprotein (AHRD V3.3 -** B9HJA6_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,396	0,379	0,096	0,214	0,117									
Solyc04g007690	SIPIN3	PIN3	C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): IPR014024 (TIGF	4,949	6,098	0,216	0,294	0,470									
Solyc04g007700	transmembrane protein (AHRD V3.3 *** AT1G14990.1)		C:GO:0016021	C:integral component of membrane			PTHR36712 (PANTHER)	15,666	14,248	18,145	15,381	17,204									
Solyc04g007705	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT5G53090.1)							0,105	0,021	0,025	0,000	0,073									

Solyc04g007710	mitogen-activated protein kinase 14	mapk14	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	27,481	32,761	14,720	14,300	17,151									
Solyc04g007720	LOW QUALITY:Histone H1 (AHRD V3.3 *-* A0A151SYJ4_CAJCA)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR005818 (SMART): IPR005818 (PF	7,790	5,420	3,420	2,325	3,264									
Solyc04g007730	fold protein (AHRD V3.3 *** AT1G23110.7)						PTHR35100:SF1 (PANTHER): PTHR3	14,790	13,577	20,876	18,483	17,085									
Solyc04g007750	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR000916 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc04g007760	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR000916 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc04g007763	Major latex-like protein (AHRD V3.3 *** B5THI3_PANGI)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	0,000	0,018	0,025	0,000	0,000									
Solyc04g007767	Major latex-like protein (AHRD V3.3 -** Q9AXU0_PRUPE)		P:GO:0006952	P:defense response			IPR023393 (G3DSA:3.30.530.GENE3	7,528	5,826	7,651	7,306	5,473									
Solyc04g007770	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	5424,950	3714,040	2907,992	2810,278	2711,707									
Solyc04g007780	MLP (AHRD V3.3 *** G8DRV9_GOSBA)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	18,212	13,292	4,584	5,647	3,336									
Solyc04g007790	MLP-like protein (AHRD V3.3 *** G8DRW0_GOSBA)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	1,024	0,771	1,263	0,521	0,401									
Solyc04g007795	Major latex-like protein (AHRD V3.3 *** K9MJR1_9ASTR)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	0,252	0,200	0,000	0,000	0,000									
Solyc04g007800	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G70810.1)						IPR000008 (SMART): IPR000008 (PF	0,867	0,754	0,852	0,953	0,590									
Solyc04g007810	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,079	0,019	0,166	0,145	0,422									
Solyc04g007820	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR000916 (PF	0,000	0,000	0,025	0,000	0,000									
Solyc04g007840	Senescence-associated protein, putative (AHRD V3.3 *** Q2HTL2_MEDTR)						PTHR33270:SF5 (PANTHER): IPR040	8,664	8,565	13,243	13,887	12,019									
Solyc04g007850	Protein BCCIP homolog (AHRD V3.3 *** A0A0V0I1F4_SOLCH)						IPR025602 (PFAM): IPR025602 (PIRS	11,188	13,902	13,856	12,735	12,183									
Solyc04g007860	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** A0A061E7Q5_THECC)		F:GO:0005545; C:GC	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART): IPR011417 (PF	102,741	99,459	117,000	111,162	110,726									
Solyc04g007870	zein-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *-* AT3G54740.8)		F:GO:0017022	F:myosin binding			IPR007656 (PFAM): IPR039306 (PAN	80,586	83,709	50,762	69,429	62,574					0,454	0,013			up
Solyc04g007880	Receptor-like kinase (AHRD V3.3 *** G7IA07_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	169,567	199,801	97,863	219,283	177,700			0,858	0,000	1,167	0,000		up	up
Solyc04g007890	HMG-Y-related protein A (AHRD V3.3 *** HMGYA_ARATH)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR000116 (PRINTS): IPR017956 (PF	124,304	145,171	87,498	93,095	97,659									
Solyc04g007900	Plant cadmium resistance 2, putative (AHRD V3.3 *** A0A061E9L3_THECC)		C:GO:0016021	C:integral component of membrane			IPR006461 (TIGRFAM): IPR006461 (F	24,395	40,291	7,919	10,711	12,202									
Solyc04g007910	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SP53_RICCO)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR000490 (PF	6,419	6,396	1,092	0,872	1,129									
Solyc04g007920	B-cell receptor-associated-like protein (AHRD V3.3 *** AT5G17190.1)		C:GO:0005783; P:GC	C:endoplasmic reticulum; P:intracellular protein transport; C:inte			IPR040463 (PFAM): IPR008417 (PAN	0,040	0,249	0,049	0,252	0,000									
Solyc04g007940	Cytochrome P450 monooxygenase (AHRD V3.3 *** A7KMF3_NICSY)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,061	0,060	0,050	0,000	0,000									
Solyc04g007950	Cysteine-rich repeat secretory 12-like protein (AHRD V3.3 *** A0A0B0NFR5_GOSAR)		C:GO:0009506; C:GC	C:plasmodesma; C:integral component of membrane; P:defense			IPR038408 (G3DSA:3.30.430.GENE3	5,545	4,719	1,825	2,176	2,595									
Solyc04g007960	Ubiquitin-conjugating enzyme, E2 (AHRD V3.3 *** A0A103XCT0_CYNCS)						SM00212 (SMART): IPR000608 (PFAI	1,162	1,154	1,689	2,528	1,955									
Solyc04g007970	Ubiquitin-conjugating enzyme, E2 (AHRD V3.3 *** A0A103XCT0_CYNCS)						SM00212 (SMART): IPR016135 (G3D	16,388	17,061	9,698	7,723	7,860									
Solyc04g007980	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	53,720	56,670	155,691	147,693	159,976									
Solyc04g007990	LOW QUALITY:ATP synthase subunit beta, chloroplastic (AHRD V3.3 --* ATPB_CALFL)		P:GO:0008150	P:biological_process			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,299	4,439	0,352	0,437	0,494	1,799	0,001					up		
Solyc04g008010	Protein VAC14 like (AHRD V3.3 *** A0A0B2Q990_GLYSO)		F:GO:0005509; P:GC	F:calcium ion binding; P:phosphatidylinositol biosynthetic proces			IPR002048 (SMART): IPR011989 (G3	21,626	18,223	25,779	31,371	27,632									
Solyc04g008020	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61180.1)		C:GO:0016021; F:GC	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR013083 (G3	26,556	17,439	22,110	22,203	19,239	-0,579	0,024					down		
Solyc04g008030	Cleavage and polyadenylation specificity factor, putative (AHRD V3.3 *** B9SJ31_RICCO)		C:GO:0016021	C:integral component of membrane			IPR022712 (SMART): IPR001279 (SM	4,564	6,048	5,076	5,382	5,330									
Solyc04g008040	Microtubule-associated protein 70-2 (AHRD V3.3 *** MP702_ARATH)		P:GO:0007010; F:GC	P:cytoskeleton organization; F:microtubule binding			IPR009768 (PFAM): mobidb-lite (MOB	18,269	19,351	1,374	0,939	1,452									
Solyc04g008050	Two-component response regulator (AHRD V3.3 *** W9QMB4_9ROSA)		P:GO:0000160; F:GC	P:phosphorelay signal transduction system; F:DNA binding			IPR001789 (SMAF ARR-B	54,014	45,021	19,521	19,191	24,204									
Solyc04g008060	Iron vacuolar transporter (AHRD V3.3 *** W8VRG3_CENCY)		F:GO:0005381; F:GC	F:iron ion transmembrane transporter activity; F:manganese ior			IPR008217 (PFAM): IPR008217 (PAN	1,937	2,699	0,570	0,490	0,753									
Solyc04g008070	cyclinSDS	SDS	C:GO:0005634	C:nucleus			IPR013763 (SMART): G3DSA:1.10.47	0,101	0,097	0,000	0,000	0,048									
Solyc04g008075	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR002160 (SMART): G3DSA:2.80.10	0,019	0,000	0,000	0,000	0,000									
Solyc04g008080	LOW QUALITY:Dirigent protein (AHRD V3.3 *** K4BNW4_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495:SF7	0,000	0,000	0,000	0,000	0,023									
Solyc04g008090	PLATZ transcription factor family protein, putative (AHRD V3.3 *** A0A061EGB3_THECC)		F:GO:0008270	F:zinc ion binding			IPR006734 (PFAM): IPR006734 (PAN	0,063	0,140	0,022	0,048	0,071									
Solyc04g008100	U-box domain-containing protein (AHRD V3.3 *** A0A0A0RAL4_9ROSI)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR013083 (G3	10,156	6,213	4,074	7,832	3,878									
Solyc04g008110	Histidine kinase (AHRD V3.3 *** Q2ACB8_MAIZE)		F:GO:0000155; P:GC	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR003594 (SM	88,575	51,570	51,887	42,230	41,687	-0,752	0,017					down		
Solyc04g008120	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q6_9SOLN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	3,615	3,415	0,299	0,201	0,357									
Solyc04g008130	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q9_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,201	0,507	0,148	0,247	0,188									
Solyc04g008140	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	0,061	0,000	0,050	0,000	0,024									
Solyc04g008150	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,042	0,062	0,000	0,000	0,000									
Solyc04g008160	hero resistance 2	help2	F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,019	0,039	0,000	0,000	0,000									
Solyc04g008170	hero resistance 3	help3	F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,038	0,000	0,147	0,048	0,024									
Solyc04g008200	LES457048 hero resistance protein 1 homologue	help1	F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	13,657	15,500	5,911	6,940	7,920									
Solyc04g008210	ETAG-A3	ETAG-A3	F:GO:0004553; C:GC	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR016455 (PIRSF): IPR010713 (PFA	10,876	8,351	16,097	27,872	27,569			0,772	0,000	0,794	0,000		up	up
Solyc04g008220	Protein OBERON 3 (AHRD V3.3 *** A0A0B2R231_GLYSO)		P:GO:0009790; P:GC	P:embryo development; P:root morphogenesis; P:maintenance			IPR004082 (PRINTS): IPR032881 (PF	7,263	6,093	6,430	6,028	6,866									
Solyc04g008230	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G48100.1)	PG6	F:GO:0004650; P:GC	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	4,848	7,009	0,715	0,675	0,591									
Solyc04g008240	Oxidoreductase, 2OG-Fe(II) oxygenase family protein (AHRD V3.3 *** A0A0K9PBA8_ZOSMR)						IPR037151 (G3DSA:2.60.120.GENE3	97,203	129,306	82,460	79,168	87,397									
Solyc04g008250	PURPLE ACID PHOSPHATASE family protein (AHRD V3.3 *** U5G823_POPTR)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR024927 (PIRSF): IPR029052 (G3D	0,019	0,114	0,359	0,320	0,094									
Solyc04g008260	PURPLE ACID PHOSPHATASE family protein (AHRD V3.3 *** U5G823_POPTR)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR024927 (PIRSF): IPR029052 (G3D	1,706	1,843	1,623	2,145	1,535									
Solyc04g008280	4-hydroxy-4-methyl-2-oxoglutarate aldolase (AHRD V3.3 *** K4BNY4_SOLLC)		F:GO:0008428; P:GC	F:ribonuclease inhibitor activity; P:regulation of RNA metabolic			G3DSA:3.50.30.40 (GENE3D): IPR01	98,257	101,163	125,028	108,295	110,468									
Solyc04g008290	microtubule-associated protein 65-7 (AHRD V3.3 *** AT1G14690.2)		P:GO:0000226; F:GC	P:microtubule cytoskeleton organization; F:microtubule binding			G3DSA:1.20.58.1520 (GENE3D): PF0	49,949	32,532	16,987	17,416	19,689	-0,591	0,032					down		
Solyc04g008295	Protein kinase superfamily protein (AHRD V3.3 *** AT1G65950.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	25,799	15,816	41,448	37,282	41,444	-0,677	0,013					down		
Solyc04g008310	Glycosyltransferase (AHRD V3.3 *** K4BNY7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR	50,233	54,445	28,745	26,702	34,360									
Solyc04g008320	Glycosyltransferase (AHRD V3.3 *-* M1CLU3_SOLTU)		C:GO:0016021; F:GC	C:integral component of membrane; F:transferase activity, trans			G3DSA:3.40.50.2000 (GENE3D): PTH	0,000	0,000	0,000	0,000	0,023									
Solyc04g008330	Glycosyltransferase (AHRD V3.3 *** M1CVU0_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR	0,538	0,413	0,075	0,097	0,024									
Solyc04g008340	IAA-alanine resistance protein 1 (AHRD V3.3 *** IAR1_ARATH)		C:GO:0016020; P:GC	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR003689 (PFAM): mobidb-lite (MOB	83,237	76,969	118,153	103,984	108,266									
Solyc04g008360	Protein OBERON 3 (AHRD V3.3 *-* A0A0B2R231_GLYSO)		P:GO:0009790; P:GC	P:embryo development; P:root morphogenesis; P:maintenance			IPR004082 (PRINTS): IPR032881 (PF	1,390	1,405	0,294	0,223	0,446									
Solyc04g008370	Serine/threonine-protein kinase (AHRD V3.3 *** M1CVL4_SOLTU)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR003609 (SMART): IPR001480 (SM	0,617	0,780	0,738	0,460	0,495									
Solyc04g008380	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN86_SOLLC)						IPR010409 (SMAF BBR-BPC	78,166	83,073	87,620	85,631	80,901									
Solyc04g008385	Serine/threonine-protein kinase (AHRD V3.3 *** M1CVL4_SOLTU)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001480 (SM	0,097	0,078	0,119	0,025	0,072									
Solyc04g008390	Serine/threonine-protein kinase (AHRD V3.3 *** M1CVL4_SOLTU)		F:GO:0004674; F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR003609 (SMART): IPR001480 (SM	1,269	0,809	0,969	1,135	0,824									
Solyc04g008410	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G03100.1)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	6,881	3,907	4,839	5,922	5,907									
Solyc04g008430	Leucine-rich receptor kinase (AHRD V3.3 *** E5F701_9BRAS)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	1,458	1,516	0,914	1,039	1,062									
Solyc04g008450	Potassium transporter (AHRD V3.3 *-* K4BP01_SOLLC)		F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): PTHR30540:SF5	1,031	1,042	0,559	0,701	0,774									
Solyc04g008455	Potassium transporter (AHRD V3.3 *** K4BP01_SOLLC)		F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): PTHR30540:SF5	1,101	1,124	0,609	0,898	1,078									
Solyc04g008460	SET-domain containing protein lysine methyltransferase family protein (AHRD V3.3 --* AT5G43990.9)							178,637	193,638	114,343	91,616	101,083									
Solyc04g008470	Defensin (AHRD V3.3 *** C1K3M7_VIGUN)		P:GO:0006952	P:defense response			IPR008176 (PRINTS): IPR003614 (SM	0,539	0,495	0,025	0,000	0,000									
Solyc04g008480	MYB transcription factor-like (AHRD V3.3 *-* A0A0K9PMY6_ZOSMR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	0,021	0,021	0,000	0,000	0,024									
Solyc04g008490	putative NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7		C:GO:0005739; F:GC	C:mitochondrion; F:	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR008698 (PFAM): mobidb-lite (MOB	45,330	45,440	62,047	53,964	53,551									
Solyc04g008500	Zinc finger protein, putative (AHRD V3.3 *** B9S7A8_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	7,620	9,427	4,544	6,010	5,279									
Solyc04g008510	UBX domain-containing protein (AHRD V3.3 *** K4BP07_SOLLC)		F:GO:0005515	F:protein binding			IPR006577 (SMART): PF14555 (PFAM	46,634	46,406	45,613	45,233	41,426									
Solyc04g008520	Outer envelope pore protein 37, chloroplastic (AHRD V3.3 *** OEP37_PEA)		F:GO:0005216; P:GC	F:ion channel activity; P:cation transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	46,388	51,257	56,429	52,063	58,081									
Solyc04g008530	TRAF-like family protein (AHRD V3.3 *** AT3G17380.1)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR008974 (G3	0,000	0,000	0,000	0,000	0,024									
Solyc04g008540	LeTH1tobamovirus multiplication 1 homolog	th1	C:GO:0016021	C:integral component of membrane			IPR009457 (PFAM): IPR040226 (PAN	25,388	18,094	28,109	29,802	28,022									
Solyc04g008550	Zinc finger transcription factor 31	C3H31	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	37,564	48,105	45,131	41,384	43,332									
Solyc04g008560	PPR containing protein (AHRD V3.3 *** AT2G02148.5)						mobidb-lite (MOBIDB_LITE): PTHR135	12,428	10,746	13,532	11,515	12,280									
Solyc04g008570	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GUB4_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	3,177	5,129	2,039	3,143	4,117									
Solyc04g008580	Ankyrin repeat family protein (AHRD V3.3 *** B9HNG0_POPTR)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	17,278	15,030	21,036	19,113	19,682									
Solyc04g008590	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** A0A0B0NLW1_GOSAR)		F:GO:0003824	F:catalytic activity			IPR005475 (SMART): IPR009014 (G3	54,688	62,332	104,222	112,086	103,972									
Solyc04g008600	Zinc knuckle family protein (AHRD V3.3 *** B9HVL9_POPTR)		P:GO:0000076; F:GC	P:DNA replication checkpoint; F:nucleic acid binding; C:nucleus;			IPR001878 (SMART): IPR012923 (PF	1,436	1,346	0,165	0,145	0,237									
Solyc04g008610	Histone acetyltransferase (AHRD V3.3 *** A0A0U5B4W5_TOBAC)		F:GO:0003712; F:GC	F:transcription core	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR013178 (SMART): IPR000433 (SM	54,614	42,664	58,205	70,064	65,146									
Solyc04g008615	MATH domain and coiled-coil domain-containing protein At3g44800 (AHRD V3.3 --* MCC14_ARATH)						mobidb-lite (MOBIDB_LITE)	0,237	0,106	0,372	0,174	0,261									
Solyc04g008620	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** B6ETT7_ARATH)		F:GO:0008289	F:lipid binding			IPR000008 (SMART): IPR000008 (PF	28,586	39,735	52,975	48,775	51,483									
Solyc04g008625	Mannose/glucose-specific lectin alpha 2 chain (AHRD V3.3 --* LEC2_LATOC)							0,021	0,000	0,025	0,048	0,071									
Solyc04g008630	Autophagy-related protein 9 (AHRD V3.3 *** A0A0K0XR24_TOBAC)		C:GO:0005794; P:GC	C:Golgi apparatus; P:autophagy; P:protein transport; C:integral			IPR007241 (PFAM): mobidb-lite (MOB	17,338	15,727	27,868	31,842	26,784									
Solyc04g008640	Conserved oligomeric Golgi complex, subunit 3 (AHRD V3.3 *** A0A103Y6H1_CYNCS)		C:GO:0005801; P:GC	C:cis-Golgi network; P:intracellular protein transport; C:membrai			IPR007265 (PFAM): IPR007265 (PAN	59,930	56,680	50,553	54,508	53,494									
Solyc04g008650	Receptor-kinase, putative (AHRD V3.3 *** B9RY46_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR013210 (PFAM): IPR032675 (G3D	6,338	12,057	1,323	1,803	1,616	0,956	0,006					up		
Solyc04g008660	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *-* G5DWI4_SILLA)		F:GO:0005515; C:GC	F:protein binding; C:cytoplasm			IPR004148 (SMART): PF16746 (PFAM	12,901	9,419	11,148	13,269	11,942									
Solyc04g008665	ADP-ribosylation factor GTPase-activating protein AGD2 (AHRD V3.3 *** AGD2_ARATH)		F:GO:0005096; F:GC	F:GTPase activator activity; F:protein binding			IPR001164 (PRINTS): IPR002110 (SM	22,178	18,658	22,488	24,233	21,566									
Solyc04g008670	Gibberellin 2-beta-dioxygenase (AHRD V3.3 *** A0A072UXE4_MEDTR)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,019	0,019	0,000	0,022	0,000									
Solyc04g008680	DBC1/CARP1-like protein (AHRD V3.3 *** A0A103XRU5_CYNCS)		F:GO:0005509; P:GC	F:calcium ion binding; P:regulation of transcription, DNA-templat			IPR025954 (SMART): IPR005123 (PF	111,247	91,466	105,386	110,481	109,578									
Solyc04g008690	ZZ-type zinc finger-containing protein 3, putative isoform 1 (AHRD V3.3 *** A0A061EGG8_THECC)		F:GO:0003677	F:DNA binding			IPR022228 (PFAM): PTHR14000 (PAN	23,548	16,905	8,324	8,052	8,739									
Solyc04g008700	Transcription elongation regulator 1 (AHRD V3.3 *** A0A1D1XFU2_9ARAE)		F:GO:0005515	F:protein binding			IPR001202 (SMART): IPR002713 (SM	54,919	50,087	55,107	54,894	52,790									
Solyc04g008710	tRNA 2-thiocytidine biosynthesis TtcA (AHRD V3.3 *-* A0A0B0N6V1_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	41,806	59,350	75,776	81,470	85,193									
Solyc04g008720	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *** K4BP28_SOLLC)		F:GO:0008017; C:GC	F:microtubule binding; C:katanin complex; P:microtubule severin			IPR020472 (PRINTS): IPR001680 (SM	17,830	14,902	13,729	14,918	13,409									
Solyc04g008730	Alpha-galactosidase (AHRD V3.3 *** K4BP29_SOLLC)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR002241 (PRINTS): IPR002241 (PF	32,431	40,396	25,215	20,822	26,504									
Solyc04g008740	Pyruvate kinase (AHRD V3.3 *** K4BP30_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS): IPR001697 (TI	314,637	302,274	444,938	392,540	401,070									
Solyc04g008750	Transcription elongation factor SPT4 homolog (AHRD V3.3 *** K4BP31_SOLLC)		C:GO:0005634; F:GC	C:nucleus; F:zinc ion binding; P:positive regulation of DNA-temp			IPR022800 (SMART): IPR009287 (PIF	32,492	33,297	32,228	27,868	30,801									
Solyc04g008760	Homoserine kinase (AHRD V3.3 *** A0A097PK94_SOLTU)		F:GO:0004413; F:GC	F:homoserine kinas	EC:2.7.1.39	Homoserine kinase	PR00958 (PRINTS): IPR013750 (PFA	12,081	10,335	21,092	16,957	18,563									
Solyc04g008770	Mitochondrial intermembrane space import and assembly protein 40 homolog (AHRD V3.3 *** MIA40_ARATH		F:GO:0015035; P:GC	F:protein disulfide oxidoreductase activity; P:protein import into			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,812	3,133	6,067	7,003	6,268									
Solyc04g008780	Dihydroflavonol 4-reductase family (AHRD V3.3 *** D7MD06_ARALL)	DFR	F:GO:0003824; F:GC	F:catalytic activity; F:coenzyme binding; P:sporopollenin biosyn			G3DSA:3.40.50.720 (GENE3D): IPR0	3,408	3,495	2,373	2,416	2,095									
Solyc04g008790	Ribosomal protein L1 (AHRD V3.3 *** A0A124SGR3_CYNCS)		P:GO:0000470; F:GC	P:maturation of LSU-rRNA; F:RNA binding; C:90S preribosome			IPR016095 (G3DSA:3.40.50.GENE3D	5,334	4,387	5,464	6,539	4,887									
Solyc04g008800	Protein translocase subunit SecA (AHRD V3.3 *** A0A0B0MG38_GOSAR)		C:GO:0005739; C:GC	C:mitochondrion; C:plastid			mobidb-lite (MOBIDB_LITE): PTHR367	21,898	24,383	35,075	32,937	32,350									
Solyc04g008810	40S ribosomal S26-like protein (AHRD V3.3 *** I3S2G2_MEDTR)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000892 (PFAM): IPR038551 (G3D	77,730	89,196	79,998	72,347	73,912									
Solyc04g008820	High mobility group protein (AHRD V3.3 *-* O49948_SOLTU)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus; P:polar nucleus fusion			IPR009071 (SMART): IPR036910 (G3	8,397	8,227	1,476	0,486	0,818					-1,588	0,002			down
Solyc04g008840	Protein FRIGIDA, putative (AHRD V3.3 *** B9SG32_RICCO)		P:GO:0009908; P:GC	P:flower development; P:cell differentiation			IPR012474 (PFAM): mobidb-lite (MOB	15,127	12,306	21,091	17,309	19,583									
Solyc04g008850	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G20015.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	1,739	4,875	0,245	0,323	0,284	1,508	0,001					up		
Solyc04g008860	protein arginine methyltransferase 6 (AHRD V3.3 *** AT3G20020.1)		P:GO:0006479; F:GC	P:protein methylation; F:methyltransferase activity			PF06325 (PFAM): G3DSA:3.40.50.15	18,880	16,819	24,000	23,573	23,515									
Solyc04g008870	Myb family transcription factor family protein (AHRD V3.3 *** B9H5N1_POPTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	3,471	3,944	3,724	3,257	2,942									
Solyc04g008880	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (AHRD V3.3 *** A0A199UNF2_ANACO)		F:GO:0005524; P:GC	F:ATP binding; P:biosynthetic process; F:ligase activity			IPR013221 (PFAM): G3DSA:3.40.139	1,552	2,323	0,424	0,270	0,447									
Solyc04g008890	Splicing factor 3B, subunit 5 (AHRD V3.3 *** A0A103XPM0_CYNCS)		P:GO:0000398	P:mRNA splicing, via spliceosome			IPR017089 (PIRSF): IPR009846 (PFA	1,309	0,952	0,661	0,665	0,849									
Solyc04g008910	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50160.1)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN	0,121	0,178	0,163	0,174	0,189									
Solyc04g008915	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50170.1)		C:GO:0016020	C:membrane			IPR004158 (PFAM): IPR004158 (PAN	0,508	0,324	0,642	0,268	0,425									
Solyc04g008920	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT3G50160.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN	0,058	0,021	0,025	0,000	0,048									
Solyc04g008930	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)						IPR004182 (SMART): IPR004182 (PF	0,339	0,430	0,477	0,805	0,448									
Solyc04g008940	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *-* A0A061E267_THECC)						IPR004182 (SMART): IPR004182 (PF	3,452	4,329	2,558	2,834	2,621									
Solyc04g008950	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)						IPR004182 (SMART): IPR004182 (PF	0,940	0,788	0,440	1,053	0,519									
Solyc04g008960	GRAM domain-containing protein / ABA-responsive protein-like protein (AHRD V3.3 *** AT5G23370.1)						IPR004182 (SMART): IPR004182 (PF	0,587	0,452	0,169	0,175	0,167									
Solyc04g008970	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)						IPR004182 (SMART): IPR011993 (G3	2,613	3,601	0,820	0,702	0,685									
Solyc04g008980	F-box/LRR protein (AHRD V3.3 *** I3SW78_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001611 (PF	11,119	7,906	9,480	6,668	7,086									
Solyc04g008990	Riboflavin biosynthesis protein ribF (AHRD V3.3 *** W9RX51_9ROSA)		F:GO:0003919; P:GC	F:FMN adenylyltran	EC:2.7.7.2	FAD synthetase	IPR014729 (G3DSA:3.40.50.GENE3D	7,629	6,839	6,820	7,322	7,860									
Solyc04g009000	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XCD9_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,841	3,702	3,151	2,863	2,470									
Solyc04g009010	Protein-S-isoprenylcysteine O-methyltransferase (AHRD V3.3 *** K4BP57_SOLLC)		F:GO:0004671; C:GC	F:protein C-terminal	EC:2.1.1.1	Protein-S-isoprenylcy	G3DSA:1.20.120.1630 (GENE3D): IPF	8,623	7,721	8,856	9,425	7,957									
Solyc04g009020	PsbB mRNA maturation factor Mbb1 (AHRD V3.3 *** W9RTZ1_9ROSA)		F:GO:0005515; P:GC	F:protein binding; P:RNA processing			IPR003107 (SMART): IPR019734 (SM	9,322	13,259	5,260	8,631	13,638			1,366	0,000				up	
Solyc04g009030	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4BP59_SOLLC)	GADPHL	P:GO:0006006; F:GC	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR020828 (SM	208,283	546,290	134,447	198,402	454,838	1,419	0,000	1,755	0,000	0,566	0,045	up	up	up
Solyc04g009040	Receptor-kinase, putative (AHRD V3.3 *** B9SZK5_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	0,000	0,021	0,000	0,000	0,000									
Solyc04g009050	Dentin sialophosphoprotein-related, putative isoform 5 (AHRD V3.3 *** A0A061E2G0_THECC)		P:GO:0006355; P:GC	P:regulation of transcription, DNA-templated; P:circadian rhythm			mobidb-lite (MOBIDB_LITE): mobidb-lit	33,785	37,721	34,803	41,402	40,179									
Solyc04g009060	CD2 antigen cytoplasmic tail-binding 2 (AHRD V3.3 *** A0A0B0NJW2_GOSAR)		C:GO:0005682	C:U5 snRNP			mobidb-lite (MOBIDB_LITE): mobidb-lit	29,797	26,568	37,022	37,424	36,574									
Solyc04g009100	Disease resistance family protein (AHRD V3.3 *-* B9NHG2_POPTR)		F:GO:0043531	F:ADP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	0,000	0,000	0,000	0,022	0,000									
Solyc04g009110	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,078	0,097	0,000	0,025	0,000									
Solyc04g009120	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	0,021	0,037	0,000	0,025	0,069									
Solyc04g009130	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): PF18052 (PFAM)	0,275	0,667	0,000	0,000	0,000									
Solyc04g009135	R2 late blight resistance protein (AHRD V3.3 *-* E0Y3W5_9SOLN)		F:GO:0043531	F:ADP binding				0,000	0,059	0,000	0,000	0,000									
Solyc04g009140	39S ribosomal protein L46, mitochondrial (AHRD V3.3 *** A0A0B2RLR6_GLYSO)		F:GO:0003735	F:structural constituent of ribosome			G3DSA:3.90.79.10 (GENE3D): mobidt	3,635	4,090	6,725	5,908	6,223									
Solyc04g009145	tRNA wybutosine-synthesizing protein 2/3/4 (AHRD V3.3 --* TYW23_ARATH)							0,078	0,039	0,050	0,025	0,024									
Solyc04g009150	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	0,000	0,000	0,000	0,025	0,000									

Solyc04g009153	Disease resistance protein (AHRD V3.3 *-* D1GEE0_BRARP)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:3.40.50.3	0,593	0,414	0,434	0,368	0,518									
Solyc04g009155	Disease resistance family protein (AHRD V3.3 *-* B9GY55_POPTR)		F:GO:0043531	F:ADP binding		IPR002182 (PFAM): PTHR43886 (PAN	0,526	0,200	0,240	0,387	0,377									
Solyc04g009157	disease resistance family protein / LRR family protein (AHRD V3.3 --* AT2G34930.1)		F:GO:0043531	F:ADP binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,636	0,295	0,461	0,580	0,522									
Solyc04g009160	Nascent polypeptide-associated complex subunit beta (AHRD V3.3 --* A0A0E0EZ19_9ORYZ)					mobidb-lite (MOBIDB_LITE): mobidb-lit	14,541	9,714	10,478	10,853	9,749									
Solyc04g009170	RING/U-box superfamily protein (AHRD V3.3 *** AT3G19950.3)		F:GO:0061630	F:ubiquitin protein ligase activity		IPR001841 (SMART): IPR039525 (PF.	4,855	4,236	5,251	4,025	5,025									
Solyc04g009180	TCP transcription factor 14	TCP14	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR017887 (PFAM TCP	6,255	4,544	3,144	4,887	5,049									
Solyc04g009190	UPF0664 stress-induced protein C29B12.11c (AHRD V3.3 *** A0A0B2PCL5_GLYSO)		F:GO:0003713: C:G(	F:transcription coactivator activity; C:nucleus; F:chromatin DNA		mobidb-lite (MOBIDB_LITE): mobidb-lit	7,251	6,887	8,963	8,734	8,593									
Solyc04g009200	glutamate 1-semialdehyde 2,1-aminomutase	GSA-AM	F:GO:0008483: F:G(	F:transaminase act EC:5.4.3.8	Glutamate-1-semiald	IPR005814 (PFAM): IPR015421 (G3D	79,977	126,829	68,463	70,932	97,775	0,693	0,025	0,511	0,001			up	up	
Solyc04g009210	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061E2B0_THECC)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (PFA	2,649	2,944	2,686	2,108	2,016									
Solyc04g009220	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T720_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (TIGF	3,211	3,140	3,214	2,846	3,084									
Solyc04g009230	Thioredoxin-like protein 4A (AHRD V3.3 *** A0A151RDS9_CAJCA)		P:GO:0000398: C:G(	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con		IPR004123 (SMART): IPR004123 (PIF	32,239	30,057	91,372	86,162	83,647									
Solyc04g009240	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:3.40.50.3	0,084	0,019	0,000	0,022	0,000									
Solyc04g009250	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): IPR032675 (G3D	0,277	0,553	0,200	0,668	0,118									
Solyc04g009260	stomatal cytokinesis defective / SCD1 protein (SCD1) (AHRD V3.3 --* AT1G49040.1)						1,504	0,636	0,713	0,666	0,541									
Solyc04g009280	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT3G57180.1)		F:GO:0005525: C:G(	F:GTP binding; C:chloroplast stroma; P:brassinosteroid mediate		mobidb-lite (MOBIDB_LITE): PTHR110	1,056	0,795	1,449	2,417	1,345									
Solyc04g009290	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): IPR032675 (G3D	2,206	2,885	3,900	6,347	4,825									
Solyc04g009300	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G57180.1)		F:GO:0005525	F:GTP binding		IPR006073 (PFAM): G3DSA:3.40.50.3	17,674	18,837	40,318	33,368	37,118									
Solyc04g009310	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4BP87_SOLLC)		F:GO:0004252: P:G(	F:serine-type endor EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): G3DSA:3.90.22	8,701	10,115	12,137	12,625	14,030									
Solyc04g009320	Hsp70 nucleotide exchange factor FES1 (AHRD V3.3 *** A0A0B0MDD7_GOSAR)		F:GO:0005515	F:protein binding		IPR000225 (SMART): IPR011989 (G3	8,417	7,380	12,195	12,488	11,402									
Solyc04g009330	Kinase family protein (AHRD V3.3 *** B9HBC9_POPTR)		P:GO:0000226: P:G(	P:microtubule cytoskeleton organization; P:mitotic cell cycle; F:(		IPR000719 (SMART): G3DSA:3.30.20	6,599	7,164	4,300	4,745	6,028									
Solyc04g009340	RING/U-box superfamily protein (AHRD V3.3 *** AT3G19895.1)					IPR013083 (G3DSA:3.30.40.GENE3D	18,305	15,589	38,943	34,462	32,320									
Solyc04g009350	Histidinol-phosphate aminotransferase (AHRD V3.3 *** W9QXS8_9ROSA)		P:GO:0000105: F:G(	P:histidine biosynth EC:2.6.1.9	Histidinol-phosphate	IPR015422 (G3DSA:3.90.1150.GENE	24,970	26,077	39,881	33,609	37,102									
Solyc04g009360	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G54520.1)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR015943 (G3	5,724	5,147	8,270	7,280	6,470									
Solyc04g009370	Protease (AHRD V3.3 *** A0A1D1YP20_9ARAE)					IPR021420 (PFAM): G3DSA:3.30.428	8,124	8,650	16,849	20,129	21,794									
Solyc04g009380	S-acyltransferase (AHRD V3.3 *** K4BP94_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic retic EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883:SF3	7,434	7,527	18,709	22,416	17,756									
Solyc04g009390	LOW QUALITY:RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *** G7K0L5_MEDTR)		F:GO:0046872	F:metal ion binding		IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc04g009400	Polynucleotidyl transferase%2C ribonuclease H fold protein with HRDC domain-containing protein (AHRD V3.3 --* AT2G32415.3)						1,271	1,700	0,959	0,985	1,225									
Solyc04g009410	Proteasome subunit beta type (AHRD V3.3 *** K4BP97_SOLLC)		F:GO:0004298: C:G(	F:threonine-type en EC:3.4.25	Acting on peptide bor	IPR001353 (PFAM): IPR029055 (G3D	97,277	109,924	120,742	114,486	108,555									
Solyc04g009420	PsbP domain protein (AHRD V3.3 *** G7JC63_MEDTR)		F:GO:0005509: C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple		IPR016123 (G3DSA:3.40.1000.GENE	5,540	4,845	3,019	2,771	4,476									
Solyc04g009430	NAD-dependent protein deacylase (AHRD V3.3 *** K4BP99_SOLLC)		F:GO:0070403	F:NAD+ binding		G3DSA:3.40.50.1220 (GENE3D): IPR(	10,465	13,059	17,722	19,124	19,847									
Solyc04g009435	NAC domain protein (AHRD V3.3 *** Q6RH27_SOLLC)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated		IPR003441 (PFAM): IPR036093 (G3D	0,000	0,043	0,071	0,120	0,071									
Solyc04g009440	NAC domain protein AY498713	NAC1	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated		IPR003441 (PFAM NAC	1,691	4,328	0,803	0,658	0,848									
Solyc04g009465	Mediator of RNA polymerase II transcription subunit 15-like protein (AHRD V3.3 *-* A0A0U3AA10_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,374	0,096	0,321	0,337	0,376									
Solyc04g009470	Mediator of RNA polymerase II transcription subunit 15a (AHRD V3.3 *-* A0A199VYD9_ANACO)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,		IPR036546 (PFAM): G3DSA:1.10.246	10,700	9,069	12,069	10,518	10,829									
Solyc04g009473	mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT2G10440.1)					mobidb-lite (MOBIDB_LITE)	4,520	4,311	6,515	6,676	5,786									
Solyc04g009475	Mediator of RNA polymerase II transcription subunit 15-like protein (AHRD V3.3 *-* A0A0U3AA10_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,049	0,024									
Solyc04g009490	Mediator of RNA polymerase II transcription subunit 15-like protein (AHRD V3.3 *-* A0A0U3AA10_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,043	0,025	0,045	0,023									
Solyc04g009500	Mediator of RNA polymerase II transcription subunit 15-like protein (AHRD V3.3 *** A0A0U3AA10_REHGL)		F:GO:0003712: P:G(	F:transcription coregulator activity; P:regulation of transcription,		G3DSA:1.10.246.20 (GENE3D): IPR0:	61,915	65,823	74,133	75,075	80,872									
Solyc04g009510	Nuclear transcription factor Y subunit B (AHRD V3.3 *-* G7L4J2_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ubiquitin-protein transferase activity; C		PR00615 (PRINTS): IPR003958 (PFA	73,521	50,701	27,055	23,557	28,526									
Solyc04g009515	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 --* B9HMA0_POPTR)						0,224	0,311	0,075	0,114	0,165									
Solyc04g009520	Nuclear transcription factor Y subunit B (AHRD V3.3 *** G7L4J2_MEDTR)		F:GO:0046982	F:protein heterodimerization activity		PR00615 (PRINTS NF-YB	0,000	0,000	0,000	0,022	0,000									
Solyc04g009530	Glutathione S-transferase (AHRD V3.3 *** A0A0N9HM59_HELAN)	GSTL1	F:GO:0005515	F:protein binding		G3DSA:3.40.30.10 (GENE3D): PF134	8,638	8,893	5,957	4,919	7,689									
Solyc04g009540	Ribosomal protein L10 (AHRD V3.3 *** A0A124SGM8_CYNCS)		C:GO:0005622: P:G(	C:intracellular; P:ribosome biogenesis		G3DSA:3.30.70.1730 (GENE3D): IPR(	21,301	37,707	31,486	43,905	58,697	0,851	0,008	0,893	0,000	0,480	0,010	up	up	up
Solyc04g009550	TONNEAU 1B family protein (AHRD V3.3 *** B9HM06_POPTR)		F:GO:0005515	F:protein binding		G3DSA:1.20.960.40 (GENE3D): IPR0(	15,190	14,599	8,123	7,035	7,995									
Solyc04g009560	TBC1 domain family member 8B (AHRD V3.3 *** W9RFJ9_9ROSA)					IPR000195 (SMART): IPR000195 (PF.	128,589	140,249	99,994	97,923	90,933									
Solyc04g009570	Nodulation receptor kinase A (AHRD V3.3 --* D8V144_SOYBN)					mobidb-lite (MOBIDB_LITE): PTHR351	8,098	7,693	8,812	8,403	8,482									
Solyc04g009580	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (AHRD V3.3 *** W9RFS6_9ROSA)		F:GO:0008444: P:G(	F:CDP-diacylglycer EC:2.7.8.5	CDP-diacylglycerol--(	G3DSA:1.20.120.1760 (GENE3D): IPI	27,114	22,431	18,159	19,684	18,402									
Solyc04g009600	TNF receptor-associated factor family protein (AHRD V3.3 *** A0A0B2QRS0_GLYSO)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding		IPR001293 (PFAM): IPR013083 (G3D	4,476	5,422	3,982	5,909	5,784									
Solyc04g009610	LOW QUALITY:Fasciclin domain-containing protein, putative isoform 1 (AHRD V3.3 *-* A0A061GR92_THEC		C:GO:0016021	C:integral component of membrane		PTHR37232 (PANTHER)	3,062	4,205	2,214	1,547	1,983									
Solyc04g009620	chorismate synthase 2 precursor	CS2	F:GO:0004107: P:G(	F:chorismate synthe EC:4.2.3.5	Chorismate synthase	IPR000453 (PFAM): IPR000453 (TIGF	6,527	6,462	8,363	9,286	9,057									
Solyc04g009630	Alpha-glucosidase (AHRD V3.3 *** L0G8H1_CAMSI)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		G3DSA:2.60.40.1760 (GENE3D): IPR(	65,223	89,328	94,197	107,299	114,202									
Solyc04g009640	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1A662_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		IPR000719 (SMART): IPR003591 (SM	1,859	28,557	8,598	10,838	13,054	3,956	0,000	0,601	0,036			up	up	
Solyc04g009650	Diphosphomevalonate decarboxylase (AHRD V3.3 *-* M1BB88_SOLTU)		F:GO:0004163: F:G(	F:diphosphomevalo EC:4.1.1.33	Diphosphomevalonat	IPR036554 (G3DSA:3.30.70.GENE3D	8,175	9,365	13,584	12,807	13,163									
Solyc04g009655	Diphosphomevalonate decarboxylase (AHRD V3.3 *** K4BPC0_SOLLC)		F:GO:0004163: F:G(	F:diphosphomevalo EC:4.1.1.33	Diphosphomevalonat	IPR014721 (G3DSA:3.30.230.GENE3I	13,576	14,105	24,601	20,736	18,732									
Solyc04g009660	LOW QUALITY:Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): IPR002182 (PFA	3,063	2,921	0,897	0,581	1,131									
Solyc04g009670	LOW QUALITY:Acyltransferase-like protein (AHRD V3.3 *-* Q589X8_TOBAC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3I	0,000	0,000	0,000	0,000	0,023									
Solyc04g009690	LOW QUALITY:Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:3.40.50.3	0,038	0,021	0,025	0,000	0,000									
Solyc04g009700	Dual specificity phosphatase domain protein (AHRD V3.3 *** A0A072W222_MEDTR)		P:GO:0006470: F:G(	P:protein dephosph EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR000340 (PF.	9,101	7,750	8,082	7,625	7,648									
Solyc04g009710	Ferredoxin family protein (AHRD V3.3 *** B9MYW6_POPTR)		F:GO:0009055: P:G(	F:electron transfer activity; P:electron transport chain; F:2 iron,		IPR010241 (TIGRFAM): IPR001041 (F	0,019	0,000	0,000	0,025	0,023									
Solyc04g009730	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RPX5_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR011990 (G3D	16,596	14,463	15,506	14,519	18,893									
Solyc04g009740	Exocyst complex component 7 (AHRD V3.3 *** A0A0B0PU57_GOSAR)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis		IPR004140 (PFAM): mobidb-lite (MOB	92,013	66,831	43,980	40,954	45,541									
Solyc04g009770	DnaJ-like protein (AHRD V3.3 *** Q38HT9_SOLTU)		F:GO:0005524: P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc		IPR001623 (PRINTS): IPR001623 (SM	778,662	656,699	658,707	612,611	595,311									
Solyc04g009780	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FQW5_THECC)		C:GO:0016021	C:integral component of membrane		IPR001841 (SMART): IPR013083 (G3	0,000	0,000	0,050	0,025	0,000									
Solyc04g009790	Protein DETOXIFICATION (AHRD V3.3 *-* K4BPD4_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpc		IPR002528 (TIGRFAM): IPR002528 (F	0,313	0,299	0,025	0,237	0,258									
Solyc04g009795	EEIG1/EHBP1 N-terminal domain-containing protein (AHRD V3.3 *** A0A103PZW1_CYNCS)					IPR019448 (PFAM): mobidb-lite (MOB	19,015	21,221	13,212	7,536	9,011					-0,810	0,004			down
Solyc04g009800	Calcium dependent protein kinase (AHRD V3.3 *** E1CFU1_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F		IPR000719 (SMART): IPR002048 (SM	75,263	182,119	112,861	134,205	123,670	1,298	0,001					up		
Solyc04g009810	Protein pelota homolog (AHRD V3.3 *** K4BPD6_SOLLC)		P:GO:0070481: P:G(	P:nuclear-transcribed mRNA catabolic process, non-stop decav		IPR005140 (SMART): IPR005140 (PF.	13,813	12,519	11,151	10,257	10,703									
Solyc04g009820	GRF1-interacting factor-like protein (AHRD V3.3 *** G7I6V2_MEDTR)		F:GO:0003713	F:transcription coactivator activity		IPR007726 (PFAM): mobidb-lite (MOB	3,205	5,446	1,584	0,678	1,829									
Solyc04g009830	Vacuolar protein sorting-associated protein 72 like (AHRD V3.3 *** A0A0B2R1L5_GLYSO)		C:GO:0005634: P:G(	C:nucleus; P:regulation of transcription, DNA-templated; P:histo		IPR013272 (SMART): IPR008895 (PF.	7,380	7,175	11,157	11,185	9,184									
Solyc04g009840	TRICHOME BIREFRINGENCE-LIKE 5 (AHRD V3.3 --* AT5G20590.2)						2,428	2,897	1,435	1,770	1,155									
Solyc04g009850	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR005123 (PFAM): IPR026992 (PFA	1,794	7,140	2,019	2,617	3,583	2,006	0,000	0,818	0,019			up	up	
Solyc04g009860	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process		IPR005123 (PFAM): IPR026992 (PFA	6,117	26,193	2,696	6,330	6,827	2,124	0,000	1,322	0,006	1,218	0,022	up	up	up
Solyc04g009900	phosphoenolpyruvate carboxylase kinase		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): PIRSF000654 (	3,185	4,959	10,707	10,558	14,247									
Solyc04g009910	phosphoenolpyruvate carboxylase kinase 1		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR000719 (PF.	3,152	3,042	6,611	5,031	7,486									
Solyc04g009920	Hexosyltransferase (AHRD V3.3 *** K4BPE7_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups		IPR029044 (G3DSA:3.90.550.GENE3I	22,920	22,430	38,730	46,454	38,222									
Solyc04g009940	Chloroplast J-like domain 1 (AHRD V3.3 *** AT1G08640.1)		C:GO:0016021	C:integral component of membrane		IPR021788 (PFAM): IPR021788 (PAN	11,651	17,138	26,963	25,050	24,617									
Solyc04g009950	cell division cycle 5	cdc5	F:GO:0003677	F:DNA binding		IPR001005 (SMAF MYB	150,988	130,720	132,807	115,833	122,847									
Solyc04g009960	L-allo-threonine aldolase-related protein (AHRD V3.3 *** Q2XPX1_SOLTU)		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:lyase activity		IPR023603 (PIRSF): IPR015422 (G3D	12,192	18,891	97,216	169,994	81,385					0,810	0,000			up
Solyc04g009970	SWIM zinc finger family protein (AHRD V3.3 *** AT1G60560.1)		F:GO:0008270	F:zinc ion binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	14,298	12,194	16,117	19,314	15,357									
Solyc04g009980	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT1G07090.1)		C:GO:0005634: P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus		IPR006936 (PFAM): IPR040222 (PAN	0,000	0,116	0,000	0,000	0,000									
Solyc04g009990	Transcription factor jumonji family protein (AHRD V3.3 *** A0A072VNF4_MEDTR)		C:GO:0005634	C:nucleus		IPR003888 (SMART): IPR003889 (SM	57,905	58,982	60,949	62,740	61,706									
Solyc04g010000	RNA-binding protein (AHRD V3.3 *** A0A0K9NRG1_ZOSMR)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR000504 (PF.	12,586	12,876	16,731	17,620	17,007									
Solyc04g010010	RNA-binding protein (AHRD V3.3 *-* A0A0K9NRG1_ZOSMR)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR000504 (PF.	0,276	1,107	0,025	0,189	0,188									
Solyc04g010020	RNA-binding protein (AHRD V3.3 *** A0A0K9NRG1_ZOSMR)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR012677 (G3	6,881	7,844	11,717	12,073	10,926									
Solyc04g010030	LOW QUALITY:Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* B9H1J2_POPTR)					IPR037047 (G3DSA:2.60.120.GENE3I	0,159	0,041	0,197	0,208	0,211									
Solyc04g010040	RNA-binding protein (AHRD V3.3 *** A0A0K9NRG1_ZOSMR)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR000504 (PF.	0,333	0,484	0,433	0,438	0,234									
Solyc04g010050	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061F0N9_THECC)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR011990 (G3D	4,256	4,260	2,976	2,720	3,075									
Solyc04g010055	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S7L1_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (TIGF	2,480	3,717	2,646	2,885	3,573									
Solyc04g010060	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9S7L1_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (TIGRFAM): IPR011990 ((	0,114	0,135	0,126	0,120	0,024									
Solyc04g010070	calcium-binding EF-hand family protein		F:GO:0005509	F:calcium ion binding		G3DSA:1.10.238.220 (GENE3D): G3D	63,297	63,947	92,400	97,921	86,674									
Solyc04g010080	Meiotically up-regulated protein 71-like protein (AHRD V3.3 *** G7KWG3_MEDTR)		F:GO:0017178: P:G(	F:diphthine-ammoni EC:6.3.1.14	Diphthine--ammonia l	IPR002761 (PFAM): IPR006175 (PFA	28,242	24,270	43,005	41,717	42,950									
Solyc04g010090	Transcription initiation factor TFIID subunit 9 (AHRD V3.3 *** TAF9_ARATH)		P:GO:0006352: F:G(	P:DNA-templated transcription, initiation; F:protein heterodimeri:		IPR003162 (PFAM): IPR009072 (G3D	14,617	14,761	20,883	19,279	19,630									
Solyc04g010100	50S ribosomal protein L33 (AHRD V3.3 *** J7FNN0_OLEEU)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR038584 (G3DSA:2.20.28.GENE3D	9,431	10,615	14,841	16,097	12,018									
Solyc04g010110	Glycosyltransferase (AHRD V3.3 *** K4BPG6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		IPR002213 (PFAM): G3DSA:3.40.50.2	20,174	21,373	31,842	32,450	32,345									
Solyc04g010120	LisH/CRA/RING-U-box domains-containing protein (AHRD V3.3 *** AT3G55070.1)		F:GO:0005515: P:G(	F:protein binding; P:negative regulation of gluconeogenesis		IPR013144 (SMART): IPR006595 (SM	35,736	28,293	62,030	57,946	51,761									
Solyc04g010130	LOW QUALITY:Chalcone synthase (AHRD V3.3 --* A0A0K9PJD4_ZOSMR)	CHS				PTHR34536:SF2 (PANTHER): PTHR3	0,662	0,586	0,608	0,412	0,519									
Solyc04g010135	myo-inositol polyphosphate 5-phosphatase 2 (AHRD V3.3 --* AT4G18010.2)					mobidb-lite (MOBIDB_LITE)	1,426	1,228	1,410	0,853	0,991									
Solyc04g010140	Clathrin adaptor complexes medium subunit family protein (AHRD V3.3 --* AT4G24550.3)						1,168	1,169	0,804	0,918	1,016									
Solyc04g010155	Pax6 (AHRD V3.3 *-* A0A0B0PQB1_GOSAR)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,037	0,000	0,000	0,000									
Solyc04g010180	Pax6 (AHRD V3.3 *-* A0A0B0PQB1_GOSAR)					mobidb-lite (MOBIDB_LITE): mobidb-lit	101,612	107,010	94,455	103,640	103,523									
Solyc04g010190	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 --* K7TWD9_MAIZE)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:integral component of men		IPR022796 (PFAM): mobidb-lite (MOB	11,692	17,272	24,176	24,933	32,916									
Solyc04g010200	ABC transporter G family member (AHRD V3.3 *** A0A0K9NPK2_ZOSMR)	ABCG8	F:GO:0005524: C:G(	F:ATP binding; C:me EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	1,136	0,930	17,319	29,570	19,983					0,776	0,000			up
Solyc04g010210	ABC transporter G family member (AHRD V3.3 *** A0A0K9NPK2_ZOSMR)	ABCG9	F:GO:0005524: C:G(	F:ATP binding; C:me EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF.	0,947	1,116	1,256	1,541	1,698									
Solyc04g010220	centrosomal protein of 135 kDa-like protein (AHRD V3.3 *** AT2G37370.3)		C:GO:0005829	C:cytosol		mobidb-lite (MOBIDB_LITE): mobidb-lit	75,583	68,331	87,521	85,959	89,268									
Solyc04g010230	Pectate lyase (AHRD V3.3 *** K4BPH7_SOLLC)		F:GO:0030570: P:G(	F:pectate lyase act EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	22,770	19,955	38,247	33,084	36,324									
Solyc04g010235	Glutathione reductase, chloroplastic (AHRD V3.3 --* GSHRP_ARATH)	GR					0,695	1,371	0,485	0,476	0,518									
Solyc04g010240	60S ribosomal protein L35 (AHRD V3.3 *** RL35_EUPES)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR001854 (TIGRFAM): G3DSA:1.10.:	20,768	24,997	19,434	16,070	18,085									
Solyc04g010250	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G39420.1)		C:GO:0016020	C:membrane		IPR000073 (PRINTS): IPR029058 (G3	118,108	80,277	7,595	3,377	10,884					-1,165	0,027			down
Solyc04g010260	Splicing factor 3B subunit-like protein (AHRD V3.3 *** G7JFE1_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:protein binding; C:nucleus		IPR004871 (PFAM): IPR015943 (G3D	85,080	76,624	100,102	94,884	94,265									
Solyc04g010270	Dirigent protein (AHRD V3.3 *** K4BPI1_SOLLC)		C:GO:0048046	C:apoplast		IPR004265 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc04g010280	cytokinin oxidase/dehydrogenase 1 (AHRD V3.3 --* AT2G41510.3)						0,885	0,908	1,905	2,204	2,260									
Solyc04g010290	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061ER80_T		F:GO:0008375: C:G(	F:acetylglucosaminyltransferase activity; C:membrane		IPR003406 (PFAM): PTHR19297 (PAN	26,952	22,088	23,686	24,161	24,685									
Solyc04g010300	ABC transporter B family protein (AHRD V3.3 *-* A0A072VSU0_MEDTR)		F:GO:0005524: C:G(	F:ATP binding; C:int EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	5,759	5,011	5,966	8,315	7,120									
Solyc04g010310	ABC transporter B family protein (AHRD V3.3 *** A0A072VSU0_MEDTR)	ABCB7	F:GO:0005524: C:G(	F:ATP binding; C:int EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	35,849	40,235	45,778	56,175	46,976									
Solyc04g010320	Cytochrome P450 (AHRD V3.3 *** Q1AGW1_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(		IPR002401 (PRINTS): IPR001128 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc04g010330	Auxin-regulated protein	ARP				IPR010369 (PFAM): IPR021182 (PIRS	1,049	0,871	0,459	0,270	0,467									
Solyc04g011340	WAT1-related protein (AHRD V3.3 *** K4BPI9_SOLLC)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport		IPR000620 (PFAM): IPR030184 (PAN	0,358	0,577	0,025	0,047	0,024									
Solyc04g011350	2-oxoglutarate dehydrogenase E1 component family protein (AHRD V3.3 *** B9HM58_POPTR)		F:GO:0004591: P:G(	F:oxoglutarate dehy EC:1.2.4.2	Oxoglutarate dehydrc	IPR005475 (SMART): G3DSA:3.40.50	39,807	34,177	65,361	56,348	71,242									
Solyc04g011360	GTP-binding protein	ypt2	F:GO:0003924: F:G(	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	99,304	91,368	169,997	155,609	143,877									
Solyc04g011370	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 --* A0A0K1ZX75_9ASTR)						57,008	63,502	68,090	62,313	59,169									
Solyc04g011380	Zinc finger C3H1 domain-containing protein, putative (AHRD V3.3 *** A0A061FU07_THECC)		C:GO:0000178: F:G(	C:exosome (RNase complex); F:RNA binding; F:protein binding		IPR019607 (PFAM): mobidb-lite (MOB	85,937	80,336	85,108	85,323	86,156									
Solyc04g011385	Zinc finger C3H1 domain-containing protein, putative (AHRD V3.3 *-* A0A061FU07_THECC)		C:GO:0000178: F:G(	C:exosome (RNase complex); F:RNA binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	18,195	12,900	15,958	18,249	16,116									
Solyc04g011390	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein heterodimerization activity		IPR001951 (PRINTS): IPR001951 (SM	38,770	39,181	6,760	2,418	4,848					-1,473	0,001			down
Solyc04g011400	UDP-glucuronate decarboxylase 1 (AHRD V3.3 *** Q6IVK5_TOBAC)		C:GO:0005737: P:G(	C:cytoplasm; P:D-x; EC:4.1.1.35	UDP-glucuronate dec	IPR016040 (PFAM): G3DSA:3.40.50.7	309,014	354,691	291,226	239,418	250,107									
Solyc04g011420	CASP-like protein (AHRD V3.3 *** K4BPJ5_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir		IPR006702 (PFAM): PTHR11615:SF1:	27,249	24,941	19,139	19,085	17,380									
Solyc04g011430	ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** AT5G59300.1)		P:GO:0000209: F:G(	P:protein polyubiquitination; F:ATP binding; P:ubiquitin-depender		SM00212 (SMART): IPR016135 (G3D	569,351	491,329	927,121	972,538	845,581									
Solyc04g011440	ethylene-responsive heat shock protein cognate 70		F:GO:0005524: C:G(	F:ATP binding; C:cy EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS): IPR013126 (PF	557,491	432,667	868,153	1012,086	874,632									
Solyc04g011450	Heat shock cognate protein 2 (AHRD V1 ***- B6SZ69_MAIZE)		F:GO:0005524	F:ATP binding		mobidb-lite (MOBIDB_LITE): PTHR193	0,000	0,000	0,000	0,025	0,000									
Solyc04g011460	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT2G37570.1)		C:GO:0009941	C:chloroplast envelope		PTHR33981 (PANTHER): PTHR33981	37,506	61,200	57,439	53,682	53,408	0,733	0,006					up		
Solyc04g011465	trichohyalin-like protein (DUF3444) (AHRD V3.3 --* AT4G27980.3)						2,179	3,998	4,227	3,883	3,018									
Solyc04g011495	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT4G26055.1)		C:GO:0016021	C:integral component of membrane		IPR027858 (PFAM): PTHR28492 (PAN	4,987	4,684	3,297	2,944	2,918									
Solyc04g011500	actin	ACTIN4	F:GO:0005524: C:G(	F:ATP binding; C:cytoplasm; C:cytoskeleton		IPR004000 (PRINTS): IPR004000 (SM	224,662	192,103	242,059	204,038	238,621									
Solyc04g011510	triosephosphate isomerase (AHRD V3.3 *** AT3G55440.1)		F:GO:0004807: P:G(	F:triose-phosphate EC:5.3.1.1	Triose-phosphate isc	IPR000652 (PFAM): IPR013785 (G3D	360,002	378,363	192,684	172,238	205,861									
Solyc04g011520	Protein kinase (AHRD V3.3 *** A3RI54_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:1.10.510.10 (GENE3D): PIRSI	10,783	13,705	29,038	42,498	25,885					0,556	0,023			up
Solyc04g011530	cytochrome oxidase complex assembly protein (AHRD V3.3 *** AT2G20390.1)					IPR014807 (PFAM): PTHR35114 (PAN	12,131	13,088	27,130	24,937	23,005									
Solyc04g011540	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G55470.1)					IPR000008 (SMART): IPR000008 (PF.	0,616	0,949	11,271	16,520	10,294									
Solyc04g011545	receptor like protein 9 (AHRD V3.3 --* AT1G58190.4)						1,265	1,092	1,035	1,160	1,339									
Solyc04g011550	ABC-2 type transporter family protein (AHRD V3.3 --* AT2G01320.4)		C:GO:0016020	C:membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	18,741	21,764	16,390	15,501	15,808									
Solyc04g011560	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G41060.3)		F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR012677 (G3	41,882	32,202	32,958	31,529	34,502									
Solyc04g011570	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT2G22120.2)		F:GO:0008270	F:zinc ion binding		IPR011016 (SMART): IPR013083 (G3	7,271	6,308	12,804	13,940	11,506									
Solyc04g011580	Pumilio, putative (AHRD V3.3 *** B9SDY2_RICCO)		F:GO:0003723	F:RNA binding		IPR001313 (SMART): IPR011989 (G3	88,250	57,731	83,143	62,731	72,136					-0,403	0,031			down

Solyc04g011600	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7KGS4_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR002123 (SMART): IPR002123 (PF	0,059	0,081	0,025	0,121	0,233									
Solyc04g011610	RING/U-box superfamily protein (AHRD V3.3 *** A0A0K9NMJ4_ZOSMR)		F:GO:0061630	F:ubiquitin protein ligase activity	IPR001841 (SMART): IPR010543 (PF	21,987	26,772	21,869	17,286	19,764									
Solyc04g011620	Peptidyl-prolyl cis-trans isomerase FKBP20-1 (AHRD V3.3 *** FK201_ARATH)		P:GO:0000413; F:G(	P:protein peptidyl-p: EC:5.2.1.8 Peptidylprolyl isomer:	G3DSA:3.10.50.40 (GENE3D): IPR00	0,980	0,998	2,063	1,892	1,671									
Solyc04g011630	Transcription factor GRAS (AHRD V3.3 *-* A0A103Y9C7_CYNCS)	GRAS			IPR005202 (PFAM GRAS	12,146	9,196	12,732	11,796	11,768									
Solyc04g011640	GRAS family transcription factor (AHRD V3.3 *-* AT2G37650.2)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	mobidb-lite (MOBIDB_LITE): PTHR31€	6,170	4,560	6,682	5,959	5,770									
Solyc04g011650	Telomere binding protein (AHRD V3.3 *** A0JBS3_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding	IPR001005 (SMAF MYB_related	14,058	14,526	49,800	49,622	45,800									
Solyc04g011670	bZIP transcription factor family protein (AHRD V3.3 *** AT5G65210.7)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	20,238	19,752	5,222	4,665	6,998									
Solyc04g011680	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc04g011690	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,234	0,995	0,047	0,050	0,565	2,047	0,005					up		
Solyc04g011700	Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 *** A0A061DIZ3_THECC)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (SMART): IPR003690 (PF	5,715	6,163	6,012	6,884	5,843									
Solyc04g011750	Protein TIC 214 (AHRD V3.3 --* TI214_VITVI)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,080	0,025	0,000	0,023									
Solyc04g011767	Pentatricopeptide repeat-containing protein At5g14770, mitochondrial (AHRD V3.3 --* PP381_ARATH)				mobidb-lite (MOBIDB_LITE): mobidb-lit	1,800	2,721	0,211	0,167	0,212									
Solyc04g011810	Glutaredoxin (AHRD V3.3 *** A0A103XEX1_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): G3DSA:3.40.3(	0,000	0,000	0,000	0,025	0,000									
Solyc04g011820	Glutaredoxin (AHRD V3.3 *** A0A103Y3D7_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): IPR011905 (TI(	0,021	0,021	0,047	0,142	0,069									
Solyc04g011880	Glutaredoxin (AHRD V3.3 *** A0A103XEX1_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): IPR011905 (TI(	0,042	0,101	0,091	0,000	0,023									
Solyc04g011900	translation initiation factor 3 subunit I (AHRD V3.3 *-* AT1G54680.3)		F:GO:0004222; F:G(	F:metalloendopeptic EC:3.4.24 Acting on peptide bor	PTHR33471 (PANTHER): PTHR33471	6,610	6,731	3,257	3,655	4,698									
Solyc04g011910	Pathogenic type III effector avirulence factor Avr cleavage site-containing protein (AHRD V3.3 *** A0A124SBZ3_CYNCS)				PTHR33882:SF2 (PANTHER): PTHR3:	0,340	0,458	0,162	0,220	0,072									
Solyc04g011940	Cytochrome P450 family protein (AHRD V3.3 *** B9NGF5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,040	0,039	0,000	0,025	0,000									
Solyc04g011950	LOW QUALITY:SBP (S-ribonuclease-binding protein) family protein (AHRD V3.3 --* G7JYN7_MEDTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination; F:ligase activity		0,019	0,021	0,000	0,000	0,000									
Solyc04g011960	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT1G53350.1)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	0,038	0,079	0,000	0,000	0,000									
Solyc04g011980	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT5G35450.2)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR032675 (G3D	0,218	0,118	0,000	0,119	0,070									
Solyc04g011990	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	0,438	1,175	0,409	1,055	1,016									
Solyc04g012000	LOW QUALITY:NBS-coding resistance gene analog (AHRD V3.3 *** B3V7S2_TOBAC)		F:GO:0043531	F:ADP binding	IPR002182 (PFAM): G3DSA:3.40.50.3	0,019	0,000	0,000	0,000	0,000									
Solyc04g012010	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): G3DSA:1.10.8.43	6,536	7,026	4,140	6,100	5,053									
Solyc04g012020	Acylsugar acyltransferase 2 (AHRD V3.3 *** K4BPQ4_SOLLC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR003480 (PFAM): IPR023213 (G3D	0,886	0,857	0,000	0,000	0,000									
Solyc04g012030	DHHC-type zinc finger family protein		C:GO:0005783; C:G(	C:endoplasmic retic EC:2.3.1.225 Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	7,180	6,412	0,688	0,795	0,635									
Solyc04g012040	26S proteasome non-ATPase regulatory subunit (AHRD V3.3 *** A0A0K9PTB7_ZOSMR)		C:GO:0005737; C:G(	C:cytoplasm; C:proteasome regulatory particle, lid subcomplex;	IPR000717 (SMART): SM00753 (SMA	10,067	10,857	10,290	13,093	11,436									
Solyc04g012050	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RA19_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,000	0,342	0,000	0,000	0,000									
Solyc04g012060	Ribonucleoside-diphosphate reductase (AHRD V3.3 *** K4BPQ8_SOLLC)		F:GO:0004748; F:G(	F:ribonucleoside-dit EC:1.17.4; EC:1.17.4 Acting on CH or CH2	IPR000788 (PRINTS): IPR013509 (PF	26,606	21,244	6,453	3,974	4,562									
Solyc04g012090	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BPR1_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR003591 (SMART): IPR000719 (SM	0,000	0,018	0,025	0,025	0,000									
Solyc04g012100	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT5G46330.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	SM00365 (SMART): IPR003591 (SMA	0,000	0,157	0,000	0,000	0,024									
Solyc04g012120	SIG5 14-3-3 family protein	sig5	F:GO:0019904	F:protein domain specific binding	IPR000308 (PRINTS): IPR023410 (SM	135,490	176,876	288,629	297,536	281,818									
Solyc04g012150	Botryococcus squalene synthase (AHRD V3.3 --* BOSS_BOTBR)					2,365	2,013	2,095	3,992	2,098									
Solyc04g012160	SNF1-related kinase	SRK2C	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): G3DS	24,189	22,081	47,514	69,289	48,743					0,546	0,000			up
Solyc04g012170	Kinase family protein (AHRD V3.3 *** D7MCM2_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001680 (SMART): IPR000719 (SM	82,449	65,113	113,350	126,300	113,578									
Solyc04g012180	Ras-related protein Rab11D (AHRD V3.3 *** RB11D_TOBAC)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	31,503	31,303	37,077	34,673	34,396									
Solyc04g012190	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	G3DSA:3.30.200.20 (GENE3D): PTHF	0,000	0,021	0,025	0,000	0,047									
Solyc04g013200	stomatal cytokinesis defective / SCD1 protein (SCD1) (AHRD V3.3 --* AT1G49040.4)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,142	0,156	0,000	0,000	0,023									
Solyc04g014210	RNA helicase DEAH-box12	DEAH12	F:GO:0003723; F:G(	F:RNA binding; F:he EC:3.6.1.15 Nucleoside-triphosph	IPR001650 (SMART): IPR007502 (SM	78,065	52,830	126,170	119,448	115,373	-0,536	0,048					down		
Solyc04g014220	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E293_THECC)		C:GO:0016021	C:integral component of membrane	IPR001841 (SMART): IPR013083 (G3	0,518	1,505	0,502	0,605	0,491	1,559	0,010					up		
Solyc04g014240	Mediator of RNA polymerase II transcription subunit 4 (AHRD V3.3 *** A0A0S2LKP4_REHGL)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription	IPR019258 (PFAM): mobidb-lite (MOB	14,660	13,849	26,826	24,872	25,845									
Solyc04g014250	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)				IPR004182 (SMART): IPR004182 (PF	52,883	49,866	87,172	79,924	76,292									
Solyc04g014260	ZF-HD homeobox protein family (AHRD V3.3 *** A0A151QZQ5_CAJCA)		F:GO:0003677	F:DNA binding	IPR006456 (TIGRI ZF-HD	0,154	0,213	0,000	0,124	0,000									
Solyc04g014270	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** K4BPT1_SOLLC)		F:GO:0003872; F:G(	F:6-phosphofructok EC:2.7.1.11 6-phosphofructokinas	IPR022953 (PRINTS): IPR000023 (PF	24,473	20,517	23,258	24,668	25,324									
Solyc04g014290	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072V4P7_MEDTR)				mobidb-lite (MOBIDB_LITE): PTHR33(	0,119	0,134	0,282	0,463	0,327									
Solyc04g014310	LOW QUALITY:Proteasome subunit alpha type-4 (AHRD V3.3 --* PSA4_SPIOL)					0,079	0,036	0,000	0,076	0,071									
Solyc04g014320	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** G7KAG0_MEDTR)				mobidb-lite (MOBIDB_LITE): PTHR33(	0,057	0,078	0,235	0,297	0,303									
Solyc04g014330	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** G7KAF8_MEDTR)				mobidb-lite (MOBIDB_LITE): PTHR33(	0,080	0,144	0,022	0,227	0,281									
Solyc04g014350	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G69350.1)					0,101	0,117	0,310	0,396	0,211									
Solyc04g014360	bHLH transcription factor 032		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,217	0,661	0,000	0,000	0,000									
Solyc04g014370	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase (AHRD V3.3 *** K4BPU1_SOLLC)		C:GO:0005789; P:G(	C:endoplasmic retic EC:4.2.1.134 Very-long-chain (3R)-	IPR007482 (PFAM): IPR007482 (PAN	17,618	14,185	12,622	11,073	11,329									
Solyc04g014380	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** AT1G09720.1)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): mobidb-lite (MOB	0,075	0,021	0,000	0,000	0,000									
Solyc04g014390	60S ribosomal protein L51, mitochondrial (AHRD V3.3 *** A0A0B2SGQ7_GLYSO)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:mitochondrial translation	IPR007741 (SMART): G3DSA:3.40.30	92,789	73,365	81,355	68,553	72,923									
Solyc04g014400	LRR receptor-like kinase (AHRD V3.3 *-* A0A072U1S2_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:carbohydrate metabc	SM00365 (SMART): IPR003591 (SMA	0,513	1,045	0,792	2,871	5,728			2,829	0,000	1,840	0,000		up	up
Solyc04g014420	HVA22-like protein (AHRD V3.3 *** K4BPU6_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004345 (PFAM): PTHR12300:SF6	0,000	0,060	0,000	0,000	0,000									
Solyc04g014425	RNA and export factor-binding protein 2 (AHRD V3.3 *-* A0A151U9H0_CAJCA)		F:GO:0003723	F:RNA binding	mobidb-lite (MOBIDB_LITE): PTHR19(	17,790	21,020	17,937	16,968	16,663									
Solyc04g014440	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT2G22620.3)		F:GO:0030246	F:carbohydrate binding	IPR029411 (PFAM): IPR029413 (PFA	0,198	0,247	0,000	0,000	0,000									
Solyc04g014460	RNA-binding family protein (AHRD V3.3 *-* A0A061H038_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	67,682	83,957	72,909	63,829	66,013									
Solyc04g014470	R2R3MYB transcription factor 20	R2R3MYB20	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,077	0,037	0,000	0,000	0,000									
Solyc04g014480	Heat-shock protein, putative (AHRD V3.3 *** B9S3B2_RICCO)	Hsp16.1B	C:GO:0005782; P:G(	C:peroxisomal matrix; P:protein folding; P:response to heat; P:r	IPR008978 (G3DSA:2.60.40.GENE3D	74,309	41,181	410,205	381,988	419,793	-0,824	0,001					down		
Solyc04g014490	LOW QUALITY:B-cell receptor-associated-like protein (AHRD V3.3 *** AT5G17190.1)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte	PTHR12701:SF12 (PANTHER): IPR00	84,390	85,535	148,821	132,326	116,683									
Solyc04g014500	Nudix hydrolase-like protein (AHRD V3.3 *** G7J9C3_MEDTR)		F:GO:0016787	F:hydrolase activity	G3DSA:3.90.79.10 (GENE3D): IPR00(	40,004	44,748	101,385	84,241	77,482									
Solyc04g014510	glutamine synthase	gts1	F:GO:0004356; P:G(	F:glutamate-ammon EC:6.3.1.2 Glutamine synthetase	IPR008146 (SMART): IPR008146 (PF	49,343	27,463	8,257	1,041	3,193	-0,818	0,000	-1,374	0,032	-2,970	0,000	down	down	down
Solyc04g014520	LOW QUALITY:Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)		C:GO:0016021	C:integral component of membrane	IPR006904 (PFAM): PTHR16007:SF2	0,168	0,115	0,000	0,000	0,000									
Solyc04g014530	Ethylene Response Factor C.2	ERF_C_2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	2,897	8,833	0,539	0,195	0,657	1,635	0,000					up		
Solyc04g014540	Zinc finger protein, putative (AHRD V3.3 *** B9T5L7_RICCO)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.60 (GENE3D): PTHF	16,413	15,031	16,436	15,036	16,001									
Solyc04g014560	Pre-mRNA splicing factor PRP38 family protein (AHRD V3.3 *** B9H3J6_POPTR)		C:GO:0071011	C:precatalytic spliceosome	IPR005037 (PFAM): mobidb-lite (MOB	59,805	58,370	78,118	76,080	73,065									
Solyc04g014570	Transmembrane 9 superfamily member (AHRD V3.3 *** K4BPW1_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM): PTHR10766:SF5	110,107	109,696	67,638	61,684	63,725									
Solyc04g014572	high mobility group B5 (AHRD V3.3 --* AT4G35570.2)					0,081	0,057	0,025	0,050	0,047									
Solyc04g014576	LOW QUALITY:DNA topoisomerase (AHRD V3.3 *-* M4CF68_BRARP)		F:GO:0008270	F:zinc ion binding	IPR010666 (PFAM): mobidb-lite (MOB	0,019	0,000	0,000	0,025	0,000									
Solyc04g014578	Ribulose bisphosphate carboxylase small chain 5, chloroplastic (AHRD V3.3 --* RBS5_ACEPE)		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane; C:integra	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,037	0,057	0,072	0,000	0,023									
Solyc04g014600	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G03270.2)		C:GO:0005737; C:G(	C:cytoplasm; C:plasma membrane; F:protein self-association	IPR006015 (PRINTS): IPR006016 (PF	59,056	36,748	141,392	122,335	105,573	-0,658	0,048					down		
Solyc04g014610	Armadillo repeat-containing protein, putative (AHRD V3.3 *** B9SB49_RICCO)		F:GO:0005515	F:protein binding	IPR000225 (SMART): IPR011989 (G3	1,968	1,779	0,942	0,540	0,518									
Solyc04g014615	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SDM1_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAI	0,000	0,021	0,025	0,000	0,000									
Solyc04g014640	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SE46_CAJCA)		F:GO:0004721; F:G(	F:phosphoprotein phosphatase activity; F:protein serine/threoni	IPR019557 (PFAM): PTHR16007:SF4	0,061	0,136	0,000	0,000	0,000									
Solyc04g014650	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	0,573	3,567	0,266	0,247	0,304	2,666	0,000					up		
Solyc04g014670	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G29150.1),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	37,317	42,980	71,935	82,294	76,224									
Solyc04g014680	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *** AT4G22290.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	93,342	74,142	23,372	20,505	26,601									
Solyc04g014700	Mediator of RNA polymerase II transcription subunit 11 (AHRD V3.3 *-* A0A0B0N6V2_GOSAR)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription	IPR019404 (PFAM): mobidb-lite (MOB	6,576	5,434	9,505	9,259	9,166									
Solyc04g014710	Autophagy-related protein 9 (AHRD V3.3 *** A0A1D1ZI98_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	6,456	6,677	7,371	7,241	6,648									
Solyc04g014720	60S ribosomal protein L6 (AHRD V3.3 *** RL6_MESCR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR005568 (PFAM): IPR000915 (PFA	266,771	300,917	211,954	201,607	203,202									
Solyc04g014730	fumarylacetoacetase (AHRD V3.3 *** AT1G12050.1)		F:GO:0004334; P:G(	F:fumarylacetoacet EC:3.7.1.2 Fumarylacetoacetase	IPR036663 (G3DSA:3.90.850.GENE3I	13,052	12,046	54,207	39,846	39,195			-0,470	0,008	-0,440	0,005		down	down
Solyc04g014740	BAG family molecular chaperone regulator 5 (AHRD V3.3 *** Q2HT37_MEDTR)		F:GO:0051087	F:chaperone binding	IPR003103 (SMART): IPR036533 (G3	14,365	13,516	11,375	8,492	9,770									
Solyc04g014750	LOW QUALITY:PENTATRICOPEPTIDE REPEAT 596 (AHRD V3.3 --* AT1G80270.5)		C:GO:0016021	C:integral component of membrane		0,177	0,161	0,025	0,025	0,000									
Solyc04g014760	Rho GDP-dissociation inhibitor 1 (AHRD V3.3 *** A0A151S024_CAJCA)		F:GO:0005094; C:G(	F:Rho GDP-dissociation inhibitor activity; C:cytoplasm	IPR000406 (PRINTS): IPR000406 (PF	8,165	6,390	9,659	10,157	8,414									
Solyc04g014770	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT5G14330.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		0,019	0,000	0,050	0,000	0,000									
Solyc04g014775	Cysteine proteinase inhibitor (AHRD V3.3 *** K4BPY2_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity	IPR000010 (SMART): G3DSA:3.10.45	1,261	0,817	0,000	0,000	0,000									
Solyc04g014780	Cysteine proteinase inhibitor (AHRD V3.3 *** K4BPY1_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity	IPR000010 (SMART): G3DSA:3.10.45	0,000	0,039	0,000	0,000	0,000									
Solyc04g014790	Cysteine proteinase inhibitor (AHRD V3.3 *** K4BPY2_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity	IPR000010 (SMART): IPR000010 (PF	2,248	3,465	0,000	0,000	0,000									
Solyc04g014800	myo-inositol monophosphatase 1	imp1	F:GO:0008934; P:G(	F:inositol monophos EC:3.1.3.25 Inositol-phosphate pl	IPR020552 (PRINTS): IPR000760 (PF	24,805	24,397	6,775	5,004	6,827									
Solyc04g014810	ARM repeat superfamily protein (AHRD V3.3 *** AT4G16490.1)		F:GO:0005515	F:protein binding	IPR000225 (SMART): IPR000225 (PF	51,494	43,924	34,898	46,426	38,956					0,413	0,012			up
Solyc04g014820	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding	IPR000504 (SMART): IPR000504 (PF	16,176	18,905	3,863	3,447	4,489									
Solyc04g014830	GRAS family transcription factor (AHRD V3.3 *** G7JLR5_MEDTR)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM GRAS	25,400	26,441	1,254	2,919	3,579			1,494	0,013				up	
Solyc04g014840	Stress associated endoplasmic reticulum protein (AHRD V3.3 *** A0A0A0KD83_CUCSA)		C:GO:0005783	C:endoplasmic reticulum	IPR010580 (PFAM): IPR010580 (PAN	0,000	0,000	0,022	0,000	0,000									
Solyc04g014850	structural maintenance of chromosomes protein (AHRD V3.3 *** AT4G17240.1)				mobidb-lite (MOBIDB_LITE): PTHR354	0,704	0,742	0,075	0,116	0,072									
Solyc04g014857	Myb/SANT-like domain-containing protein (AHRD V3.3 *** A0A103XYT3_CYNCS)				PTHR31704 (PANTHER): PTHR31704	0,000	0,043	0,047	0,022	0,024									
Solyc04g014870	RNA-dependent RNA polymerase6a	RDR6a	F:GO:0003676; F:G(	F:nucleic acid bindi EC:2.7.7.48 RNA-directed RNA pc	IPR000504 (SMART): IPR007855 (PF	45,969	44,886	41,791	46,522	41,576									
Solyc04g014875	Chalcone--flavonone isomerase (AHRD V3.3 --* CFI_ORYSJ)	CHI				1,823	1,241	2,462	2,030	1,585									
Solyc04g014880	Outward rectifying potassium channel protein (AHRD V3.3 *** AT5G55630.2)		F:GO:0005267; F:G(	F:potassium channel activity; F:calcium ion binding; C:membran	IPR003280 (PRINTS): G3DSA:1.10.23	0,019	0,018	0,000	0,000	0,000									
Solyc04g014885	Receptor-like kinase (AHRD V3.3 *-* A0A072TRW0_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:1.10.510	0,019	0,021	0,000	0,000	0,000									
Solyc04g014900	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): IPR003591 (SM	4,904	18,190	2,432	2,043	2,202	1,914	0,000					up		
Solyc04g014910	Receptor-like kinase (AHRD V3.3 *-* A0A072TRW0_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	11,558	11,737	11,647	11,669	11,679									
Solyc04g014920	LOW QUALITY:Unknown protein (AHRD V3.3)					0,021	0,000	0,000	0,000	0,000									
Solyc04g014930	Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 --* Q2MGS1_MEDTR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE)	1,113	0,885	1,200	1,400	0,894									
Solyc04g014940	Glucose-1-phosphate adenylyltransferase family protein (AHRD V3.3 --* AT2G21590.7)		C:GO:0016021	C:integral component of membrane		0,355	0,171	0,363	0,265	0,188									
Solyc04g014950	Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 *-* Q2MGS1_MEDTR)		C:GO:0016020	C:membrane	IPR007577 (PFAM): PTHR12042:SF3	3,204	3,009	2,239	2,209	2,390									
Solyc04g014960	Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 *-* Q2MGS1_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR007652 (PFAM): PTHR12042:SF3	5,169	4,691	4,134	3,780	3,348									
Solyc04g014970	Protein TIC 214 (AHRD V3.3 --* TI214_POPAL)					0,534	0,334	0,140	0,147	0,141									
Solyc04g014990	Glycosyltransferase (AHRD V3.3 *** K4BNY7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	5,363	10,098	2,688	2,992	3,709	0,935	0,023					up		
Solyc04g015000	Kinase-like protein (AHRD V3.3 *-* A8BL37_PRUAV)		F:GO:0004672; P:G(	F:protein kinase activity; P:protein phosphorylation	IPR001245 (PFAM): IPR032675 (G3D	0,000	0,041	0,000	0,000	0,000									
Solyc04g015010	Microtubule-associated protein 70-5 (AHRD V3.3 *** A0A0B0MZW7_GOSAR)		P:GO:0007010; F:G(	P:cytoskeleton organization; F:microtubule binding	IPR009768 (PFAM): IPR009768 (PAN	0,526	0,538	0,647	1,455	1,526									
Solyc04g015020	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT4G16380.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	136,633	120,733	111,158	103,955	114,609									
Solyc04g015030	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** I3STQ6_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D): G3DS	0,289	0,507	0,992	1,665	0,165									
Solyc04g015040	Peptidyl-prolyl cis-trans isomerase FKBP16-3 (AHRD V3.3 *** W9R3C3_9ROSA)		P:GO:0000413; F:G(	P:protein peptidyl-p: EC:5.2.1.8 Peptidylprolyl isomer:	IPR001179 (PFAM): G3DSA:3.10.50.4	9,682	15,983	8,868	7,236	14,367	0,752	0,033	0,691	0,002			up	up	
Solyc04g015050	Trafficking protein particle complex subunit (AHRD V3.3 *** A0A0K9NWI1_ZOSMR)		C:GO:0030008; P:G(	C:TRAPP complex; P:Golgi vesicle transport	IPR016696 (PIRSF): G3DSA:3.30.138	0,417	0,429	0,390	0,611	0,399									
Solyc04g015060	Nuclear transcription factor Y protein (AHRD V3.3 *-* I3TAW1_MEDTR)		C:GO:0030008; F:G(	C:TRAPP complex; F:protein heterodimerization activity; P:Golo	PR00615 (PRINTS NF-YB	0,113	0,301	0,000	0,000	0,000									
Solyc04g015070	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G47710.4)				IPR000008 (PRINTS): IPR000008 (SM	9,941	11,954	5,401	5,387	6,018									
Solyc04g015075	Somatic embryogenesis receptor kinase (AHRD V3.3 --* E2IXG3_MEDTR)		C:GO:0016021	C:integral component of membrane		0,000	0,021	0,000	0,000	0,072									
Solyc04g015080	oxidoreductase, 2OG-Fe(II) oxygenase family protein (AHRD V3.3 *** AT2G22260.6)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR037151 (G3DSA:2.60.120.GENE3I	1,773	1,488	1,807	2,264	2,308									
Solyc04g015100	Thiolase family protein (AHRD V3.3 *** AT5G47720.4)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR002155 (TIGRFAM): IPR020616 (F	53,804	50,050	238,041	267,669	211,514									
Solyc04g015110	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT1G12150.2)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac	IPR008545 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc04g015120	U-box domain-containing protein 33 (AHRD V3.3 *-* W9RCI3_9ROSA)				IPR014729 (G3DSA:3.40.50.GENE3D	0,178	0,185	0,282	0,220	0,307									
Solyc04g015130	Protein kinase (AHRD V3.3 *** Q02494_MAIZE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	61,430	59,281	43,665	41,843	43,379									
Solyc04g015140	Low PSII Accumulation 3 (AHRD V3.3 --* AT1G73060.1)				mobidb-lite (MOBIDB_LITE)	0,233	0,328	1,606	1,851	1,724									
Solyc04g015150	Phosphoglycolate phosphatase (AHRD V3.3 *** M1BQX5_SOLTU)		F:GO:0016791	F:phosphatase activity	IPR006357 (TIGRFAM): IPR006349 (T	7,086	8,470	13,277	11,457	13,079									
Solyc04g015160	C2 and GRAM domain-containing protein (AHRD V3.3 *** W9RQD0_9ROSA)		C:GO:0016021	C:integral component of membrane	IPR000008 (PRINTS): IPR004182 (SM	7,569	6,889	4,916	6,804	6,374									
Solyc04g015170	Nuclear inhibitor of protein phosphatase 1 (AHRD V3.3 *** A0A0B2S918_GLYSO)		F:GO:0005515	F:protein binding	IPR000253 (SMART): IPR000253 (PF	21,327	22,369	28,720	32,079	31,559									
Solyc04g015180	DNA-directed RNA polymerase II subunit rpb4 (AHRD V3.3 *** A0A151T6X0_CAJCA)		F:GO:0000166; F:G(	F:nucleotide binding; F:catalytic activity; P:cellular metabolic prc	IPR038324 (G3DSA:1.20.1250.GENE	36,569	32,849	49,790	46,511	45,825									
Solyc04g015190	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SGA7_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012946 (SMART): G3DSA:3.20.20	25,137	26,868	19,506	15,992	19,330									
Solyc04g015200	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** K4BQ23_SOLLC)		F:GO:0003872; F:G(	F:6-phosphofructok EC:2.7.1.11 6-phosphofructokinas	IPR022953 (PRINTS): G3DSA:3.40.5(	14,971	13,403	59,493	58,935	52,396									
Solyc04g015210	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	8,656	9,328	4,113	6,715	5,487					0,709	0,008			up
Solyc04g015220	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR032675 (G3D	0,019	0,043	0,000	0,000	0,000									
Solyc04g015260	LOW QUALITY:acetyl-CoA carboxylase carboxyl transferase subunit beta (AHRD V3.3 --* ATCG00500.1)					0,228	0,000	0,000	0,000	0,000									
Solyc04g015270	Hexosyltransferase (AHRD V3.3 *** M1CLK3_SOLTU)	GAUT4	F:GO:0047262	F:polygalacturonate EC:2.4.1.43 Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	109,273	90,555	73,869	73,445	72,698									
Solyc04g015280	Zinc finger, RING-type (AHRD V3.3 *** A2Q5E8_MEDTR)				IPR001841 (SMART): IPR013083 (G3	6,259	5,978	3,748	3,221	3,912									
Solyc04g015290	Myb family transcription factor APL (AHRD V3.3 *** M5WGF6_PRUPE)		F:GO:0003677	F:DNA binding	IPR006447 (TIGRI G2-like	18,161	17,669	22,061	21,946	20,562									
Solyc04g015300	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G17150.1)				IPR029058 (G3DSA:3.40.50.GENE3D	11,937	11,781	12,130	11,654	13,002									
Solyc04g015330	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT3G52155.3)				IPR013078 (SMART): IPR013078 (PF	7,135	7,444	14,527	14,224	14,632									
Solyc04g015340	Carboxypeptidase (AHRD V3.3 *** K4BQ37_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	24,982	34,287	170,820	292,580	184,211					0,780	0,000			up
Solyc04g015350	Phosphatidylinositol 3-kinase (AHRD V3.3 *** Q8GUA6_MEDTR)		F:GO:0016303; P:G(	F:1-phosphatidylino EC:2.7.1.137 Phosphatidylinositol 3	IPR000403 (SMART): IPR002420 (SM	39,445	36,244	68,228	70,650	65,244									
Solyc04g015360	GATA transcription factor (AHRD V3.3 *** K4BQ39_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ior	IPR000679 (SMAF GATA	83,533	15,656	14,282	92,339	55,728	-2,390	0,000	1,958	0,000	2,690	0,000	down	up	up

Solyc04g015370	Acyl carrier protein (AHRD V3.3 *** K4BQ40_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR036736 (G3DSA:1.10.1200.GENE	75,413	76,257	84,665	93,686	91,201									
Solyc04g015380	LOW QUALITY:GDSL esterase/lipase EXL3, putative (AHRD V3.3 *** A0A061GMX5_THECC)		C:GO:0005739; C:G(	C:mitochondrion; C:plastid			PTHR35097:SF1 (PANTHER): PTHR3!	0,021	0,000	0,022	0,000	0,000									
Solyc04g015390	GDSL esterase/lipase EXL3, putative (AHRD V3.3 *** A0A061GMX5_THECC)		C:GO:0005739; C:G(	C:mitochondrion; C:plastid			PTHR35097:SF1 (PANTHER): PTHR3!	3,297	1,776	0,513	0,173	0,351									
Solyc04g015400	GDSL esterase/lipase EXL3, putative (AHRD V3.3 *** A0A061GMX5_THECC)		C:GO:0005739; C:G(	C:mitochondrion; C:plastid			PTHR35097:SF1 (PANTHER): PTHR3!	6,215	6,548	10,932	8,772	9,127									
Solyc04g015430	GDSL esterase/lipase EXL3, putative (AHRD V3.3 *-* A0A061GMX5_THECC)		C:GO:0005739; C:G(	C:mitochondrion; C:plastid			PTHR35097:SF1 (PANTHER): PTHR3!	0,099	0,138	0,715	0,418	0,353									
Solyc04g015440	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061GHJ7_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	14,160	13,305	22,456	20,987	24,133									
Solyc04g015450	extensin X55684		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR000640 (SM	31,419	37,368	36,608	42,410	43,960									
Solyc04g015460	Serine/threonine-protein kinase (AHRD V3.3 *** K4BQ48_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,431	1,028	0,072	0,260	0,188									
Solyc04g015470	Phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *** B9RJA3_RICCO)		F:GO:0005524; F:G(	F:ATP binding; F:1-(	EC:2.7.1.68	1-phosphatidylinosito	IPR002498 (SMART): IPR003409 (SM	17,735	13,777	4,587	3,205	3,478									
Solyc04g015480	BTB/POZ domain-containing protein TNFAIP1 isoform 2 (AHRD V3.3 *** A0A061DKW6_THECC)						IPR022203 (PFAM): mobidb-lite (MOB	21,515	25,579	69,510	65,380	67,096									
Solyc04g015490	Mg-protoporphyrin IX chelatase (AHRD V3.3 *** K4BQ51_SOLLC)	CHLH/I/D	F:GO:0005524; P:G(	F:ATP binding; P:ch	EC:6.6.1.1	Magnesium chelatase	IPR002035 (SMART): IPR003593 (SM	33,134	53,922	43,335	38,603	60,425	0,729	0,001	0,477	0,003			up	up	
Solyc04g015500	B3 domain-containing transcription factor VRN1 (AHRD V3.3 *-* W9SKQ9_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	13,454	13,238	16,576	15,068	13,860									
Solyc04g015510	LOW QUALITY:Invertase/pectin methylesterase inhibitor family protein (AHRD V3.3 *** B9N451_POPTR)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (SMART): IPR006501 (PF.	0,021	0,113	0,000	0,000	0,000									
Solyc04g015520	Remorin family protein (AHRD V3.3 *** A0A061F452_THECC)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR005516 (PFAM): mobidb-lite (MOB	15,606	18,328	20,813	33,852	20,845					0,705	0,000			up
Solyc04g015530	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G57510.1)	PG15 (PS-2)	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,160	0,135	3,613	7,677	3,960					1,086	0,000			up
Solyc04g015540	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072UCS3_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,057	0,116	0,044	0,000	0,000									
Solyc04g015560	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR036881 (G3	58,722	50,307	20,849	16,434	22,180									
Solyc04g015570	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 16 (AHRD V3.3 *** W9RRL3_9ROS		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR000058 (SMAF C2H2	4,861	4,480	4,494	4,237	4,569									
Solyc04g015580	Protein EFR3 B (AHRD V3.3 *** A0A1D1ZEH0_9ARAE)		P:GO:0072659	P:protein localization to plasma membrane			IPR039786 (PANTHER): PTHR12444:(	10,290	8,981	7,166	8,726	7,055									
Solyc04g015585	Ozone-responsive stress related protein (AHRD V3.3 *** I0J1A6_9ORYZ)		C:GO:0016020	C:membrane			IPR009515 (PFAM): PTHR34267:SF1	15,352	21,127	45,441	47,416	42,108									
Solyc04g015590	Dihydroflavonol-4-reductase-like protein (AHRD V3.3 *** G7IPP8_MEDTR)	DFR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	0,144	0,451	0,611	0,561	0,495									
Solyc04g015600	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072U3C5_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART): IPR032675 (G3	6,801	5,222	4,946	4,947	4,939									
Solyc04g015610	imidazolonepropionase (Protein of unknown function, DUF642) (AHRD V3.3 *** AT2G41810.1)						IPR008979 (G3DSA:2.60.120.GENE3I	0,000	0,064	0,169	0,660	0,211									
Solyc04g015620	imidazolonepropionase (Protein of unknown function, DUF642) (AHRD V3.3 *** AT2G41810.1)						IPR006946 (PFAM): IPR008979 (G3D	7,336	10,899	5,680	10,795	9,813			0,787	0,002	0,931	0,000		up	up
Solyc04g015660	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151RU32_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAI	0,000	0,000	0,050	0,000	0,000									
Solyc04g015680	insulin degrading enzyme	ide	F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			G3DSA:3.30.830.10 (GENE3D): IPR0:	169,937	159,777	191,429	207,115	195,813									
Solyc04g015690	Insulin degrading enzyme (AHRD V3.3 *** Q93YG9_SOLLC)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			IPR011765 (PFAM): G3DSA:3.30.830	17,213	18,157	8,198	10,107	10,308									
Solyc04g015710	SANTA (SANT associated) protein (AHRD V3.3 *-* A0A072VWG5_MEDTR)		C:GO:0000778; C:G(	C:condensed nuclear chromosome kinetochore; C:membrane			IPR015216 (PFAM): mobidb-lite (MOB	0,949	0,810	0,552	0,489	0,376									
Solyc04g015740	transmembrane protein, putative (DUF288) (AHRD V3.3 *** AT2G41770.1)		C:GO:0016021	C:integral component of membrane			IPR005049 (PFAM): mobidb-lite (MOB	28,103	17,808	11,572	12,334	12,840									
Solyc04g015750	Magnesium chelatase H subunit (AHRD V3.3 *** F8SPG3_CAMSI)	CHLH/GUN5	P:GO:0015995; F:G(	P:chlorophyll biosyr	EC:6.6.1.1	Magnesium chelatase	IPR022571 (PFAM): IPR011771 (TIGF	137,912	226,124	458,468	354,174	505,202									
Solyc04g015760	Protein N-terminal glutamine amidohydrolase (AHRD V3.3 *** NTAQ1_ARATH)		F:GO:0008418; F:G(	F:protein-N-terminal asparagine amidohydrolase activity; F:prot			IPR023128 (PFAM): IPR037132 (G3D	4,248	4,065	4,364	4,736	4,571									
Solyc04g015765	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_PLAOC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM)	0,040	0,039	0,050	0,000	0,046									
Solyc04g015830	villin 2 (AHRD V3.3 *** AT2G41740.2)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly			IPR007122 (PRINTS): IPR003128 (SM	276,010	237,388	259,994	271,228	268,275									
Solyc04g015850	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G57400.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR349	25,013	11,869	4,483	3,694	3,693	-1,046	0,015					down		
Solyc04g015940	ARM repeat superfamily protein (AHRD V3.3 *** AT4G23540.1)						IPR012978 (PFAM): IPR011989 (G3D	25,436	24,882	20,764	21,944	19,162									
Solyc04g015950	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H9T6_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	9,648	7,610	10,075	11,741	11,789									
Solyc04g015960	NAC domain-containing protein, putative (AHRD V3.3 --* B9S9K8_RICCO)	NAC037	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	2,106	1,273	1,782	3,725	2,081					1,059	0,001			up
Solyc04g015970	ABC transporter family protein (AHRD V3.3 *** B9H9T2_POPTR)	ABCA1	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	48,777	42,721	55,693	56,529	54,981									
Solyc04g015980	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1A662_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART): SM00365 (SMA	3,229	6,527	1,589	2,157	1,980	1,043	0,010					up		
Solyc04g016000	SolycHsfB3a	HSF-11	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	0,061	0,242	0,249	0,241	0,420									
Solyc04g016010	Thioredoxin reductase (AHRD V3.3 *** M1C6N0_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00368 (PRINTS): IPR000103 (PRII	3,190	1,947	2,672	2,652	2,518									
Solyc04g016015	Thioredoxin reductase (AHRD V3.3 *** M1C6N0_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:cell redox homeostasis; P:oxidatio			IPR000103 (PRINTS): PR00368 (PRII	0,000	0,000	0,000	0,000	0,047									
Solyc04g016030	transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT2G36430.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN	0,021	0,000	0,000	0,000	0,000									
Solyc04g016050	Mitochondrial GTPase 1 (AHRD V3.3 *** A0A0B2PDD2_GLYSO)		F:GO:0005525	F:GTP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	5,286	4,083	4,576	4,302	5,226									
Solyc04g016060	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT2G41660.1)						IPR006460 (PFAM): IPR006460 (TIGF	0,221	0,431	0,047	0,069	0,047									
Solyc04g016070	LOW QUALITY:MADS-box transcription factor (AHRD V3.3 *** A0A023JBP0_9ROSI)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM): PTHR11945 (PAI	0,000	0,000	0,000	0,025	0,000									
Solyc04g016080	Kinesin-like protein (AHRD V3.3 *** A0A1B6Q1A3_SORBI)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,136	0,231	0,000	0,000	0,024									
Solyc04g016130	F-box/LRR-repeat protein family (AHRD V3.3 *** A0A151TR18_CAJCA)		F:GO:0005515	F:protein binding			IPR019494 (SMART): IPR019494 (PF.	30,630	26,804	42,718	43,559	44,966									
Solyc04g016160	Glycosyltransferase, putative (AHRD V3.3 *** B9T5B7_RICCO)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR019494 (SMART): IPR013702 (PF.	4,282	3,480	1,800	1,453	1,478									
Solyc04g016170	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE:	0,038	0,126	0,099	0,197	0,117									
Solyc04g016175	RNA-binding protein (AHRD V3.3 *-* Q941H9_TOBAC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	1,451	1,411	1,574	1,754	1,745									
Solyc04g016177	Glycosyltransferase (AHRD V3.3 *** M1CLQ4_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,792	1,200	0,655	0,528	0,729									
Solyc04g016190	Glycosyltransferase (AHRD V3.3 *** K4BQB9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,000	0,018	0,000	0,073	0,047									
Solyc04g016200	Glycosyltransferase (AHRD V3.3 *** Q8RXA4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	3,596	4,901	0,305	0,460	0,703									
Solyc04g016210	Glycosyltransferase (AHRD V3.3 *** K4BQC1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	3,291	4,322	1,002	1,041	1,031									
Solyc04g016220	Glycosyltransferase (AHRD V3.3 *** M1CLQ4_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	129,467	160,064	15,110	10,454	19,781									
Solyc04g016230	Glycosyltransferase (AHRD V3.3 *** M1DUF2_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,234	0,985	0,049	0,072	0,069									
Solyc04g016235	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9T205_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,000	0,022	0,000	0,000									
Solyc04g016240	Nucleoporin interacting component (Nup93/Nic96-like) family protein (AHRD V3.3 *** AT2G41620.1)		C:GO:0005643; F:G(	C:nuclear pore; F:structural constituent of nuclear pore			IPR007231 (PFAM): IPR007231 (PAN	102,668	80,988	71,099	63,876	69,833									
Solyc04g016250	Mitochondrial glycoprotein family protein (AHRD V3.3 *** AT2G41600.7)		C:GO:0005759	C:mitochondrial matrix			IPR036561 (G3DSA:3.10.280.GENE3I	0,558	0,790	0,789	0,545	0,896									
Solyc04g016260	Calcium-transporting ATPase (AHRD V3.3 *** M1AYJ8_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR001757 (PRINTS): PR00119 (PRII	27,047	85,065	10,902	11,811	12,578	1,677	0,000					up		
Solyc04g016270	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G27110.2)							0,577	2,911	0,391	0,288	0,426	2,366	0,000					up		
Solyc04g016280	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT3G10290.1)		C:GO:0005794; F:G(	C:Golgi apparatus; F:pyrimidine nucleotide-sugar transmembran			IPR004853 (PFAM): PTHR44010 (PAI	0,000	0,021	0,000	0,050	0,000									
Solyc04g016290	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G27370.4)		P:GO:0006353	P:DNA-templated transcription, termination			IPR011112 (SMART): IPR011112 (PF.	5,596	4,163	1,970	2,002	1,960									
Solyc04g016295	threonine-tRNA ligase 2 (AHRD V3.3 *** AT3G57320.1)						PTHR38377 (PANTHER): SSF46966 (	4,288	6,012	8,128	9,454	6,871									
Solyc04g016330	Glycerol-3-phosphate dehydrogenase [NAD(+)] (AHRD V3.3 *** K4BQD3_SOLLC)		F:GO:0004367; P:G(	F:glycerol-3-phosph	EC:1.1.1.8; EC:1.1.1	Glycerol-3-phosphate	IPR006168 (PRINTS): IPR013328 (G3	62,768	52,883	4,271	5,053	5,253									
Solyc04g016350	40S ribosomal protein S4 (AHRD V3.3 *** RS4_SOLTU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR038237 (G3DSA:2.40.50.GENE3D	7,241	7,036	7,244	6,828	6,734									
Solyc04g016360	S-formylglutathione hydrolase (AHRD V3.3 *** K4BQD6_SOLLC)		F:GO:0018738; P:G(	F:S-formylglutathior	EC:3.1.2.12	S-formylglutathione h	IPR014186 (TIGRFAM): IPR000801 (F	155,519	144,017	143,738	113,563	139,035									
Solyc04g016370	DNA helicase INO80-like protein (AHRD V3.3 *** AT3G57300.4)		F:GO:0003677; F:G(	F:DNA binding; F:A[illegible]	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR014001 (SMART): IPR001650 (SM	40,116	38,942	46,324	50,817	47,700									
Solyc04g016380	Ribosome biogenesis protein brix, putative (AHRD V3.3 *** B9SUS1_RICCO)		P:GO:0000027; C:G(	P:ribosomal large subunit assembly; C:nucleolus			IPR007109 (SMART): IPR007109 (PF.	30,569	35,288	40,375	35,936	35,812									
Solyc04g016390	50S ribosomal protein L33 (AHRD V3.3 *** J7FNN0_OLEEU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR038584 (G3DSA:2.20.28.GENE3D	0,000	0,019	0,022	0,000	0,000									
Solyc04g016400	Calcium-binding EF-hand family protein (AHRD V3.3 *** AT5G04170.1)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF.	7,649	6,973	5,516	5,876	6,514									
Solyc04g016410	DnaJ (AHRD V3.3 *-* S6G1R4_ORYSJ)		F:GO:0005515	F:protein binding			IPR001623 (PRINTS): IPR001623 (SM	47,549	34,722	41,733	42,716	40,580									
Solyc04g016420	Mediator of RNA polymerase II transcription subunit 23 (AHRD V3.3 *-* A0A061EVL7_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,738	0,838	0,733	0,692	0,634									
Solyc04g016430	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ8_SOLLC)		P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	IPR016167 (G3DSA:3.30.43.GENE3D	0,338	0,137	0,096	0,196	0,283									
Solyc04g016440	Transmembrane proteins 14C (AHRD V3.3 *** AT3G57280.1)		C:GO:0016020	C:membrane			IPR005349 (PFAM): G3DSA:1.20.58.1	1,695	1,995	1,330	1,793	1,125									
Solyc04g016460	receptor-like kinase in flowers 1 (AHRD V3.3 --* AT1G29750.2)							0,021	0,043	0,835	1,182	0,544									
Solyc04g016470	LEQA L.esculentum TomQ'a beta(1,3)glucanase	tomqa	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00(	22,125	49,243	327,379	310,120	404,007									
Solyc04g016480	SUN-like protein 12	SUN12	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR000048 (PF.	6,788	6,529	5,466	4,876	5,438									
Solyc04g016490	purple acid phosphatase 16 (AHRD V3.3 *** AT3G10150.2)		F:GO:0016787	F:hydrolase activity			IPR011230 (PIRSF): IPR004843 (PFA	2,224	2,251	0,605	0,557	1,053									
Solyc04g016510	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A0K9PSA6_ZOSMR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,000	0,000	0,022	0,000	0,000									
Solyc04g016520	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase (AHRD V3.3 *** W9		F:GO:0003975; P:G(	F:UDP-N-acetylgluc	EC:2.7.8.13; EC:2.7.	Phospho-N-acetylmu	IPR000715 (PFAM): mobidb-lite (MOB	43,838	41,293	52,518	50,202	47,965									
Solyc04g016530	DNA-(apurinic or apyrimidinic site) lyase (AHRD V3.3 *** K4BQF3_SOLLC)		F:GO:0004518; P:G(	F:nuclease activity; P:DNA repair			IPR003034 (SMART): IPR005135 (PF.	9,311	8,665	12,888	14,366	13,621									
Solyc04g016540	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2Q1K7_GLYSO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	12,200	8,290	9,880	10,478	10,318									
Solyc04g016550	Folylpolyglutamate synthase (AHRD V3.3 *** FPGS2_ARATH)		F:GO:0004326; F:G(	F:tetrahydrofolylpol	EC:6.3.2.17	Tetrahydrofolate syn	IPR001645 (TIGRFAM): IPR036565 ((	9,638	8,817	8,674	8,323	10,408									
Solyc04g016560	Folylpolyglutamate synthase (AHRD V3.3 --* W9RJD3_9ROSA)		F:GO:0004326; F:G(	F:tetrahydrofolylpol	EC:6.3.2.17	Tetrahydrofolate synthase		0,019	0,037	0,025	0,025	0,000									
Solyc04g016590	global transcription factor C (AHRD V3.3 --* AT4G10710.2)							5,388	3,938	2,437	1,746	1,931									
Solyc04g017593	SBP (S-ribonuclease-binding protein) family protein (AHRD V3.3 --* A0A072UPG0_MEDTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination; F:ligase activity				0,692	0,435	0,910	0,968	0,709									
Solyc04g017595	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 *-* U5G6X7_POPTR)		F:GO:0016307; P:G(	F:phosphatidylinositol phosphate kinase activity; P:phosphatidy			IPR002498 (SMART): IPR002498 (PF.	0,932	0,918	1,191	1,153	0,853									
Solyc04g017620	F-box family protein (AHRD V3.3 *** B9H429_POPTR)	ARC3					IPR005174 (PFAM): PTHR44259 (PAI	35,409	29,375	37,882	47,088	41,197									
Solyc04g017650	PAX-interacting protein 1 (AHRD V3.3 *** W9RS25_9ROSA)						IPR001357 (SMART): IPR036420 (G3	23,742	24,033	36,227	40,150	49,716			0,453	0,006				up	
Solyc04g017670	F-box protein (AHRD V3.3 *** H6VUS4_9ROSI)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): PTH	0,235	0,271	0,292	0,593	0,283									
Solyc04g017680	50S ribosomal protein L22, putative (AHRD V3.3 *** B9SDL6_RICCO)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005727 (TIGRFAM): IPR001063 (F	12,504	13,585	19,653	19,419	18,255									
Solyc04g017685	mitogen-activated protein kinase 14 (AHRD V3.3 --* AT4G36450.1)							0,000	0,018	0,025	0,022	0,000									
Solyc04g017690	ERD15 (AHRD V3.3 *** A0EPI4_CAPAN)						IPR009818 (PFAM): mobidb-lite (MOB	245,042	253,399	549,745	511,701	426,319									
Solyc04g017700	N-acetylglucosaminyl transferase component family protein (AHRD V3.3 *** B9H9G1_POPTR)		P:GO:0006506; C:G(	P:GPI anchor biosy	EC:2.4.1.198	Phosphatidylinositol	IPR007720 (PFAM): PTHR21329:SF3	11,774	8,275	10,597	11,027	10,488									
Solyc04g017710	Zinc finger transcription factor 32	C3H32	P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; F:me			IPR000504 (SMART): IPR000571 (SM	70,728	66,585	73,421	75,635	75,794									
Solyc04g017720	Gibberellin-regulated family protein (AHRD V3.3 *** A0A061EVH9_THECC)						IPR003854 (PFAM): PTHR23201:SF8	0,269	0,618	0,000	0,000	0,000									
Solyc04g017730	LOW QUALITY:30S ribosomal protein S2, chloroplastic (AHRD V3.3 --* RR2_LEMMI)						IPR025558 (PFAM): mobidb-lite (MOB	0,218	0,000	0,099	0,022	0,213									
Solyc04g017740	LOW QUALITY:pyridoxal-phosphate-dependent serine hydroxymethyltransferase, putative (DUF632) (AHRD V3.3 --* AT3G51290.3)						PTHR38223 (PANTHER)	0,021	0,043	0,000	0,000	0,000									
Solyc04g017750	Plant calmodulin-binding-like protein (AHRD V3.3 *-* G7KRQ7_MEDTR)		F:GO:0005516	F:calmodulin binding			IPR012417 (SMART): IPR012417 (PF.	51,448	84,824	22,827	22,049	25,269	0,748	0,003					up		
Solyc04g017770	LOW QUALITY:Oxygen evolving enhancer protein 1 (AHRD V3.3 *-* F2XX49_LITCN)		C:GO:0009523; C:G(	C:photosystem II; C:plastid; P:photosynthesis; C:thylakoid membrane				0,021	0,000	0,000	0,000	0,000									
Solyc04g017807	CTC-interacting domain 11 (AHRD V3.3 --* AT1G32790.2)							0,019	0,041	0,000	0,000	0,000									
Solyc04g018050	LOW QUALITY:sequence-specific DNA binding transcription factor ATNDX (AHRD V3.3 --* AT4G03090.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc04g018060	LOW QUALITY:GAMMA carbonic anhydrase (AHRD V3.3 *-* G5DWW8_SILLA)							0,040	0,000	0,000	0,025	0,000									
Solyc04g018063	Cytochrome P450, putative (AHRD V3.3 *-* B9S4U5_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3I	0,418	0,338	0,393	0,508	0,726									
Solyc04g018080	mediator of RNA polymerase II transcription subunit 15a-like protein (AHRD V3.3 *-* AT1G15780.3)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR036546 (PFAM): G3DSA:1.10.246	6,918	5,508	7,503	6,317	5,871									
Solyc04g018100	Sodium/hydrogen exchanger, putative, expressed (AHRD V3.3 *** D8L9T1_WHEAT)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR006153 (PFAM): PTHR10110:SF8	5,338	6,368	1,836	1,691	1,903									
Solyc04g018110	Hop-interacting protein THI026 (AHRD V3.3 *** G8Z256_SOLLC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF.	235,031	141,159	123,044	242,664	156,113	-0,711	0,043			0,983	0,000	down		up
Solyc04g018120	LOW QUALITY:Pattern formation protein EMB30 (AHRD V3.3 --* A0A0B2S8Q4_GLYSO)							0,482	0,753	2,289	3,695	1,891									
Solyc04g018130	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G04300.2)							0,664	0,493	1,076	2,194	1,459									
Solyc04g018140	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT3G58940.2)							0,063	0,239	0,292	0,383	0,213									
Solyc04g018147	DnaJ heat shock amino-terminal domain protein (AHRD V3.3 --* AT5G53150.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,079	0,059	0,000	0,000	0,000									
Solyc04g018170	LOW QUALITY:Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_ATRBE)							0,019	0,000	0,000	0,000	0,000									
Solyc04g018177	ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9SSN0_RICCO)		F:GO:0000166; F:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase: Nucleoside-triphosphate phosphat		0,019	0,000	0,000	0,000	0,000									
Solyc04g018190	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_VITVI)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PANTHER)	0,000	0,000	0,000	0,025	0,024									
Solyc04g018250	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_PIPCE)		C:GO:0009536; F:G(	C:plastid; F:nucleotidyltransferase activity			G3DSA:1.10.1790.20 (GENE3D): SSF	0,000	0,000	0,022	0,025	0,000									
Solyc04g018300	LOW QUALITY:Allene oxide cyclase 4, chloroplastic (AHRD V3.3 --* AOC4_ARATH)						mobidb-lite (MOBIDB_LITE)	0,019	0,000	0,000	0,000	0,000									
Solyc04g019310	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50120.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): PTHR31549:SF6	0,042	0,043	0,025	0,000	0,000									
Solyc04g019315	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT4G38900.3)							0,427	0,225	0,497	0,362	0,234									
Solyc04g024340	Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** AT1G24350.3)		C:GO:0016021	C:integral component of membrane			IPR003832 (PFAM): mobidb-lite (MOB	12,955	12,106	24,351	25,323	23,131									
Solyc04g024380	LOW QUALITY:haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 --* AT1G56500.3)							0,019	0,000	0,050	0,047	0,024									
Solyc04g024420	Proteasome subunit beta type (AHRD V3.3 *** K4BQP1_SOLLC)		F:GO:0004298; C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000243 (PRINTS): IPR001353 (PF	15,177	17,809	30,108	30,331	28,770									
Solyc04g024430	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT1G08260.1)							13,431	9,525	11,610	10,255	10,136									
Solyc04g024500	CCR4-NOT transcription complex subunit (AHRD V3.3 *** AT5G18420.2)		C:GO:0030014	C:CCR4-NOT complex			IPR019312 (PANTHER)	21,512	21,478	30,588	30,259	30,722									
Solyc04g024510	CCR4-NOT transcription complex subunit (AHRD V3.3 *-* AT5G18420.3)		C:GO:0030014	C:CCR4-NOT complex			IPR019312 (PFAM): IPR019312 (PAN	11,386	11,942	17,678	17,625	16,587									
Solyc04g024520	Protein TSSC4 (AHRD V3.3 *** A0A0B0PXY2_GOSAR)		F:GO:0005515	F:protein binding			IPR029338 (PANTHER)	7,786	7,547	4,407	4,259	4,829									
Solyc04g024530	Actin-related family protein (AHRD V3.3 *** B9HTF8_POPTR)		F:GO:0005524; C:G(	F:ATP binding; C:Arp2/3 protein complex; P:Arp2/3 complex-me			IPR004000 (SMART): G3DSA:3.30.42	40,585	38,034	63,576	67,078	62,212									
Solyc04g024540	Protein Ycf2 (AHRD V3.3 *-* A0A0K0K9F0_9CARY)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,085	0,025	0,075	0,000									
Solyc04g024570	NADH dehydrogenase subunit (AHRD V3.3 *-* Q8HSD5_9SOLN)		F:GO:0003735; C:G(	F:structural constitu	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR018393 (PRINTS): PR01434 (PRII	0,000	0,000	0,025	0,000	0,000									
Solyc04g024580	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PANTHER): IPR027417 (:	0,000	0,021	0,025	0,000	0,000									
Solyc04g024590	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G03330.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS): G3DSA:3.40.5(	37,491	36,282	44,687	40,153	39,072									
Solyc04g024710	OTU domain-containing (AHRD V3.3 *** A0A0B0PQ69_GOSAR)						IPR003323 (PFAM): G3DSA:3.90.70.8	12,534	11,011	12,995	13,864	13,032									
Solyc04g024730	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT1G31850.4)							0,021	0,039	0,022	0,000	0,023									
Solyc04g024770	LOW QUALITY:Two pore calcium channel protein 1 (AHRD V3.3 --* TPC1_HORVU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,018	0,000	0,000	0,000									
Solyc04g024780	LOW QUALITY:DUF1645 family protein (AHRD V3.3 *** G7K1D1_MEDTR)		F:GO:0016874	F:ligase activity			IPR012442 (PFAM): PTHR33095:SF3	1,104	0,906	0,172	0,195	0,211									
Solyc04g024810	plant-specific transcription factor YABBY family protein (AHRD V3.3 --* AT2G26580.2)						mobidb-lite (MOBIDB_LITE)	0,000	1,950	0,000	0,000	0,873	7,644	0,000					up		
Solyc04g024820	LOW QUALITY:Cysteine proteinase 3 (AHRD V3.3 --* CYSP3_VASCU)						mobidb-lite (MOBIDB_LITE)	0,000	1,423	0,025	0,000	0,615									
Solyc04g024840	GDSL lipase-like protein (AHRD V3.3 *** H6U1I8_TANCI)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	2,089	1,339	0,741	1,210	0,826									
Solyc04g024885	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM): IPR036408 (G3D	0,081	0,061	0,125	0,125	0,142									
Solyc04g024940	F-box family protein		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	21,720	22,270	24,936	26,862	23,791									

Solyc04g024950	LOW QUALITY:MATH domain/coiled-coil protein (AHRD V3.3 --* AT2G42475.1)							0,000	0,018	0,000	0,000	0,000									
Solyc04g024960	LOW QUALITY:AP-1 complex subunit mu (AHRD V3.3 --* A0A0K9PPH1_ZOSMR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,986	1,717	1,502	1,393	1,739									
Solyc04g025040	Pre-mRNA splicing Prp18-interacting factor (AHRD V3.3 --* AT3G45950.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	92,657	88,072	76,483	73,740	84,112									
Solyc04g025120	ATPase (AHRD V3.3 *-* A0A0K9PK69_ZOSMR)		F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	7,263	8,291	12,159	9,240	11,252									
Solyc04g025130	LOW QUALITY:Ribonuclease H (AHRD V3.3 --* Q2HRG4_MEDTR),Pfam:PF13456		F:GO:0003676: F:GC	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond	IPR002156 (PFAM): PTHR35218 (PAN	0,080	0,059	0,025	0,000	0,069									
Solyc04g025160	ATPase (AHRD V3.3 *** Q9ST64_SOLTU)		F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	21,592	27,205	36,507	31,549	39,002									
Solyc04g025170	ABC transporter G family member (AHRD V3.3 *-* A0A0K9PAR3_ZOSMR)	ABCG57	F:GO:0005524: C:GC	F:ATP binding; C:pl	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR19241 (PANTHER): PTHR19241	7,055	6,930	6,901	7,069	6,936									
Solyc04g025180	ABC transporter G family-like protein (AHRD V3.3 *-* A0A072UJT7_MEDTR)		F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	15,764	14,575	14,219	15,822	15,807									
Solyc04g025190	LOW QUALITY:DnaJ heat shock amino-terminal domain protein (AHRD V3.3 --* AT5G53150.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,036	0,022	0,000	0,024									
Solyc04g025210	DUF668 family protein (AHRD V3.3 *** A0A072VPK0_MEDTR)		C:GO:0005739: C:GC	C:mitochondrion; C:plasma membrane			IPR021864 (PFAM): IPR007700 (PFA	14,336	21,830	16,726	16,164	15,540									
Solyc04g025260	Endoplasmic reticulum metallopeptidase 1 (AHRD V3.3 *** A0A151SE95_CAJCA)		C:GO:0005783: C:GC	C:endoplasmic reticulum; C:integral component of membrane			G3DSA:3.40.630.10 (GENE3D): IPR0	43,010	42,082	47,448	50,572	52,425									
Solyc04g025280	Pleckstrin-like (PH) and lipid-binding START domain protein (AHRD V3.3 *** G7IRU5_MEDTR)		F:GO:0008289	F:lipid binding			IPR009769 (PFAM): PTHR12136 (PAN	0,000	0,018	0,000	0,000	0,000									
Solyc04g025290	Peptide chain release factor 2 (AHRD V3.3 *** W9RF34_9ROSA)		C:GO:0005737: P:GC	C:cytoplasm; P:translational termination; F:translation release fa			IPR005139 (SMART): IPR000352 (PF	10,825	15,028	25,857	26,967	29,447									
Solyc04g025300	sgs3 innate immune response protein	sgs3	P:GO:0031047	P:gene silencing by RNA			IPR005381 (PFAM): IPR038588 (G3D	51,236	50,969	69,106	64,533	67,246									
Solyc04g025377	Glucose-6-phosphate isomerase, cytosolic 1 (AHRD V3.3 --* G6PI1_CLACO)							0,000	0,021	0,022	0,074	0,024									
Solyc04g025400	Lipid phosphate phosphatase (AHRD V3.3 *** H9NED0_TOBAC)		F:GO:0008195: C:GC	F:phosphatidate ph	EC:3.1.3.4	Phosphatidate phosp	IPR000326 (SMART): IPR000326 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc04g025440	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G23460.1)	PG12-2	F:GO:0004650: P:GC	F:polygalacturonas	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	5,658	6,263	4,558	4,127	3,926									
Solyc04g025450	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *-* U7DVH1_POPTR)		F:GO:0003824	F:catalytic activity			PTHR43859 (PANTHER): PTHR43859	5,323	5,153	2,992	3,419	3,288									
Solyc04g025477	CDPK-related kinase (AHRD V3.3 *-* AT3G50530.2)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,000	0,021	0,000	0,000	0,000									
Solyc04g025510	Non-structural maintenance of chromosome element 4 (AHRD V3.3 --* A0A103YHY4_CYNCS)		P:GO:0006259: P:GC	P:DNA metabolic process; P:cellular response to DNA damage stimulus; C:intracellular organelle				0,000	0,058	0,000	0,000	0,000									
Solyc04g025530	glutamate decarboxylase (AHRD V3.3 *** AT5G17330.1)		F:GO:0004351: P:GC	F:glutamate decarb	EC:4.1.1.15	Glutamate decarboxy	IPR010107 (TIGRFAM): IPR002129 (F	0,306	3,625	1,222	1,013	1,113	3,571	0,000					up		
Solyc04g025540	anthranilate phosphoribosyltransferase (AHRD V3.3 *** AT1G70570.1)		F:GO:0003921: C:GC	F:GMP synthase ac	EC:6.3.5.2	GMP synthase (gluta	IPR035902 (G3DSA:3.40.1030.GENE	22,597	24,232	52,962	49,070	52,168									
Solyc04g025550	Outer arm dynein light chain 1 protein (AHRD V3.3 --* AT1G48540.3)							0,377	0,367	0,165	0,344	0,306									
Solyc04g025560	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00175 (SMA	9,416	10,576	4,691	2,759	5,136									
Solyc04g025570	CW-type zinc-finger protein (AHRD V3.3 --* A0A072UF28_MEDTR)		F:GO:0008270	F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,080	0,039	0,025	0,025	0,071									
Solyc04g025600	AIG2-like (avirulence induced gene) family protein (AHRD V3.3 *-* AT3G28940.1)							0,019	0,018	0,000	0,000	0,000									
Solyc04g025610	low-molecular-weight cysteine-rich 82 (AHRD V3.3 -** AT2G04425.1)							0,299	0,991	1,104	2,474	2,003					1,150	0,011			up
Solyc04g025650	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** A0A072UIU6_MEDTR)		F:GO:0071949	F:FAD binding			PR00420 (PRINTS): IPR036188 (G3D	14,996	81,268	2,305	1,623	3,527	2,459	0,000					up		
Solyc04g025670	Anticodon-binding domain protein (AHRD V3.3 *-* G7LFG2_MEDTR)						IPR019181 (PFAM): IPR039683 (PAN	26,937	26,351	17,151	14,841	16,839									
Solyc04g025715	Protein LSM12 like (AHRD V3.3 *** A0A0B2PMF4_GLYSO)						IPR019181 (PFAM): IPR039683 (PAN	19,401	18,521	12,837	13,062	14,906									
Solyc04g025730	LOW QUALITY:root hair specific 6 (AHRD V3.3 --* AT1G51880.1)							0,084	0,229	0,122	0,097	0,072									
Solyc04g025735	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (AHRD V3.3 *-* A0A1D1ZH66_9ARAE)		F:GO:0003826: C:GC	F:alpha-ketoacid dehydrogenase activity; C:mitochondrial alpha-ketoglutarate dehydrogenase complex;				0,040	0,043	0,046	0,000	0,000									
Solyc04g025770	beta-D-xylosidase 4 (AHRD V3.3 --* AT5G64570.1)							0,513	0,418	0,237	0,289	0,141									
Solyc04g025860	LOW QUALITY:HJTR2GH1 protein (AHRD V3.3 *-* E0Y3W0_9SOLN)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc04g025870	AP-1 complex subunit gamma-2 (AHRD V3.3 *** AP1G2_ARATH)		P:GO:0006886: P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR008152 (SMART): IPR011989 (G3	41,024	38,286	37,156	38,534	38,649									
Solyc04g025880	Potassium transporter (AHRD V3.3 *** M0ZY66_SOLTU)		F:GO:0015079: C:GC	F:potassium ion transmembrane transporter activity; C:membra			IPR003855 (TIGRFAM): IPR003855 (F	0,450	0,917	0,288	1,049	0,445									
Solyc04g025930	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *-* AT2G17410.3)		F:GO:0003677	F:DNA binding			IPR001606 (PFAM): IPR036431 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc04g025940	Trehalose-6-phosphate synthase-6 (AHRD V3.3 *** A0A0S2A6P6_HEVBR)		F:GO:0003824: P:GC	F:catalytic activity; P:trehalose biosynthetic process			IPR006379 (TIGRFAM): IPR001830 (F	39,186	29,927	55,064	58,496	57,018									
Solyc04g025990	Potassium transporter (AHRD V3.3 *** M1B2Z4_SOLTU)		F:GO:0015079: C:GC	F:potassium ion transmembrane transporter activity; C:membra			IPR003855 (PFAM): IPR003855 (TIGF	64,945	58,215	43,368	38,695	43,465									
Solyc04g025993	Zinc finger, RanBP2-type (AHRD V3.3 *-* A0A103YGP3_CYNCS)		F:GO:0003723: C:GC	F:RNA binding; C:nucleus; P:response to abscisic acid; F:metal ion binding; P:3'-UTR-mediated mRNA s				0,094	0,043	0,000	0,025	0,000									
Solyc04g026000	Nucleoporin GLE1 (AHRD V3.3 *-* A0A151U933_CAJCA)		C:GO:0005643: P:GC	C:nuclear pore; P:poly(A)+ mRNA export from nucleus				0,000	0,000	0,000	0,022	0,023									
Solyc04g026020	Sieve element occlusion c (AHRD V3.3 *** E2FKK0_9SOLN)		P:GO:0010088	P:phloem development			IPR027942 (PFAM): IPR027944 (PFA	1,387	1,983	0,025	0,025	0,023									
Solyc04g026030	Spermidine synthase (AHRD V3.3 *** SPDE_NICSY)		F:GO:0003824: P:GC	F:catalytic activity; P:polyamine metabolic process			IPR037163 (G3DSA:2.30.140.GENE3	30,936	35,976	45,904	36,968	42,152									
Solyc04g026080	Kinesin-like calmodulin-binding protein (AHRD V3.3 *-* A0A0B2SMC1_GLYSO)						PTHR33499 (PANTHER): PTHR33499	0,021	0,000	0,022	0,000	0,000									
Solyc04g026100	Ribosomal protein S16 (AHRD V3.3 *** A9P8S1_POPTR)		F:GO:0003735: C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000754 (PFAM): IPR014721 (G3D	134,210	155,273	99,185	88,923	91,244									
Solyc04g026110	Disease resistance family protein (AHRD V3.3 *** B9GY55_POPTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	5,297	3,815	1,230	1,789	1,336									
Solyc04g026150	Homeobox leucine zipper protein (AHRD V3.3 --* A0A072TYN2_MEDTR)		F:GO:0003677: C:GC	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-templated; F:lipid binding; F:sequence-spe				0,000	0,118	0,072	0,045	0,071									
Solyc04g026200	Ubiquitin-like-specific protease 1D (AHRD V3.3 *-* ULP1D_ARATH)		P:GO:0006508: F:GC	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:1.10.418.20 (GENE3D): IPR0	9,479	9,491	8,617	9,637	8,967									
Solyc04g026210	Kinase family protein (AHRD V3.3 *-* B9GH93_POPTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	0,297	0,161	0,168	0,098	0,142									
Solyc04g026220	Sentrin/sumo-specific protease, putative (AHRD V3.3 *-* B9SH87_RICCO)		P:GO:0006508: F:GC	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:1.10.418.20 (GENE3D): IPR0	0,000	0,000	0,000	0,000	0,047									
Solyc04g026223	Ubiquitin-like-specific protease 1D (AHRD V3.3 *-* A0A0B2R587_GLYSO)		P:GO:0006508: F:GC	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM): G3DSA:3.40.395	0,512	0,275	0,408	0,604	0,827									
Solyc04g026227	Peptidase C48, SUMO/Sentrin/Ubl1 (AHRD V3.3 --* A0A118JXG9_CYNCS)		P:GO:0006508: F:GC	P:proteolysis; F:peptidase activity; F:cysteine-type peptidase activity				0,021	0,000	0,000	0,000	0,000									
Solyc04g026230	Kinase like protein (AHRD V3.3 *-* O23334_ARATH)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	0,021	0,041	0,121	0,372	0,166									
Solyc04g026235	Kinase family protein (AHRD V3.3 *** B9GH93_POPTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	0,587	0,555	0,490	0,839	0,970									
Solyc04g026250	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7K1C9_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc04g026255	C2 domain-containing protein (AHRD V3.3 --* D7KLT5_ARALL)							0,237	0,296	0,337	0,430	0,353									
Solyc04g026270	S3 self-incompatibility locus-linked pollen 3.15 protein (AHRD V3.3 *-* Q7XAE6_PETIN)		C:GO:0005783: C:GC	C:endoplasmic reticulum; C:integral component of membrane; P			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,023	0,791	0,482	0,741	0,800									
Solyc04g026271	S3 self-incompatibility locus-linked pollen 3.15 protein (AHRD V3.3 *-* Q7XAE6_PETIN)		C:GO:0005783: C:GC	C:endoplasmic reticulum; C:integral component of membrane			IPR019144 (PFAM): IPR019144 (PTH	16,926	14,711	18,467	21,940	21,438									
Solyc04g026272	S3 self-incompatibility locus-linked pollen 3.15 protein (AHRD V3.3 *-* Q7XAE6_PETIN)		C:GO:0016021	C:integral component of membrane			PTHR21650 (PANTHER)	0,283	0,196	0,293	0,267	0,165									
Solyc04g026274	S3 self-incompatibility locus-linked pollen 3.15 protein (AHRD V3.3 *-* Q7XAE6_PETIN)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE)	0,195	0,099	0,169	0,196	0,258									
Solyc04g026276	S3 self-incompatibility locus-linked pollen 3.15 protein (AHRD V3.3 *-* Q7XAE6_PETIN)		C:GO:0005783: C:GC	C:endoplasmic reticulum; C:integral component of membrane				0,115	0,079	0,049	0,050	0,071									
Solyc04g026300	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT3G43570.1)							1,788	1,236	0,988	1,184	1,339									
Solyc04g026310	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_SOLLC)		F:GO:0003677: F:GC	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007642 (PFAM)	0,000	0,000	0,000	0,025	0,023									
Solyc04g026315	Activating signal cointegrator 1 (AHRD V3.3 *-* A0A0B0NUV2_GOSAR)							2,323	1,689	0,816	0,829	1,294									
Solyc04g026350	Centrin (AHRD V3.3 *** Q9SQI5_TOBAC)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	139,432	116,476	147,636	134,744	131,406									
Solyc04g026360	AP-1 complex subunit mu-1 (AHRD V3.3 *** AP1M1_ARATH)		P:GO:0006886: P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS): G3DSA:2.60.4C	7,945	7,757	8,937	7,130	7,384									
Solyc04g026370	LOW QUALITY:RNA-directed DNA polymerase, putative (AHRD V3.3 --* A2Q3P3_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,079	0,022	0,047	0,071									
Solyc04g026380	AP-1 complex subunit mu (AHRD V3.3 *** G5DWW9_SILLA)		P:GO:0006886: P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS): IPR028565 (PF	11,537	12,981	12,384	12,212	12,702									
Solyc04g028440	ATP-dependent protease LA (Lon) domain protein (AHRD V3.3 --* A0A072V4D0_MEDTR)							0,000	0,000	0,025	0,000	0,000									
Solyc04g028460	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT4G00830.6)		F:GO:0016874	F:ligase activity			PTHR33095 (PANTHER): PTHR33095	0,021	0,000	0,000	0,000	0,000									
Solyc04g028470	GDSL lipase-like protein (AHRD V3.3 *** H6U1I8_TANCI)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,019	0,021	0,000	0,000	0,000									
Solyc04g028560	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* W9SFC2_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	8,996	8,843	11,521	12,595	11,955									
Solyc04g028565	30S ribosomal protein S18, chloroplastic (AHRD V3.3 *** RR18_TOBAC)		F:GO:0003723: C:GC	F:RNA binding; C:plastid; C:intracellular organelle part				0,021	0,019	0,000	0,025	0,046									
Solyc04g028570	Lysine-specific demethylase REF6 (AHRD V3.3 *-* A0A0B2P9C9_GLYSO)		F:GO:0003676: C:GC	F:nucleic acid binding; C:nucleus; F:methyltransferase activity; I			IPR003347 (PFAM): G3DSA:2.60.120	0,000	0,000	0,000	0,045	0,000									
Solyc04g028580	Lysine-specific demethylase (AHRD V3.3 *-* A0A199W5D5_ANACO)		F:GO:0003676: C:GC	F:nucleic acid binding; C:nucleus; F:methyltransferase activity; I			IPR003347 (SMART): IPR003349 (SM	2,755	2,714	4,294	4,929	5,537									
Solyc04g039650	Ribose-phosphate pyrophosphokinase 3 (AHRD V3.3 *-* M8BK22_AEGTA)		F:GO:0000287: F:GC	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	SM01400 (SMART): IPR029099 (PFAI	9,855	8,220	13,732	13,487	14,375									
Solyc04g039670	ATP-citrate synthase, putative (AHRD V3.3 *** B9SHC9_RICCO)		F:GO:0005524	F:ATP binding			IPR016102 (G3DSA:3.40.50.GENE3D	13,647	14,673	2,997	2,006	3,261									
Solyc04g039675	Ribose-phosphate pyrophosphokinase 4 (AHRD V3.3 *-* KPRS4_ARATH)		F:GO:0000287: F:GC	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	IPR025558 (PFAM): G3DSA:3.40.50.2	5,719	6,431	9,327	7,764	8,541									
Solyc04g039730	Receptor-like kinase (AHRD V3.3 *** A0A0K9NTZ6_ZOSMR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	10,915	10,149	19,285	24,488	18,096									
Solyc04g039760	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524: C:GC	F:ATP binding; C:chloroplast			IPR003959 (PFAM): IPR008543 (PFA	0,000	0,041	0,025	0,175	0,000									
Solyc04g039800	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* A0A0X8IHH4_9GENT)		P:GO:0006091: C:GC	P:generation of pre	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM): PTHR45564 (PAI	0,060	0,059	0,000	0,176	0,070									
Solyc04g039810	Photosystem I assembly protein Ycf4 (AHRD V3.3 *** YCF4_GOSHI)		C:GO:0009522: P:GC	C:photosystem I; P:photosynthesis; C:integral component of me			IPR003359 (PFAM): PTHR33288:SF4	0,057	0,167	0,050	0,125	0,303									
Solyc04g039820	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 *** ACCD_SOL		F:GO:0003989: P:GC	P:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR000438 (PRINTS): G3DSA:3.90.22	0,019	0,124	0,174	0,275	0,139									
Solyc04g039830	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 *** ACCD_SOL		F:GO:0003989: P:GC	P:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	PTHR42995 (PANTHER): PTHR42995	0,000	0,128	0,251	0,175	0,096									
Solyc04g039840	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_VIGUN)		P:GO:0015977: F:GC	P:carbon fixation; F	EC:4.1.1.39	Ribulose-bisphospha	IPR017443 (PFAM): IPR036422 (G3D	0,059	0,291	0,322	0,374	0,357									
Solyc04g039850	LOW QUALITY:ATP synthase subunit beta (AHRD V3.3 *-* ATCG00480.1)		F:GO:0005524	F:ATP binding			IPR000194 (PFAM): G3DSA:3.40.50.3	0,176	0,866	0,215	0,269	0,307									
Solyc04g039900	Glutaredoxin family protein (AHRD V3.3 *** AT3G57070.1)		F:GO:0009055: F:GC	F:electron transfer activity; F:protein disulfide oxidoreductase a			G3DSA:3.40.30.10 (GENE3D): IPR00	0,021	0,039	0,000	0,000	0,000									
Solyc04g039920	12-oxophytodienoate reductase-like protein (AHRD V3.3 *-* OPRL_SOLLC)		F:GO:0010181: F:GC	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	0,021	0,000	0,022	0,000	0,000									
Solyc04g039930	12-oxophytodienoate reductase-like protein (AHRD V3.3 *-* OPRL_SOLLC)		F:GO:0003824	F:catalytic activity			IPR013785 (G3DSA:3.20.20.GENE3D	0,224	0,278	0,168	0,241	0,187									
Solyc04g039940	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IHS8_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	6,320	5,371	4,423	5,521	4,349									
Solyc04g039945	12-oxophytodienoate reductase (AHRD V3.3 *-* H6VGI0_9MAGN)		F:GO:0010181: F:GC	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	1,114	0,813	0,452	0,509	0,538									
Solyc04g039950	Mediator of RNA polymerase II transcription subunit 13 like (AHRD V3.3 *** A0A0B2QWJ7_GLYSO)		F:GO:0003712: P:GC	F:transcription coregulator activity; P:regulation of transcription			IPR021643 (PFAM): IPR009401 (PFA	115,223	98,894	166,651	179,222	169,153									
Solyc04g039960	Calcium-binding EF-hand family protein (AHRD V3.3 *-* AT1G29020.2)		F:GO:0005509: C:GC	F:calcium ion binding; C:integral component of membrane; P:tra			PTHR44326:SF3 (PANTHER): PTHR4	0,182	0,262	0,119	0,067	0,117									
Solyc04g039990	NBS-LRR disease resistance protein (AHRD V3.3 *** C6FF78_SOYBN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): PF18052 (PFAM)	0,418	0,357	0,287	0,623	0,212									
Solyc04g040000	polypyrimidine tract-binding protein 1 (AHRD V3.3 --* AT3G01150.4)							0,533	0,690	0,319	0,388	0,235									
Solyc04g040090	Strictosidine synthase-like protein (AHRD V3.3 *** A7WPL3_TOBAC)		P:GO:0009058: F:GC	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR018119 (PFAM): IPR011042 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc04g040110	Kinesin motor family protein (AHRD V3.3 *** B9H942_POPTR)		F:GO:0003777: F:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	15,386	13,499	7,127	6,402	7,399									
Solyc04g040120	Fatty acid desaturase (AHRD V3.3 *** I3RV99_9ERIC)		P:GO:0006629: F:GC	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR005804 (PFAM): IPR021863 (PFA	0,021	0,114	0,000	0,000	0,000									
Solyc04g040130	Fatty acid desaturase (AHRD V3.3 *** I3RV99_9ERIC)		P:GO:0006629: F:GC	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR021863 (PFAM): IPR005804 (PFA	0,451	1,168	3,331	3,543	13,372									
Solyc04g040160	Pheophorbide A oxygenase, putative (AHRD V3.3 *** B9T573_RICCO)		F:GO:0010277: F:GC	F:chlorophyllide a o	EC:1.13.12; EC:1.14	Acting on single donc	IPR036922 (G3DSA:2.102.10.GENE3	46,306	55,792	10,895	10,404	21,768			0,992	0,000				up	
Solyc04g040170	DNA-directed RNA polymerase II, putative (AHRD V3.3 *** B9ST46_RICCO)		F:GO:0003677: F:GC	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR005571 (PFAM): IPR000783 (PFA	10,665	9,964	13,826	11,210	11,123									
Solyc04g040180	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9SZS6_RICCO)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	6,129	15,516	46,780	69,510	41,592	1,367	0,018			0,574	0,000	up		up
Solyc04g040200	Cellular retinaldehyde-binding/triple function, C-terminal (AHRD V3.3 *** Q2HW59_MEDTR)						IPR001251 (SMART): IPR001251 (PF	45,493	43,697	27,110	23,813	29,913									
Solyc04g040210	cysteine-rich TM module stress tolerance protein (AHRD V3.3 *** AT5G04080.1)		C:GO:0005886: C:GC	C:plasma membrane; C:integral component of membrane			IPR028144 (PFAM): mobidb-lite (MOB	66,228	70,875	41,797	44,711	50,180									
Solyc04g040220	BTB/POZ ankyrin repeat protein (AHRD V3.3 *** G3LSH3_LOTJA)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR002110 (SM	0,078	0,261	0,000	0,000	0,024									
Solyc04g040230	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT3G10200.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): PTHR10108:SF3	0,477	0,200	0,380	0,685	0,424									
Solyc04g045300	LOW QUALITY:Glucose-1-phosphate adenylyltransferase family protein (AHRD V3.3 --* AT4G39210.2)							0,000	0,039	0,144	0,000	0,164									
Solyc04g045315	Gag-pol polyprotein, putative (AHRD V3.3 *-* Q60CW7_SOLTU)		F:GO:0003676: F:GC	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): mobidb-lite (MO	0,081	0,039	0,316	0,429	0,234									
Solyc04g045330	Glycosyltransferase (AHRD V3.3 *-* M1AXT7_SOLTU)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			G3DSA:3.40.50.2000 (GENE3D): PTH	0,061	0,059	0,344	0,418	0,094									
Solyc04g045340	Phosphoglucomutase, putative (AHRD V3.3 *** B9SP64_RICCO)		P:GO:0005975: F:GC	P:carbohydrate metabolic process; F:intramolecular transferase			IPR005841 (PRINTS): IPR005845 (PF	402,728	385,086	432,744	369,622	415,218									
Solyc04g045430	Trihelix transcription factor GTL1-like protein (AHRD V3.3 *** A0A0B0NPR3_GOSAR)						G3DSA:1.10.10.6C Trihelix	41,251	30,452	65,209	62,894	58,649									
Solyc04g045440	Phosphoenolpyruvate/phosphate translocator 2, chloroplastic (AHRD V3.3 --* PPT2_ORYSJ)							0,405	0,252	0,192	0,245	0,186									
Solyc04g045470	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G35510.1)		P:GO:0006004: C:GC	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	22,007	17,575	16,733	18,454	16,454									
Solyc04g045475	O-fucosyltransferase family protein (AHRD V3.3 *-* AT1G35510.1)		P:GO:0006004: C:GC	P:fucose metabolic process; C:integral component of membrane			PTHR31288:SF8 (PANTHER): PTHR3	4,950	4,209	3,549	4,103	3,558									
Solyc04g045480	Ubiquitin thioesterase (AHRD V3.3 *** K4BRH8_SOLLC)		P:GO:0016579: F:GC	P:protein deubiquitination; F:hydrolase activity			IPR019400 (PFAM): G3DSA:1.20.130	50,269	52,345	80,896	87,159	77,954									
Solyc04g045520	Eukaryotic translation initiation factor 3 subunit A (AHRD V3.3 --* EIF3A_MAIZE)							0,101	0,139	0,277	0,100	0,190									
Solyc04g045530	DNA primase large subunit (AHRD V3.3 *** K4BRI2_SOLLC)		F:GO:0003896: P:GC	F:DNA primase acti	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:1.20.930.80 (GENE3D): IPR0	5,085	7,294	2,736	1,889	3,030									
Solyc04g045540	Ycf1 (AHRD V3.3 *** A0A168RD69_SOLME)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,050	0,000									
Solyc04g045550	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZG15_SOLCE)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM): PTHR33163:SF1	0,000	0,021	0,000	0,097	0,000									
Solyc04g045560	Squamosa promoter-binding protein 3		F:GO:0003677: C:GC	F:DNA binding; C:nucleus			IPR004333 (PFAN SBP	1,770	2,306	1,166	1,474	2,018									
Solyc04g045580	phosphoribosylformylglycinamidine synthase (AHRD V3.3 *** AT1G27385.1)						IPR007454 (PFAM): G3DSA:3.30.70.2	11,137	13,561	19,178	18,053	22,300									
Solyc04g045590	Alpha-ketoglutarate-dependent dioxygenase alkB (AHRD V3.3 *** G5DX61_SILLA)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR037151 (G3DSA:2.60.120.GENE3	8,665	10,095	16,931	15,807	15,911									
Solyc04g045600	Protein kinase family protein (AHRD V3.3 *** F4JTH2_ARATH)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	8,821	9,578	2,443	2,232	2,722									
Solyc04g045620	NADH-ubiquinone oxidoreductase subunit (AHRD V3.3 *** A0A1D1YMQ7_9ARAE)						IPR035204 (PFAM): IPR035204 (PAN	40,445	45,658	76,779	66,526	69,412									
Solyc04g045630	CTD small phosphatase-like protein (AHRD V3.3 *** A0A0K9Q658_ZOSMR)		F:GO:0016791	F:phosphatase activity			IPR004274 (SMART): IPR023214 (G3	15,558	13,833	19,759	22,087	18,833									
Solyc04g045650	Exostosin family protein (AHRD V3.3 *** AT1G67410.1)		P:GO:0006486: F:GC	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM): PTHR11062:SF4	16,967	10,324	21,080	19,132	19,846	-0,689	0,019					down		
Solyc04g045660	MLH1	MLH1	F:GO:0005524: P:GC	F:ATP binding; P:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013507 (SMART): IPR002099 (TIC	17,049	16,574	15,262	14,480	17,020									
Solyc04g047680	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 --* A0A151TC71		C:GO:0000943	C:retrotransposon nucleocapsid			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,163	0,340	0,124	0,047	0,140									
Solyc04g047690	Vesicle transport protein, Got1/SFT2-like protein (AHRD V3.3 *** A0A103XF84_CYNCS)		C:GO:0016021: P:GC	C:integral component of membrane; P:vesicle-mediated transpo			IPR007305 (PFAM): IPR011691 (PAN	4,508	4,495	4,035	3,581	3,930									
Solyc04g047720	ER membrane protein complex subunit-like protein (AHRD V3.3 *** AT1G65270.3)		C:GO:0005774: C:GC	C:vacuolar membrane; C:endoplasmic reticulum			IPR029615 (PTHR21397:PANTHER):	45,605	46,266	59,318	55,061	55,204									
Solyc04g047723	LOW QUALITY:Endonuclease/exonuclease/phosphatase family protein (AHRD V3.3 *** G7IDH2_MEDTR)		F:GO:0003677: F:GC	F:DNA binding; F:endonuclease activity; P:DNA repair; P:nuclei			IPR036691 (G3DSA:3.60.10.GENE3D	0,237	0,229	0,187	0,199	0,258									
Solyc04g047727	ER membrane protein complex subunit-like protein, putative (AHRD V3.3 *-* G7KRL1_MEDTR)		C:GO:0005774: C:GC	C:vacuolar membrane; C:endoplasmic reticulum			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,041	0,025	0,022	0,000									
Solyc04g047750	Alpha-taxilin (AHRD V3.3 *** A0A0B0PMY2_GOSAR)		F:GO:0019905	F:syntaxin binding			IPR026183 (PFAM): mobidb-lite (MOB	22,707	23,229	30,219	29,594	29,873									
Solyc04g047760	Unknown protein (AHRD V3.3)							0,019	0,021	0,000	0,000	0,000									
Solyc04g047770	VHS domain-containing protein (AHRD V3.3 *** A0A061GBA9_THECC)		P:GO:0006886	P:intracellular protein transport			IPR002014 (SMART): IPR013809 (PF	156,675	134,186	183,096	195,591	183,513									
Solyc04g048900	Calreticulin (AHRD V3.3 *** G7KRL3_MEDTR)		F:GO:0005509: C:GC	F:calcium ion binding; C:endoplasmic reticulum; P:protein foldinc			IPR001580 (PRINTS): IPR009169 (PII	53,201	110,659	39,225	35,238	49,171	1,082	0,003					up		
Solyc04g048950	MACPF domain-containing protein (AHRD V3.3 *** A0A0B2S5Z8_GLYSO)		C:GO:0005886: P:GC	C:plasma membrane; P:plant-type hypersensitive response			IPR020864 (SMART): IPR020864 (PF	15,419	14,055	14,199	17,211	13,854									
Solyc04g048980	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_ACUOB)		F:GO:0004386	F:helicase activity			IPR018904 (PFAM)	0,000	0,021	0,000	0,076	0,000									
Solyc04g049007	cAMP-dependent protein kinase inhibitor-like protein (AHRD V3.3 --* AT3G43153.1)							0,000	0,018	0,000	0,000	0,000									
Solyc04g049010	ethylene insensitive 5/7	ein57	F:GO:0003676: F:GC	F:nucleic acid bindi	EC:3.1.13; EC:3.1.1!	Acting on ester bond	G3DSA:3.30.110.100 (GENE3D): IPR0	82,685	69,573	97,865	94,508	91,115									
Solyc04g049070	alpha glucosidase II	gluii	F:GO:0004553: P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR013780 (G3DSA:2.60.40.GENE3D	119,950	112,901	183,421	172,492	168,108									

Solyc04g049080	Tetraspanin family protein (AHRD V3.3 *** I3SAK4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR018499 (PFAM): PTHR32191 (PAI	6,258	5,321	3,778	4,580	4,081									
Solyc04g049090	SlMlo1	Mlo1	P:GO:0006952; C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	0,056	0,121	0,000	0,022	0,024									
Solyc04g049100	Protein kinase superfamily protein (AHRD V3.3 *-* AT3G56760.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,019	0,018	0,025	0,025	0,000									
Solyc04g049120	Nuclear receptor corepressor 1 (AHRD V3.3 *** A0A0B2NZZ3_GLYSO)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	122,622	137,151	123,461	126,602	122,912									
Solyc04g049130	Iron-sulfur cluster biosynthesis family protein (AHRD V3.3 *** A0A097PNI2_SOLLC)		C:GO:0009941; C:G(	C:chloroplast envelope; C:integral component of membrane			PTHR10072:SF43 (PANTHER): PTHR	12,391	16,707	24,345	25,338	25,537									
Solyc04g049135	transmembrane protein (AHRD V3.3 --* AT2G41945.3)							2,374	3,880	4,941	4,705	4,550									
Solyc04g049140	Transcription factor jumonji (JmjC) domain protein (AHRD V3.3 *** A0A072VKD6_MEDTR)		C:GO:0000785; F:G(	C:chromatin; F:transcription regulatory region sequence-specifi			IPR003347 (SMART): IPR003347 (PF	51,875	48,902	56,220	51,444	53,565									
Solyc04g049150	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT3G05090.3)							6,788	5,292	10,290	9,651	9,729									
Solyc04g049160	Calcium dependent protein kinase (AHRD V3.3 *** Q93XI9_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): IPR002048 (SM	32,991	36,439	49,244	51,595	49,133									
Solyc04g049180	Transmembrane protein 115 (AHRD V3.3 *** A0A0B2NZA3_GLYSO)		P:GO:0006890; C:G(	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			SM01160 (SMART): IPR013861 (PFAI	50,090	49,565	39,873	36,438	35,808									
Solyc04g049224	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103S9G9_CYNCS)		F:GO:0005515	F:protein binding			IPR033443 (PFAM): IPR011990 (G3D	1,735	1,352	1,606	2,026	1,512									
Solyc04g049226	Pentatricopeptide repeat-containing protein, mitochondrial (AHRD V3.3 *-* A0A0B2Q4X7_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,375	1,113	1,449	2,059	1,243									
Solyc04g049240	Photosystem II protein D1 (AHRD V3.3 --* PSBA_CRYJA)							1,550	1,960	1,798	2,319	1,741									
Solyc04g049260	30S ribosomal protein S12, chloroplastic (AHRD V3.3 *** RR12_HELAN)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR006032 (PRINTS): IPR006032 (PF	0,120	0,372	0,147	0,199	0,190									
Solyc04g049330	V-type proton ATPase subunit G (AHRD V3.3 *** A0A0B2RXB3_GLYSO)		C:GO:0016471; F:G(	C:vacuolar proton-t	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR005124 (PFAM): G3DSA:1.20.5.62	154,539	127,298	257,357	215,385	229,721									
Solyc04g049340	Tryptophan/tyrosine permease (AHRD V3.3 *** A0A061FPP3_THECC)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:integral component o			IPR018227 (PFAM): PTHR32195:SF1(	0,543	0,745	0,075	0,076	0,210									
Solyc04g049350	chorismate synthase 1 precursor	CS1	F:GO:0004107; P:G(	F:chorismate synth	EC:4.2.3.5	Chorismate synthase	IPR000453 (TIGRFAM): IPR000453 (I	68,061	87,268	178,980	165,388	171,525									
Solyc04g049355	Para-aminobenzoate synthase (AHRD V3.3 *-* V5L0F7_SOLNI)		P:GO:0006541; C:G(	P:glutamine metabo	EC:2.6.1.85	Aminodeoxychorismate synthase		0,224	0,396	0,364	0,364	0,376									
Solyc04g049360	aminodeoxychorismate synthase/glutamine amidotransferase		P:GO:0009396	P:folic acid-containing compound biosynthetic process			PR00099 (PRINTS): PR00097 (PRINT	14,624	23,043	21,781	31,904	31,367	0,683	0,013	0,524	0,007	0,554	0,003	up	up	up
Solyc04g049375	ATP-citrate lyase B-1 (AHRD V3.3 --* AT3G06650.2)							0,000	0,021	0,000	0,000	0,000									
Solyc04g049380	Protein kinase superfamily protein (AHRD V3.3 *** AT2G39190.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR025558 (PFAM): IPR004147 (PFA	31,849	37,560	38,484	43,981	57,630			0,579	0,000				up	
Solyc04g049390	Kinase superfamily protein isoform 1 (AHRD V3.3 *-* A0A061FUY1_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PTHR10566:SF44 (PANTHER): PTHR	15,169	19,941	19,293	22,723	29,603			0,615	0,000				up	
Solyc04g049410	Cysteine proteinases superfamily protein (AHRD V3.3 --* AT3G62940.4)						mobidb-lite (MOBIDB_LITE): PTHR372	4,855	4,595	5,688	6,986	5,720									
Solyc04g049450	Protein disulfide-isomerase (AHRD V3.3 *** K4BRS2_SOLLC)		F:GO:0003756; P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	PR00421 (PRINTS): IPR005792 (TIGF	88,160	88,433	78,909	77,872	74,999									
Solyc04g049480	LOW QUALITY:PAS domain-containing protein tyrosine kinase family protein (AHRD V3.3 --* AT3G06640.3)						mobidb-lite (MOBIDB_LITE)	0,000	0,018	0,000	0,000	0,000									
Solyc04g049490	Membrane trafficking VPS53 family protein (AHRD V3.3 *** AT1G50500.4)		C:GO:0000938; P:G(	C:GARP complex; P:retrograde transport, endosome to Golgi			IPR007234 (PFAM): mobidb-lite (MOB	71,438	77,943	107,813	107,735	105,335									
Solyc04g049550	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (AHRD V3.3 *** W9RFS6_9ROSA)		F:GO:0008444; P:G(	F:CDP-diacylglycer	EC:2.7.8.5	CDP-diacylglycerol--	IPR004570 (TIGRFAM): G3DSA:1.20.	12,460	14,113	28,475	27,356	26,297									
Solyc04g049555	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G13400.2)						IPR026992 (PFAM): IPR027443 (G3D	10,948	9,031	9,588	8,882	9,312									
Solyc04g049590	LOW QUALITY:Ribosomal protein S3 (AHRD V3.3 *-* I3NTU0_SOLLC)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:mitochon			PTHR35928 (PANTHER)	0,000	0,000	0,000	0,050	0,070									
Solyc04g049610	LOW QUALITY:Unknown protein (AHRD V3.3)							0,021	0,019	0,047	0,022	0,117									
Solyc04g049620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G13400.1)						IPR027443 (G3DSA:2.60.120.GENE3I	8,417	8,272	7,486	6,920	7,637									
Solyc04g049630	Dipeptidyl peptidase family member 6 (AHRD V3.3 *** A0A0B0PQJ9_GOSAR)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity			IPR001375 (PFAM): IPR029058 (G3D	38,938	38,124	47,193	47,285	48,363									
Solyc04g049640	Protein kinase-like protein (AHRD V3.3 *-* Q6TKQ5_VITAE)		F:GO:0004672; P:G(	F:protein kinase activity; P:protein phosphorylation			IPR001245 (PFAM): G3DSA:1.10.510.	0,918	0,998	0,517	0,404	0,447									
Solyc04g049650	Kinase family protein (AHRD V3.3 *-* D7LYF0_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200.	0,333	0,473	0,288	0,097	0,166									
Solyc04g049660	DVA-1 polyprotein (AHRD V3.3 *** A0A0B0N1N3_GOSAR)						IPR027921 (PFAM): mobidb-lite (MOB	10,572	12,285	14,851	14,437	13,516									
Solyc04g049670	Pseudo-response regulator (AHRD V3.3 *** X5I0R0_IPONI)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:protein binding			IPR010402 (PFAM): G3DSA:3.40.50.2	364,544	402,467	263,075	251,675	269,712									
Solyc04g049673	50S ribosomal protein L20, chloroplastic (AHRD V3.3 *** RK20_CARPA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR005813 (PFAM): IPR005813 (PAN	0,042	0,083	0,022	0,025	0,000									
Solyc04g049677	Pseudo-response regulator (AHRD V3.3 *-* X5I0R0_IPONI)		P:GO:0000160; C:G(	P:phosphorelay signal transduction system; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	81,149	78,876	52,638	55,306	54,932									
Solyc04g049690	Adenylate kinase (AHRD V3.3 *** A0A103XGY7_CYNCS)		F:GO:0004017; F:G(	F:adenylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS): PF00406 (PFAI	41,470	32,039	44,305	43,092	40,340									
Solyc04g049710	Tonneau protein 1b (AHRD V3.3 *** G7IAX0_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.960.40 (GENE3D): IPR0(	17,309	17,615	23,918	18,597	19,880									
Solyc04g049720	Leukotriene A-4 hydrolase, putative (AHRD V3.3 *** B9SD61_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:metallopeptidase activity; F:zinc ion binding			IPR014782 (PRINTS): IPR015211 (SM	30,092	30,703	33,888	25,878	33,754									
Solyc04g049730	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_VITVI)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007083 (PFAM): IPR038120 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc04g049770	Regulator of nonsense transcripts 2 (AHRD V3.3 *** W9QEG3_9ROSA)		P:GO:0000184; F:G(	P:nuclear-transcribed mRNA catabolic process, nonsense-medi			IPR003890 (SMART): IPR016021 (G3	103,140	92,533	116,684	110,598	112,632									
Solyc04g049780	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TCY2_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid			PTHR44381 (PANTHER): PTHR44381	0,000	0,021	0,000	0,000	0,000									
Solyc04g049790	Membrane steroid-binding protein (AHRD V3.3 *** G5DXK7_SILLA)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			IPR001199 (SMART): IPR001199 (PF	14,597	12,453	23,355	21,448	18,889									
Solyc04g049800	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VBB0_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (SMAF AP2	1,113	2,465	1,677	2,103	3,056	1,167	0,021	0,856	0,045			up	up	
Solyc04g049840	CCR4-NOT transcription complex subunit 4 (AHRD V3.3 *-* A0A0B0N9G8_GOSAR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ubiquitin-protein transferase activity; C			IPR003954 (SMART): IPR013083 (G3	12,581	11,547	5,941	5,606	6,653									
Solyc04g049850	Sporulation protein RMD1 (AHRD V3.3 *** A0A0B2PBW6_GLYSO)						IPR003734 (PFAM): PTHR16255 (PAI	25,576	20,934	31,962	32,097	30,558									
Solyc04g049860	LOW QUALITY:Rho guanine nucleotide exchange factor (AHRD V3.3 *-* AT1G49290.1)						PTHR33527:SF2 (PANTHER): PTHR3:	0,350	0,233	0,000	0,000	0,000									
Solyc04g049890	D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein (AHRD V3.3 *** AT3G5497(		F:GO:0003824	F:catalytic activity			IPR001544 (PFAM): G3DSA:3.20.10.1	2,943	3,082	5,328	4,376	3,869									
Solyc04g049910	Nuclear transcription factor Y subunit B (AHRD V3.3 *** G7L4J2_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	13,526	10,841	13,602	13,313	12,790									
Solyc04g049920	RNA-binding region-containing protein, putative (AHRD V3.3 *** B9SD37_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	1,849	1,539	0,022	0,025	0,000									
Solyc04g049930	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 --* AT4G08940.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	45,378	41,788	52,599	52,834	54,160									
Solyc04g049940	LOW QUALITY:Auxin-responsive GH3 family protein (AHRD V3.3 --* AT4G37390.1)							3,806	4,688	5,507	5,482	5,333									
Solyc04g049950	Serine/threonine-protein kinase ATM (AHRD V3.3 *-* A0A0B0MKV0_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	29,085	32,668	37,598	34,217	35,232									
Solyc04g049960	Low temperature and salt responsive protein family (AHRD V3.3 *** AT2G38905.1)		C:GO:0016021	C:integral component of membrane			IPR000612 (PFAM): IPR000612 (PAN	0,471	1,214	0,074	0,351	0,000									
Solyc04g049965	threonyl and alanyl tRNA synthetase second additional domain-containing protein (AHRD V3.3 --* AT3G16565.5)						mobidb-lite (MOBIDB_LITE)	2,112	2,412	1,668	1,355	1,223									
Solyc04g049970	complex 1 protein, LYR family protein (AHRD V3.3 *** AT5G51960.2),Pfam:PF13233						IPR039443 (PFAM): PTHR35763 (PAI	1,587	2,348	1,723	1,520	1,720									
Solyc04g050010	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)						IPR004883 (PFAM LBD	0,133	0,054	0,000	0,000	0,000									
Solyc04g050040	mitochondrial substrate carrier family protein (AHRD V3.3 *** AT2G35800.1)		F:GO:0005509; F:G(	F:calcium ion binding; F:transmembrane transporter activity			IPR018108 (PFAM): IPR023395 (G3D	25,513	26,967	21,956	18,924	24,204									
Solyc04g050050	SUN-like protein 13	SUN13	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR025064 (PF	4,068	3,778	8,568	9,779	11,421									
Solyc04g050060	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT2G22760.2)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,047									
Solyc04g050070	Myb-like transcription factor family protein (AHRD V3.3 *** G7KXD8_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			PTHR31314:SF21 G2-like	0,040	0,021	0,022	0,000	0,000									
Solyc04g050080	MYB-related transcription factor (AHRD V3.3 *-* A0A059PRQ3_SALMI)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,000	0,000	0,000	0,025	0,000									
Solyc04g050140	vacuolar sorting-associated protein (DUF946) (AHRD V3.3 *** AT3G04350.1)						IPR009291 (PFAM): PTHR42656 (PAI	12,716	25,845	8,448	8,709	9,634	1,048	0,014					up		
Solyc04g050150	RNA helicase DEAH-box13	DEAH13	F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR001650 (SM	44,014	39,717	42,818	43,403	45,457									
Solyc04g050160	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT1G08600.4)		F:GO:0005524	F:ATP binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,038	0,079	0,050	0,170	0,164									
Solyc04g050170	Clavata1 receptor kinase family protein (AHRD V3.3 *** B9I5Q8_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS): IPR000719 (SMA	1,295	1,168	0,865	1,182	0,683									
Solyc04g050180	Major pollen allergen Pha a 5.1 (AHRD V3.3 --* MPA51_PHAAQ)							8,938	9,064	11,581	11,449	11,021									
Solyc04g050190	heme oxygenase-like, multi-helical (AHRD V3.3 *** AT5G32470.1)		F:GO:0016787	F:hydrolase activity			IPR004305 (PFAM): IPR016084 (G3D	34,154	29,043	31,544	28,387	30,493									
Solyc04g050220	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT3G25460.1)							0,000	0,000	0,000	0,025	0,000									
Solyc04g050225	RNA binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT3G12640.4)							2,712	2,726	1,967	1,469	2,442									
Solyc04g050240	Vacuolar protein sorting-associated (AHRD V3.3 *** J7G2X3_ROSRU)		C:GO:0005768; C:G(	C:endosome; C:cytosol; P:intracellular protein transport; F:prote			IPR014752 (G3DSA:2.60.40.GENE3D	43,694	45,177	69,796	63,101	60,131									
Solyc04g050245	DNA repair protein recA, putative (AHRD V3.3 --* Q6ASS3_ORYSJ)							3,934	3,734	4,267	4,495	3,731									
Solyc04g050250	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G65810.3)							0,342	0,249	0,247	0,200	0,117									
Solyc04g050270	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G04310.2)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	10,187	10,640	16,440	16,090	17,782									
Solyc04g050300	LOW QUALITY:Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT5G56040.1)							0,161	0,195	0,214	0,194	0,164									
Solyc04g050305	Nucleolar histone methyltransferase-related protein (AHRD V3.3 --* AT1G45248.3)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,937	1,027	0,827	1,157	0,850									
Solyc04g050310	Ribosomal protein S5/Elongation factor G/III/V family protein (AHRD V3.3 --* AT1G56070.3)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,040	0,000	0,000	0,047	0,023									
Solyc04g050330	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR020783 (PF	0,057	0,021	0,000	0,000	0,000									
Solyc04g050340	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036769 (G3DSA:1.10.10.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc04g050345	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR020783 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc04g050370	60S ribosomal protein L12 (AHRD V3.3 *** K7WTX4_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036769 (G3DSA:1.10.10.GENE3D	1,065	1,152	0,239	0,146	0,210									
Solyc04g050380	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR036769 (G3	0,019	0,041	0,000	0,000	0,023									
Solyc04g050390	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR020783 (PF	0,624	0,657	0,099	0,092	0,047									
Solyc04g050410	60S ribosomal protein L12 (AHRD V3.3 *** W9R6G5_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036769 (G3DSA:1.10.10.GENE3D	0,000	0,000	0,000	0,025	0,000									
Solyc04g050413	60S ribosomal protein L12 (AHRD V3.3 *-* Q6RJY1_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR020783 (PFAM): IPR036769 (G3D	0,000	0,018	0,000	0,000	0,024									
Solyc04g050417	60S ribosomal protein L12 (AHRD V3.3 *** W9R6G5_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036769 (G3DSA:1.10.10.GENE3D	0,000	0,043	0,022	0,000	0,000									
Solyc04g050440	ammonium transporter	amt2	F:GO:0008519; C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR001905 (TIGRFAM): IPR029020 ((	0,040	0,057	0,025	0,025	0,024									
Solyc04g050470	LOW protein: ammonium transporter 1-like protein (AHRD V3.3 *** AT5G37360.1)		C:GO:0016021	C:integral component of membrane			PTHR36802 (PANTHER)	26,893	31,415	40,850	43,345	41,712									
Solyc04g050480	Exosome complex component CSL4 (AHRD V3.3 *** A0A0B0MMJ8_GOSAR)		C:GO:0000178; F:G(	C:exosome (RNase complex); F:RNA binding; P:RNA processin			G3DSA:2.40.50.100 (GENE3D): IPR0	9,770	10,188	11,937	9,398	10,960									
Solyc04g050490	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)		C:GO:0016021	C:integral component of membrane			IPR004314 (PFAM): IPR025521 (PFA	15,776	10,900	1,090	0,571	0,676									
Solyc04g050510	Translational activator GCN1, putative (AHRD V3.3 *** B9S7P8_RICCO)		P:GO:0006417; F:G(	P:regulation of translation; F:protein kinase regulator activity; F			IPR034085 (SMART): IPR011989 (G3	107,530	108,179	96,899	89,275	94,600									
Solyc04g050520	Translational activator GCN1-like protein (AHRD V3.3 *** A0A072U5F0_MEDTR)		P:GO:0006417; F:G(	P:regulation of translation; F:protein kinase regulator activity; F			IPR011989 (G3DSA:1.25.10.GENE3D	58,321	49,211	45,903	50,687	47,898									
Solyc04g050540	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9S7Q8_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	20,666	24,974	30,394	26,779	36,785									
Solyc04g050550	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T3S4_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	14,219	11,194	12,204	13,526	12,687									
Solyc04g050560	Glutathione S-transferase family protein (AHRD V3.3 *-* B9GKJ1_POPTR)		F:GO:0016740	F:transferase activity			G3DSA:1.20.1050.10 (GENE3D): PTH	2,676	2,484	2,162	2,882	3,268									
Solyc04g050565	OSBP(oxysterol binding protein)-related protein 2A (AHRD V3.3 --* AT4G22540.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,372	4,816	5,509	4,644	5,468									
Solyc04g050570	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RSX5_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	1,066	1,042	0,051	0,000	0,071									
Solyc04g050620	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW6_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	18,093	27,951	2,450	2,709	5,916	0,655	0,016					up		
Solyc04g050670	Terpene cyclase/mutase family member (AHRD V3.3 *-* U5FII5_POPTR)		C:GO:0016020; F:G(	C:membrane; F:isomerase activity			G3DSA:1.50.10.20 (GENE3D): PTHR1	0,021	0,000	0,000	0,000	0,000									
Solyc04g050690	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SDM1_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,109	0,025	0,000	0,189									
Solyc04g050700	Inosine-uridine preferring nucleoside hydrolase, putative (AHRD V3.3 *-* B9RSW6_RICCO)		C:GO:0016021; F:G(	C:integral component of membrane; F:hydrolase activity			IPR036452 (G3DSA:3.90.245.GENE3I	0,000	0,000	0,000	0,000	0,024									
Solyc04g050720	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7K0L5_MEDTR)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,694	3,761	3,219	3,482	3,664									
Solyc04g050730	GDSL-motif esterase/acyltransferase/lipase		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,499	0,392	0,000	0,000	0,000									
Solyc04g050750	Dehydration responsive element binding transcription factor (AHRD V3.3 *-* W6FFW7_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,234	0,658	0,321	0,152	0,047									
Solyc04g050760	U11/U12 small nuclear ribonucleoprotein (AHRD V3.3 *** AT3G04160.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	21,303	16,627	23,189	24,418	22,914									
Solyc04g050775	U-box domain-containing protein 9 (AHRD V3.3 *-* A0A151TXT5_CAJCA)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:nucleus; C:cytoplasm;			PTHR23315:SF75 (PANTHER): PTHR:	0,000	0,000	0,000	0,000	0,023									
Solyc04g050780	U-box domain-containing protein (AHRD V3.3 *** A0A0K9NXH9_ZOSMR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR000225 (SMART): IPR003613 (SM	0,142	0,076	0,022	0,000	0,000									
Solyc04g050790	Pathogenic type III effector avirulence factor Avr cleavage site-containing protein (AHRD V3.3 *** A0A118JW76_CYNCS)						mobidb-lite (MOBIDB_LITE): PTHR336	0,341	0,192	0,071	0,000	0,071									
Solyc04g050820	myo-inositol-1-phosphate synthase 1 (AHRD V3.3 *** AT4G39800.1)		F:GO:0004512; P:G(	F:inositol-3-phosph	EC:5.5.1.4	Inositol-3-phosphate	IPR002587 (PFAM): IPR002587 (PIRS	2,376	3,605	1,549	3,835	1,382					1,318	0,007			up
Solyc04g050840	Protein Ycf2 (AHRD V3.3 *-* U3R4Y1_9ASTE)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,000	0,024									
Solyc04g050850	Protein Ycf2 (AHRD V3.3 *-* YCF2_COFAR)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,019	0,000	0,000	0,076	0,024									
Solyc04g050860	myo-inositol-1-phosphate synthase 1 (AHRD V3.3 *-* AT4G39800.1)		F:GO:0004512; P:G(	F:inositol-3-phosph	EC:5.5.1.4	Inositol-3-phosphate	G3DSA:3.40.50.720 (GENE3D): IPR0(	0,077	0,041	0,025	0,022	0,000									
Solyc04g050895	CBL-interacting protein kinase 6 (AHRD V3.3 --* CIPK6_ORYSJ)							0,159	0,156	0,071	0,000	0,047									
Solyc04g050920	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase (AHRD V3.3 *** A0A1D1Z955_9ARAE)						mobidb-lite (MOBIDB_LITE): PTHR354	32,066	32,293	6,747	6,240	7,941									
Solyc04g050930	violaxanthin de-epoxidase	vde	C:GO:0009507; F:G(	C:chloroplast; F:vio	EC:1.1.99.3	Acting on diphenols a	IPR010788 (PFAM): IPR012674 (G3D	9,244	22,106	20,501	23,437	38,891	1,284	0,000	0,920	0,000			up	up	
Solyc04g050940	Tyrosine kinase family protein (AHRD V3.3 *** G7L302_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,019	0,021	0,000	0,025	0,023									
Solyc04g050950	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR023393 (G3	2,407	4,177	0,452	0,750	2,077			2,154	0,000				up	
Solyc04g050960	Homeodomain-like (AHRD V3.3 *-* Q2HV80_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): mobidt	31,176	21,249	30,236	28,424	29,039									
Solyc04g050990	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): PTHR32278 (PAI	2,898	1,958	2,077	1,487	2,063									
Solyc04g051020	50S ribosomal L18 (AHRD V3.3 *** A0A0B0N185_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.420.100 (GENE3D): IPR(	0,160	0,119	0,074	0,147	0,120									
Solyc04g051025	L18 ribosomal protein Heart Stopper (AHRD V3.3 *-* A0A0I9RJ77_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation				0,295	0,261	0,196	0,331	0,260									
Solyc04g051030	LOW QUALITY:50S ribosomal L18 (AHRD V3.3 *** A0A0B0N185_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.420.100 (GENE3D): IPR(	0,038	0,064	0,025	0,000	0,072									
Solyc04g051080	LOW QUALITY:Two-component response regulator (AHRD V3.3 *** W9RKG5_9ROSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding			IPR006447 (TIGRI ARR-B	0,000	0,039	0,000	0,000	0,000									
Solyc04g051100	trichome birefringence-like protein (DUF828) (AHRD V3.3 --* AT2G40160.3)							1,821	1,533	2,495	2,326	2,079									
Solyc04g051103	RING/U-box superfamily protein (AHRD V3.3 --* AT1G14180.2)							0,870	0,511	1,031	1,129	0,800									
Solyc04g051120	Transmembrane protein, putative (AHRD V3.3 *** G7JST7_MEDTR)		C:GO:0009941; C:G(	C:chloroplast envelope; C:integral component of membrane			PTHR33825:SF11 (PANTHER): PTHR:	11,330	10,800	24,687	27,382	24,960									
Solyc04g051125	Serine/threonine protein phosphatase family protein (AHRD V3.3 --* AT1G03445.2)						mobidb-lite (MOBIDB_LITE)	1,100	1,294	2,300	2,753	2,616									
Solyc04g051140	Phospholipase D (AHRD V3.3 *-* K4B675_SOLLC)		F:GO:0003824; F:G(	F:catalytic activity; F:phospholipase D activity; F:calcium ion bi			IPR015679 (PANTHER): PTHR18896:	0,040	0,021	0,025	0,050	0,023									
Solyc04g051150	UDP-glucose:sterol glucosyltransferase (AHRD V3.3 *** O22678_AVESA)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:transferase activity, trans			G3DSA:3.40.50.2000 (GENE3D): IPR(	5,229	8,498	3,563	3,370	4,423									
Solyc04g051180	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061FJ80_THECC)		F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ior			IPR008217 (PFAM): PTHR31851:SF3(	0,276	0,274	0,096	0,123	0,071									
Solyc04g051190	CYP97A29	CYP97A3	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	20,951	26,451	23,994	25,767	31,675			0,397	0,019				up	
Solyc04g051200	Alpha-1,4-glucan-protein synthase [UDP-forming], putative (AHRD V3.3 *** B9RFU2_RICCO)		F:GO:0016866; P:G(	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR037595 (PFAM): IPR004901 (PIRS	32,082	40,120	49,268	46,890	44,938									
Solyc04g051205	UDP-arabinopyranose mutase (AHRD V3.3 *** AT4G30390.1)							6,312	7,213	9,498	12,850	10,021									
Solyc04g051240	exocyst subunit exo70 family protein A1 (AHRD V3.3 --* AT5G03540.1)							0,276	0,425	0,406	0,515	0,522									
Solyc04g051247	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,059	0,082	0,000	0,174	0,070									
Solyc04g051280	Transmembrane protein, putative (AHRD V3.3 *-* A0A072VMC3_MEDTR)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			mobidb-lite (MOBIDB_LITE): mobidb-lit	46,326	37,336	50,528	70,299	64,386					0,480	0,016			up
Solyc04g051283	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061FVD3_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM): IPR025525 (PFA	0,096	0,041	0,000	0,000	0,000									
Solyc04g051287	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT5G42905.1)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis				0,346	0,453	0,171	0,242	0,379									
Solyc04g051310	transmembrane protein (AHRD V3.3 *** AT5G16520.1)		C:GO:0016021	C:integral component of membrane			PTHR37254 (PANTHER)	55,233	127,520	43,442	39,468	42,941	1,231	0,002					up		

Solyc04g051340	Like-COV protein (AHRD V3.3 *** G7JAD5_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane			IPR007462 (PFAM): mobidb-lite (MOB	30,475	30,639	30,211	30,584	27,779									
Solyc04g051350	Ribonucleoside-diphosphate reductase (AHRD V3.3 *** K4BS95_SOLLC)		F:GO:0004748; F:G(	F:ribonucleoside-di	EC:1.17.4; EC:1.17.4	Acting on CH or CH(2	IPR000788 (PRINTS): IPR005144 (PF	18,352	20,888	7,664	5,523	7,547									
Solyc04g051360	Ethylene Response Factor D.1	ERF_D_1	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,863	18,656	1,892	0,441	0,935	4,459	0,000					up		
Solyc04g051370	26S proteasome non-ATPase regulatory subunit (AHRD V3.3 *** A0A0K9PTB7_ZOSMR)		C:GO:0005737; C:G(	C:cytoplasm; C:proteasome regulatory particle, lid subcomplex;			IPR000717 (SMART): SM00753 (SMA	98,572	101,884	132,508	139,853	124,711									
Solyc04g051390	LOW QUALITY:Cation-transporting P-type ATPase (AHRD V3.3 --* A0A103XPK3_CYNCS)							0,475	0,543	0,247	0,319	0,281									
Solyc04g051400	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *-* G7LC68_MEDTR)		P:GO:0016579; F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM): G3DSA:3.90.70.1	0,021	0,000	0,000	0,000	0,000									
Solyc04g051410	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** G7LC68_MEDTR)		P:GO:0016579; F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM): PTHR44509 (PAN	3,042	3,192	2,631	3,052	2,447									
Solyc04g051420	root meristem growth factor (AHRD V3.3 -** AT5G64770.1)		F:GO:0008083	F:growth factor activity			IPR039337 (PANTHER): PTHR33743:	0,881	0,685	0,000	0,000	0,000									
Solyc04g051450	TSL-kinase interacting 1-like protein (AHRD V3.3 *-* A0A0B0PPU6_GOSAR)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): PTHR216	7,949	7,079	5,028	5,324	5,339									
Solyc04g051460	Protein kinase family protein (AHRD V3.3 *-* Q9LQ29_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	2,761	2,086	0,124	0,117	0,188									
Solyc04g051470	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 *** G7IBW0_MEDTR)						IPR021899 (PFAM): PTHR33193:SF7	6,622	1,943	5,456	3,368	4,355	-1,739	0,000					down		
Solyc04g051480	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XF42_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,778	0,517	0,457	0,477	0,472									
Solyc04g051490	essential meiotic endonuclease 1B (AHRD V3.3 *-* AT2G22140.1)		F:GO:0003677; F:G(	F:DNA binding; F:nuclease activity; C:nucleus; P:DNA repair; C:			IPR006166 (PFAM): G3DSA:1.10.150	8,981	23,113	1,777	2,372	2,946	1,391	0,000					up		
Solyc04g051500	Transporter-related family protein (AHRD V3.3 *** A9PB03_POPTR)		C:GO:0000139; F:G(	C:Golgi membrane; F:UDP-galactose transmembrane transporte			IPR004853 (PFAM): PTHR44060:SF3	13,585	14,061	12,822	13,810	15,471									
Solyc04g051510	curl-3		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	107,641	81,900	24,239	29,777	44,219			0,862	0,004				up	
Solyc04g051540	WRKY transcription factor 13	WRKY13	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,019	0,021	0,000	0,025	0,023									
Solyc04g051570	spatacsin carboxy-terminus protein (AHRD V3.3 *** AT4G39420.2)						IPR028107 (PFAM): mobidb-lite (MOB	86,573	75,086	91,845	91,016	97,231									
Solyc04g051580	(DB244) meloidogyne-induced giant cell protein	TOMTRALTBR	F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR023395 (G3	7,398	10,310	3,254	2,719	3,631									
Solyc04g051590	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SW88_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR012946 (PF	0,040	0,019	0,000	0,025	0,000									
Solyc04g051600	tRNA(His) guanylyltransferase 2 (AHRD V3.3 *** THG2_ARATH)		F:GO:0000287; P:G(	F:magnesium ion binding; P:tRNA modification; F:tRNA guanylyl			IPR024956 (PFAM): IPR038469 (G3D	14,246	12,566	19,636	21,907	18,818									
Solyc04g051610	violaxanthin de-epoxidase-like protein (AHRD V3.3 *** AT2G21860.1)		C:GO:0009507; F:G(	C:chloroplast; F:vio	EC:1.1.99.3	Acting on diphenols a	IPR010788 (PFAM): IPR012674 (G3D	1,865	1,617	1,568	1,302	1,814									
Solyc04g051620	Terpene synthase (AHRD V3.3 *** G5CV47_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc04g051630	LOW QUALITY:ABC transporter G family member 39 (AHRD V3.3 --* AB39G_ARATH)							0,021	0,000	0,000	0,025	0,024									
Solyc04g051640	Purple acid phosphatase (AHRD V3.3 *** M1D307_SOLTU)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	1,097	0,799	0,794	0,678	0,800									
Solyc04g051650	Purple acid phosphatase (AHRD V3.3 *** M1D309_SOLTU)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR025733 (PFAM): IPR029052 (G3D	1,400	1,760	1,057	1,405	1,316									
Solyc04g051660	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT4G39470.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	10,722	14,376	12,301	10,024	11,647									
Solyc04g051670	RNA cytidine acetyltransferase (AHRD V3.3 *** K4BSC6_SOLLC)		F:GO:0005524; F:G(	F:ATP binding; F:N-	EC:2.3.1.5	Arylamine N-acetyltra	IPR027992 (PFAM): G3DSA:3.40.630	45,280	43,757	42,741	43,616	41,465									
Solyc04g051690	WRKY transcription factor 51	WRKY51	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,124	2,535	0,527	1,015	1,463	4,310	0,000					up		
Solyc04g051700	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G64813.3)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	16,987	24,789	13,576	12,485	10,871									
Solyc04g051710	thionin-like protein (AHRD V3.3 *** AT5G64816.4)		C:GO:0016021	C:integral component of membrane			IPR038934 (PANTHER)	12,352	13,172	10,783	11,127	9,282									
Solyc04g051720	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT5G64820.1)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): PTHR354	0,000	0,000	0,025	0,000	0,000									
Solyc04g051730	Cytochrome P450 (AHRD V3.3 *** A0A061DIB1_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,132	0,246	1,264	3,692	0,876									
Solyc04g051760	LOW QUALITY:U6 snRNA phosphodiesterase-like protein (AHRD V3.3 --* AT5G51170.4)							0,000	0,000	0,000	0,025	0,000									
Solyc04g051768	Cytochrome P450 (AHRD V3.3 *** A0A124SBZ5_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,222	0,186	0,000	0,000	0,000									
Solyc04g051780	Programmed cell death protein 2-like protein (AHRD V3.3 *** A0A0B0MYF6_GOSAR)		C:GO:0005737	C:cytoplasm			IPR007320 (PFAM): mobidb-lite (MOB	28,341	29,093	26,710	24,186	25,170									
Solyc04g051785	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 --* AT3G24200.2)		F:GO:0003677; C:G(	F:DNA binding; C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,039	0,000	0,022	0,000									
Solyc04g051790	LOW QUALITY:Transposon protein, putative, mutator sub-class (AHRD V3.3 *-* Q60DJ3_ORYSJ)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding; C:membrane; C:integral comp			IPR004332 (PFAM): PTHR31973 (PAN	0,000	0,021	0,022	0,000	0,000									
Solyc04g051800	ABC transporter family protein (AHRD V3.3 *** AT5G09930.1)	ABCF1	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	112,575	112,810	206,344	182,848	255,567									
Solyc04g051820	RPM1-interacting protein 4 (RIN4) family protein (AHRD V3.3 *** G7LBA7_MEDTR)						PTHR33882 (PANTHER): PTHR33882	46,957	57,175	31,938	36,098	45,759			0,516	0,044				up	
Solyc04g051830	Developmentally-regulated GTP-binding protein 1 (AHRD V3.3 *** A0A0B2PPN5_GLYSO)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR006073 (PF	46,664	50,014	44,265	42,054	38,831									
Solyc04g051850	embryo defective 1303 (AHRD V3.3 *** AT1G56200.2)		C:GO:0009507; P:G(	C:chloroplast; P:chloroplast organization; P:thylakoid membrane			mobidb-lite (MOBIDB_LITE): IPR0402	90,939	99,531	97,662	86,199	93,339									
Solyc04g051860	shikimate kinase precursor	SK	F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.71	Shikimate kinase	PR01100 (PRINTS): IPR031322 (PFA	22,100	22,372	38,619	35,190	35,890									
Solyc04g051870	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 *** AT4G39550.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR006652 (SM	15,835	15,448	12,852	13,009	15,002									
Solyc04g051880	LOW QUALITY:Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 --* A0A061		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DNA-templated				0,634	0,487	0,308	0,386	0,304									
Solyc04g052930	LOW QUALITY:SPX domain-containing membrane protein Os02g45520 (AHRD V3.3 --* SPXM1_ORYSJ)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,101	0,019	0,050	0,170	0,024									
Solyc04g052990	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT1G29500.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc04g053000	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G21210.2)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAN	2,477	0,219	0,025	0,072	0,000	-3,419	0,000					down		
Solyc04g053010	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175 (PAN	2,848	0,421	0,000	0,022	0,000	-2,683	0,000					down		
Solyc04g053020	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175:SF2	0,021	0,036	0,000	0,000	0,000									
Solyc04g053030	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175 (PAN	0,019	0,117	0,000	0,000	0,000									
Solyc04g053040	Coatomer subunit delta (AHRD V3.3 --* B4G0V4_MAIZE)							0,000	0,000	0,000	0,072	0,000									
Solyc04g053050	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *-* B9GL08_POPTR)		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductio			IPR026992 (PFAM): IPR027443 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc04g053055	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,040	0,142	0,000	0,000	0,000									
Solyc04g053080	OTU-like cysteine protease family protein (AHRD V3.3 *** B9I9W0_POPTR)		C:GO:0005829	C:cytosol			IPR003323 (PFAM): G3DSA:3.90.70.8	480,867	299,454	380,602	316,980	290,587	-0,656	0,008	-0,392	0,007			down	down	
Solyc04g053110	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR014025 (PRINTS): IPR002109 (PF	0,182	0,484	0,072	0,025	0,071									
Solyc04g053120	4-alpha-glucanotransferase (AHRD V3.3 *** K4BSG9_SOLLC)		F:GO:0004134; P:G(	F:4-alpha-glucanotr	EC:2.4.1.25	4-alpha-glucanotrans	G3DSA:3.20.20.80 (GENE3D): IPR00	90,438	107,238	43,438	29,311	43,896					-0,564	0,000			down
Solyc04g053130	Stress enhanced protein 2 (AHRD V3.3 *** K7XKQ9_SOLTU)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:response to wounding; C:i			PTHR36490 (PANTHER): SSF103511	447,283	247,013	1218,474	1092,115	1240,478	-0,830	0,000					down		
Solyc04g053140	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT2G21990.1)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006460 (TIGRFAM): IPR006460 (F	0,105	0,061	0,326	0,144	0,307									
Solyc04g053145	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT3G61950.3)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR357	1,326	1,298	0,994	1,469	1,132									
Solyc04g054140	E3 ubiquitin-protein ligase RKP (AHRD V3.3 *** W9RJE5_9ROSA)		F:GO:0005515	F:protein binding			IPR003877 (SMART): G3DSA:2.60.12	64,730	68,360	70,559	74,543	71,097									
Solyc04g054145	kinectin-like protein (AHRD V3.3 --* AT5G66250.3)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,059	0,047	0,050	0,000									
Solyc04g054150	Nuclear transcription factor Y protein (AHRD V3.3 *** G7LB97_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	0,241	0,292	0,141	0,072	0,094									
Solyc04g054170	CPR5, putative (AHRD V3.3 *** G7JA92_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:systemic acquired resistance; P:trichome morphoc			PTHR35322 (PANTHER)	12,768	11,251	15,537	14,486	14,498									
Solyc04g054180	Myosin-H heavy chain (AHRD V3.3 *** A0A151TQJ2_CAJCA)		P:GO:1900034	P:regulation of cellular response to heat			mobidb-lite (MOBIDB_LITE): mobidb-lit	29,716	29,686	22,629	20,386	20,493									
Solyc04g054190	ABC1 protein (AHRD V3.3 *** D2XP29_MAIZE)		P:GO:0007623; P:G(	P:circadian rhythm; P:response to high light intensity; C:chlorop			IPR004147 (PFAM): PTHR10566:SF1	107,820	111,865	122,854	115,568	166,309			0,434	0,018				up	
Solyc04g054200	Receptor protein kinase, putative (AHRD V3.3 *** B9T1C2_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	24,769	20,616	29,904	36,109	29,567									
Solyc04g054220	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,040	0,000	0,000	0,000	0,000									
Solyc04g054225	Cytochrome P450 CYP736A121 (AHRD V3.3 *-* A0A0B4VSP1_SALMI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PFAM): IPR036396 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc04g054250	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,042	0,021	0,000	0,025	0,000									
Solyc04g054257	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,763	0,468	0,065	0,075	0,070									
Solyc04g054260	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,813	1,241	3,721	3,694	2,907									
Solyc04g054270	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T1C7_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,623	3,477	4,674	4,436	5,297									
Solyc04g054290	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HFU9_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR032867 (F	3,428	3,282	2,717	3,358	3,000									
Solyc04g054310	Alanine-glyoxylate aminotransferase, putative (AHRD V3.3 *** B9T1D1_RICCO)		F:GO:0008483; F:G(	F:transaminase activity; F:pyridoxal phosphate binding			IPR015421 (G3DSA:3.40.640.GENE3I	18,225	21,400	123,654	153,642	111,092									
Solyc04g054320	leucine-zipper transcription factor	nitf	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	9,857	7,271	9,339	8,745	10,943									
Solyc04g054330	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT2G22120.2)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR011016 (PF	16,022	14,106	22,860	23,075	21,800									
Solyc04g054340	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT5G65440.9)						PTHR36067 (PANTHER)	1,782	2,328	0,907	0,650	0,916									
Solyc04g054370	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G41400.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	16,505	13,411	9,111	5,198	8,844					-0,805	0,018			down
Solyc04g054380	Terpene synthase (AHRD V3.3 *** G5CV47_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR036965 (G3D	0,000	0,080	0,000	0,000	0,000									
Solyc04g054400	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061DJT5_THECC)		F:GO:0000140; F:G(	F:acylglycerone-ph	EC:1.1.1.11; EC:3.1.	Acylglycerone-phosp	IPR002347 (PRINTS): IPR002347 (PF	10,772	11,077	21,311	19,829	19,780									
Solyc04g054410	Regulation of nuclear pre-mRNA domain-containing 1B (AHRD V3.3 *** A0A0B0P8L0_GOSAR)		F:GO:0000993; C:G(	F:RNA polymerase II complex binding; C:RNA polymerase II, ho			IPR006569 (SMART): IPR008942 (G3	10,142	9,683	17,144	16,866	16,659									
Solyc04g054430	Retrovirus-related Pol polyprotein from transposon 17.6 (AHRD V3.3 --* A0A151SX10_CAJCA)							11,082	12,640	19,422	15,267	17,128									
Solyc04g054440	LOW QUALITY:chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR001650 (SM	0,533	0,979	0,333	0,100	0,494									
Solyc04g054460	Glycine-rich family protein (AHRD V3.3 *** B9MTF6_POPTR)		C:GO:0009507	C:chloroplast			mobidb-lite (MOBIDB_LITE): PTHR354	20,111	24,855	37,246	39,551	40,137									
Solyc04g054470	NAD(P)H-quinone oxidoreductase subunit 3, chloroplastic (AHRD V3.3 --* NU3C_AGRST)							30,408	26,195	44,346	45,559	45,456									
Solyc04g054475	Formation of crista junctions protein 1 (AHRD V3.3 *** A0A1D1ZJH3_9ARAE)		C:GO:0005743; C:G(	C:mitochondrial inner membrane; C:integral component of memb			IPR025558 (PFAM): IPR019133 (PFA	0,160	0,180	0,146	0,262	0,235									
Solyc04g054480	U-box domain-containing protein (AHRD V3.3 *** A0A0K9NX58_ZOSMR)		F:GO:0005515	F:protein binding			IPR000008 (SMART): IPR000225 (SM	600,767	406,440	78,713	60,705	85,564									
Solyc04g054490	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061DI57_THECC)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032861 (PF	9,542	7,945	3,895	4,881	5,172									
Solyc04g054500	metal ion binding protein		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	31,516	31,146	14,404	3,265	10,282					-2,135	0,000			down
Solyc04g054510	FK506-binding protein 16-2 (AHRD V3.3 *** AT4G39710.3)		F:GO:0003676; P:G(	F:nucleic acid binding; P:transcription, DNA-templated; P:mRNA			IPR001222 (SMART): G3DSA:2.20.25	3,624	4,115	5,023	5,553	4,360									
Solyc04g054520	FK506-binding protein 16-2 (AHRD V3.3 *** AT4G39710.3)		P:GO:0000413; F:G(	P:protein peptidyl-pi	EC:5.2.1.8	Peptidylprolyl isomer	G3DSA:3.10.50.40 (GENE3D): IPR00	0,098	0,157	0,000	0,045	0,118									
Solyc04g054650	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G09770.1)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,041	0,000	0,000	0,000									
Solyc04g054685	MADS-box transcription factor (AHRD V3.3 *-* A2PZF4_ALSLI)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRINTS): IPR002100 (SM	0,000	0,039	0,000	0,000	0,000									
Solyc04g054690	ascorbate oxidase	ao	F:GO:0005507; C:G(	F:copper ion binding; C:extracellular region; F:oxidoreductase a			IPR011706 (PFAM): IPR001117 (PFA	40,345	50,776	6,840	7,246	10,560									
Solyc04g054700	GTF2H2 (AHRD V3.3 *** A0A097PR28_PRUPE)		C:GO:0000439; P:G(	C:transcription factor TFIIH core complex; P:nucleotide-excisior			IPR004595 (SMART): IPR002035 (SM	47,094	34,691	40,529	43,328	37,758									
Solyc04g054710	aspartate aminotransferase (AHRD V3.3 *** AT2G22250.3)	PAT	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015422 (G3DSA:3.90.1150.GENE	55,762	56,467	118,428	117,852	118,963									
Solyc04g054720	APOLLO (AHRD V3.3 *-* U5U5S3_9BRAS)		F:GO:0003676	F:nucleic acid binding			IPR013520 (SMART): IPR036397 (G3	0,084	0,176	0,000	0,000	0,000									
Solyc04g054730	Sulfate transporter (AHRD V3.3 *** A7YGJ3_POPCN)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR011547 (PFAM): IPR001902 (TIGF	18,164	17,746	12,782	19,989	22,555			0,814	0,001	0,649	0,042		up	up
Solyc04g054740	myo-inositol-1-phosphate synthase	inps	F:GO:0004512; P:G(	F:inositol-3-phospha	EC:5.5.1.4	Inositol-3-phosphate	IPR002587 (PFAM): IPR013021 (PFA	42,176	43,071	25,782	22,899	24,502									
Solyc04g054745	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT5G64360.7)							0,368	0,540	0,215	0,246	0,190									
Solyc04g054760	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)						IPR007650 (PFAM): mobidb-lite (MOB	3,816	5,147	6,246	8,796	6,335									
Solyc04g054770	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 --* AT5G45790.2)							0,492	0,509	0,268	0,341	0,261									
Solyc04g054780	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_SILLA)							3,522	3,054	2,438	3,131	3,412									
Solyc04g054790	Domain of Uncharacterized protein function, putative (AHRD V3.3 *-* A0A061GWB6_THECC)						IPR010369 (PFAM): mobidb-lite (MOB	0,237	0,143	0,000	0,000	0,070									
Solyc04g054800	UPSTREAM OF FLC protein (DUF966) (AHRD V3.3 *** AT5G10150.4)						IPR010369 (PFAM): mobidb-lite (MOB	1,772	2,791	0,216	0,365	0,471									
Solyc04g054810	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *** A0A103XBC9_CYNCS),Pfam:PF01190		C:GO:0005615	C:extracellular space			PF01190 (PFAM): PTHR31614 (PANT	724,527	747,084	830,138	882,477	805,286									
Solyc04g054820	phosphoglycerate/bisphosphoglycerate mutase (AHRD V3.3 *** AT1G78050.1)		F:GO:0004619; P:G(	F:phosphoglycerate	EC:5.4.2.1	Intramolecular transfe	IPR013078 (SMART): IPR013078 (PF	19,860	27,210	16,600	22,073	19,032									
Solyc04g054830	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** A0A151RRQ5_CAJCA)		P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART): IPR036691 (G3	0,042	0,077	1,615	3,202	0,824									
Solyc04g054840	Ethylene insensitive 3 family protein (AHRD V3.3 *** AT5G10120.1),Pfam:PF04873		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus			IPR006957 (PFAM EIL	0,123	0,064	0,025	0,025	0,023									
Solyc04g054880	bZIP transcription factor (DUF630 and DUF632) (AHRD V3.3 *** AT2G27090.2)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM): IPR006868 (PFA	41,875	30,405	29,587	26,049	25,356									
Solyc04g054890	Acyl-coenzyme A oxidase (AHRD V3.3 *** K4BSN7_SOLLC)		F:GO:0003997; C:G(	F:acyl-CoA oxidase	EC:1.3.3.6	Acyl-CoA oxidase	G3DSA:1.20.140.10 (GENE3D): IPR0(	16,507	18,324	103,648	109,099	105,357									
Solyc04g054900	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** A0A0B0PI24_GOSAR)						mobidb-lite (MOBIDB_LITE): PTHR339	4,056	4,955	2,584	2,012	2,115									
Solyc04g054910	Ethylene-responsive element binding-factor (AHRD V3.3 *** K9UTK3_JATCU)	ERF.H10	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	186,798	148,372	101,996	145,674	134,306					0,516	0,007			up
Solyc04g054930	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** M1BUG9_SOLTU)		F:GO:0003824; P:G(	F:catalytic activity; P:trehalose biosynthetic process			G3DSA:3.30.70.1020 (GENE3D): IPR(	21,495	15,831	9,359	10,771	10,096									
Solyc04g054950	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		C:GO:0016021; F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS): IPR002347 (PF	0,415	1,446	0,737	0,539	1,390									
Solyc04g054980	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)		F:GO:0004096; F:G(	F:catalase activity;	EC:1.11.1.7; EC:1.1	Peroxidase; Catalase	IPR001024 (PFAM): IPR037060 (G3D	561,727	497,985	227,110	141,769	219,465					-0,677	0,000			down
Solyc04g054990	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)		F:GO:0005515	F:protein binding			IPR001024 (PFAM): G3DSA:2.60.60.2	59,857	46,691	11,565	4,801	9,619					-1,267	0,000			down
Solyc04g055000	tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *** AT5G65160.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	7,567	3,899	0,194	0,333	0,329									
Solyc04g055010	Protein SCO1, mitochondrial-like protein (AHRD V3.3 *** A0A0B0NQD3_GOSAR)		C:GO:0016021; P:G(	C:integral component of membrane; P:copper ion homeostasis			G3DSA:3.40.30.10 (GENE3D): IPR00	20,688	18,483	16,912	16,892	17,549									
Solyc04g055020	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (AHRD V3.3 *** K4BSQ1_SOLLC)		P:GO:0006099; F:G(	P:tricarboxylic acid cycle; F:electron transfer activity; F:iron-sul			IPR004489 (TIGRFAM): PF13534 (PF	0,465	1,047	0,223	0,203	0,023									
Solyc04g055030	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (AHRD V3.3 *** K4BSQ1_SOLLC)		P:GO:0006099; F:G(	P:tricarboxylic acid cycle; F:electron transfer activity; F:iron-sul			PF13534 (PFAM): IPR012675 (G3DS/	1,175	2,928	0,444	1,385	0,046									
Solyc04g055050	VQ motif-containing protein (AHRD V3.3 *-* AT4G39720.4)		P:GO:0008150	P:biological_process			IPR008889 (PFAM): mobidb-lite (MOB	11,678	8,108	13,542	12,158	12,967									
Solyc04g055060	Serine/threonine-protein phosphatase 7 long form like (AHRD V3.3 --* A0A0B2QDN2_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,080	0,257	0,143	0,072	0,071									
Solyc04g055080	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): G3D	2,406	2,648	1,542	2,084	1,578									
Solyc04g055090	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7J3T5_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	14,375	24,471	0,931	1,241	1,361	0,794	0,008					up		
Solyc04g055100	LOW QUALITY:Plant/F17O14-7 protein (AHRD V3.3 *** G7KY86_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR010605 (PFAM): mobidb-lite (MOB	0,061	0,076	0,000	0,000	0,000									
Solyc04g055110	ARM-repeat/Tetratricopeptide repeat (TPR)-containing protein		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	30,842	26,888	49,386	46,706	40,940									
Solyc04g055120	peroxisomal ABC transporter 1 (AHRD V3.3 *** AT4G39850.4)	ABCD1	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	124,663	114,564	209,030	231,576	207,260									
Solyc04g055160	N-lysine methyltransferase (AHRD V3.3 *** AT1G78150.2)						IPR025131 (PFAM): mobidb-lite (MOB	3,691	5,555	2,682	2,144	2,300									
Solyc04g055170	annexin p35	an35	F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR009118 (PF	3,334	2,100	2,368	2,475	2,420									
Solyc04g055180	(DB215) meloidogyne-induced giant cell protein						IPR006571 (SMART): IPR006571 (PF	28,933	21,341	36,281	29,549	29,983									
Solyc04g055190	Membrane-bound O-acyltransferase family MBOAT protein (AHRD V3.3 *** G7ID88_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR004299 (PFAM): PTHR13285 (PAN	12,046	11,096	17,390	21,222	16,578									
Solyc04g055200	Asparagine synthetase, putative (AHRD V3.3 *** B9SZ39_RICCO)		F:GO:0004066; P:G(	F:asparagine synth	EC:6.3.5.4	Asparagine synthase	IPR006426 (PIRSF): IPR001962 (PFA	41,896	44,371	48,033	40,133	43,841									
Solyc04g055207	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT4G35050.1)							3,714	2,709	0,352	0,507	0,632									
Solyc04g055230	cystathionine beta-lyase (AHRD V3.3 *-* AT3G57050.5)		F:GO:0030170	F:pyridoxal phosphate binding			PTHR11808:SF50 (PANTHER): IPR00	0,101	0,178	0,050	0,218	0,000									
Solyc04g055250	Adenine deaminase 2 (AHRD V3.3 *-* A0A0B0PKM7_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR34064 (PANTHER): PTHR34064	15,540	18,303	2,162	2,212	3,231									
Solyc04g055260	S-adenosyl-L-methionine:benzoic acid/salicylic acid carboxyl methyltransferase (AHRD V3.3 *** H9BID1_NI(		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	0,115	1,068	0,000	0,000	0,000									
Solyc04g056260	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G64970.1)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR018108 (PF	1,269	1,164	0,284	0,145	0,094									
Solyc04g056270	ER66	er66	F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR002110 (SMAF CAMTA	188,730	382,971	150,676	138,194	158,611	1,044	0,013					up		
Solyc04g056280	cyclin dependent kinase C	cdkc	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	33,085	33,855	38,834	37,578	36,837									
Solyc04g056290	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** A0A072TTI7_MEDTR)		P:GO:0016579; F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	11,016	8,462	9,538	8,697	9,000									

Solyc04g056310	Myb transcription factor (AHRD V3.3 *-* A0A072V9U0_MEDTR)	R2R3MYB53	F:GO:0003677	F:DNA binding		IPR001005 (SMAF MYB	0,040	0,000	0,022	0,000	0,071									
Solyc04g056320	Protein SENSITIVE TO PROTON RHIZOTOXICITY 1 (AHRD V3.3 *** W9QND6_9ROSA)		F:GO:0003676	F:nucleic acid binding		IPR013087 (SMAF C2H2	31,574	30,626	9,790	9,793	10,741									
Solyc04g056330	AIG2-like (Avirulence induced protein) family protein (AHRD V3.3 *** G7KF20_MEDTR)		F:GO:0061929	F:gamma-glutamyla EC:4.3.2.8	Gamma-glutamylamir	IPR009288 (PFAM): G3DSA:3.10.490	3,132	3,973	1,234	1,088	1,348									
Solyc04g056340	Tyrosine phosphatase family protein (AHRD V3.3 *** AT3G02800.1)		F:GO:0016791	F:phosphatase activity		IPR020428 (PRINTS): IPR004861 (PF	10,962	19,869	4,998	3,507	4,911									
Solyc04g056350	zinc finger (C2H2 type) family protein (AHRD V3.3 *** AT3G02790.1)					mobidb-lite (MOBIDB_LITE): PTHR212	122,241	109,816	158,671	149,674	140,582									
Solyc04g056370	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UHC2_ANACO)		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	11,755	12,033	18,271	16,406	18,368									
Solyc04g056380	Seipin (AHRD V3.3 *** A0A0B0N0V2_GOSAR)		P:GO:0019915	P:lipid storage		IPR009617 (PFAM): mobidb-lite (MOB	13,065	12,088	2,814	2,807	3,323									
Solyc04g056390	isopentenyl diphosphate isomerase	IPI1	F:GO:0004452; P:G(	F:isopentenyl-dipho EC:5.3.3.2	Isopentenyl-diphospt	IPR011876 (TIGRFAM): IPR011876 (F	139,666	139,790	464,974	399,024	421,483									
Solyc04g056410	DNA repair/recombination protein (AHRD V3.3 *** AT3G19210.1)		F:GO:0005524	F:ATP binding		IPR001650 (SMART): IPR014001 (SM	3,668	3,937	1,083	0,699	1,103									
Solyc04g056430	basic leucine zipper/W2 domain protein (AHRD V3.3 *** AT1G06010.1)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	12,008	11,521	13,928	10,289	11,796									
Solyc04g056440	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *-* AT3G23530.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PR00419 (PRINTS): IPR036188 (G3D	0,000	0,043	0,000	0,000	0,023									
Solyc04g056450	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *** AT3G23510.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PF02353 (PFAM): G3DSA:3.40.50.15(	0,236	0,124	0,000	0,000	0,000									
Solyc04g056480	26S proteasome non-ATPase regulatory subunit 3 (AHRD V3.3 --* A0A072V347_MEDTR)		P:GO:0006511; C:G(	P:ubiquitin-dependent protein catabolic process; C:proteasome		mobidb-lite (MOBIDB_LITE)	0,019	0,000	0,000	0,000	0,000									
Solyc04g056491	E3 ubiquitin-protein ligase CHIP (AHRD V3.3 *-* A0A199VLN1_ANACO)					IPR004252 (PFAM): PTHR33144:SF8	0,019	0,000	0,000	0,000	0,000									
Solyc04g056494	BZIP transcription factor family protein (AHRD V3.3 *-* B9IHM4_POPTR)		C:GO:0016020	C:membrane		PTHR37616 (PANTHER)	0,000	0,021	0,000	0,000	0,000									
Solyc04g056498	Pyridoxamine 5'-phosphate oxidase family protein (AHRD V3.3 --* AT2G04690.5)		C:GO:0005737; P:G(	C:cytoplasm; P:poly(A)+ mRNA export from nucleus; C:nuclear (		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc04g056510	BZIP family transcription factor (AHRD V3.3 *-* A0A0K9PLB3_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc		PTHR37616 (PANTHER)	0,021	0,000	0,000	0,000	0,000									
Solyc04g056530	L18 ribosomal protein Heart Stopper (AHRD V3.3 *** A0A0I9RJ77_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR005484 (PFAM): G3DSA:3.30.420	2,666	2,866	5,203	4,015	3,778									
Solyc04g056540	Riboflavin biosynthesis RibD (AHRD V3.3 *** A0A0B0NJC0_GOSAR)		F:GO:0008703; F:G(	F:5-amino-6-(5-pho EC:3.5.4.26; EC:1.1.	Diaminohydroxypho	IPR012816 (TIGRFAM): IPR024072 ((	15,576	14,617	43,870	39,394	43,496									
Solyc04g056560	Protein phosphatase-2c, putative (AHRD V3.3 *** B9RM68_RICCO)		F:GO:0004722; P:G(	F:protein serine/thr EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	50,402	41,207	52,949	48,503	47,212									
Solyc04g056580	AT1G65230-like protein (AHRD V3.3 *** A0A097PRZ6_SOLLC)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane		IPR018790 (PFAM): PTHR36334 (PAI	28,843	45,477	17,769	25,752	46,177	0,684	0,035	1,372	0,000			up	up	
Solyc04g056590	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G02740.1)		F:GO:0004190; P:G(	F:aspartic-type end EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	16,101	17,804	26,041	31,176	25,615									
Solyc04g056600	Na+/H+ antiporter 2	nhx2	P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral		IPR006153 (PFAM): mobidb-lite (MOB	24,557	22,694	33,682	39,123	35,378									
Solyc04g056610	Isopentenyl-diphosphate delta-isomerase (AHRD V3.3 *** A0A0B0PDY5_GOSAR)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast; C:integral component of membra		PTHR36074 (PANTHER)	13,445	12,234	28,819	29,787	24,898									
Solyc04g056630	CBS domain-containing family protein (AHRD V3.3 *** B9N159_POPTR)		C:GO:0005773	C:vacuole		IPR000644 (SMART): G3DSA:3.10.58	55,629	47,873	69,306	61,808	68,724									
Solyc04g056640	Leucine rich repeat receptor like protein CLAVATA2 (AHRD V3.3 *** F8WS85_SOLLC)		F:GO:0005515	F:protein binding		PR00019 (PRINTS): IPR003591 (SMA	3,834	4,116	1,149	0,864	1,151									
Solyc04g056650	ABC transporter family protein (AHRD V3.3 *** A0A097P9U3_HEVBR)	ABCI5	F:GO:0005524; F:G(	F:ATP binding; F:AT EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	21,280	24,900	42,044	42,721	42,233									
Solyc04g056680	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)		P:GO:0007165	P:signal transduction		IPR025886 (PFAM): PTHR32278 (PAI	0,217	0,236	0,000	0,075	0,000									
Solyc04g056690	F-box protein (AHRD V3.3 *-* A0A1D1Y009_9ARAE)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): PTH	0,021	0,000	0,000	0,025	0,024									
Solyc04g056700	LOW QUALITY:Pleiotropic drug resistance ABC transporter (AHRD V3.3 --* W0TSU1_ACAMN)		F:GO:0000166; F:G(	F:nucleotide binding; F:ATP binding; C:plasma membrane; C:membrane; C:integral component of membr			0,000	0,172	0,000	0,000	0,142									
Solyc04g056710	F-box family protein (AHRD V3.3 *-* AT2G02240.1)		P:GO:0007165	P:signal transduction		IPR025886 (PFAM): PTHR32278:SF2	0,040	2,687	0,000	0,000	0,682	5,792	0,000					up		
Solyc04g056730	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 --* AT5G63020.1)						0,304	6,464	0,025	0,072	4,047	4,353	0,000					up		
Solyc04g056735	F-box family protein (AHRD V3.3 *** A0A061EJY2_THECC)		P:GO:0007165	P:signal transduction		PTHR32278 (PANTHER): PTHR32278	0,000	0,532	0,000	0,000	0,094									
Solyc04g056740	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *** AT4G36590.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity		IPR002100 (PRIN' M-type_MADS	0,384	0,059	0,000	0,000	0,000									
Solyc04g056743	Cytochrome P450 (AHRD V3.3 *-* Q9AVQ2_SOLTU)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; C:membrane; C:integral component of membrane; F:oxidc			0,075	0,057	0,000	0,000	0,000									
Solyc04g056744	Cytochrome P450 (AHRD V3.3 *-* Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc		IPR036396 (G3DSA:1.10.630.GENE3	0,132	0,000	0,000	0,000	0,000									
Solyc04g056745	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative (AHRD V3.3 *-* A0AC		F:GO:0003682	F:chromatin binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	2,659	0,950	0,000	0,101	0,000									
Solyc04g056746	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SM34_RICCO)		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	4,389	2,713	3,794	3,988	4,148									
Solyc04g056748	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THECC)		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM): PTHR23272 (PAI	1,082	0,746	0,885	0,822	0,988									
Solyc04g057780	ENHANCED DISEASE RESISTANCE 2 (AHRD V3.3 --* AT4G19040.3)						1,627	1,167	1,492	1,570	1,413									
Solyc04g057783	BED zinc finger,hAT family dimerization domain (AHRD V3.3 --* A0A061G8Z6_THECC)		F:GO:0003677	F:DNA binding		IPR025525 (PFAM)	0,082	0,083	0,000	0,025	0,070									
Solyc04g057787	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THECC)		F:GO:0046983	F:protein dimerization activity		PTHR23272 (PANTHER): PTHR23272	0,193	0,293	0,187	0,170	0,142									
Solyc04g057830	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7K362_MEDTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:heme binding; P:electron transpor		IPR025322 (PFAM): PTHR33052 (PAI	0,623	1,931	0,199	0,151	0,168									
Solyc04g057840	LOW QUALITY:Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)		F:GO:0043531	F:ADP binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,040	0,078	0,000	0,022	0,000									
Solyc04g057850	LOW QUALITY:Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)		F:GO:0043531	F:ADP binding		PTHR33463:SF6 (PANTHER): PTHR3:	0,057	0,165	0,193	0,100	0,141									
Solyc04g057860	60S ribosomal protein L27 (AHRD V3.3 *** A0A0V0HNB9_SOLCH)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR001141 (PFAM): IPR038655 (G3D	1,107	1,341	0,634	0,750	0,867									
Solyc04g057870	plastid transcriptionally active 6 (AHRD V3.3 *** AT1G21600.2)		C:GO:0009508; C:G(	C:plastid chromosome; C:chloroplast nucleoid; P:plastid transcri		PTHR35994 (PANTHER)	37,631	47,826	71,748	68,963	79,181									
Solyc04g057880	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9NPD3_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C EC:2.1.1.43	Histone-lysine N-met	IPR006560 (SMART): IPR001214 (SM	21,483	17,767	28,851	35,428	32,728									
Solyc04g057890	ganglioside-induced differentiation-associated protein 1	GSTF6	F:GO:0005515	F:protein binding		G3DSA:3.40.30.10 (GENE3D): PF134	2,627	1,743	7,292	8,519	6,464									
Solyc04g057910	Yippee family putative zinc-binding protein (AHRD V3.3 --* AT2G40110.4)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:metal ion bi		mobidb-lite (MOBIDB_LITE): mobidb-lit	14,951	3,398	0,109	0,000	0,023	-2,110	0,000					down		
Solyc04g057920	LOW QUALITY:Protein yippee-like (AHRD V3.3 *** K4C9V4_SOLLC)		F:GO:0046872	F:metal ion binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,135	0,019	0,000	0,000	0,000									
Solyc04g057930	Kinase family protein (AHRD V3.3 *** B9H7J5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR006016 (PF	76,156	69,104	99,893	81,276	80,148									
Solyc04g057940	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061EZ85_THECC)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot		IPR001680 (SMART): IPR003613 (SM	22,865	27,215	2,325	4,104	3,434									
Solyc04g057950	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,174	0,062	0,075	0,051	0,071									
Solyc04g057960	Peroxisome biogenesis protein 1 (AHRD V3.3 *** A0A061GC53_THECC)		F:GO:0005524; C:G(	F:ATP binding; C:pe EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR015342 (PF	38,505	28,597	36,914	34,975	38,052									
Solyc04g057970	ATPase, V1 complex, subunit B protein (AHRD V3.3 --* AT4G38510.5)					mobidb-lite (MOBIDB_LITE): PTHR341	12,500	8,971	10,359	9,439	9,799									
Solyc04g057980	Orange Ripening	ORR	F:GO:0016655; P:G(	F:oxidoreductase activity, acting on NAD(P)H, quinone or simila		IPR018922 (PFAM): mobidb-lite (MOB	4,498	14,712	0,380	0,990	2,752	1,735	0,000	2,799	0,000			up	up	
Solyc04g057990	Zinc finger transcription factor 33	C3H33	F:GO:0046872	F:metal ion binding		IPR000571 (SMAF C3H	65,196	50,170	65,433	68,920	74,868									
Solyc04g057993	30S ribosomal protein S8, putative (AHRD V3.3 *-* B9SR47_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		G3DSA:3.30.1490.10 (GENE3D): IPR(	18,431	20,792	13,420	13,781	12,007									
Solyc04g057997	30S ribosomal protein S8, putative (AHRD V3.3 *-* B9SR47_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR000630 (PFAM): G3DSA:3.30.149(	3,018	3,610	2,218	1,771	1,954									
Solyc04g058000	Laccase (AHRD V3.3 *-* F6HJA9_VITVI)		F:GO:0005507; P:G(	F:copper ion binding; P:oxidation-reduction process		IPR001117 (PFAM): IPR011707 (PFA	0,936	2,216	0,025	0,096	0,047									
Solyc04g058010	PTB domain engulfment adapter (AHRD V3.3 --* AT2G04790.9)						0,164	0,163	0,075	0,092	0,094									
Solyc04g058040	Laccase (AHRD V3.3 *** K4DG13_SOLLC)		F:GO:0005507; P:G(	F:copper ion binding; P:oxidation-reduction process		IPR001117 (PFAM): IPR011707 (PFA	0,387	0,761	0,025	0,000	0,000									
Solyc04g058060	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)		C:GO:0016020	C:membrane		IPR004314 (PFAM): IPR025521 (PFA	37,264	41,510	23,925	19,462	22,143									
Solyc04g058065	UDP-sugar pyrophosphorylase (AHRD V3.3 *** USP_CUCME)		F:GO:0070569	F:uridylyltransferase activity		IPR002618 (PFAM): IPR029044 (G3D	0,294	0,213	0,221	0,245	0,235									
Solyc04g058070	UDP-sugar pyrophosphorylase (AHRD V3.3 *** AT5G52560.1)		F:GO:0070569	F:uridylyltransferase activity		IPR029044 (G3DSA:3.90.550.GENE3	13,499	11,817	11,165	10,587	9,810									
Solyc04g058080	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *-* B9RKF7_RICCO)					IPR012946 (SMART): IPR012946 (PF	0,115	0,234	0,050	0,025	0,000									
Solyc04g058090	Phosphoribosylformylglycinamidine cyclo-ligase (AHRD V3.3 *** A0A061DT32_THECC)		F:GO:0004641; P:G(	F:phosphoribosylfor EC:6.3.3.1	Phosphoribosylformy	IPR036921 (G3DSA:3.30.1330.GENE	48,799	53,339	46,699	43,183	45,872									
Solyc04g058100	Metallothionein-like protein type 2 (AHRD V3.3 *** MT2X_SOLLC)		F:GO:0046872	F:metal ion binding		IPR000347 (PFAM): IPR000347 (PAN	0,139	0,132	0,454	0,429	0,306									
Solyc04g058110	Serine/threonine-protein kinase (AHRD V3.3 *** M1CVM1_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phosphc	IPR000719 (SMART): IPR001480 (SM	5,731	9,443	1,467	2,305	2,956	0,747	0,022	1,003	0,021			up	up	
Solyc04g058130	calcium-dependent protein kinase 29 (AHRD V3.3 --* AT1G76040.4)		C:GO:0005634; P:G(	C:nucleus; P:cellular response to DNA damage stimulus		mobidb-lite (MOBIDB_LITE): mobidb-lit	5,265	4,419	6,050	6,589	6,283									
Solyc04g058140	GTPase obg (AHRD V3.3 *** A0A1D1XZG9_9ARAE)		F:GO:0005525	F:GTP binding		IPR006073 (PRINTS): IPR006073 (PF	25,229	22,264	30,934	31,419	30,054									
Solyc04g058150	Metallothionein-like protein (AHRD V3.3 *** A8DUB1_SOLLC)		F:GO:0046872	F:metal ion binding		IPR000347 (PFAM): PTHR33543:SF1	455,247	443,068	121,629	90,564	115,620					-0,422	0,026			down
Solyc04g058160	Calcium-binding protein (AHRD V3.3 *** A0A1B0WUT3_SOLHA)		F:GO:0005509	F:calcium ion binding		IPR002048 (SMART): G3DSA:1.10.23	0,000	0,039	0,000	0,000	0,000									
Solyc04g058170	Calcium-binding protein (AHRD V3.3 *** A0A1B0WUT3_SOLHA)		F:GO:0005509	F:calcium ion binding		IPR002048 (SMART): G3DSA:1.10.23	1,936	3,127	0,902	2,787	2,272			1,311	0,026	1,599	0,001		up	up
Solyc04g058180	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G77260.1)		F:GO:0008168	F:methyltransferase activity		IPR004159 (PFAM): G3DSA:3.40.50.1	19,947	17,729	28,966	23,575	25,791									
Solyc04g058190	PHD finger family protein (AHRD V3.3 *** B9GTY7_POPTR)		C:GO:0000123; C:G(	C:histone acetyltrar EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR001965 (SMART): G3DSA:2.30.30	2,882	2,560	1,949	1,898	2,067									
Solyc04g058200	Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *** A0A061FHS4_THECC)		F:GO:0005515	F:protein binding		IPR019734 (SMART): PF13428 (PFAM	1,814	1,529	2,392	2,272	2,122									
Solyc04g063200	LOW QUALITY:PH01B035L11.21 protein (AHRD V3.3 --* L0P1Q5_9POAL)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,000	0,000									
Solyc04g063210	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_MESCR)		F:GO:0008171	F:O-methyltransferase activity		IPR002935 (PFAM): G3DSA:3.40.50.1	5,857	6,245	1,715	0,839	2,108									
Solyc04g063230	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G64030.1)		F:GO:0008168	F:methyltransferase activity		G3DSA:3.40.50.150 (GENE3D): IPR(	399,937	380,780	97,785	77,607	103,189									
Solyc04g063240	STAY-GREEN-like protein (AHRD V3.3 *** AT1G44000.1)		P:GO:0009658	P:chloroplast organization		IPR024438 (PFAM): PTHR31750:SF2	10,724	11,873	4,647	5,777	6,954									
Solyc04g063245	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc		IPR001128 (PRINTS): IPR002401 (PF	1,524	0,960	0,093	0,123	0,186									
Solyc04g063280	ENTH/VHS/GAT family protein (AHRD V3.3 *** A0A072V220_MEDTR)		C:GO:0005622; P:G(	C:intracellular; P:intracellular protein transport		IPR002014 (SMART): IPR014645 (PIF	151,351	193,213	139,883	128,169	134,864									
Solyc04g063290	40S ribosomal protein S2 (AHRD V3.3 *** K7WJZ4_SOLTU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio		G3DSA:3.30.160.770 (GENE3D): IPR(	177,436	212,476	185,977	162,042	172,562									
Solyc04g063300	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SVS3_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (TIGF	1,396	1,951	1,822	1,926	1,829									
Solyc04g063320	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 --* AT3G53680.2)						1,688	1,666	0,911	0,992	0,914									
Solyc04g063330	LOW QUALITY:with no lysine (K) kinase 5 (AHRD V3.3 --* AT3G51630.2)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis			0,063	0,075	0,025	0,000	0,000									
Solyc04g063340	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H7L3_POPTR)		F:GO:0005515	F:protein binding		IPR002885 (TIGRFAM): IPR002885 (I	2,785	2,252	2,182	3,167	3,254									
Solyc04g063345	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 --* RBL_PHUST)						0,373	0,475	0,295	0,315	0,307									
Solyc04g063350	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** A0A178WNY2_ARATH)		F:GO:0016624	F:oxidoreductase activity, acting on the aldehyde or oxo group (		G3DSA:3.40.50.970 (GENE3D): IPR(	3,121	3,273	8,928	18,165	14,640					1,027	0,001			up
Solyc04g063360	ATP-dependent zinc metalloprotease FTSH (AHRD V3.3 *** W9S040_9ROSA)		F:GO:0004222; F:G(	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): IPR003959 (PF	34,396	38,437	60,437	58,208	61,053									
Solyc04g063370	Receptor-like kinase (AHRD V3.3 *** A0A072V0S7_MEDTR)		F:GO:0004713; F:G(	F:protein tyrosine k EC:2.7.1	Transferring phosphc	IPR020635 (SMART): G3DSA:3.30.20	0,040	0,055	0,072	0,123	0,047									
Solyc04g063380	F-box family protein (AHRD V3.3 *** B9H7L8_POPTR)		F:GO:0005515	F:protein binding		IPR006553 (SMART): IPR001810 (PF	37,169	27,612	53,540	48,155	50,860									
Solyc04g063390	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9S2N8_RICCO)					IPR001623 (PRINTS): IPR001623 (SM	0,038	0,021	0,000	0,025	0,000									
Solyc04g063400	F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding		IPR001810 (SMART): G3DSA:1.20.12	7,390	7,799	12,792	12,993	12,633									
Solyc04g063440	F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding		IPR001810 (SMART): IPR013187 (PF	0,019	0,076	0,000	0,000	0,000									
Solyc04g064440	F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding		IPR001810 (SMART): IPR013187 (PF	0,056	0,057	0,000	0,000	0,000									
Solyc04g064470	Squamosa promoter-binding-like protein (AHRD V3.3 *-* A0A072V7X4_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus		IPR004333 (PFAM SBP	12,262	13,072	8,710	11,337	11,391									
Solyc04g064480	F-box family protein (AHRD V3.3 --* AT1G19160.1)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): IPR	19,858	20,843	18,159	19,963	20,460									
Solyc04g064490	Hexosyltransferase (AHRD V3.3 *** K4BT40_SOLLC)	GAUT10	F:GO:0047262	F:polygalacturonate EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	31,933	25,948	28,970	28,554	25,616									
Solyc04g064500	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G43900.1)		F:GO:0004722; P:G(	F:protein serine/thr EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	36,522	36,394	69,683	74,782	77,102									
Solyc04g064510	GTP-binding family protein (AHRD V3.3 *** B9HES5_POPTR)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	54,951	54,883	98,936	97,011	91,534									
Solyc04g064520	Transmembrane protein, putative (AHRD V3.3 *** G7LHG7_MEDTR)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	11,780	10,652	19,775	20,767	17,746									
Solyc04g064530	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072V150_MEDTR)		C:GO:0016021	C:integral component of membrane		PTHR33133:SF5 (PANTHER): PTHR3:	2,798	24,554	3,007	6,138	9,228	3,153	0,000	1,608	0,000	1,024	0,018	up	up	up
Solyc04g064540	R2R3MYB transcription factor 115	R2R3MYB115	F:GO:0003677	F:DNA binding		IPR001005 (SMAF MYB	0,000	0,039	0,000	0,025	0,000									
Solyc04g064550	gras6	GRAS6	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR005202 (PFAM GRAS	35,535	31,650	19,173	37,530	31,369			0,705	0,000	0,969	0,000		up	up
Solyc04g064560	Small RNA degrading nuclease (AHRD V3.3 *** A0A072VFB2_MEDTR)		F:GO:0003676	F:nucleic acid binding		IPR013520 (SMART): IPR013520 (PF	11,615	11,877	15,217	17,266	16,564									
Solyc04g064570	Ribosome maturation SBDS (AHRD V3.3 *** A0A0B0ME10_GOSAR)		P:GO:0042256	P:mature ribosome assembly		IPR019783 (PFAM): IPR002140 (TIGF	27,408	24,958	32,231	28,453	29,202									
Solyc04g064590	MAP kinase kinase kinase 33	MAPKKK33	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): G3DSA:1.10.51	0,479	0,525	0,392	0,411	0,497									
Solyc04g064600	Structural maintenance of chromosomes protein (AHRD V3.3 --* V4NTQ4_EUTSA)					PTHR34808:SF2 (PANTHER): PTHR3-	6,444	5,758	0,022	0,000	0,000									
Solyc04g064610	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT52_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:sugar transmembrane tra		G3DSA:1.20.1280.290 (GENE3D): IPI	0,301	1,046	5,346	7,521	5,693									
Solyc04g064620	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT53_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:sugar transmembrane tra		G3DSA:1.20.1280.290 (GENE3D): IPI	2,553	1,799	0,192	0,072	0,047									
Solyc04g064630	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT54_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:sugar transmembrane tra		G3DSA:1.20.1280.290 (GENE3D): IPI	1,860	1,591	0,094	0,607	0,498									
Solyc04g064640	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT55_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:sugar transmembrane tra		IPR004316 (PFAM): G3DSA:1.20.128	1,396	1,146	1,353	1,809	1,694									
Solyc04g064650	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XXL8_CYNCS)		F:GO:0005515	F:protein binding		IPR002885 (PFAM): IPR002885 (PFA	1,414	1,409	1,771	1,797	1,457									
Solyc04g064670	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** A0A0F7GXL4_9ROSI)		F:GO:0005509; C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple		IPR016123 (G3DSA:3.40.1000.GENE	33,386	49,013	17,751	18,032	25,870	0,580	0,022	0,540	0,002			up	up	
Solyc04g064680	Exostosin family protein (AHRD V3.3 *** AT1G21480.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc		IPR004263 (PFAM): mobidb-lite (MOB	48,299	40,896	36,182	34,569	32,536									
Solyc04g064690	Peroxidase (AHRD V3.3 *** K4BT60_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activi EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	6,717	8,089	0,240	0,290	0,258									
Solyc04g064700	Transcription elongation factor SPT5 (AHRD V3.3 *** K4BT61_SOLLC)		P:GO:0006357; P:G(	P:regulation of transcription by RNA polymerase II; P:regulation		IPR006645 (SMART): IPR005824 (SM	127,083	117,178	134,612	126,024	128,184									
Solyc04g064705	LOW QUALITY:Maturase K (AHRD V3.3 --* Q7YM20_9MAGN)					IPR025558 (PFAM): mobidb-lite (MOB	0,155	0,341	0,209	0,248	0,235									
Solyc04g064710	Alcohol dehydrogenase (AHRD V3.3 *** Q42953_TOBAC)		P:GO:0055114	P:oxidation-reduction process		IPR013154 (PFAM): G3DSA:3.40.50.7	4,263	8,048	2,351	5,308	0,606									
Solyc04g064720	Maltose excess protein 1 (AHRD V3.3 *** A0A0C5DIX1_CAMSI)		F:GO:0005363; C:G(	F:maltose transmembrane transporter activity; C:chloroplast en		IPR034628 (PANTHER)	13,498	24,294	4,713	5,493	10,683	0,874	0,001	1,171	0,000			up	up	
Solyc04g064730	Leucine-rich repeat (LRR) family protein (AHRD V3.3 --* AT1G80080.1)						0,247	0,164	0,165	0,173	0,235									
Solyc04g064740	TRICHOME BIREFRINGENCE-LIKE 7 (AHRD V3.3 *** AT1G48880.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace		IPR025846 (PFAM): IPR026057 (PFA	0,575	1,351	1,156	1,070	0,896									
Solyc04g064750	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061FHU2_THECC)		F:GO:0004185; F:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR029058 (G3DSA:3.40.50.GENE3D	4,654	6,122	4,262	4,589	4,748									
Solyc04g064760	Carboxypeptidase (AHRD V3.3 *** K4BT67_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): G3DSA:3.40.5(	5,258	6,911	1,532	2,706	2,485									
Solyc04g064763	Zinc finger CCCH domain-containing protein 38 (AHRD V3.3 *** W9QM16_9ROSA)		F:GO:0046872	F:metal ion binding		IPR000571 (SMART): PF18044 (PFAI	83,859	85,685	103,938	90,243	103,811									
Solyc04g064765	exostosin family protein (AHRD V3.3 --* AT3G57630.3)		F:GO:0046872	F:metal ion binding		mobidb-lite (MOBIDB_LITE): mobidb-lit	15,753	15,016	19,960	16,201	19,118									
Solyc04g064790	Hexosyltransferase (AHRD V3.3 *** K4BT70_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups		IPR002495 (PFAM): IPR029044 (G3D	34,870	28,257	42,088	41,454	40,690									
Solyc04g064795	zinc finger CCCH domain protein (AHRD V3.3 *-* AT2G10553.1)		F:GO:0046872	F:metal ion binding		IPR000571 (SMART): G3DSA:1.10.15	3,576	3,640	3,475	3,640	4,005									
Solyc04g064800	Zinc finger transcription factor 35	C3H35	F:GO:0046872	F:metal ion binding		IPR000571 (SMAF C3H	0,021	0,000	0,025	0,000	0,024									
Solyc04g064810	integral membrane metal-binding family protein (DUF2296) (AHRD V3.3 *** AT4G31080.1)		P:GO:0071786	P:endoplasmic reticulum tubular network organization		IPR019273 (PFAM): mobidb-lite (MOB	71,347	98,036	80,880	71,572	80,713									
Solyc04g064820	vacuolar protein sorting 45 (AHRD V3.3 *** AT1G77140.1)		P:GO:0006904	P:vesicle docking involved in exocytosis		IPR001619 (PIRSF): G3DSA:3.90.83(	19,595	17,085	20,715	23,269	21,007									
Solyc04g064830	transcriptional factor B3 family protein (AHRD V3.3 *** AT4G31690.1)		F:GO:0003677	F:DNA binding		IPR003340 (SMAF B3	6,663	5,105	5,951	5,763	5,731									
Solyc04g064850	Organic solute transporter ostalpha protein (AHRD V3.3 *** A0A072V0U4_MEDTR)		P:GO:0007033; C:G(	P:vacuole organization; C:plant-type vacuole membrane; C:inte		IPR005178 (PFAM): mobidb-lite (MOB	9,675	8,579	25,026	32,265	24,505									
Solyc04g064860	LOW QUALITY:Transcription factor, MADS-box (AHRD V3.3 *** A0A103YHS3_CYNCS)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity		IPR002100 (PRIN' M-type_MADS	2,231	1,502	1,150	1,466	1,199									
Solyc04g064870	protein early flowering 2-like					G3DSA:3.10.450.50 (GENE3D): PTHF	3,175	12,390	18,860	52,192	42,999	1,988	0,000	1,186	0,000	1,475	0,000	up	up	up
Solyc04g064880	Pathogen-related protein (AHRD V3.3 *** A0A1D1XC89_9ARAE)					G3DSA:3.10.450.50 (GENE3D): PTHF	0,119	1,098	2,750	11,015	5,624					2,007	0,000			up
Solyc04g064890	LOW QUALITY:suppressor of npr1-1 constitutive 4 (AHRD V3.3 --* AT1G66980.4)						4,167	2,421	0,881	0,559	0,678									
Solyc04g064900	Endoglucanase (AHRD V3.3 *-* A0A067LEU1_JATCU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR012341 (G3DSA:1.50.10.GENE3D	13,599	9,473	2,771	1,548	1,782									

Solyc04g064910	Endoglucanase (AHRD V3.3 *-* V4SJ00_9ROSI)		F:GO:0003824	F:catalytic activity			IPR012341 (G3DSA:1.50.10.GENE3D	0,698	0,661	0,136	0,245	0,257									
Solyc04g064920	Glycolipid transfer protein domain-containing protein (AHRD V3.3 *** A0A118JYI2_CYNCS)		C:GO:0005737: P:G(	C:cytoplasm; P:intermembrane lipid transfer; F:intermembrane li			IPR014830 (PFAM): IPR036497 (G3D	0,233	0,383	0,194	0,245	0,326									
Solyc04g064930	Peroxiredoxin (AHRD V3.3 *** G8JBE2_9ORYZ)		F:GO:0016209: F:G(	F:antioxidant activity; F:oxidoreductase activity; P:cell redox ho			IPR000866 (PFAM): G3DSA:3.40.30.1	7,698	11,471	10,620	11,622	15,537			0,546	0,011				up	
Solyc04g064940	Receptor protein kinase (AHRD V3.3 *** Q9FEU2_PINSY)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	2,061	1,430	0,191	0,171	0,284									
Solyc04g064943	Filament-plant-like protein (AHRD V3.3 *-* A0A072V4F5_MEDTR)						IPR008587 (PFAM): PTHR31580 (PAI	0,057	0,000	0,000	0,000	0,047									
Solyc04g070960	Dof zinc finger protein (AHRD V3.3 *-* W9S6D3_9ROSA)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM: Dof	0,040	0,064	0,000	0,000	0,024									
Solyc04g070970	ABC transporter family protein (AHRD V3.3 *** B9IIG9_POPTR)	ABCG10	F:GO:0005524: C:G(	F:ATP binding; C:m(	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	17,085	11,630	2,716	0,885	1,725					-1,594	0,001			down
Solyc04g070980	cycloartenol synthase 1	cas1	C:GO:0016021: F:G(	C:integral component of membrane; F:intramolecular transferas(			G3DSA:1.50.10.20 (GENE3D): PTHR1	24,846	21,991	6,687	3,613	5,835					-0,884	0,031			down
Solyc04g070983	Terpene cyclase/mutase family member (AHRD V3.3 *** K4BT90_SOLLC)		F:GO:0003824	F:catalytic activity			IPR001330 (PFAM): IPR032696 (PFA	34,311	31,544	8,658	5,854	8,841									
Solyc04g070985	adenine phosphoribosyl transferase 3 (AHRD V3.3 -** AT4G22570.2)						mobidb-lite (MOBIDB_LITE)	0,482	0,372	0,168	0,095	0,166									
Solyc04g070990	E4/E8 binding protein 1		F:GO:0003677	F:DNA binding			IPR003656 (PFAM): mobidb-lite (MOB	23,376	26,285	41,783	39,659	37,612									
Solyc04g071000	clade XIII lectin receptor kinase		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,939	0,732	1,354	1,192	1,365									
Solyc04g071005	Phytochrome B (AHRD V3.3 --* PHYB_ORYSJ)							2,392	2,857	3,155	3,313	3,162									
Solyc04g071010	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G42130.1)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	29,299	32,328	39,954	42,387	41,757									
Solyc04g071030	U-box domain-containing family protein (AHRD V3.3 *** B9HEI4_POPTR)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR003613 (PF	63,390	18,934	27,092	81,478	28,852	-1,718	0,000			1,592	0,000	down		up
Solyc04g071040	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHF		F:GO:0046872	F:metal ion binding			IPR000408 (PRINTS): IPR000306 (SM	115,286	159,041	70,056	64,914	68,434									
Solyc04g071050	RNA-binding protein with multiple splicing (AHRD V3.3 *** W9SPG0_9ROSA)		F:GO:0003723	F:RNA binding			mobidb-lite (MOBIDB_LITE): PTHR105	11,024	12,600	17,632	16,456	15,391									
Solyc04g071060	ROP uanine nucleotide exchange factor 10 (AHRD V3.3 --* AT5G19560.5)		F:GO:0003676: F:G(	F:nucleic acid binding; F:RNA binding; F:protein kinase activity;			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,953	0,681	0,047	0,301	0,071									
Solyc04g071070	Extensin (AHRD V3.3 *** Q06446_SOLTU)		F:GO:0005199: P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			IPR006706 (PFAM): mobidb-lite (MOB	9,882	8,693	77,848	63,931	88,085									
Solyc04g071075	Auxin efflux carrier family protein (AHRD V3.3 --* AT1G76530.3)							1,131	0,844	7,826	6,413	8,729									
Solyc04g071080	Extensin (AHRD V3.3 *** Q06446_SOLTU)		F:GO:0005199: P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			IPR006706 (PFAM): mobidb-lite (MOB	0,133	0,202	0,075	0,192	0,070									
Solyc04g071085	Hydroxyproline-rich glycoprotein (AHRD V3.3 *** Q8H9E0_SOLTU)		F:GO:0005199: P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			IPR006706 (PFAM): mobidb-lite (MOB	18,240	43,965	21,904	13,815	12,770	1,297	0,020					up		
Solyc04g071120	Protein kinase, putative (AHRD V3.3 *** B9T446_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	10,338	7,853	8,412	12,446	10,471					0,570	0,016			up
Solyc04g071130	F-box family protein (AHRD V3.3 *** AT1G76920.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	20,450	21,158	23,958	23,588	24,079									
Solyc04g071140	Serine decarboxylase (AHRD V3.3 *** SDC1_ARATH)		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015421 (G3DSA:3.40.640.GENE3	21,837	19,281	16,855	16,418	15,632									
Solyc04g071150	Cytochrome P450 family protein (AHRD V3.3 *** A0A072U8X2_MEDTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	0,753	0,856	4,682	5,832	3,776									
Solyc04g071160	BZIP transcription factor (AHRD V3.3 *** A0A0K9NU16_ZOSMR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR004827 (SMAF: bZIP	40,528	34,607	74,965	67,349	64,109									
Solyc04g071165	Vacuolar iron transporter (AHRD V3.3 *** A0A199VAI8_ANACO)		C:GO:0005623: P:G(	C:cell; P:ion transport; C:membrane; F:transition metal ion trans			IPR008217 (PFAM): PTHR31851:SF3	13,060	10,688	11,417	12,004	14,146									
Solyc04g071180	COMPLEX 1 LYR-like protein (AHRD V3.3 *** AT3G17300.3)						IPR008011 (PFAM): PTHR13166:SF1	12,564	13,353	13,892	10,991	12,744									
Solyc04g071260	Actin (AHRD V3.3 *** ACT_GOSHI)		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): IPR004000 (SM	0,180	0,115	0,571	0,691	0,733									
Solyc04g071270	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** A0A061FZW6_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,000	0,000	0,025	0,000	0,000									
Solyc04g071280	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5GR08_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	6,971	5,325	7,018	7,499	7,137									
Solyc04g071285	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 --* AT5G57200.1)							1,352	1,862	2,154	2,242	2,566									
Solyc04g071290	Mitochondrial substrate carrier family protein (AHRD V3.3 *-* AT5G42130.1)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	2,546	1,600	2,881	2,769	3,116									
Solyc04g071300	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_VITVI)		P:GO:0046034: P:G(	P:ATP metabolic process; P:proton transmembrane transport			IPR004100 (PFAM): G3DSA:3.40.50.3	0,078	0,715	0,096	0,123	0,164									
Solyc04g071310	CDK-activating kinase assembly factor-related		C:GO:0005675: P:G(	C:transcription factor TFIIH holo complex; P:nucleotide-excision			IPR015877 (PFAM): mobidb-lite (MOB	20,319	25,383	21,581	19,407	23,382									
Solyc04g071320	ubiquitin interaction motif-containing protein (AHRD V3.3 *** AT1G43690.1)		C:GO:0005829: F:G(	C:cytosol; F:cysteir	EC:3.4.18	Acting on peptide bor	IPR025257 (SMART): IPR025257 (PF	20,552	19,249	24,746	26,266	25,197									
Solyc04g071330	Armadillo repeat-containing protein, putative (AHRD V3.3 *** B9SB49_RICCO)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	13,840	12,815	16,499	17,677	15,487									
Solyc04g071340	fructose-1%2C6-bisphosphatase%2C cytosolic		P:GO:0005975: F:G(	P:carbohydrate met	EC:3.1.3.23; EC:3.1.	Sugar-phosphatase;	IPR028343 (PRINTS): G3DSA:3.40.1(	35,225	66,452	16,909	18,568	35,700	0,941	0,000	1,072	0,000			up	up	
Solyc04g071350	Exocyst complex component, putative (AHRD V3.3 *** B9T2G4_RICCO)		C:GO:0000145: P:G(	C:exocyst; P:Golgi to plasma membrane transport			IPR039481 (PFAM): mobidb-lite (MOB	129,564	126,499	122,412	133,832	122,703									
Solyc04g071360	Trihelix transcription factor GT-2-like protein (AHRD V3.3 *** A0A0B0MXN8_GOSAR)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR001005 (SMAF: Trihelix	79,238	43,481	29,862	33,513	35,908	-0,839	0,001					down		
Solyc04g071400	WAT1-related protein (AHRD V3.3 *** K4BTD2_SOLLC)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF2	1,474	1,142	0,044	0,000	0,000									
Solyc04g071420	Thioredoxin superfamily protein (AHRD V3.3 *** AT2G31840.2)		P:GO:0006355: C:G(	P:regulation of transcription, DNA-templated; C:chloroplast stror			mobidb-lite (MOBIDB_LITE): PTHR346	22,374	22,932	19,444	15,685	22,691									
Solyc04g071440	Tubby-like F-box protein (AHRD V3.3 *** K4BTD6_SOLLC)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS): IPR001810 (PF	20,198	18,263	23,585	23,128	20,799									
Solyc04g071470	WD40-repeat-containing domain-containing protein (AHRD V3.3 *** A0A103XXC8_CYNCS)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	9,900	9,736	5,939	4,397	5,719									
Solyc04g071480	LOW QUALITY:Plant/F1M20-13 protein (AHRD V3.3 *** G7IBZ7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR008511 (PFAM): PTHR31509 (PAI	184,551	122,923	121,213	311,773	193,238					1,364	0,000			up
Solyc04g071490	Heat shock family protein (AHRD V3.3 *-* B9GTI4_POPTR)	Hsp37.0	C:GO:0016021	C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,103	0,060	0,025	0,025	0,047									
Solyc04g071500	Cupredoxin superfamily protein (AHRD V3.3 *** AT1G21090.1)						IPR008972 (G3DSA:2.60.40.GENE3D	0,271	0,179	0,000	0,000	0,023									
Solyc04g071510	Transcription factor, putative (AHRD V3.3 *** B9SE72_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR004827 (SMAF: bZIP	14,515	13,040	17,963	18,281	16,751									
Solyc04g071520	Transcription elongation factor (TFIIS) family protein (AHRD V3.3 *** AT5G09850.5)		C:GO:0005634	C:nucleus			IPR003617 (SMART): IPR017923 (PF	0,201	0,272	2,291	3,490	2,092									
Solyc04g071523	UPF0496 protein (AHRD V3.3 *** A0A0B2QAE4_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR007749 (PFAM): IPR007749 (PAN	0,098	0,120	0,903	1,153	0,730									
Solyc04g071540	Sterol glucosyltransferase (AHRD V3.3 *** Q2I015_9SOLA)		P:GO:0005975: F:G(	P:carbohydrate metabolic process; F:transferase activity, trans			G3DSA:3.40.50.2000 (GENE3D): G3D	11,240	8,946	28,340	37,303	25,136									
Solyc04g071560	Sphingomyelin synthetase family protein (AHRD V3.3 *** AT1G43580.1)		C:GO:0009506: C:G(	C:plasmodesma; C:integral component of membrane; P:sphingo			IPR025749 (PFAM): PTHR21290 (PAI	20,447	20,409	11,149	9,102	12,065									
Solyc04g071565	Thioredoxin family protein (AHRD V3.3 *** A9PGA7_POPTR)		P:GO:0006662: F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored(			PR00421 (PRINTS): IPR005746 (TIGF	4,244	5,771	10,506	10,520	10,041									
Solyc04g071570	SET domain protein (AHRD V3.3 *** G7IQD7_MEDTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	10,570	8,781	9,867	9,908	8,805									
Solyc04g071580	ASR2	Asr_2					IPR003496 (PFAM): mobidb-lite (MOB	15,625	25,149	7,566	10,522	7,764									
Solyc04g071590	Abscisic acid stress ripening 3%2C ASR3						IPR003496 (PFAM): mobidb-lite (MOB	0,462	3,596	0,332	0,270	0,258	2,960	0,000					up		
Solyc04g071600	Abscisic acid stress ripening 5						IPR003496 (PFAM): mobidb-lite (MOB	0,058	0,300	0,236	0,530	0,425									
Solyc04g071610	Abscicic acid stress ripening 1	ASR1					IPR003496 (PFAM): mobidb-lite (MOB	8251,460	6530,682	11981,249	9369,528	8135,760			-0,561	0,029				down	
Solyc04g071615	ASR4 (AHRD V3.3 *** Q2QJT5_SOLLC)						IPR003496 (PFAM): mobidb-lite (MOB	71,230	67,321	20,790	20,074	26,464									
Solyc04g071620	Abscicic acid stress ripening 4	Asr4					IPR003496 (PFAM): mobidb-lite (MOB	11,236	12,238	2,699	2,515	3,443									
Solyc04g071630	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_CHLSC)						PTHR33674:SF3 (PANTHER): PTHR3:	4,669	3,143	11,027	8,570	8,424									
Solyc04g071650	Cellulose synthase (AHRD V3.3 *** M1A8I3_SOLTU)		C:GO:0016020: F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (l	IPR029044 (G3DSA:3.90.550.GENE3	542,351	405,220	22,131	9,693	19,089					-1,190	0,001			down
Solyc04g071660	U-box domain-containing protein kinase family protein (AHRD V3.3 --* AT2G45910.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	14,587	12,768	2,646	1,660	2,495									
Solyc04g071670	LOW QUALITY:Receptor-like protein kinase FERONIA (AHRD V3.3 --* A0A0B2PCR8_GLYSO)							0,139	0,135	0,072	0,072	0,119									
Solyc04g071680	Receptor protein kinase, putative (AHRD V3.3 *** B9SAG6_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR001611 (PF	1,877	1,673	0,384	0,489	0,490									
Solyc04g071690	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT1G76010.2)		F:GO:0003676	F:nucleic acid binding			IPR002775 (PFAM): IPR036882 (G3D	0,040	0,079	0,000	0,072	0,024									
Solyc04g071700	5-formyltetrahydrofolate cyclo-ligase (AHRD V3.3 *** A0A103XXD3_CYNCS)		C:GO:0005737: F:G(	C:cytoplasm; F:ligase activity			IPR024185 (G3DSA:3.40.50.GENE3D	6,977	8,555	7,868	7,873	11,609			0,561	0,029				up	
Solyc04g071710	Like-COV protein (AHRD V3.3 *** G7JAD5_MEDTR)		C:GO:0005768: C:G(	C:endosome; C:trans-Golgi network; C:integral component of m			IPR007462 (PFAM): mobidb-lite (MOB	18,524	20,654	26,986	27,076	22,737									
Solyc04g071715	Spo11/DNA topoisomerase VI, subunit A protein (AHRD V3.3 --* AT3G13170.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,817	1,159	0,912	0,988	1,248									
Solyc04g071730	Syntaxin-81-like protein (AHRD V3.3 *** A0A0B0PVL2_GOSAR)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport			G3DSA:1.20.5.110 (GENE3D): IPR01!	24,397	24,282	32,318	31,020	28,043									
Solyc04g071750	Tubby-like F-box protein (AHRD V3.3 *** K4BTG5_SOLLC)		F:GO:0005515	F:protein binding			IPR000007 (PFAM): IPR025659 (G3D	27,516	34,040	12,344	11,700	13,228									
Solyc04g071755	Tubby-like F-box protein (AHRD V3.3 *** K4BTG5_SOLLC)		C:GO:0005929: F:G(	C:cilium; F:phosphatidylinositol binding; P:protein localization to			IPR000007 (PRINTS): IPR000007 (PF	17,718	21,628	7,490	7,839	8,692									
Solyc04g071770	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RA19_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,242	4,591	10,006	13,798	7,858	4,227	0,000					up		
Solyc04g071780	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	5,150	7,703	5,625	5,051	10,906			0,945	0,001				up	
Solyc04g071790	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	0,269	0,199	0,068	0,022	0,046									
Solyc04g071800	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	178,065	182,172	10,439	2,702	13,561					-1,944	0,004			down
Solyc04g071807	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	0,059	0,118	0,000	0,000	0,000									
Solyc04g071820	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	0,059	0,019	0,000	0,000	0,000									
Solyc04g071860	S-acyltransferase (AHRD V3.3 *** K4BTH3_SOLLC)		C:GO:0016021: F:G(	C:integral compone	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	26,092	36,248	17,449	17,020	17,015									
Solyc04g071870	Receptor-like kinase (AHRD V3.3 *** G7IBW3_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	20,883	35,587	11,694	16,460	13,591									
Solyc04g071880	Pyrophosphate-energized membrane proton pump (AHRD V3.3 *** G5DWK6_SILLA)		F:GO:0004427: F:G(	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (PFAM): IPR004131 (TIGF	102,735	122,017	90,784	94,485	94,551									
Solyc04g071890	Peroxidase (AHRD V3.3 *** K4BTH6_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	31,256	60,885	35,822	19,354	22,956	0,987	0,004			-0,883	0,019	up		down
Solyc04g071900	Peroxidase (AHRD V3.3 *** K4BTH7_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	43,629	33,555	47,404	19,915	29,139					-1,249	0,000			down
Solyc04g071920	Protein kinase-like protein (AHRD V3.3 *** A0A087GP50_ARAAL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,355	0,225	0,072	0,048	0,000									
Solyc04g071930	one-helix protein 2 (AHRD V3.3 *** AT1G34000.1)		C:GO:0009535: P:G(	C:chloroplast thylakoid membrane; P:response to light intensity			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,658	18,999	8,077	9,185	16,897	1,003	0,000	1,060	0,000			up	up	
Solyc04g071940	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561		F:GO:0004316: C:G(	F:3-oxoacyl-[acyl-ca	EC:2.3.1.85; EC:1.1.	Fatty-acid synthase;	IPR002347 (PRINTS): IPR002347 (PF	13,080	16,685	33,297	34,823	29,203									
Solyc04g071960	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	0,000	0,000	0,025	0,000	0,024									
Solyc04g071970	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561		P:GO:0009642: F:G(	P:response to light intensity; F:oxidoreductase activity; P:oxidat			IPR002347 (PRINTS): IPR002347 (PF	24,976	37,852	11,529	11,574	13,424	0,627	0,015					up		
Solyc04g071980	Holocarboxylase synthetase (AHRD V3.3 *** G7IEW6_MEDTR)						IPR029196 (PFAM): IPR016549 (PIRS	19,051	18,538	32,408	31,669	28,989									
Solyc04g071990	GIGANTEA (AHRD V3.3 *** F2Z6M2_IPONI)		P:GO:2000028	P:regulation of photoperiodism, flowering			IPR026211 (PRINTS): mobidb-lite (MO	103,167	102,329	155,353	150,103	146,085									
Solyc04g072000	Chitinase (AHRD V3.3 *** A0A1B1HY32_9APIA)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR001002 (SMART): IPR016283 (PIF	0,040	1,594	0,044	0,025	0,048									
Solyc04g072010	carboxypeptidase D (AHRD V3.3 *** AT1G71696.2)		F:GO:0004181: P:G(	F:metallocarboxype	EC:3.4.17	Acting on peptide bor	IPR000834 (PRINTS): IPR000834 (SM	22,471	19,887	22,672	25,003	24,842									
Solyc04g072020	Choline/ethanolamine kinase (AHRD V3.3 *** W9S6I0_9ROSA),Pfam:PF01633		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			PF01633 (PFAM): G3DSA:3.30.200.2(	10,104	22,942	7,127	9,569	9,403	1,209	0,001					up		
Solyc04g072030	Dynamin-related protein (AHRD V3.3 *** A0A1B0UTC3_TOBAC)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR003130 (SM	24,305	29,222	8,082	8,041	8,492									
Solyc04g072050	Transmembrane protein, putative (AHRD V3.3 *** I3SNC1_MEDTR)		C:GO:0005773: C:G(	C:vacuole; C:integral component of membrane			IPR009943 (PFAM): IPR009943 (PAN	30,760	33,318	35,622	35,951	43,198									
Solyc04g072060	Rab family GTPase (AHRD V3.3 *** D8RRT7_SELML)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	13,225	14,425	12,638	13,324	13,010									
Solyc04g072070	WRKY transcription factor 55	WRKY55	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR003657 (SMAF: WRKY	0,569	0,772	0,022	0,050	0,095									
Solyc04g072110	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *** A0A1D1ZH74_9ARAE)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	43,394	54,505	55,401	48,395	49,141									
Solyc04g072130	Programmed cell death protein 4 (AHRD V3.3 *** A0A151SX73_CAJCA)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR003891 (SMART): IPR003891 (PF	0,021	0,039	0,000	0,000	0,048									
Solyc04g072140	tRNA pseudouridine synthase (AHRD V3.3 *-* K4BTK1_SOLLC)		P:GO:0001522: F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			G3DSA:3.30.70.580 (GENE3D): IPR0(	3,913	4,974	5,820	5,699	5,086									
Solyc04g072145	tRNA pseudouridine synthase (AHRD V3.3 *** K4BTK1_SOLLC)		P:GO:0001522: F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR020097 (PFAM): IPR020095 (G3D	5,262	6,116	7,014	5,914	6,598									
Solyc04g072150	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T6B6_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	0,254	0,220	0,219	0,169	0,116									
Solyc04g072160	HSP20-like chaperones superfamily protein (AHRD V3.3 *** A0A061FJ96_THECC)	ddtfr8	C:GO:0005634: C:G(	C:nucleus; C:cytosol; P:protein folding; F:chaperone binding; P:(			IPR008978 (G3DSA:2.60.40.GENE3D	38,468	30,220	151,701	143,143	153,037									
Solyc04g072180	Sphingoid base hydroxylase 2 (AHRD V3.3 *** A0A061FL55_THECC)		F:GO:0005506: P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR11863 (PAI	2,948	1,685	1,740	1,448	1,789									
Solyc04g072190	Sphingoid base hydroxylase 2 (AHRD V3.3 *-* A0A061FL55_THECC)		F:GO:0000170: F:G(	F:sphingosine hydroxylase activity; F:monooxygenase activity;			PTHR11863:SF91 (PANTHER): PTHR	2,187	2,605	1,305	1,267	1,505									
Solyc04g072200	FRIGIDA-like protein, putative (AHRD V3.3 *** A0A061G6R8_THECC)		P:GO:0007275	P:multicellular organism development			IPR012474 (PFAM): mobidb-lite (MOB	8,208	7,239	6,237	4,955	6,187									
Solyc04g072220	NAC domain protein, (AHRD V3.3 *** A0A061FKH8_THECC)	NAC039	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS: NAC	72,431	77,571	51,143	57,577	55,886									
Solyc04g072230	ABC1 family protein (AHRD V3.3 *-* D7KYY4_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PTHR10566:SF83 (PANTHER): PTHR	7,887	8,928	19,413	18,877	18,828									
Solyc04g072235	Protein kinase superfamily protein (AHRD V3.3 *** AT1G71810.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM): PTHR10566:SF8:	10,228	11,841	25,853	27,217	27,957									
Solyc04g072240	Oxidoreductase family protein (AHRD V3.3 *** AT4G09670.1)		F:GO:0016491	F:oxidoreductase activity			G3DSA:3.40.50.720 (GENE3D): G3DS	20,285	19,700	90,445	78,421	85,018									
Solyc04g072250	Heat-shock protein, putative (AHRD V3.3 *** B9SMA2_RICCO)	Hsp17.9	P:GO:0006457: P:G(	P:protein folding; P:response to heat; P:response to salt stress;			IPR008978 (G3DSA:2.60.40.GENE3D	1,421	5,463	2,246	5,949	0,580									
Solyc04g072260	Midasin (AHRD V3.3 *-* K4BTL3_SOLLC)		P:GO:0000027: F:G(	P:ribosomal large s(	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	41,232	40,111	28,280	24,332	28,727									
Solyc04g072265	Midasin (AHRD V3.3 *** K4BTL3_SOLLC)		F:GO:0005524: F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR011704 (PF	31,317	20,424	15,370	17,038	17,842									
Solyc04g072280	Laccase (AHRD V3.3 *** A0A022Q9N6_ERYGU)		F:GO:0005507: P:G(	F:copper ion bindin(	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR008972 (G3DSA:2.60.40.GENE3D	0,000	0,021	0,022	0,000	0,000									
Solyc04g072290	Exocyst complex component SEC6 (AHRD V3.3 *** SEC6_ARATH)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			G3DSA:1.10.357.70 (GENE3D): G3DS	61,957	49,087	72,388	80,537	72,322									
Solyc04g072310	Elicitor peptide 1 (AHRD V3.3 --* A0A087GE76_ARAAL)		P:GO:0045087	P:innate immune response			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,316	0,359	0,000	0,000	0,047									
Solyc04g072340	LOW QUALITY:thiamin pyrophosphokinase1 (AHRD V3.3 --* AT1G02880.4)							0,000	0,000	0,000	0,000	0,024									
Solyc04g072360	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT5G02930.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,117	0,117	0,150	0,453	0,190									
Solyc04g072370	Bidirectional sugar transporter SWEET (AHRD V3.3 --* A0A0D2PUV2_GOSRA)							0,042	0,342	0,096	0,097	0,047									
Solyc04g072375	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT1G63840.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR001841 (PF	0,471	2,444	0,162	0,219	0,234	2,389	0,005					up		
Solyc04g072380	electron protein, putative (Protein of unknown function, DUF547) (AHRD V3.3 *-* AT1G43020.1)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR000591 (SMART): IPR002109 (PF	5,478	5,634	1,367	1,468	1,623									
Solyc04g072390	Methyltransferase-like (AHRD V3.3 *** Q6Z8K5_ORYSJ)		P:GO:0002098: F:G(	P:tRNA wobble uridine modification; F:tRNA (uracil) methyltrans(			IPR013216 (PFAM): PTHR13069 (PAI	16,698	18,179	23,218	23,708	22,171									
Solyc04g072400	Plant/F7F23-4 protein (AHRD V3.3 *** G7IJR9_MEDTR)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:chloroplast envelope			mobidb-lite (MOBIDB_LITE): PTHR317	23,397	26,357	125,045	127,523	138,784									
Solyc04g072410	Trafficking protein particle complex subunit-like protein (AHRD V3.3 *** A2Q3F3_MEDTR)		P:GO:0043087: P:G(	P:regulation of GTPase activity; P:Golgi vesicle transport			G3DSA:3.30.1380.20 (GENE3D): IPR(	4,938	5,055	7,959	6,531	7,469									
Solyc04g072440	DNA-directed RNA polymerase II, putative (AHRD V3.3 *** B9T6K6_RICCO)		F:GO:0000149: P:G(	F:SNARE binding; P:SNARE complex assembly			IPR018791 (PFAM): mobidb-lite (MOB	39,149	33,910	69,566	66,840	67,970									
Solyc04g072450	Zinc finger CCCH domain-containing protein 54 (AHRD V3.3 --* C3H54_ORYSJ)						mobidb-lite (MOBIDB_LITE): mobidb-lit	48,968	63,352	21,752	18,609	23,420									
Solyc04g072460	bZIP transcription factor family protein (AHRD V3.3 *** AT5G65210.7)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR004827 (SMAF: bZIP	24,734	21,470	17,045	22,997	21,412									
Solyc04g072465	Tyrosine aminotransferase (AHRD V3.3 --* W9QNC8_9ROSA)		C:GO:0016020	C:membrane				0,021	0,000	0,000	0,000	0,000									
Solyc04g072470	Defensin (AHRD V3.3 *** Q8W4V6_CAPAN)		P:GO:0006952	P:defense response			IPR003614 (SMART): IPR036574 (G3	4,049	14,454	3,601	9,329	0,813									
Solyc04g072480	phosphopantothenate-cysteine ligase-like protein (AHRD V3.3 *** AT5G02080.5)		F:GO:0016874	F:ligase activity			IPR035929 (G3DSA:3.40.50.GENE3D	0,019	0,037	0,000	0,000	0,000									
Solyc04g072490	Epidermal patterning factor (AHRD V3.3 *** A0A072V8D7_MEDTR)		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): IPR039455 (PANTH	4,139	3,743	8,754	7,278	7,580									
Solyc04g072500	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G07900.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR038538 (G3	3,595	3,288	5,639	4,132	4,844									
Solyc04g072510	Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 *** A0A061EP78_THECC)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR038538 (G3	8,430	9,249	10,926	10,233	10,322									
Solyc04g072520	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G07900.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR038538 (G3	6,675	5,529	6,421	6,786	5,843									
Solyc04g072530	Mitochondrial transcription termination factor family protein (AHRD V3.3 *-* AT5G64950.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR003690 (PF	3,033	2,271	2,696	3,811	2,752									
Solyc04g072540	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G07900.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR003690 (PF	4,090	4,102	3,380	3,344	3,511									
Solyc04g072550	Transcription termination factor, mitochondrial (AHRD V3.3 *** A0A1D1XYW6_9ARAE)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DI			IPR003690 (SMART): IPR003690 (PF	2,314	1,962	1,453	1,955	1,482									
Solyc04g072560	Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *** A0A061FL82_THECC)		P:GO:0015031	P:protein transport			IPR005061 (PFAM): G3DSA:1.20.126(	22,775	27,345	11,849	12,544	13,068									
Solyc04g072570	Receptor-like kinase (AHRD V3.3 *** A0A0K9PIY0_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:signaling receptor binding; F:ATP bir			IPR000719 (SMART): IPR013210 (PF	14,054	14,074	1,862	2,527	2,260									
Solyc04g072580	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** M1CMU7_SOLTU)		F:GO:0003872: F:G(	F:6-phosphofructok	EC:2.7.1.11	6-phosphofructokinas	IPR022953 (PRINTS): IPR012004 (PII	0,021	0,018	0,050	0,000	0,024									

Solyc04g072590	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT5G02930.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,280	0,059	0,144	0,213	0,234									
Solyc04g072600	ATP binding microtubule motor family protein (AHRD V3.3 --* AT5G42490.2)							0,120	0,019	0,094	0,144	0,189									
Solyc04g072605	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** K4BTP5_SOLLC)		F:GO:0003872: F:GO	F:6-phosphofructok	EC:2.7.1.11	6-phosphofructokinas	IPR022953 (PRINTS): IPR000023 (PF	0,455	0,419	0,491	0,578	0,540									
Solyc04g072610	FAR1-related sequence 11 (AHRD V3.3 --* AT1G10240.2)							1,801	2,328	2,283	1,992	1,997									
Solyc04g072620	LOW QUALITY:sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 --* AT2G45700.2)							1,522	4,802	0,603	0,645	0,512	1,675	0,022					up		
Solyc04g072630	F-box and Leucine Rich Repeat domains containing protein, putative isoform 1 (AHRD V3.3 *** A0A061FNK		C:GO:0005773	C:vacuole			IPR019448 (PFAM): mobidb-lite (MOB	90,151	60,937	28,848	25,507	25,845									
Solyc04g072640	Membrane-anchored ubiquitin-fold protein (AHRD V3.3 *** A0A0K9NMY0_ZOSMR)		F:GO:0005515	F:protein binding			IPR039540 (PFAM): G3DSA:3.10.20.9	14,713	18,825	14,867	17,470	16,358									
Solyc04g072650	LOW QUALITY:FANTASTIC four protein, putative (DUF3049) (AHRD V3.3 *-* AT1G77932.1)						IPR021410 (PFAM): PTHR33155 (PAN	0,252	0,316	0,025	0,000	0,000									
Solyc04g072660	60S ribosomal protein L30 (AHRD V3.3 *** RL30_LUPLU)		F:GO:0003723: F:GO	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR029064 (G3DSA:3.30.1330.GENE	100,687	96,476	53,342	51,431	52,327									
Solyc04g072670	Apoptotic chromatin condensation inducer in the nucleus (AHRD V3.3 *-* A0A1D1XLP8_9ARAE)		F:GO:0003676	F:nucleic acid binding			IPR003034 (SMART): IPR036361 (G3	125,449	121,902	145,980	152,480	150,447									
Solyc04g072690	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061DI57_THECC)		F:GO:0004190: P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	9,561	7,163	13,011	13,365	12,788									
Solyc04g072700	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT4G08570.1)		P:GO:0030001: F:GO	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): PTHR	0,075	0,041	0,000	0,000	0,047									
Solyc04g072740	Sulfate transporter, putative (AHRD V3.3 *** B9RJF7_RICCO)		F:GO:0008271: P:GO	F:secondary active sulfate transmembrane transporter activity;			IPR002645 (PFAM): IPR036513 (G3D	1,698	2,890	0,921	0,560	1,222									
Solyc04g072760	Sulfate transporter (AHRD V3.3 *** S6A1Z9_NICAT)		C:GO:0005886: F:GO	C:plasma membrane; F:secondary active sulfate transmembran			IPR011547 (PFAM): IPR036513 (G3D	0,974	0,970	0,707	1,683	0,873									
Solyc04g072780	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)						IPR007650 (PFAM): mobidb-lite (MOB	1,200	0,995	0,541	0,342	0,236									
Solyc04g072790	Cellulose synthase (AHRD V3.3 *** M1AK99_SOLTU)		C:GO:0016020: F:GO	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR013083 (G3DSA:3.30.40.GENE3D	3,699	5,676	0,173	0,380	0,069									
Solyc04g072810	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G22180.4)						IPR001251 (SMART): IPR036865 (G3	16,228	14,257	5,474	5,437	6,379									
Solyc04g072815	1-aminocyclopropane-1-carboxylate synthase CMW33 (AHRD V3.3 --* 1A11_CUCMA)							2,080	1,407	0,679	0,712	0,658									
Solyc04g072830	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G30100.2)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	PF13087 (PFAM): G3DSA:3.40.50.300	40,824	37,306	87,431	109,484	79,303									
Solyc04g072840	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT4G30100.2)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,299	0,273	0,448	0,808	0,564									
Solyc04g072850	Beta-D-xylosidase (AHRD V3.3 *** H1AC33_SOLLC)		F:GO:0004553: P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR026891 (SM	77,139	52,674	0,626	0,446	0,634									
Solyc04g072860	Beta-D-xylosidase (AHRD V3.3 *** H1AC33_SOLLC)		F:GO:0004553: P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR026891 (SM	4,922	3,997	3,127	2,919	3,549									
Solyc04g072870	Beta-D-xylosidase (AHRD V3.3 *** H1AC33_SOLLC)		F:GO:0004553: P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR026891 (SM	0,040	0,101	0,000	0,000	0,000									
Solyc04g072880	CycH1_2	CycH1_2	P:GO:0000079: P:GO	P:regulation of cycli	EC:2.7.11; EC:2.7.1	Transferring phospho	IPR013763 (SMART): G3DSA:1.10.47	18,346	18,421	42,190	42,662	39,173									
Solyc04g072890	Transducin/WD40 repeat protein (AHRD V3.3 *-* G8A379_MEDTR)		F:GO:0008168: P:GO	F:methyltransferase activity; P:methylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	47,346	42,943	60,834	68,804	74,792									
Solyc04g072895	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G78070.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	91,448	93,879	135,198	146,111	156,197									
Solyc04g072900	dehydration-responsive element binding protein 3	ERF.H12	F:GO:0003677: F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINT ERF	137,934	151,625	99,541	161,521	116,017					0,701	0,001			up
Solyc04g072910	Endoplasmic reticulum vesicle transporter protein (AHRD V3.3 *** AT1G36050.2)		C:GO:0005774: C:GO	C:vacuolar membrane; C:endoplasmic reticulum; C:Golgi appara			IPR012936 (PFAM): IPR039542 (PFA	61,014	65,317	100,897	99,101	95,143									
Solyc04g072920	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4BTS9_SOLLC)		F:GO:0003824: P:GO	F:catalytic activity; P:trehalose biosynthetic process			G3DSA:3.30.70.1020 (GENE3D): IPR	7,905	6,619	4,221	5,910	4,777									
Solyc04g072930	F-box protein (AHRD V3.3 *** W9S0P0_9ROSA)		F:GO:0005515	F:protein binding			PTHR31215 (PANTHER): IPR001810	21,395	34,967	21,193	16,149	18,843	0,735	0,009					up		
Solyc04g072940	Succinate dehydrogenase cytochrome b560 subunit (AHRD V3.3 --* C560_MARPO)							4,540	2,532	1,037	1,497	1,131									
Solyc04g073940	TPR repeat-containing thioredoxin TTL1-like protein (AHRD V3.3 *** A0A0B2PI95_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13432 (PFAM	0,057	0,112	0,000	0,025	0,000									
Solyc04g073950	VQ motif-containing family protein (AHRD V3.3 *** B9H742_POPTR)		F:GO:0016301: P:GO	F:kinase activity; P:phosphorylation			IPR008889 (PFAM): mobidb-lite (MOB	19,438	20,133	37,488	43,731	31,114									
Solyc04g073960	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021: P:GO	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM): G3DSA:1.20.125	7,521	5,774	5,178	9,492	7,462					0,871	0,000			up
Solyc04g073970	N-lysine methyltransferase (AHRD V3.3 *** AT1G78150.3)						IPR025131 (PFAM): mobidb-lite (MOB	45,833	39,593	18,953	18,574	17,324									
Solyc04g073980	pumilio 7 (AHRD V3.3 *-* AT1G78160.2)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR011989 (G3	1,350	1,447	1,930	1,189	1,694									
Solyc04g073990	annexin p34	an34	F:GO:0005509: F:GO	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR009118 (PF	1075,047	820,098	682,038	592,036	665,896									
Solyc04g074000	Receptor protein kinase, putative (AHRD V3.3 *** A0A061FG24_THECC)		F:GO:0004672: F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): SM00365 (SMAR	0,142	0,869	0,172	1,235	1,830									
Solyc04g074020	Receptor protein kinase, putative (AHRD V3.3 *** A0A061FG24_THECC)		F:GO:0004713: F:GO	F:protein tyrosine k	EC:2.7.1	Transferring phospho	PR00019 (PRINTS): IPR003591 (SMA	0,063	0,289	0,065	0,363	0,429									
Solyc04g074030	Receptor protein kinase, putative (AHRD V3.3 *** A0A061FG24_THECC)		F:GO:0004672: F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): SM00365 (SMAR	0,021	0,119	0,022	0,239	0,451									
Solyc04g074040	Serine/arginine rich splicing factor, putative (AHRD V3.3 *** B9SZR9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR003954 (SMART): IPR000504 (SM	193,764	202,872	213,350	186,239	199,935									
Solyc04g074050	Receptor protein kinase, putative (AHRD V3.3 *** A0A061FG24_THECC)		F:GO:0004713: F:GO	F:protein tyrosine k	EC:2.7.1	Transferring phospho	PR00019 (PRINTS): SM00365 (SMAR	0,056	0,500	0,121	0,097	0,072									
Solyc04g074070	Sugar transporter protein 4	STP4	C:GO:0016021: F:GO	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI	0,239	0,607	0,000	0,000	0,023									
Solyc04g074090	Nucleolar complex protein 3 like (AHRD V3.3 *** A0A0B2PDL3_GLYSO)		F:GO:0003682: C:GO	F:chromatin binding; C:nucleolus			IPR011501 (PFAM): IPR005612 (PFA	24,303	24,556	20,383	20,545	21,390									
Solyc04g074100	Senescence-associated protein, putative (AHRD V3.3 *** Q2HTL2_MEDTR)						PTHR33270:SF5 (PANTHER): IPR040	27,151	39,285	39,513	36,646	34,782									
Solyc04g074110	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)						IPR005181 (PFAM): IPR036514 (G3D	10,001	8,459	1,228	1,612	0,941									
Solyc04g074120	Synaptonemal complex protein 1 (AHRD V3.3 *** A0A151TZS6_CAJCA)						PTHR23160:SF3 (PANTHER): PTHR2	3,728	3,123	2,769	2,816	2,755									
Solyc04g074130	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G64970.1)		F:GO:0022857: P:GO	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR023395 (G3	8,419	9,144	5,180	5,363	6,831									
Solyc04g074140	transmembrane protein (AHRD V3.3 *-* AT1G34630.2)						IPR026749 (PANTHER): PTHR12459:	13,883	9,087	16,209	17,833	15,960									
Solyc04g074145	transmembrane protein (AHRD V3.3 *** AT1G34630.1)		C:GO:0016021	C:integral component of membrane			IPR026749 (PANTHER): PTHR12459:	20,004	15,669	25,820	28,287	23,903									
Solyc04g074150	Protein trm112, putative (AHRD V3.3 *** B9SWY6_RICCO)		F:GO:0046982	F:protein heterodimerization activity			IPR005651 (PFAM): G3DSA:2.20.25.1	13,504	13,938	16,624	15,881	13,461									
Solyc04g074160	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GTQ2_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,281	4,676	3,441	4,414	3,996									
Solyc04g074165	Hydroxyproline-rich glycoprotein (AHRD V3.3 -** B9HM75_POPTR)		C:GO:0016020	C:membrane			IPR039346 (PANTHER): PTHR35725:	2,085	2,471	0,902	1,330	1,539									
Solyc04g074180	cryptochrome 1	cry1a	P:GO:0009785: F:GO	P:blue light signaling pathway; F:blue light photoreceptor activity			IPR002081 (PRINTS): IPR014729 (G3	56,802	34,705	52,139	58,411	50,905	-0,682	0,048					down		
Solyc04g074190	Protein phosphatase 2C-like (AHRD V1 ***- A2Q6E4_MEDTR)		F:GO:0004722: P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART): IPR001932 (SM	6,775	5,249	11,425	12,475	8,722									
Solyc04g074220	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G09430.1)		F:GO:0016787	F:hydrolase activity			IPR000073 (PRINTS): IPR029058 (G3	2,282	2,927	2,115	2,259	1,814									
Solyc04g074230	SIG74 14-3-3 family protein	sig74	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR023410 (SM	48,612	51,797	247,290	230,567	197,136									
Solyc04g074240	5-adenylylsulfate reductase-like protein (AHRD V3.3 *** A0A072UZH9_MEDTR)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	99,568	75,169	122,742	119,524	106,895									
Solyc04g074250	Methyl-CpG-binding domain-containing protein 8 (AHRD V3.3 *-* A0A199UGF7_ANACO)		F:GO:0003677	F:DNA binding			IPR013087 (SMAF C2H2	10,395	7,270	7,164	8,313	7,539									
Solyc04g074270	Leucine-rich repeat-containing protein (AHRD V3.3 *** A0A103XBY7_CYNCS)		F:GO:0005515	F:protein binding			SM00365 (SMART): IPR003591 (SMA	101,563	138,664	76,089	97,839	107,900									
Solyc04g074280	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT4G08940.1)		P:GO:0006979	P:response to oxidative stress			IPR021099 (PFAM): PTHR31476:SF1	3,186	2,986	4,079	4,275	3,967									
Solyc04g074290	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G78240.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	173,811	192,041	66,598	67,088	74,395									
Solyc04g074300	40S ribosomal protein S2 (AHRD V3.3 *** K7WJZ4_SOLTU)		F:GO:0003723: F:GO	F:RNA binding; F:structural constituent of ribosome; P:translatio			G3DSA:3.30.160.770 (GENE3D): IPR	326,887	340,041	233,720	196,728	214,428									
Solyc04g074310	RNA-binding family protein, putative (AHRD V3.3 *-* A0A061G9K2_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	7,176	5,187	0,168	0,236	0,258									
Solyc04g074320	Protein TRANSPARENT TESTA 1-like protein (AHRD V3.3 *** A0A0B0MYQ3_GOSAR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,019	0,000	0,000	0,000	0,000									
Solyc04g074330	Glycosyltransferase (AHRD V3.3 *** K4BTX1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR	0,236	0,257	0,068	0,072	0,000									
Solyc04g074380	Glycosyltransferase (AHRD V3.3 *-* M1D1E1_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,000	0,019	0,000	0,000	0,024									
Solyc04g074390	Glycosyltransferase (AHRD V3.3 *** M1D1E1_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR	0,021	0,124	0,050	0,022	0,094									
Solyc04g074410	Phosphate-responsive 1 family protein (AHRD V3.3 *** A0A061FGW0_THECC)						IPR006766 (PFAM): IPR006766 (PAN	188,227	33,318	25,465	74,498	68,888	-2,474	0,000	1,431	0,000	1,548	0,000	down	up	up
Solyc04g074420	Phosphate-responsive 1 family protein (AHRD V3.3 *-* AT4G08950.1)						IPR006766 (PFAM): PTHR31279:SF3	27,165	6,742	1,945	6,408	4,197	-1,987	0,000			1,700	0,000	down		up
Solyc04g074430	Phosphate-responsive 1 family protein (AHRD V3.3 *-* A0A061FGW0_THECC)						IPR006766 (PFAM): PTHR31279:SF3	61,898	14,220	5,561	21,085	12,055	-2,096	0,000			1,914	0,000	down		up
Solyc04g074440	Phosphate-responsive 1 family protein (AHRD V3.3 *** A0A061FGW0_THECC)						IPR006766 (PFAM): PTHR31279:SF3	128,382	15,855	9,660	37,533	17,298	-2,992	0,000	0,835	0,019	1,956	0,000	down	up	up
Solyc04g074450	Phosphate-responsive 1 family protein (AHRD V3.3 *** AT4G08950.1)						IPR006766 (PFAM): IPR006766 (PAN	268,451	34,753	34,627	165,240	107,424	-2,926	0,000	1,629	0,000	2,254	0,000	down	up	up
Solyc04g074470	Phosphate-induced protein 1 (AHRD V3.3 *** A0A103XX62_CYNCS)						IPR006766 (PFAM): PTHR31279:SF8	0,460	0,561	0,125	0,295	0,071									
Solyc04g074480	DAHP synthase 2 precursor	DAHPS2	F:GO:0003849: P:GO	F:3-deoxy-7-phospt	EC:2.5.1.54	3-deoxy-7-phosphoh	IPR002480 (TIGRFAM): IPR013785 (G	155,294	239,644	113,174	83,320	103,308	0,652	0,042			-0,439	0,034	up		down
Solyc04g074490	F-box protein (AHRD V3.3 *** A0A0B2PIF2_GLYSO)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR003347 (SM	73,413	129,282	110,715	83,531	98,219	0,840	0,022					up		
Solyc04g074500	Protein kinase (AHRD V3.3 *** Q40264_MESCR)		F:GO:0004672: F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	9,040	11,517	19,335	22,988	19,005									
Solyc04g074510	tft3 14-3-3	tft3	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR023410 (SM	143,381	144,342	67,667	56,358	65,086									
Solyc04g074520	VQ motif-containing protein, putative (AHRD V3.3 *** A0A061FFT9_THECC)		P:GO:1901001	P:negative regulation of response to salt stress			IPR008889 (PFAM): mobidb-lite (MOB	10,510	8,547	8,798	10,104	7,870									
Solyc04g074530	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9R8J1_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): IPR013154 (PFA	5,115	5,534	2,662	4,140	6,491			1,288	0,000				up	
Solyc04g074540	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9R8J1_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): IPR013154 (PFA	0,138	0,085	0,050	0,115	0,165									
Solyc04g074545	RAD3-like DNA-binding helicase protein (AHRD V3.3 --* AT1G79890.3)							3,215	3,050	4,543	4,163	4,338									
Solyc04g074550	Cytochrome c oxidase subunit 6B (AHRD V3.3 *** A0A151TZY7_CAJCA)		C:GO:0005739	C:mitochondrion			IPR036549 (G3DSA:1.10.10.GENE3D	53,838	57,597	81,570	72,772	72,699									
Solyc04g074560	LOW QUALITY:syntaxin of plants 124 (AHRD V3.3 --* AT1G61290.2)		P:GO:0006355	P:regulation of transcription, DNA-templated				26,386	27,436	22,746	22,484	20,840									
Solyc04g074570	LOW QUALITY:cysteine-rich RLK (RECEPTOR-like protein kinase) 5 (AHRD V3.3 --* AT4G23130.3)							22,685	21,868	20,695	19,112	19,396									
Solyc04g074580	Histone H3 (AHRD V3.3 *** K7VSQ3_MAIZE)		C:GO:0000786: F:GO	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS): IPR000164 (SM	244,902	360,387	271,844	258,542	257,167									
Solyc04g074590	Seryl-tRNA synthetase family protein (AHRD V3.3 --* B9GUZ6_POPTR)		F:GO:0000166: F:GO	F:nucleotide binding; F:aminoacyl-tRNA ligase activity; P:tRNA aminoacylation for protein translation				1,905	2,538	2,084	2,579	2,585									
Solyc04g074620	LOW QUALITY:Topoisomerase I (AHRD V3.3 --* F5HPU4_9GENT)						mobidb-lite (MOBIDB_LITE)	0,040	0,019	0,000	0,000	0,000									
Solyc04g074630	Seryl-tRNA synthetase (AHRD V3.3 *** AT1G11870.2)		F:GO:0004828: F:GO	F:serine-tRNA ligas	EC:6.1.1.11	Serine--tRNA ligase	IPR002317 (PRINTS): IPR002317 (TI	8,648	10,137	9,262	8,571	9,850									
Solyc04g074640	Ascorbate peroxidase (AHRD V3.3 *** W8E036_JATCU)		F:GO:0004601: P:GO	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS): IPR002016 (PF	3,085	20,860	0,637	2,370	3,518	2,781	0,000	2,457	0,000			up	up	
Solyc04g074660	Protein FRA10AC1 like (AHRD V3.3 *** A0A0B2RYX4_GLYSO)						IPR019129 (PFAM): mobidb-lite (MOB	0,040	0,000	0,000	0,022	0,047									
Solyc04g074670	O-fucosyltransferase family protein (AHRD V3.3 *** A0A061FG90_THECC)		P:GO:0006004: F:GO	P:fucose metabolic process; F:transferase activity, transferring			IPR024709 (PIRSF): IPR019378 (PFA	37,425	34,351	19,313	17,173	17,613									
Solyc04g074680	Avr9/Cf-9 rapidly elicited protein, putative (AHRD V3.3 *** A0A072TTE4_MEDTR)						IPR008004 (PFAM): mobidb-lite (MOB	7,169	4,370	0,916	1,511	1,667									
Solyc04g074690	Ribosomal protein L27/L41, mitochondrial (AHRD V3.3 *** A0A118JZK9_CYNCS)		F:GO:0003735: C:GO	F:structural constituent of ribosome; C:mitochondrial large ribos			IPR019189 (PFAM): IPR019189 (PAN	12,639	14,076	16,166	17,209	16,289									
Solyc04g074700	LES17306 homeodomain protein	h52	F:GO:0003700: P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRINT HD-ZIP	5,332	5,293	1,283	1,456	1,678									
Solyc04g074710	Queuine tRNA-ribosyltransferase catalytic subunit 1 (AHRD V3.3 *** K4BU09_SOLLC)		F:GO:0008479: P:GO	F:queuine tRNA-ribo	EC:2.4.2.29	tRNA-guanine(34) tra	IPR036511 (G3DSA:3.20.20.GENE3D	0,570	2,080	0,123	0,075	0,117	1,858	0,003					up		
Solyc04g074720	FAM91A1-like protein (AHRD V3.3 *** G7J6Q2_MEDTR)						IPR028091 (PFAM): IPR028097 (PFA	31,183	46,274	15,230	14,935	15,870									
Solyc04g074730	Arabinogalactan-protein (AHRD V3.3 *** Q40380_NICAL)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	116,825	135,940	106,786	156,879	138,077					0,558	0,003			up
Solyc04g074740	Blue copper protein, putative (AHRD V3.3 *** B9RJR1_RICCO)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	2,350	1,931	0,240	0,120	0,353									
Solyc04g074750	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT4G09040.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	6,570	9,615	5,266	5,573	8,128									
Solyc04g074760	BEST plant protein match is: (TAIR:plant.1) protein, putative (AHRD V3.3 *** G7J4G3_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,122	3,081	1,861	1,510	2,238									
Solyc04g074770	Phage capsid scaffolding protein (GPO) serine peptidase (AHRD V3.3 *-* G7KAI6_MEDTR)						PTHR33735 (PANTHER): PTHR33735	0,778	2,924	0,124	0,073	0,187	1,929	0,014					up		
Solyc04g074780	Phage capsid scaffolding protein (GPO) serine peptidase (AHRD V3.3 *** G7KAI6_MEDTR)						G3DSA:1.10.287.950 (GENE3D): PTH	0,076	0,041	0,000	0,050	0,047									
Solyc04g074790	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FG67_THECC)		C:GO:0016021: P:GO	C:integral component of membrane; P:protein ubiquitination			IPR001841 (SMART): IPR001841 (PF	1,915	1,456	2,253	2,306	2,029									
Solyc04g074800	Craniofacial development protein 1 (AHRD V3.3 *** A0A151SCQ0_CAJCA)						IPR011421 (PFAM): mobidb-lite (MOB	0,434	0,241	0,477	0,484	0,588									
Solyc04g074810	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT1G72210.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	1,036	1,709	0,406	0,143	0,163									
Solyc04g074820	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FLH6_THECC)		C:GO:0016021: F:GO	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	0,483	0,180	0,237	0,504	0,352									
Solyc04g074830	LOW QUALITY:ENTH/ANTH/VHS superfamily protein, putative (AHRD V3.3 *** A0A061FE62_THECC)		F:GO:0005543	F:phospholipid binding			IPR008942 (G3DSA:1.25.40.GENE3D	2,272	3,061	8,550	12,692	9,934									
Solyc04g074840	Protein DETOXIFICATION (AHRD V3.3 *** K4BU22_SOLLC)		P:GO:0006855: F:GO	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	1,090	0,731	864,605	1323,766	834,390					0,618	0,005			up
Solyc04g074850	ripening regulated protein DDTFR18	ddtfr18	P:GO:0006855: F:GO	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	42,921	43,086	194,891	205,812	187,643									
Solyc04g074860	Mate efflux family protein (AHRD V1 **-- D7MN36_ARALY)		P:GO:0006855: F:GO	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	18,393	13,051	16,137	14,333	15,623									
Solyc04g074870	Purine permease-like protein (AHRD V3.3 *** G7J4H5_MEDTR)		F:GO:0005215: C:GO	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): PTHR31376:SF1 (F	14,377	10,757	4,905	5,456	6,983									
Solyc04g074880	Purine permease-like protein (AHRD V3.3 *** G7J4H5_MEDTR)		F:GO:0005215: C:GO	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): mobidb-lite (MOBID	0,080	0,043	0,022	0,067	0,071									
Solyc04g074900	40S ribosomal protein S21 (AHRD V3.3 *** K4BU28_SOLLC)		F:GO:0003735: C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001931 (PIRSF): IPR038579 (G3D	0,294	0,557	0,314	0,162	0,189									
Solyc04g074910	40S ribosomal protein S21 (AHRD V3.3 *** M0ZPV5_SOLTU)		F:GO:0003735: C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001931 (PFAM): IPR001931 (PIRS	129,651	115,110	104,562	99,948	102,207									
Solyc04g074920	Photosystem I assembly protein Ycf3 (AHRD V3.3 --* YCF3_CHLVU)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM): IPR007657 (PAN	0,096	0,128	0,000	0,051	0,024									
Solyc04g074930	transmembrane protein (AHRD V3.3 *** AT4G33590.1)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM): mobidb-lite (MOB	0,042	0,041	0,069	0,217	0,236									
Solyc04g074940	Target SNARE coiled-coil domain-containing protein (AHRD V3.3 *** A0A103XBX5_CYNCS)		P:GO:0015031: C:GO	P:protein transport; C:integral component of Golgi membrane			G3DSA:1.20.5.110 (GENE3D): PTHR1	2,397	2,346	3,646	4,048	2,888									
Solyc04g074950	dihydrofolate reductase (AHRD V3.3 *** AT4G24380.1)		C:GO:0005634: C:GO	C:nucleus; C:cytoplasm			IPR029058 (G3DSA:3.40.50.GENE3D	15,913	57,758	7,218	8,108	10,269	1,880	0,001					up		
Solyc04g074960	dihydrofolate reductase (AHRD V3.3 *** AT4G24380.1)		C:GO:0005634: C:GO	C:nucleus; C:cytoplasm			IPR005645 (PFAM): IPR029058 (G3D	12,767	15,775	24,051	22,871	21,272									
Solyc04g074980	TRANSPORT INHIBITOR RESPONSE 1 protein, putative (AHRD V3.3 *** B9RJT7_RICCO)		F:GO:0000822: P:GO	F:inositol hexakisphosphate binding; P:auxin-activated signaling			IPR006553 (SMART): G3DSA:1.20.12	57,174	56,788	41,436	40,586	42,786									
Solyc04g074990	ZF-HD homeobox protein family (AHRD V3.3 *-* A0A151RTI4_CAJCA)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 ZF-HD	0,536	1,138	0,122	0,073	0,256									
Solyc04g075000	Kinase family protein (AHRD V3.3 *** D7KCW3_ARALL)		F:GO:0004672: F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001245 (PF	5,143	5,074	2,153	1,682	2,359									
Solyc04g075010	LOW QUALITY:auxin response factor 9 (AHRD V3.3 --* AT4G23980.2)							0,019	0,060	0,022	0,022	0,024									
Solyc04g076010	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT1G43770.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	48,465	44,240	28,029	21,880	22,375									
Solyc04g076020	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7J574_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR011990 (G3	33,233	28,709	45,810	43,728	44,709									
Solyc04g076030	Basic helix-loop-helix (BHLH) DNA-binding superfamily (AHRD V3.3 *-* A0A0K9NNV3_ZOSMR)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	122,787	114,194	107,694	127,730	108,478									
Solyc04g076040	cyclinD5_1	CycD5_1	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	29,585	25,505	10,958	9,621	10,951									
Solyc04g076050	Protein CutA, chloroplastic (AHRD V3.3 *** A0A0B2PMZ2_GLYSO)		P:GO:0010038	P:response to metal ion			IPR004323 (PFAM): IPR015867 (G3D	19,639	18,814	53,647	51,825	55,339									
Solyc04g076060	tft10	tft10	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR023410 (SM	148,565	135,318	143,886	127,015	126,986									
Solyc04g076080	Chaperone protein DnaJ (AHRD V3.3 *** W9S894_9ROSA)		C:GO:0005634: C:GO	C:nucleus; C:cytoplasm			IPR001623 (PRINTS): IPR001623 (SM	8,093	7,833	11,045	9,099	11,682									
Solyc04g076090	glucose-6-phosphate isomerase	gpi	F:GO:0004347: P:GO	F:glucose-6-phosph	EC:5.3.1.9	Glucose-6-phosphate	IPR001672 (PRINTS): G3DSA:3.40.50	106,916	103,734	182,729	161,108	175,895									
Solyc04g076100	Pesticidal crystal cry8Ba (AHRD V3.3 *** A0A0B0MPH2_GOSAR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,457	14,439	2,778	4,601	3,757									
Solyc04g076110	RING finger protein (AHRD V3.3 *** AT5G49710.3)						mobidb-lite (MOBIDB_LITE): PTHR338	18,693	22,425	29,886	30,271	27,556									
Solyc04g076120	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)		F:GO:0004185: P:GO	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PFAM): G3DSA:3.40.50.1	1,200	0,841	1,439	1,677	1,996									
Solyc04g076130	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)		F:GO:0004185: P:GO	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	G3DSA:3.40.50.12670 (GENE3D): IPF	0,137	0,199	0,100	0,193	0,141									
Solyc04g076140	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9NLF4_ZOSMR)		P:GO:0007165	P:signal transduction			IPR000198 (SMART): IPR001849 (SM	6,309	8,396	3,176	3,450	3,165									
Solyc04g076150	LOW QUALITY:Peptide upstream ORF protein (AHRD V3.3 *** G7J561_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33597:SF11 (PANTHER): PTHR	0,059	0,036	0,047	0,022	0,047									
Solyc04g076157	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TSU1_ACAMN)		F:GO:0005524: C:GO	F:ATP binding; C:pla	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,000	0,000	0,000	0,000	0,047									
Solyc04g076180	Cell division cycle protein 48 (AHRD V3.3 *** U5FI94_POPTR)		F:GO:0005515: F:GO	F:protein binding; F:ATP binding			IPR001487 (PRINTS): IPR001487 (SM	48,970	43,934	40,401	39,253	42,336									
Solyc04g076200	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G09740.2)						IPR006015 (PRINTS): IPR006016 (PF	57,873	51,585	89,654	91,528	75,096									

Solyc04g076210	Ubiquitin carboxyl-terminal hydrolase 16 (AHRD V3.3 *** A0A0B2PIM3_GLYSO)		P:GO:0016579; F:G(	P:protein deubiquitii	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM); G3DSA:3.30.60.1	79,651	82,336	101,226	100,500	95,388									
Solyc04g076220	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7J554_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D); IPR(	2,170	2,549	7,680	11,070	5,926									
Solyc04g076230	AP-4 complex subunit mu (AHRD V3.3 *** AP4M_ARATH)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS); G3DSA:2.60.4(	76,338	82,150	101,197	90,589	91,316									
Solyc04g076240	bHLH transcription factor 033		P:GO:0006355	P:regulation of transcription, DNA-templated			PTHR12565:SF30_bHLH	0,082	0,000	0,000	0,000	0,000									
Solyc04g076250	PWWP domain protein (AHRD V3.3 --* G7J551_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	43,214	44,619	49,781	46,857	44,629									
Solyc04g076260	thionin-like protein (AHRD V3.3 *** AT5G64816.4)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); IPR0389;	2,499	2,158	2,057	1,591	2,160									
Solyc04g076280	MADS box transcription factor (AHRD V3.3 *** Q6RF31_POPTO)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINTS); IPR002100 (SM	0,238	0,388	0,194	0,072	0,118									
Solyc04g076290	O-fucosyltransferase family protein (AHRD V3.3 *** AT4G24530.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM); IPR024709 (PIRS	26,807	22,199	18,065	13,924	16,297									
Solyc04g076300	Mechanosensitive ion channel protein 2, chloroplastic (AHRD V3.3 *-* A0A0B2PMX7_GLYSO)		C:GO:0009526; P:G(	C:plastid envelope; P:chloroplast fission; C:integral component			mobidb-lite (MOBIDB_LITE); mobidb-lit	10,043	15,027	1,758	1,942	3,615			1,035	0,018				up	
Solyc04g076303	Mechanosensitive ion channel-like protein (AHRD V3.3 *** G7J535_MEDTR)		C:GO:0016020; P:G(	C:membrane; P:transmembrane transport			IPR006685 (PFAM); PTHR43634:SF3	11,222	18,543	1,811	2,519	4,324			1,243	0,005				up	
Solyc04g076307	zinc finger (ubiquitin-hydrolase) domain-containing protein (AHRD V3.3 --* AT2G42160.3)							0,404	0,476	0,072	0,241	0,259									
Solyc04g076310	Kinesin-like protein (AHRD V3.3 *** K4BU69_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	0,956	1,213	0,071	0,142	0,071									
Solyc04g076330	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199VX93_ANACO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,538	4,411	1,447	1,804	1,648									
Solyc04g076340	Ribosomal RNA small subunit methyltransferase A (AHRD V3.3 *** A0A0B0NTG7_GOSAR)						PTHR34464 (PANTHER)	43,494	15,611	16,915	13,604	12,995	-1,448	0,000					down		
Solyc04g076350	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *-* AT2G22560.1)		F:GO:0003779	F:actin binding			IPR011684 (PFAM); mobidb-lite (MOB	0,550	0,436	0,618	0,802	0,564									
Solyc04g076355	UDP-Glycosyltransferase / trehalose-phosphatase family protein (AHRD V3.3 --* AT1G68020.3)							0,000	0,000	0,050	0,075	0,024									
Solyc04g076360	Myb family transcription factor family protein (AHRD V3.3 *** B9GN48_POPTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB_related	12,459	11,457	11,241	12,885	11,254									
Solyc04g076370	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SK37_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (TIGF	2,335	2,021	2,287	1,828	1,858									
Solyc04g076380	NADPH--cytochrome P450 reductase (AHRD V3.3 *** K4BU76_SOLLC)		F:GO:0003958; F:G(	F:NADPH-hemoprot	EC:1.6.2.4	NADPH--hemoproteir	IPR001709 (PRINTS); IPR001094 (PF	414,580	359,285	219,787	191,766	232,315									
Solyc04g076390	Cysteinyl-tRNA synthetase, putative (AHRD V3.3 *** B9RP10_RICCO)		F:GO:0004817; F:G(	F:cysteine-tRNA lig	EC:6.1.1.16	Cysteine--tRNA ligas	IPR024909 (PRINTS); IPR015273 (SM	16,952	18,111	9,638	10,772	13,430									
Solyc04g076400	Protein VERNALIZATION INSENSITIVE 3 (AHRD V3.3 *** W9SPV3_9ROSA)						IPR032881 (PFAM); PTHR21736 (PAN	2,482	3,627	0,172	0,148	0,378									
Solyc04g076410	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT4G24500.3)		P:GO:0000398; P:G(	P:mRNA splicing, via spliceosome; P:production of miRNAs invo			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,504	2,066	2,285	2,816	2,857									
Solyc04g076420	dsRNA-binding protein		F:GO:0003725	F:double-stranded RNA binding			IPR014720 (SMART); IPR014720 (PF.	23,126	22,093	41,680	44,814	36,880									
Solyc04g076430	Geranylgeranyl transferase type-2 subunit alpha (AHRD V3.3 *** W9QC24_9ROSA)		F:GO:0005515; C:G(	F:protein binding; C:Rab-protein geranylgeranyltransferase com			PR00019 (PRINTS); G3DSA:1.25.40.1	23,646	24,549	27,359	28,565	26,875									
Solyc04g076440	LOW QUALITY:Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *-* A0A061FLU3_THECC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,058	0,097	0,075	0,025	0,024									
Solyc04g076460	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	29,511	49,631	27,058	36,766	33,191	0,777	0,001			0,445	0,014	up		up
Solyc04g076470	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G65520.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR001440 (PF.	13,013	8,994	17,610	15,788	13,556									
Solyc04g076480	MAP kinase kinase kinase 34	MAPKKK34	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS); IPR000719 (SM	11,377	9,846	2,378	2,296	2,352									
Solyc04g076500	BEACH domain-containing lvsC (AHRD V3.3 *** A0A0B0MIE6_GOSAR)						G3DSA:2.60.120.200 (GENE3D); PF1	31,853	23,902	26,315	34,900	33,171									
Solyc04g076510	BEACH domain-containing protein (AHRD V3.3 *** A0A118JZ86_CYNCS)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR000409 (SM	79,583	72,902	76,700	82,189	79,634									
Solyc04g076520	F-box family protein (AHRD V3.3 *** A0A061DJ93_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR001810 (PF.	85,963	78,891	58,788	75,887	63,213					0,370	0,031			up
Solyc04g076525	GATA transcription factor (AHRD V3.3 *-* G7J4K3_MEDTR)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:I			IPR010399 (SMART); IPR000679 (SM	0,388	0,241	0,334	0,174	0,378									
Solyc04g076527	GATA transcription factor, putative (AHRD V3.3 *** B9SN00_RICCO)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:I			IPR010399 (SMART); IPR000679 (SM	0,057	0,082	0,069	0,025	0,140									
Solyc04g076530	GATA transcription factor, putative (AHRD V3.3 *** B9SN00_RICCO)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:I			IPR000679 (SMAF_GATA	1,903	1,734	2,031	2,507	2,579									
Solyc04g076540	Golgi-body localization protein domain isoform 4 (AHRD V3.3 *** A0A061FEK5_THECC)		C:GO:0016021	C:integral component of membrane			IPR019441 (SMART); IPR019441 (PF.	126,397	93,387	147,364	166,834	157,374									
Solyc04g076550	Golgi-body localization protein domain isoform 4 (AHRD V3.3 *-* A0A061FEK5_THECC)		C:GO:0016021	C:integral component of membrane			PTHR15678:SF8 (PANTHER); PTHR1!	26,347	19,209	28,013	36,272	33,286									
Solyc04g076560	Sas10/Utp3/C1D (AHRD V3.3 *** A0A103YDJ6_CYNCS)		P:GO:0000462; C:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSI			IPR007146 (PFAM); mobidb-lite (MOB	35,017	38,367	32,718	31,987	31,333									
Solyc04g076570	Crt (AHRD V3.3 *** A0A0B0PUG4_GOSAR)		P:GO:0002229; C:G(	P:defense response to oomycetes; C:chloroplast; C:integral coi			IPR013936 (PFAM); mobidb-lite (MOB	2,015	1,817	2,344	3,233	3,344									
Solyc04g076580	Transcription initiation factor TFIID subunit 7 (AHRD V3.3 *-* A0A151RD52_CAJCA)		C:GO:0005669; P:G(	C:transcription factor TFIID complex; P:transcription initiation fr			IPR006751 (SMART); IPR006751 (PF.	12,397	11,423	23,836	20,750	20,413									
Solyc04g076600	CHCH-like protein (AHRD V3.3 *-* A0A103XM78_CYNCS)		C:GO:0043231	C:intracellular membrane-bounded organelle			PTHR13523 (PANTHER); PTHR13523	0,197	0,238	0,046	0,073	0,116									
Solyc04g076610	HVA22-like protein (AHRD V3.3 *** A0A0D2U873_GOSRA)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	IPR003604 (SMART); IPR036397 (G3	1,185	2,425	1,257	1,831	1,665									
Solyc04g076620	E3 ubiquitin-protein ligase UPL1-like protein (AHRD V3.3 *** G7JYH3_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	IPR003604 (SMART); IPR015940 (SM	441,010	338,371	449,400	472,083	469,827									
Solyc04g076630	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09890.4)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR029411 (PFAM); IPR010325 (PFA	1,124	1,199	4,117	4,724	5,772									
Solyc04g076640	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09890.4)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR029411 (PFAM); IPR029413 (PFA	0,077	0,132	0,000	0,000	0,023									
Solyc04g076650	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09890.4)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR010325 (PFAM); IPR029411 (PFA	0,173	1,623	0,467	2,251	0,654					2,262	0,000			up
Solyc04g076660	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09910.1)		F:GO:0003824; P:G(	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR010325 (PFAM); IPR029411 (PFA	21,870	25,622	11,287	9,366	12,544									
Solyc04g076670	TRAF-type zinc finger domain-containing 1 (AHRD V3.3 *** A0A0B0MEE8_GOSAR)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	45,773	44,161	75,965	71,999	72,087									
Solyc04g076690	Protein with RNI-like/FBD-like domain (AHRD V3.3 --* AT3G26930.1)							1,059	0,816	1,587	3,461	1,456					1,137	0,001			up
Solyc04g076700	MADS-box transcription factor (AHRD V3.3 *** G7IS85_MEDTR)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINTS); IPR002100 (SM	5,761	5,650	6,247	7,337	6,831									
Solyc04g076710	COBRA-like protein 11 precursor (AHRD V3.3 --* AT4G27110.1)							1,924	2,280	5,151	10,710	5,721					1,056	0,000			up
Solyc04g076715	DNA-binding family protein (AHRD V3.3 -** A0A0K1ETQ6_9ROSI)						mobidb-lite (MOBIDB_LITE)	0,343	0,306	0,244	0,100	0,188									
Solyc04g076720	WD repeat domain phosphoinositide-interacting 3 (AHRD V3.3 *-* A0A0B0P0U0_GOSAR)		P:GO:0006914; P:G(	P:autophagy; P:organelle organization			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,533	1,819	1,228	0,937	1,857									
Solyc04g076730	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7JEX2_MEDTR)		P:GO:0006952	P:defense response			IPR040273 (PANTHER)	0,081	0,452	0,044	0,098	0,117									
Solyc04g076740	Protein TIC 20, chloroplastic (AHRD V3.3 *** A0A0B2STH9_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR005691 (PFAM); IPR005691 (TIGF	5,096	5,029	4,062	3,540	4,450									
Solyc04g076745	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT5G08750.9)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,018	0,000	0,000	0,000									
Solyc04g076770	Peroxidase (AHRD V3.3 *** K4BUB5_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS); IPR000823 (PF	1,676	2,122	0,140	0,092	0,120									
Solyc04g076780	Oligopeptide transporter, putative (AHRD V3.3 *** B9SMX8_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004648 (TIGRFAM); IPR004813 (F	57,811	50,654	12,006	7,759	10,705									
Solyc04g076790	Serine hydroxymethyltransferase (AHRD V3.3 *** M1A7K0_SOLTU)		F:GO:0004372; P:G(	F:glycine hydroxym	EC:2.1.2.1	Glycine hydroxymeth	IPR001085 (PIRSF); IPR015421 (G3E	176,175	134,983	236,217	218,892	199,965									
Solyc04g076800	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199W533_ANACO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,167	4,911	2,962	3,071	3,903									
Solyc04g076810	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BUB9_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF.	44,079	42,553	43,257	47,577	45,111									
Solyc04g076820	Octicosapeptide/Phox/Bem1p domain-containing protein (AHRD V3.3 *** T2DP86_PHAVU)		F:GO:0005515	F:protein binding			IPR000270 (SMART); IPR000270 (PF.	56,897	48,951	193,492	180,293	171,735									
Solyc04g076830	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT1G58280.2)						IPR013078 (SMART); PIRSF000709 (	40,195	37,001	95,956	106,977	96,335									
Solyc04g076850	entire	IAA9	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-i			IPR033389 (PFAM); G3DSA:3.10.20.9	1027,551	1028,845	771,708	584,559	735,160					-0,397	0,044			down
Solyc04g076860	Zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 *** AT5G49665.1)		F:GO:0003676; C:G(	F:nucleic acid binding; C:plasma membrane; P:gravitropism; P:p			IPR001841 (SMART); IPR002035 (SM	2,996	7,120	8,537	8,404	8,040	1,270	0,002					up		
Solyc04g076870	Glutamyl-tRNA reductase (AHRD V3.3 *** A0A0V0IMC1_SOLCH)	HEMA/GluTR	F:GO:0008883; P:G(	F:glutamyl-tRNA rec	EC:1.2.1.7	Glutamyl-tRNA reduc	IPR006151 (PFAM); G3DSA:3.40.50.7	87,491	134,974	72,231	82,970	115,429			0,672	0,000				up	
Solyc04g076880	phosphoenolpyruvate carboxykinase		F:GO:0004612; F:G(	F:phosphoenolpyru	EC:4.1.1.49; EC:4.1.	Phosphoenolpyruvate	G3DSA:2.170.8.10 (GENE3D); IPR01:	117,786	141,373	401,905	548,259	373,589					0,452	0,005			up
Solyc04g076890	Ubiquitin-fold modifier-conjugating enzyme 1 (AHRD V3.3 *** M1A7G9_SOLTU)		F:GO:0071568; P:G(	F:UFM1 transferase activity; P:protein K69-linked ufmylation			IPR016135 (G3DSA:3.10.110.GENE3	0,218	0,224	0,233	0,317	0,116									
Solyc04g076900	Symplekin (AHRD V3.3 *-* A0A151SP17_CAJCA)						IPR032460 (PFAM); IPR011989 (G3D	6,572	5,681	6,527	8,720	7,502									
Solyc04g076910	Symplekin (AHRD V3.3 *** A0A0B2PKU6_GLYSO)						IPR022075 (PFAM); IPR011989 (G3D	26,526	25,846	25,804	31,640	28,586									
Solyc04g076920	beta3-glucuronyltransferase	pglcat1	F:GO:0015018; C:G(	F:galactosylgalacto	EC:2.4.1.17; EC:2.4.	Glucuronosyltransfer	IPR029044 (G3DSA:3.90.550.GENE3I	17,394	17,487	12,296	12,249	13,974									
Solyc04g076940	PHD type transcription factor with transmembrane domain protein (PTM) (AHRD V3.3 --* AT5G35210.2)							10,573	7,067	8,530	8,708	8,235									
Solyc04g076950	Protein DETOXIFICATION (AHRD V3.3 *** K4BUD2_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM); IPR002528 (F	0,752	1,070	1,080	1,373	1,560									
Solyc04g076960	SlSUT4	SUT4	C:GO:0005887; F:G(	C:integral component of plasma membrane; F:sucrose transmer			PTHR19432:SF38 (PANTHER); PTHR	6,697	5,472	6,849	5,375	7,077									
Solyc04g076965	Sucrose transporter (AHRD V3.3 *-* Q9FVJ6_SOLLC),Pfam:PF13347		C:GO:0005887; F:G(	C:integral component of plasma membrane; F:sucrose transmer			G3DSA:1.20.1250.20 (GENE3D); PF1	5,298	4,166	6,106	5,097	7,242									
Solyc04g076970	transcription factor-like protein (AHRD V3.3 *** AT1G58330.1)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindii			IPR025422 (PFAM); PTHR22952 (PAN	1,506	2,896	0,386	0,195	0,563									
Solyc04g076980	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *-* AT1G09970.2)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR013210 (PFAM); IPR032675 (G3D	66,340	68,225	21,093	27,132	30,457			0,525	0,037				up	
Solyc04g076990	Receptor protein kinase CLAVATA1, putative (AHRD V3.3 *** B9R6R4_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	130,088	154,307	44,160	51,199	62,021			0,487	0,021				up	
Solyc04g077000	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GE38_THECC)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR002867 (SMART); G3DSA:1.20.12	4,603	3,508	8,409	6,907	6,012									
Solyc04g077010	Receptor protein kinase, putative (AHRD V3.3 *** B9R6R5_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART); IPR000719 (SM	11,814	13,391	9,636	9,353	10,310									
Solyc04g077020	Tubulin alpha chain (AHRD V3.3 *** TBA_PRUDU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002452 (PRINTS); IPR000217 (PF	705,168	618,230	92,962	70,812	104,445									
Solyc04g077030	Xylulose kinase, putative (AHRD V3.3 *** A0A061FE36_THECC)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:phosphotransferase activi			IPR018484 (PFAM); G3DSA:3.30.420	8,659	11,587	23,987	29,950	25,730									
Solyc04g077040	Xylulose kinase, putative (AHRD V3.3 *** A0A061FE36_THECC)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:phosphotransferase activi			G3DSA:3.30.420.40 (GENE3D); G3DS	24,912	20,990	24,713	24,458	27,378									
Solyc04g077050	Amino acid transporter (AHRD V3.3 *** P93561_SOLTU)		C:GO:0005886; F:G(	C:plasma membrane; F:acidic amino acid transmembrane trans			IPR013057 (PFAM); PTHR22950:SF2	94,348	233,677	33,196	44,619	53,942	1,331	0,005	0,697	0,022			up	up	
Solyc04g077060	RNA-binding KH domain protein (AHRD V3.3 *** G7J415_MEDTR)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR036612 (G3	51,755	50,443	64,559	55,960	59,386									
Solyc04g077100	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4BUE7_SOLLC)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylti	G3DSA:3.90.228.10 (GENE3D); IPR0	4,368	2,445	2,483	3,458	2,738									
Solyc04g077110	Succinate dehydrogenase assembly factor 1, mitochondrial (AHRD V3.3 *-* A0A0B0PRI9_GOSAR)							0,175	0,261	0,392	0,334	0,375									
Solyc04g077120	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4BUE9_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.134; EC:2.	Inositol-tetrakisphosı	IPR008656 (PIRSF); PF17927 (PFAM	21,158	34,570	9,519	10,657	14,346	0,733	0,012					up		
Solyc04g077140	DUF1005 family protein (AHRD V3.3 *** G7J413_MEDTR)						IPR010410 (PFAM); mobidb-lite (MOB	5,287	2,619	0,627	0,952	1,360	-0,988	0,043					down		
Solyc04g077150	Ergosterol biosynthetic protein 28 (AHRD V3.3 *** A0A0B2RYC5_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR005352 (PFAM); IPR005352 (PAN	9,536	9,223	13,853	12,027	12,772									
Solyc04g077160	myb-like protein X (AHRD V3.3 *-* AT4G33740.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR337	3,647	4,266	0,809	0,454	1,079									
Solyc04g077170	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *** AT4G37810.1),Pfam:PF17181		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM); IPR039455 (PANTH	0,121	0,167	0,574	0,555	0,566									
Solyc04g077180	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G10040.2)						IPR007751 (PFAM); mobidb-lite (MOB	0,353	0,366	0,184	0,239	0,284									
Solyc04g077190	Endo-1,4-beta-xylanase A (AHRD V3.3 *** A0A0B2QB53_GLYSO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001000 (SMART); IPR001000 (PF.	7,709	10,152	0,955	1,353	1,431									
Solyc04g077210	Knotted 1	tkn1	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR005541 (SMAF_TALE	1,046	1,311	1,507	0,956	0,847									
Solyc04g077220	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001356 (SMAF_HD-ZIP	2,292	5,179	7,186	9,497	7,993	1,199	0,016					up		
Solyc04g077230	Indole-3-acetaldehyde oxidase (AHRD V3.3 --* ALDO1_MAIZE)							3,812	26,823	1,929	4,084	4,559	2,836	0,000	1,235	0,000	1,078	0,005	up	up	up
Solyc04g077240	SlBCAT6	BCAT6	F:GO:0004084; P:G(	F:branched-chain-a	EC:2.6.1.42	Branched-chain-amir	G3DSA:3.20.10.10 (GENE3D); G3DS/	0,319	1,804	0,327	0,273	1,290	2,498	0,000					up		
Solyc04g077250	carbohydrate esterase, putative (DUF303) (AHRD V3.3 --* AT4G34215.2)							0,056	0,041	0,100	0,048	0,048									
Solyc04g077260	blind-like3	R2R3MYB87	F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB	0,040	0,019	0,142	0,095	0,116									
Solyc04g077270	Serine/threonine-protein kinase (AHRD V3.3 *** M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); IPR003609 (SM	24,853	63,655	12,989	13,587	19,422	1,379	0,003					up		
Solyc04g077280	Serine/threonine-protein kinase (AHRD V3.3 *** M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR003609 (SMART); IPR000719 (SM	1,531	3,159	1,049	0,832	1,181	1,067	0,036					up		
Solyc04g077290	YEATS family protein (AHRD V3.3 *** AT5G45600.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR005033 (PFAM); IPR038704 (G3D	0,593	0,724	0,724	0,645	0,942									
Solyc04g077295	Protein kinase family protein (AHRD V3.3 --* F4JJH9_ARATH)		F:GO:0000166; F:G(	F:nucleotide binding; F:protein kinase activity; F:protein serine/threonine kinase activity; F:ATP binding;				0,101	0,039	0,025	0,000	0,119									
Solyc04g077300	Serine/threonine-protein kinase (AHRD V3.3 *** K4BUH1_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001480 (SMART); IPR003609 (SM	0,000	0,000	0,000	0,025	0,000									
Solyc04g077310	Serine/threonine-protein kinase (AHRD V3.3 *-* K4BUH3_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR001480 (SM	0,019	0,000	0,000	0,000	0,000									
Solyc04g077330	Serine/threonine-protein kinase (AHRD V3.3 *-* M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); IPR003609 (SM	0,178	0,204	0,158	0,124	0,117									
Solyc04g077333	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 --* AT3G14980.6)							0,000	0,000	0,000	0,000	0,023									
Solyc04g077340	Serine/threonine-protein kinase (AHRD V3.3 *** M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR003609 (SMART); IPR001480 (SM	3,048	2,241	0,891	0,537	0,891									
Solyc04g077360	Serine/threonine-protein kinase (AHRD V3.3 *** M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR001480 (SMART); IPR000719 (SM	0,000	0,000	0,000	0,022	0,048									
Solyc04g077370	Serine/threonine-protein kinase (AHRD V3.3 *** M1A1I5_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); IPR001480 (SM	0,000	0,039	0,025	0,050	0,071									
Solyc04g077390	ARK2 product/receptor-like serine/threonine protein kinase ARK2 (AHRD V1 *-** Q9S972_ARATH)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR001480 (SMART); IPR003609 (SM	1,997	11,125	1,629	2,484	5,346	2,497	0,000	1,708	0,000			up	up	
Solyc04g077400	Early-responsive to dehydration protein-like (AHRD V1 **-- Q5JKX1_ORYSJ)		C:GO:0016020	C:membrane			IPR032880 (PFAM); IPR027815 (PFA	0,021	0,099	0,000	0,000	0,000									
Solyc04g077410	1-aminocyclopropane-1-carboxylate synthase 5	ACS5	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			PR00753 (PRINTS); IPR015421 (G3D	0,019	0,021	0,000	0,000	0,000									
Solyc04g077420	transmembrane protein (AHRD V3.3 *** AT3G49720.3)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D); mobic	11,783	10,673	18,027	18,045	15,324									
Solyc04g077430	Chaperone DnaJ (AHRD V3.3 *** A0A0B0NK31_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR001623 (PRINTS); IPR001623 (SM	6,200	8,241	7,930	8,332	7,966									
Solyc04g077440	Squalene monooxygenase (AHRD V3.3 *** Q506K3_DATIN)		F:GO:0004506; C:G(	F:squalene monoox	EC:1.14.13.132; EC:	Acting on paired dono	PR00420 (PRINTS); PF13450 (PFAM)	125,211	85,731	23,381	16,404	25,864									
Solyc04g077450	DNA binding protein (AHRD V3.3 *** AT3G12210.2)						mobidb-lite (MOBIDB_LITE); PTHR215	3,099	2,836	0,882	0,975	0,730									
Solyc04g077460	Amino acid transporter (AHRD V3.3 *** A0A061FF30_THECC)		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM); PTHR22950 (PAN	11,142	9,479	4,224	4,382	4,992									
Solyc04g077470	Cellulose synthase-like protein (AHRD V3.3 *** L0ASJ1_POPTO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity			PF13641 (PFAM); IPR029044 (G3DS/	98,525	46,169	32,021	90,374	76,941	-1,066	0,000	1,260	0,000	1,497	0,000	down	up	up
Solyc04g077480	bHLH transcription factor 034	bHLH034	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF_bHLH	6,108	4,589	2,687	3,274	3,333									
Solyc04g077490	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VCJ1_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN'_AP2	1,830	2,353	0,097	0,050	0,117									
Solyc04g077500	transmembrane protein (AHRD V3.3 *** AT1G44920.1)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane			IPR021414 (PFAM); mobidb-lite (MOB	28,711	37,782	33,875	35,062	38,811									
Solyc04g077510	Growth-regulating factor (AHRD V3.3 *** A0A072VEY4_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten			IPR014978 (SMAF_GRF	7,916	11,102	0,688	0,772	0,793									
Solyc04g077520	RNA-binding family protein, putative (AHRD V3.3 *** A0A061FF68_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR012677 (G3	7,874	7,276	12,205	11,648	10,281									
Solyc04g077540	Kinesin-like protein (AHRD V3.3 *** K4BUJ1_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	2,084	2,125	0,291	0,445	0,445									
Solyc04g077555	BZIP transcription factor family protein (AHRD V3.3 *** B9GNM4_POPTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMART); G3DSA:1.20.5.1	0,281	0,077	0,574	1,023	0,542									
Solyc04g077560	CW7 (AHRD V3.3 *** AT1G59520.1)						IPR019141 (PFAM); PTHR21477 (PAN	30,735	24,710	32,233	36,115	33,407									
Solyc04g077570	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072V1Y9_MEDTR)						mobidb-lite (MOBIDB_LITE); PTHR340	0,474	0,393	0,428	0,487	0,520									
Solyc04g077580	Phytosulfokines 3, putative (AHRD V3.3 *** A0A061FFM9_THECC)		C:GO:0005576; F:G(	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM); IPR009438 (PAN	0,360	0,621	0,099	0,300	0,024									
Solyc04g077590	Protein PHLOEM PROTEIN 2-LIKE A10 (AHRD V3.3 *** P2A10_ARATH)		C:GO:0016021	C:integral component of membrane			PTHR21477 (PANTHER); PTHR21477	15,658	16,540	15,830	14,891	17,132									
Solyc04g077600	BSD domain-containing family protein (AHRD V3.3 *** B9IBP6_POPTR)						IPR005607 (SMART); IPR005607 (PF.	30,618	33,242	37,049	33,971	36,128									
Solyc04g077610	U-box domain-containing family protein (AHRD V3.3 *** B9GNN0_POPTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART); IPR011989 (G3	20,058	12,102	12,694	18,517	13,947	-0,701	0,020			0,544	0,007	down		up
Solyc04g077615	Serine carboxypeptidase-like 7 (AHRD V3.3 *-* W9SMT8_9ROSA)		F:GO:0004185; F:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR019734 (SM	0,077	0,043	0,247	0,141	0,165									
Solyc04g077640	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	0,000	0,000	0,384	0,239	0,143									
Solyc04g077650	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	1,307	2,171	26,548	28,457	23,157									
Solyc04g077660	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NXQ5_ZOSMR)		F:GO:0005515	F:protein binding			IPR019734 (SMART); G3DSA:3.10.50	3,718	2,940	4,018	2,957	3,357									
Solyc04g077670	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	7,470	7,646	1,929	1,246	1,824									
Solyc04g077680	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT4G07410.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR001680 (PF.	33,264	31,071	37,730	35,998	33,606									
Solyc04g077690	LOW QUALITY:At4g33800-like protein (AHRD V3.3 *** A0A068F620_BRANA)		P:GO:0009690	P:cytokinin metabolic process			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,283	0,727	0,000	0,025	0,117									
Solyc04g077720	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM); PTHR11119:SF5:	0,021	0,000	0,022	0,000	0,023									
Solyc04g077740	Zinc finger protein Sdr4 (AHRD V3.3 *** M9NJT2_ORYSA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,807	2,323	5,266	5,743	4,193									

Solyc04g077745	NADH-ubiquinone oxidoreductase-like protein (AHRD V3.3 *-* AT5G67590.1)		F:GO:0016651: P:G(	F:oxidoreductase activity, acting on NAD(P)H: P:electron transp			IPR006885 (PFAM): IPR038532 (G3D	2,349	1,664	2,469	2,524	2,741									
Solyc04g077750	LOW QUALITY:NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial (AHRD V3.3 --* A0A1D1XFJ9_9ARAE)							0,993	0,611	1,223	0,989	1,443									
Solyc04g077760	LOW QUALITY:Exocyst complex component 7 (AHRD V3.3 *** W9RYK4_9ROSA)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			G3DSA:1.20.1280.170 (GENE3D): IPF	0,000	0,019	0,000	0,000	0,000									
Solyc04g077770	LOW QUALITY:Caffeic acid 3-O-methyltransferase (AHRD V3.3 --* COMT1_PRUDU)							0,000	0,000	0,000	0,025	0,000									
Solyc04g077775	F-box protein (AHRD V3.3 *** W9R463_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	7,903	7,299	9,911	8,598	8,890									
Solyc04g077780	Transcription factor LIM (AHRD V3.3 *** V9LXM6_TOBAC)		F:GO:0046872	F:metal ion binding			IPR001781 (SMART): IPR001781 (PF	85,960	85,583	29,383	28,936	40,366									
Solyc04g077790	GPN-loop GTPase (AHRD V3.3 *** A0A0K9PFH6_ZOSMR)		F:GO:0005525: F:G(	F:GTP binding; F:hydrolase activity			G3DSA:3.40.50.300 (GENE3D): IPR0(	21,333	21,742	25,110	25,742	23,086									
Solyc04g077810	LOW QUALITY:ZCF37, putative (AHRD V3.3 *** A0A061F7D6_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,197	6,600	8,609	4,854									
Solyc04g077820	ZCW7 (AHRD V3.3 *** AT1G59600.1)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	15,067	15,951	36,747	42,229	33,561									
Solyc04g077830	LOW QUALITY:Tetratricopeptide repeat protein 7A (AHRD V3.3 *** A0A0B2PIX3_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	0,221	0,178	0,047	0,022	0,071									
Solyc04g077835	F-box family protein (AHRD V3.3 *-* D7MPB2_ARALL)		F:GO:0005515	F:protein binding			PTHR44829 (PANTHER): IPR015915 (	0,755	1,292	2,193	2,159	2,077									
Solyc04g077840	F-box family protein (AHRD V3.3 --* D7MPB2_ARALL)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR036047 (SUP	0,542	0,701	1,209	0,651	0,921									
Solyc04g077850	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PK99_ZOSMR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	10,245	12,036	9,924	13,929	10,074					0,492	0,050			up
Solyc04g077860	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9R708_RICCO)		P:GO:0010223: F:G(	P:secondary shoot	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	6,221	5,491	8,558	11,231	11,049									
Solyc04g077870	Calcium-transporting ATPase (AHRD V3.3 *** M1BXT8_SOLTU)		F:GO:0005388: F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRI	12,195	14,979	25,680	26,940	26,643									
Solyc04g077910	LOW QUALITY:D5-type cyclin (AHRD V3.3 *** A8Y917_POPTR)		P:GO:0000079: C:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			G3DSA:1.10.472.10 (GENE3D): IPR0(	0,000	0,000	0,000	0,000	0,023									
Solyc04g077920	Interferon-related developmental regulator family protein (AHRD V3.3 *** B9IBS1_POPTR)						IPR007701 (PFAM): IPR006921 (PFA	77,087	88,553	120,565	152,927	130,184									
Solyc04g077925	Activating signal cointegrator 1 complex subunit 2 (AHRD V3.3 *-* W9QVC0_9ROSA)		F:GO:0003723	F:RNA binding			PTHR21494:SF0 (PANTHER): PTHR2	3,299	2,498	4,162	4,567	3,981									
Solyc04g077930	Ubiquitin system component Cue protein (AHRD V3.3 --* AT1G27752.1)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	5,580	4,868	6,269	6,637	6,684									
Solyc04g077940	SPOC domain protein (AHRD V3.3 *** A0A0C3UJQ2_MEDTR)		F:GO:0003676	F:nucleic acid binding			PR01217 (PRINTS): IPR000504 (SMA	42,860	42,907	46,277	46,393	44,685									
Solyc04g077950	nucleic acid binding protein (AHRD V3.3 *-* AT1G27750.1)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,065	0,969	0,927	0,975	0,681									
Solyc04g077960	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT2G14760.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,060	0,064	0,118	0,291	0,398									
Solyc04g077970	Adenine phosphoribosyltransferase-like (AHRD V3.3 *** Q2V997_SOLTU)		F:GO:0003999: C:G(	F:adenine phosphoi	EC:2.4.2.7	Adenine phosphoribo	IPR005764 (TIGRFAM): IPR000836 (F	658,742	539,247	676,733	583,130	631,467									
Solyc04g077980	C2H2-type zinc finger protein		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	277,820	54,760	63,311	220,381	87,507	-2,319	0,000			1,803	0,000	down		up
Solyc04g077990	LOB domain-containing protein, putative (AHRD V3.3 *** B9SND0_RICCO)						IPR004883 (PFAM LBD	12,819	11,705	3,630	2,558	4,180									
Solyc04g078000	QWRF motif protein (DUF566) (AHRD V3.3 *** AT1G49890.1)		C:GO:0005737: C:G(	C:cytoplasm; C:centrosome; C:nuclear microtubule; P:centrosoi			IPR007573 (PFAM): mobidb-lite (MOB	7,552	9,815	8,640	7,904	8,689									
Solyc04g078010	Glycosyl hydrolase family 35 protein, putative (AHRD V3.3 *** A0A061FGE0_THECC)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,544	0,572	0,000	0,000	0,000									
Solyc04g078030	Elongation factor 4 (AHRD V3.3 *** A0A0B0NVR5_GOSAR)						PTHR33181:SF4 (PANTHER): PTHR3:	0,021	0,000	0,000	0,000	0,000									
Solyc04g078040	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT5G43140.1)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM): PTHR11266:SF4:	0,255	0,576	0,244	0,195	0,165									
Solyc04g078050	Transcription initiation factor, putative (AHRD V3.3 *** B9R722_RICCO)		C:GO:0005669: P:G(	C:transcription factor TFIID complex; P:DNA-templated transcrip			IPR007900 (PFAM): IPR022003 (PFA	36,659	30,087	55,025	52,980	46,786									
Solyc04g078060	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT1G75810.1)		C:GO:0016021	C:integral component of membrane			PTHR37714 (PANTHER)	2,326	1,885	7,999	9,655	5,605									
Solyc04g078070	Zinc finger protein 706 (AHRD V3.3 *** A0A090M711_OSTTA)						IPR039438 (PFAM): IPR007513 (PFA	352,291	354,700	456,150	434,256	390,755									
Solyc04g078090	Acyl-CoA-binding domain protein (AHRD V3.3 *-* A0A072VPF6_MEDTR)		F:GO:0000062	F:fatty-acyl-CoA binding			IPR014352 (G3DSA:1.20.80.GENE3D	22,717	19,347	124,890	187,751	104,215					0,591	0,009			up
Solyc04g078110	serine protease SBT1	sbt1	F:GO:0004252: P:G(	F:serine-type endoi	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	24,031	15,051	34,066	52,368	30,978					0,624	0,000			up
Solyc04g078120	Ankyrin repeat family protein (AHRD V3.3 *** A0A097PRV4_SOLLC)		F:GO:0005515: F:G(	F:protein binding; F:	EC:2.1.1.125	Transferring one-carl	IPR002110 (SMART): IPR017408 (PIF	7,476	7,424	6,121	5,622	6,275									
Solyc04g078130	Syntaxin-61-like protein (AHRD V3.3 *** A0A0B0PXY6_GOSAR)		C:GO:0016020: P:G(	C:membrane; P:Golgi vesicle transport			IPR015260 (PFAM): G3DSA:1.20.58.9	28,243	30,837	23,706	25,834	25,667									
Solyc04g078140	Cytochrome B5 (AHRD V3.3 *** Q9ZSP7_PETHY)		C:GO:0016021: F:G(	C:integral component of membrane; F:heme binding; F:metal ior			IPR001199 (PRINTS): IPR001199 (SM	0,412	0,535	0,251	0,209	0,237									
Solyc04g078150	glycine-rich protein (AHRD V3.3 -** AT4G10330.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:heme binding; F:metal ior			mobidb-lite (MOBIDB_LITE)	6,441	7,654	12,774	11,532	11,166									
Solyc04g078160	C5orf35 (AHRD V3.3 *** AT5G23200.1)						IPR040415 (PANTHER): PTHR33524::	5,180	4,664	6,880	5,263	5,734									
Solyc04g078190	glutamyl-tRNA (Gln) amidotransferase subunit A (DUF620) (AHRD V3.3 *** AT3G19540.1)						IPR006873 (PFAM): mobidb-lite (MOB	6,980	8,093	2,545	2,463	3,168									
Solyc04g078200	Gibberellin regulated protein (AHRD V3.3 *-* A0A103XWU1_CYNCS)						IPR003854 (PFAM): PTHR23201 (PAI	0,058	0,021	0,022	0,000	0,023									
Solyc04g078210	Pumilio-like protein (AHRD V3.3 *** A0A0B0N664_GOSAR)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR011989 (G3	0,079	0,037	0,025	0,022	0,047									
Solyc04g078220	Metal transporter (AHRD V3.3 --* G5DVW2_SILLA)		C:GO:0016021: P:G(	C:integral component of membrane; P:metal ion transport; F:metal ion transmembrane transporter activi				0,000	0,000	0,000	0,000	0,000									
Solyc04g078240	Metal transporter (AHRD V3.3 --* Q84LR0_SOLLC)		C:GO:0016021: P:G(	C:integral component of membrane; P:metal ion transport; F:me			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,021	0,000	0,000	0,000									
Solyc04g078250	metal transporter Nramp2	Nramp2	C:GO:0016020: P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR001046 (PRINTS): IPR001046 (TI(	30,850	27,369	24,709	22,372	22,886									
Solyc04g078270	Cytochrome P450 family protein (AHRD V3.3 *** B9NFM5_POPTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,040	0,021	0,050	0,025	0,048									
Solyc04g078280	microtubule-associated protein 65-7 (AHRD V3.3 --* AT1G14690.2)							0,871	0,650	0,636	0,843	0,377									
Solyc04g078290	Cytochrome P450 (AHRD V3.3 *** A0A103XWR5_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	5,605	14,887	2,302	3,102	5,529	1,432	0,001	1,247	0,003			up	up	
Solyc04g078300	MADS-box transcription factor family protein (AHRD V3.3 *** G7ZXM5_MEDTR)		F:GO:0000977: P:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	1,257	1,497	0,074	0,625	0,047									
Solyc04g078310	cyclin A3_1	CycA3_2	C:GO:0005634	C:nucleus			IPR013763 (SMART): IPR004367 (SM	1,180	0,901	0,000	0,095	0,093									
Solyc04g078320	WD40 repeat-like protein (AHRD V3.3 *** I0YVP9_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	28,956	23,841	45,220	39,526	41,025									
Solyc04g078340	Cytochrome P450 (AHRD V3.3 *** C5NM78_TOBAC)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	2,788	4,857	3,572	5,825	5,883			0,718	0,022	0,709	0,027		up	up
Solyc04g078350	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT5G42830.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,061	0,082	0,000	0,072	0,024									
Solyc04g078360	Cytochrome P450, putative (AHRD V3.3 *** B9R747_RICCO)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,021	0,021	0,022	0,000	0,000									
Solyc04g078370	Cytochrome P450 (AHRD V3.3 *** C5NM78_TOBAC)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	9,793	14,342	0,282	0,140	0,282									
Solyc04g078380	RAN GTPase activating protein 2 (AHRD V3.3 *-* AT5G19320.2)		F:GO:0005515: C:G(	F:protein binding; C:nuclear envelope; C:Golgi apparatus; C:nuc			IPR025265 (PFAM): IPR038214 (G3D	88,101	90,249	91,834	77,813	86,368									
Solyc04g078390	F-box family protein (AHRD V3.3 *** AT4G24210.1)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	47,298	38,126	46,042	41,454	44,143									
Solyc04g078400	Mortality factor 4 like 1 (AHRD V3.3 *** A0A0K9PQT8_ZOSMR)		C:GO:0005634: P:G(	C:nucleus; P:chromatin organization; P:regulation of transcriptio			IPR000953 (SMART): IPR008676 (PIF	1,011	0,788	2,263	1,816	1,320									
Solyc04g078410	Serine/threonine-protein kinase (AHRD V3.3 *** M0ZUR7_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001480 (SM	0,302	0,095	0,050	0,025	0,047									
Solyc04g078420	R2R3MYB transcription factor 70	R2R3MYB70	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	130,995	75,152	143,572	245,211	217,828	-0,776	0,018	0,598	0,001	0,774	0,000	down	up	up
Solyc04g078440	Carbohydrate esterase plant-like protein (AHRD V3.3 *-* G7J707_MEDTR)		C:GO:0016020	C:membrane			IPR036514 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,515	0,898	0,234									
Solyc04g078450	pollen-specific LRR extensin-like protein (AHRD V3.3 --* AT2G25920.1)						mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,417	0,287	0,188									
Solyc04g078460	L-asparaginase (AHRD V3.3 *** Q84L89_SOYBN)		F:GO:0016787	F:hydrolase activity			IPR000246 (PFAM): G3DSA:3.60.20.3	2,480	4,407	23,336	35,682	20,714					0,617	0,028			up
Solyc04g078470	D-type cyclin-3	cycd3c3	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	0,293	0,462	0,000	0,048	0,000									
Solyc04g078480	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0C4W2P6_GINBI)		C:GO:0009507: P:G(	C:chloroplast; P:chloroplast organization; P:chloroplast rRNA pro			PF11523 (PFAM): G3DSA:3.10.450.4(	8,919	10,152	14,967	14,042	14,119									
Solyc04g078490	F-box protein (AHRD V3.3 *** W9R4Y4_9ROSA)		F:GO:0005515	F:protein binding			IPR006553 (SMART): G3DSA:1.20.12	45,147	43,910	59,433	63,912	57,651									
Solyc04g078500	cyclinJ18	J18	P:GO:0000079: C:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR006671 (PFAM): G3DSA:1.10.472	1,808	1,722	3,672	3,894	3,182									
Solyc04g078510	Rer1 family protein (AHRD V3.3 *** AT4G39220.2)		C:GO:0016021	C:integral component of membrane			IPR004932 (PFAM): PTHR10743:SF1	51,134	50,922	51,667	53,493	48,117									
Solyc04g078520	Serine/threonine-protein kinase WNK (AHRD V3.3 *-* A0A0K9PLE0_ZOSMR)						IPR025610 (PFAM): PTHR13902 (PAI	11,736	6,650	2,505	6,058	3,944					1,275	0,000			up
Solyc04g078530	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR036514 (G3DSA:3.40.50.GENE3D	0,146	0,079	0,022	0,000	0,023									
Solyc04g078540	Cysteine protease (AHRD V3.3 *** Q9ST61_SOLTU)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): IPR013201 (SM	17,362	20,511	19,065	21,723	19,833									
Solyc04g078550	WRKY transcription factor 7	WRKY7	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	101,365	91,227	49,526	97,382	70,475			0,505	0,002	0,977	0,000		up	up
Solyc04g078560	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PL83_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,059	0,000	0,000	0,000									
Solyc04g078590	Receptor protein kinase, putative (AHRD V3.3 *** B9T4U3_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	4,807	6,089	0,071	0,069	0,190									
Solyc04g078600	50S ribosomal protein L4 (AHRD V3.3 *** A0A1D1XFF1_9ARAE)						mobidb-lite (MOBIDB_LITE): PTHR355	26,533	21,502	73,519	61,146	65,976									
Solyc04g078610	Kinesin-like protein (AHRD V3.3 *** A0A0V0IYA4_SOLCH)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	37,797	28,030	24,926	24,120	22,744									
Solyc04g078620	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** A9PAA6_POPTR)		F:GO:0019789	F:SUMO transferase activity			SM00212 (SMART): IPR016135 (G3D	17,790	17,782	22,089	18,533	20,074									
Solyc04g078630	SPla/RYanodine receptor (SPRY) domain protein (AHRD V3.3 *** G7J6Y7_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR12864 (PANTHER): PTHR12864	0,738	2,574	0,813	0,871	0,589	1,818	0,000					up		
Solyc04g078640	Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9P1G2_ZOSMR)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	5,308	12,297	57,040	58,749	48,592	1,235	0,036					up		
Solyc04g078650	wuschel related homobox 4	WOX4	F:GO:0003677	F:DNA binding			IPR001356 (SMAF WOX	0,771	0,885	0,268	0,121	0,236									
Solyc04g078660	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G42830.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,563	1,152	0,795	0,637	0,729									
Solyc04g078670	NAC domain protein (AHRD V3.3 *** S5RUW2_9ROSA)	NAC040	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	25,368	13,758	7,829	14,381	9,620	-0,857	0,001			0,873	0,000	down		up
Solyc04g078680	RING/U-box superfamily protein (AHRD V3.3 *** AT5G42940.2)		P:GO:0016567: F:G(	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga:			IPR001841 (SMART): IPR013083 (G3	132,940	183,309	86,439	83,922	98,995									
Solyc04g078690	bHLH transcription factor 035		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	5,104	6,170	3,509	3,851	4,047									
Solyc04g078700	Kinase family protein (AHRD V3.3 *** B9ICA0_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	17,508	13,999	9,660	9,631	10,953									
Solyc04g078710	Subtilisin-like protease (AHRD V3.3 *** A0A151U5K8_CAJCA)		F:GO:0004252: P:G(	F:serine-type endoi	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	0,000	0,301	0,025	0,025	0,000									
Solyc04g078720	Subtilisin-like protease (AHRD V3.3 *** A0A151U5K8_CAJCA)		F:GO:0004252: P:G(	F:serine-type endoi	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	0,239	1,151	0,068	0,025	0,072									
Solyc04g078730	Subtilisin-like protease (AHRD V3.3 *** A0A151U5K8_CAJCA)		F:GO:0004252: P:G(	F:serine-type endoi	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): PF17766 (PFAI	5,973	18,628	0,755	0,300	0,918									
Solyc04g078740	Subtilisin-like protease (AHRD V3.3 *** W9SHY0_9ROSA)		F:GO:0004252: P:G(	F:serine-type endoi	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.3(	0,320	0,236	0,442	1,061	0,892									
Solyc04g078750	Late embryogenesis abundant protein (AHRD V3.3 *** G7LCF7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	107,222	67,438	43,609	70,760	77,557	-0,643	0,016	0,827	0,000	0,699	0,000	down	up	up
Solyc04g078760	CONSTANS interacting protein 4	CIP4	F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			IPR017066 (PIRSF): IPR013083 (G3D	18,995	19,791	35,369	32,198	29,933									
Solyc04g078770	SolycHsfB4a	HSF-07	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	0,420	0,467	0,046	0,000	0,000									
Solyc04g078780	Transducin/WD40 repeat protein (AHRD V3.3 *** A0A072VH71_MEDTR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	16,272	15,778	16,560	15,643	14,177									
Solyc04g078790	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT3G50330.1)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,021	0,000	0,790	0,886	0,238									
Solyc04g078800	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM): IPR029058 (G3D	0,021	0,345	0,309	0,122	0,094									
Solyc04g078810	Remorin (AHRD V3.3 *** Q00M66_SOYBN)		C:GO:0005886	C:plasma membrane			IPR005516 (PFAM): mobidb-lite (MOB	19,769	23,442	119,875	148,272	99,874									
Solyc04g078820	annexin 7	AnnSl7	F:GO:0005509: F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS): IPR018502 (SM	64,339	72,866	73,267	71,500	74,209									
Solyc04g078830	THO complex, subunit 5 (AHRD V3.3 *** A0A118JYT6_CYNCS)		C:GO:0000228: C:G(	C:nuclear chromosome; C:THO complex part of transcription ex			IPR019163 (PFAM): mobidb-lite (MOB	44,303	47,993	31,861	31,712	36,210									
Solyc04g078840	AREB	AREB	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	0,703	0,828	0,908	0,651	0,825									
Solyc04g078850	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0C4VYP8_CYCRE)	dcl	C:GO:0009507: P:G(	C:chloroplast; P:chloroplast organization; P:chloroplast rRNA pro			G3DSA:3.10.450.40 (GENE3D): PF11	2,799	4,148	7,108	8,732	7,723									
Solyc04g078860	Glutamate receptor (AHRD V3.3 *** G5EKN1_SOLLC)		F:GO:0004970: C:G(	F:ionotropic glutamate receptor activity; C:membrane			IPR001320 (SMART): G3DSA:3.40.19	1,399	1,986	1,252	0,933	0,958									
Solyc04g078870	Protein kinase family protein (AHRD V3.3 *** AT5G09890.1)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR000961 (SM	24,107	25,168	35,475	33,949	29,997									
Solyc04g078880	Cold regulated gene 27, putative isoform 1 (AHRD V3.3 *** A0A061FC20_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,098	0,079	0,334	0,050	0,141									
Solyc04g078890	Coenzyme Q-binding protein COQ10, mitochondrial (AHRD V3.3 *** A0A1D1YUM5_9ARAE)						IPR023393 (G3DSA:3.30.530.GENE3I	6,758	7,141	12,416	12,889	10,527									
Solyc04g078900	ABA 8'-hydroxylase	cyp707a1	F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	11,772	7,249	4,592	5,776	4,822									
Solyc04g078910	Thioredoxin, putative (AHRD V3.3 *** B9R7C2_RICCO)		P:GO:0006662: F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			IPR013766 (PFAM): G3DSA:3.40.30.1	2,528	3,380	4,057	6,555	6,393									
Solyc04g078920	Peroxisomal multifunctional enzyme type 2 (AHRD V3.3 *** A0A0B2RV47_GLYSO)		C:GO:0005777: C:G(	C:peroxisome; C:cytosol; P:fatty acid beta-oxidation; P:respons			IPR003033 (PFAM): IPR036527 (G3D	44,559	41,058	123,177	131,676	114,533									
Solyc04g078930	Alpha-amylase (AHRD V3.3 *** K4BUX7_SOLLC)		F:GO:0004556: F:G(	F:alpha-amylase ac	EC:3.2.1.1	Alpha-amylase	IPR006046 (PRINTS): IPR006047 (SM	3,694	3,498	3,534	3,293	4,646									
Solyc04g078940	Protein CYPRO4 (AHRD V3.3 *** A0A0B0NUW9_GOSAR)	dem	F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	2,671	2,859	0,798	0,707	1,060									
Solyc04g078950	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *-* WEB1_ARATH)						IPR008545 (PFAM): mobidb-lite (MOB	6,832	6,204	7,545	4,593	6,597					-0,712	0,006			down
Solyc04g078960	Plasma membrane ATPase (AHRD V3.3 --* PMA1_DUNBI)							1,493	0,967	1,188	1,347	1,673									
Solyc04g078970	WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT-like protein (DUF827) (AHRD V3.3 *-* AT2G26570.2)						IPR008545 (PFAM): mobidb-lite (MOB	4,904	3,439	5,321	3,573	4,829									
Solyc04g078980	Hexosyltransferase (AHRD V3.3 *** K4BUY2_SOLLC)		C:GO:0005794: P:G(	C:Golgi apparatus;	EC:2.4.1.17	Glucuronosyltransfer	IPR002495 (PFAM): IPR029044 (G3D	1,254	1,219	0,212	0,145	0,331									
Solyc04g078990	Hexosyltransferase (AHRD V3.3 *** K4BUY3_SOLLC)		C:GO:0005794: P:G(	C:Golgi apparatus;	EC:2.4.1.17	Glucuronosyltransfer	IPR002495 (PFAM): IPR029044 (G3D	0,630	0,727	0,069	0,100	0,167									
Solyc04g079000	Protein TIC 22, chloroplastic-like protein (AHRD V3.3 *** A0A0B0PIL8_GOSAR)		P:GO:0015031	P:protein transport			IPR007378 (PFAM): G3DSA:3.40.135(	18,176	22,166	52,849	50,504	52,730									
Solyc04g079040	Serine carboxypeptidase, putative (AHRD V3.3 *-* Q9FX26_ARATH)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	G3DSA:3.40.50.12670 (GENE3D): IPI	0,195	0,387	0,022	0,025	0,070									
Solyc04g079047	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y3_RICCO)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	0,040	0,021	0,000	0,000	0,000									
Solyc04g079050	Glycosyltransferase (AHRD V3.3 *** M1AUC6_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,000	0,000	0,000	0,000	0,023									
Solyc04g079060	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	2,616	2,674	2,401	1,842	2,066									
Solyc04g079070	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	7,210	6,357	0,355	0,220	0,188									
Solyc04g079080	LOW QUALITY:Calcium-binding EF-hand (AHRD V3.3 *-* A0A103YCM4_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	0,061	0,036	0,025	0,050	0,023									
Solyc04g079090	phosphatidic acid phosphohydrolase 2 (AHRD V3.3 *-* AT5G42870.2)						IPR031315 (SMART): IPR007651 (PF	18,021	15,790	16,130	17,768	19,428									
Solyc04g079100	phosphatidic acid phosphohydrolase 2 (AHRD V3.3 *-* AT5G42870.1)						IPR031315 (SMART): IPR013209 (PF	46,385	37,694	40,085	38,541	40,685									
Solyc04g079110	LOW QUALITY:BRI1 kinase inhibitor 1 (AHRD V3.3 *** A0A061FJ36_THECC)		C:GO:0005886: F:G(	C:plasma membrane; F:kinase inhibitor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,478	2,080	0,761	0,952	1,274									
Solyc04g079120	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G47380.1)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	44,506	44,516	35,649	39,576	55,252			0,629	0,005				up	
Solyc04g079125	B3 domain-containing protein (AHRD V3.3 *** A0A0B2P5H6_GLYSO)		F:GO:0003677	F:DNA binding			IPR003340 (SMART): IPR015300 (G3	0,238	0,153	0,025	0,025	0,048									
Solyc04g079140	Transmembrane 53 (AHRD V3.3 *** A0A0B0ME54_GOSAR)		C:GO:0005777	C:peroxisome			IPR008547 (PFAM): IPR029058 (G3D	13,922	9,637	16,326	14,168	15,896									
Solyc04g079150	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HVN1_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,606	2,087	1,329	1,367	1,128									
Solyc04g079160	Peptidyl-prolyl cis-trans isomerase-like 3 (AHRD V3.3 *-* A0A0B2PVH2_GLYSO)		C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane			G3DSA:3.50.4.10 (GENE3D): PTHR3:	13,397	10,198	17,071	17,262	15,475									
Solyc04g079170	BRCT domain-containing DNA repair protein (AHRD V3.3 --* AT4G03130.2)		C:GO:0016021	C:integral component of membrane			PTHR36324 (PANTHER)	0,084	0,153	0,256	0,315	0,213									
Solyc04g079180	Succinate dehydrogenase 5 (AHRD V3.3 *** A0A061FCR8_THECC)						IPR025397 (PFAM): IPR025397 (PAN	88,031	88,390	196,768	164,467	181,891									
Solyc04g079190	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G47480.1)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	20,928	19,882	20,439	22,946	17,762									
Solyc04g079200	26S proteasome non-ATPase regulatory subunit, putative (AHRD V3.3 *** B9R7G0_RICCO)		F:GO:0005515: F:G(	F:protein binding; F:Lys63-specific deubiquitinase activity			IPR000555 (SMART): G3DSA:3.40.14	79,212	93,089	129,776	141,188	124,801									
Solyc04g079210	Patatin (AHRD V3.3 *** A0A0V0I1U4_SOLCH)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): PTH	0,021	0,483	0,099	0,147	0,234									
Solyc04g079230	Patatin (AHRD V3.3 *-* G7I4H1_MEDTR)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR(	0,057	0,371	0,025	0,069	0,094									
Solyc04g079240	Patatin (AHRD V3.3 *** K4BV08_SOLLC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR(	0,021	0,000	0,069	0,025	0,024									
Solyc04g079250	Patatin (AHRD V3.3 *** K4BV09_SOLLC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR(	0,042	0,335	0,000	0,000	0,024									
Solyc04g079260	Patatin (AHRD V3.3 *** K4BV10_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM): G3DSA:3.40.109	0,000	0,000	0,000	0,095	0,000									
Solyc04g079270	Sorting and assembly machinery component 50 like (AHRD V3.3 *** A0A0B2S280_GLYSO)		C:GO:0019867	C:outer membrane			IPR000184 (PFAM): IPR010827 (PFA	56,886	52,647	82,089	79,298	75,016									
Solyc04g079280	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G34310.1)		F:GO:0004392: P:G(	F:heme oxygenase	EC:1.14.99.3	Acting on paired don	IPR011989 (G3DSA:1.25.10.GENE3D	8,299	7,367	6,554	7,394	6,669									
Solyc04g079290	heme oxygenase 2	ho2	F:GO:0004392: P:G(	F:heme oxygenase	EC:1.14.99.3	Acting on paired don	IPR016951 (PIRSF): IPR016053 (PFA	1,189	1,222	1,282	1,134	1,295									

Solyc04g079300	Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** AT4G11800.1)		F:GO:0016787	F:hydrolase activity			IPR004843 (PFAM): IPR029052 (G3D	3,551	7,241	10,048	13,430	10,785									
Solyc04g079310	RNA-binding protein (AHRD V3.3 *** A0A0K9NR72_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	31,114	29,403	4,608	3,985	5,796									
Solyc04g079315	RNA binding protein (AHRD V3.3 *** E3NYS6_9FABA)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	27,425	28,497	4,504	2,960	5,232									
Solyc04g079320	Uroporphyrinogen-III synthase (AHRD V3.3 *** W8TFM0_TOBAC)	HEMD/UROS	F:GO:0004852: P:G(	F:uroporphyrinogen	EC:4.2.1.75	Uroporphyrinogen-III	G3DSA:3.40.50.10090 (GENE3D): IPF	30,811	40,057	40,561	44,547	48,964									
Solyc04g079330	Carboxypeptidase (AHRD V3.3 *** K4BV17_SOLLC)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	0,037	0,060	0,000	0,048	0,024									
Solyc04g079340	transcription factor, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G42690.5)						IPR025757 (PFAM): IPR006869 (PFA	16,114	11,918	1,560	1,087	1,643									
Solyc04g079350	LOW QUALITY:calmodulin-binding protein (DUF1645) (AHRD V3.3 *** AT2G15760.1)		C:GO:0005886	C:plasma membrane			IPR012442 (PFAM): mobidb-lite (MOB	3,549	4,350	27,492	25,757	23,190									
Solyc04g079360	R2R3MYB transcription factor 77	R2R3MYB77	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	3,732	4,131	1,390	5,549	1,902					1,988	0,000			up
Solyc04g079370	Serpin (AHRD V3.3 *** Q5GN36_CUCSA)		C:GO:0005615	C:extracellular space			IPR023796 (SMART): G3DSA:3.30.49	0,081	0,116	0,096	0,047	0,095									
Solyc04g079375	Serpin-like protein (AHRD V3.3 *-* G7J5S6_MEDTR)		C:GO:0005615	C:extracellular space			G3DSA:3.30.497.10 (GENE3D): IPR02	0,040	0,162	0,051	0,050	0,000									
Solyc04g079390	Gamma-tubulin complex component (AHRD V3.3 *** K4BV23_SOLLC)		C:GO:0000922: C:G(	C:spindle pole; C:microtubule organizing center; P:microtubule n			IPR040457 (PFAM): PF17681 (PFAM)	16,384	13,343	19,452	19,708	20,380									
Solyc04g079400	MAP kinase kinase kinase 35	MAPKKK35	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	21,255	44,875	11,697	15,018	16,941	1,100	0,022					up		
Solyc04g079410	Primosome PriB/single-strand DNA-binding, putative (AHRD V3.3 *** A0A061FCZ9_THECC)		F:GO:0003697	F:single-stranded DNA binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	16,291	13,399	21,828	23,652	22,236									
Solyc04g079430	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7I4I7_MEDTR)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM): mobidb-lite (MOB	152,264	223,695	146,659	152,174	153,897									
Solyc04g079440	Serpin-like protein (AHRD V3.3 *** Q8GT65_CITPA)		C:GO:0005615	C:extracellular space			IPR023796 (SMART): G3DSA:3.30.49	61,777	91,719	57,063	62,037	60,938									
Solyc04g079450	Serpin-like protein (AHRD V3.3 *-* G7J5S6_MEDTR)		C:GO:0005615	C:extracellular space			IPR023796 (PFAM): G3DSA:2.30.39.1	0,586	1,869	0,394	0,201	0,399	1,686	0,012					up		
Solyc04g079460	Serpin-like protein (AHRD V3.3 *-* Q8GT65_CITPA)		C:GO:0005615	C:extracellular space			IPR023796 (PFAM): G3DSA:3.30.497	1,297	3,190	0,680	0,468	0,923									
Solyc04g079470	Serpin-like protein (AHRD V3.3 *** Q8GT65_CITPA)		C:GO:0005615	C:extracellular space			IPR023796 (SMART): IPR023796 (PF	20,734	68,095	12,185	15,919	13,981	1,738	0,000					up		
Solyc04g079475	Serpin-like protein (AHRD V3.3 *-* G7IXX4_MEDTR)		C:GO:0005615	C:extracellular space			G3DSA:2.30.39.10 (GENE3D): IPR02	0,000	0,000	0,000	0,025	0,000									
Solyc04g079480	Serpin-like protein (AHRD V3.3 *** Q8GT65_CITPA)		C:GO:0005615	C:extracellular space			IPR023796 (SMART): IPR023796 (PF	7,544	6,793	5,624	5,778	6,647									
Solyc04g079490	Serpin-like protein (AHRD V3.3 *-* G7IW05_MEDTR)		C:GO:0005615	C:extracellular space			G3DSA:2.10.300.20 (GENE3D): IPR02	0,197	0,021	0,097	0,097	0,047									
Solyc04g079500	LOW QUALITY:TRICHOME BIREFRINGENCE-LIKE 11 (AHRD V3.3 --* AT5G19160.2)							0,000	0,021	0,000	0,000	0,000									
Solyc04g079520	Major facilitator superfamily protein (AHRD V3.3 *** A0A061FB74_THECC)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	1,330	0,988	0,222	0,751	0,238									
Solyc04g079530	Major facilitator superfamily protein (AHRD V3.3 *** A0A061FB74_THECC)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	34,803	31,280	155,404	199,966	151,038									
Solyc04g079540	Tunicamycin induced 1 (AHRD V3.3 *** A0A097PPQ0_9LILI)						PTHR34454 (PANTHER): PTHR34454	13,068	10,543	17,793	17,255	14,623									
Solyc04g079550	Processing peptidase (AHRD V3.3 *** G7J5Q2_MEDTR)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity; C:membrane			IPR000223 (PRINTS): G3DSA:2.10.1(	115,463	104,820	88,956	113,135	102,385									
Solyc04g079560	Amino acid transporter family protein (AHRD V3.3 *** B9MVJ1_POPTR)		P:GO:0003333: C:G(	P:amino acid transmembrane transport; C:plasma membrane; F:			IPR013057 (PFAM): mobidb-lite (MOB	42,543	27,268	0,853	0,169	0,423									
Solyc04g079570	LOW QUALITY:Dof zinc finger protein (AHRD V3.3 *** W9QMS6_9ROSA)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	1,875	2,058	0,685	0,307	0,400									
Solyc04g079590	B3 domain-containing protein (AHRD V3.3 *** W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	16,553	13,399	20,679	19,038	19,796									
Solyc04g079600	Homeodomain-like superfamily protein (AHRD V3.3 *** AT5G42630.1)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	0,140	0,136	0,075	0,075	0,116									
Solyc04g079640	Cytochrome P450 (AHRD V3.3 *** A0A103YCJ3_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	90,160	95,462	102,617	105,162	133,430			0,376	0,023				up	
Solyc04g079660	Cytochrome P450 (AHRD V3.3 *** A0A103YCJ3_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	6,714	8,294	11,264	20,074	21,484			0,926	0,000	0,833	0,000		up	up
Solyc04g079680	Cytochrome P450 (AHRD V3.3 *** A0A103YCJ3_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	4,950	6,266	5,863	8,096	8,626									
Solyc04g079690	Dual-specific kinase DSK1 (AHRD V3.3 *** Q9FVN2_TOBAC)		F:GO:0004713: F:G(	F:protein tyrosine k	EC:2.7.1	Transferring phospho	IPR020635 (SMART): IPR001245 (PF	16,136	9,098	6,928	5,211	6,230									
Solyc04g079710	Kinase, putative (AHRD V3.3 *** B9S8Q9_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,236	1,242	0,097	0,198	0,234									
Solyc04g079730	allene oxide synthase	aos	F:GO:0004497: F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR002403 (PRINTS): IPR036396 (G3	16,222	119,440	3,570	1,637	2,993	2,899	0,000			-1,121	0,014	up		down
Solyc04g079740	tRNA-processing ribonuclease BN (AHRD V3.3 *** AT1G48460.1)		C:GO:0009941: C:G(	C:chloroplast envelope; C:integral component of membrane			PTHR33918 (PANTHER): PTHR33918	3,826	5,131	7,771	6,458	6,706									
Solyc04g079760	Structural constituent of ribosome, putative (AHRD V3.3 *** A0A061EZC6_THECC)		C:GO:0016021	C:integral component of membrane			IPR005134 (PFAM): PTHR31721:SF3	0,123	0,228	0,096	0,297	0,119									
Solyc04g079770	DNA-directed RNA polymerase subunit beta (DUF616) (AHRD V3.3 *** AT5G42660.1)		P:GO:0006672: C:G(	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): PTHR12956:SF1	11,600	10,058	12,340	11,855	11,856									
Solyc04g079780	RING/U-box superfamily protein (AHRD V3.3 *** AT2G16090.1)		F:GO:0003735: F:G(	F:structural constituent of ribosome; F:ubiquitin-protein transfer			IPR002867 (SMART): IPR014721 (G3	0,388	0,350	0,340	0,338	0,330									
Solyc04g079790	30S ribosomal protein S9 (AHRD V3.3 *** A9PB01_POPTR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014721 (G3DSA:3.30.230.GENE3	0,362	0,463	0,972	0,482	0,637									
Solyc04g079800	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR032675 (G3D	8,215	8,171	10,097	9,491	9,618									
Solyc04g079810	F-box/FBD/LRR protein (AHRD V3.3 *-* A0A072VCC9_MEDTR)		F:GO:0016874	F:ligase activity			IPR006566 (SMART): IPR006566 (PF	5,838	5,810	7,737	7,047	6,483									
Solyc04g079820	Inositol polyphosphate 5-phosphatase I (AHRD V3.3 *** G7I5A8_MEDTR)		P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART): IPR036691 (G3	0,019	0,217	0,122	0,119	0,093									
Solyc04g079830	BEL1-like homeodomain protein 2 (AHRD V3.3 *** A0A0B2SBB1_GLYSO)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006563 (SMAF TALE	4,296	3,133	1,328	0,542	1,290									
Solyc04g079840	Protein DA1-related 1 (AHRD V3.3 *** A0A199UXH9_ANACO)		F:GO:0043130: F:G(	F:ubiquitin binding; F:metal ion binding			IPR003903 (SMART): IPR001781 (SM	8,657	8,608	8,030	7,349	7,661									
Solyc04g079845	Protein DA1-related 1 (AHRD V3.3 *-* A0A1D1YPA3_9ARAE)		F:GO:0043130: F:G(	F:ubiquitin binding; F:metal ion binding			IPR022087 (PFAM): PTHR24209 (PAN	2,752	3,108	2,182	2,327	2,519									
Solyc04g079850	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061FCS7_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	14,004	18,748	7,122	8,242	8,098									
Solyc04g079860	Hexosyltransferase (AHRD V3.3 *** K4BV65_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR029044 (G3DSA:3.90.550.GENE3	6,845	12,991	2,283	1,227	1,393	0,951	0,010					up		
Solyc04g079870	Seryl-tRNA synthetase, putative (AHRD V3.3 *** B9RKX9_RICCO)		F:GO:0004828: F:G(	F:serine-tRNA ligas	EC:6.1.1.11	Serine--tRNA ligase	IPR002317 (PRINTS): IPR002314 (PF	0,019	0,021	0,025	0,050	0,071									
Solyc04g079880	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** B2LWM4_RICCO)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART): IPR002123 (PF	3,548	4,103	2,244	3,175	3,046									
Solyc04g079900	metalloendopeptidase / zinc ion binding protein (AHRD V3.3 *** AT5G42620.2)		F:GO:0004222: P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR001577 (PRINTS): IPR013111 (PF	98,073	51,490	60,207	39,611	56,154	-0,901	0,004			-0,601	0,000	down		down
Solyc04g079910	Calcium uniporter protein, mitochondrial (AHRD V3.3 *** A0A0B2QLC6_GLYSO)		P:GO:0051560	P:mitochondrial calcium ion homeostasis			IPR006769 (PFAM): PTHR13462:SF1	0,096	0,258	0,000	0,000	0,024									
Solyc04g079920	Pre-mRNA-splicing factor CWC22-like protein (AHRD V3.3 *-* W9SDK4_9ROSA)		F:GO:0003723: F:G(	F:RNA binding; F:protein binding			IPR003891 (SMART): IPR003890 (SM	32,788	30,394	31,060	27,467	29,433									
Solyc04g079930	Histone deacetylase complex subunit SAP30 (AHRD V3.3 *** A0A0B0N115_GOSAR)		F:GO:0005515	F:protein binding			IPR038291 (G3DSA:1.10.720.GENE3	7,913	6,000	6,165	3,907	4,432									
Solyc04g079940	NAC domain-containing protein (AHRD V3.3 *** A0A060A1D2_BOENI)	NAC041	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	32,261	51,207	18,501	22,350	24,824									
Solyc04g079950	Methyltransferase-like protein (AHRD V3.3 *** A0A072VF70_MEDTR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:methyltransferase activity; P:methylati			IPR007757 (PFAM): mobidb-lite (MOB	5,925	5,807	9,336	10,063	9,089									
Solyc04g079960	geranylgeranyl pyrophosphate synthase 2	GGPS2	P:GO:0008299	P:isoprenoid biosynthetic process			IPR000092 (PFAM): IPR008949 (G3D	7,985	13,609	30,992	32,858	41,663	0,795	0,030	0,423	0,011			up	up	
Solyc04g079970	RUB1 conjugating enzyme	rce1	F:GO:0005524: F:G(	F:ATP binding; F:NEDD8 transferase activity; P:protein neddyla			SM00212 (SMART): IPR016135 (G3D	506,333	448,488	502,347	557,839	497,434									
Solyc04g079980	BRASSINAZOLE-RESISTANT 1 protein, putative (AHRD V3.3 *** B9R7Q4_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:transcription, DNA			IPR008540 (PFAM BES1	42,169	62,019	21,606	23,381	27,750	0,582	0,045					up		
Solyc04g079990	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** A0A061FDE4_THECC)		P:GO:0006284: F:G(	P:base-excision rep	EC:3.2.2.21; EC:3.2.	DNA-3-methyladenine	G3DSA:1.10.340.30 (GENE3D): IPR0(	3,469	2,414	0,707	0,764	0,799									
Solyc04g080000	Peroxisomal membrane protein 11A (AHRD V3.3 *** W9SHI0_9ROSA)		C:GO:0005779: P:G(	C:integral component of peroxisomal membrane; P:peroxisome			IPR008733 (PFAM): mobidb-lite (MOB	15,116	11,967	23,825	26,054	22,606									
Solyc04g080010	Glycosyltransferase (AHRD V3.3 *** K4BV80_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	28,115	22,020	21,376	20,729	21,584									
Solyc04g080020	Acyltransferase, putative (AHRD V3.3 *** B9R7Q7_RICCO)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART): IPR002123 (PF	16,642	14,762	22,274	21,591	20,798									
Solyc04g080030	PPPDE putative thiol peptidase family protein (AHRD V3.3 *** AT1G47740.3)						IPR008580 (SMART): IPR008580 (PF	7,481	8,506	3,904	3,971	3,664									
Solyc04g080040	Heat shock protein binding protein, putative (AHRD V3.3 *** B9R7Q9_RICCO)						IPR036869 (G3DSA:1.10.287.GENE3	3,475	2,836	1,415	1,587	2,123									
Solyc04g080050	EXS family protein (AHRD V3.3 *** B9MXW8_POPTR)		C:GO:0016021	C:integral component of membrane			IPR004342 (PFAM): PTHR10783:SF4	13,882	12,814	14,168	19,892	16,407					0,491	0,021			up
Solyc04g080060	APO protein 4 (AHRD V3.3 *** W9QHQ1_9ROSA)		F:GO:0003723	F:RNA binding			IPR023342 (PFAM): PTHR10388 (PAN	3,616	4,692	6,891	8,152	7,988									
Solyc04g080080	Glycosyltransferase (AHRD V3.3 *** K4BV87_SOLLC)		C:GO:0000139: C:G(	C:Golgi membrane; C:integral component of membrane; F:transf			IPR005069 (PFAM): mobidb-lite (MOB	29,028	28,180	27,894	24,957	24,940									
Solyc04g080090	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G16580.1)		F:GO:0003824	F:catalytic activity			IPR001932 (PFAM): IPR036457 (G3D	0,973	1,007	0,415	0,421	0,706									
Solyc04g080100	Cytochrome P450 family protein (AHRD V3.3 *** B9GP38_POPTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	25,496	24,714	43,028	42,450	41,363									
Solyc04g080110	Accumulation of photosystem 2 (AHRD V3.3 *-* A0A068REC1_9MAGN)		F:GO:0003723	F:RNA binding			IPR023342 (PFAM): PTHR10388 (PAN	0,934	0,989	0,822	0,763	1,110									
Solyc04g080120	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	1,883	1,493	1,756	1,511	1,836									
Solyc04g080130	Zinc finger protein (AHRD V3.3 *** K9P0T0_9ROSI)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	10,721	17,057	0,964	1,355	1,455									
Solyc04g080140	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (AHRD V3.3 *** A0A061FJS0_THECC)						IPR025150 (PFAM): PTHR37193 (PAN	48,187	36,215	53,866	45,886	48,172									
Solyc04g080145	COP9 signalosome complex subunit 4 (AHRD V3.3 *-* S5QCB8_TOBAC)		C:GO:0008180	C:COP9 signalosome			IPR037754 (PTHR10855:PANTHER):	0,021	0,000	0,000	0,000	0,024									
Solyc04g080150	60S ribosomal protein L11 (AHRD V3.3 *-* RL11_ORYSJ)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022803 (G3DSA:3.30.1440.GENE	0,123	0,083	0,235	0,217	0,095									
Solyc04g080160	COP9 signalosome complex subunit 4 (AHRD V3.3 *** S5QCB8_TOBAC)		C:GO:0008180	C:COP9 signalosome			SM00753 (SMART): IPR000717 (SMA	29,358	28,986	54,090	53,894	48,535									
Solyc04g080170	Kinase, putative (AHRD V3.3 *** B9R7R7_RICCO)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): G3DSA:1.10.51	34,216	18,128	25,703	23,114	25,306	-0,887	0,003					down		
Solyc04g080180	Plant/F18O14-17 protein (AHRD V3.3 *** A0A072VF81_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	35,991	30,671	35,096	30,985	32,639									
Solyc04g080190	Outer envelope pore protein 24B, chloroplastic (AHRD V3.3 *** OP24B_ARATH)		F:GO:0022843: P:G(	F:voltage-gated cation channel activity; P:regulation of ion trans			IPR034626 (PANTHER): PTHR35284:	19,797	26,950	21,896	20,510	23,121									
Solyc04g080200	Endoribonuclease Dicer-like protein (AHRD V3.3 *-* A0A0B0MLI3_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,902	5,708	2,507	2,291	2,193									
Solyc04g080210	LOW QUALITY:ovate family protein 9	OFP9	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (TIGRFAM): IPR006458 (F	0,000	0,036	0,000	0,000	0,000									
Solyc04g080220	DUF620 family protein (DUF620) (AHRD V3.3 *** AT1G75160.1)						IPR006873 (PFAM): IPR006873 (PAN	0,661	0,823	0,400	0,372	0,355									
Solyc04g080230	Sugar transporter, putative (AHRD V3.3 *-* B9S6G4_RICCO)		C:GO:0016021	C:integral component of membrane			IPR010608 (PFAM): mobidb-lite (MOB	41,581	59,799	28,792	24,718	21,979			-0,392	0,037				down	
Solyc04g080240	GYF domain-containing protein (AHRD V3.3 *** AT5G42950.1)		F:GO:0005515	F:protein binding			IPR003169 (SMART): IPR035445 (G3	202,874	174,188	296,062	324,555	309,978									
Solyc04g080250	Deoxyuridine 5'-triphosphate nucleotidohydrolase (AHRD V3.3 *** DUT_ARATH)		F:GO:0004170: P:G(	F:dUTP diphosphata	EC:3.6.1.23; EC:3.6.	dUTP diphosphatase	IPR036157 (G3DSA:2.70.40.GENE3D	0,061	0,175	9,309	13,045	9,670									
Solyc04g080260	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9R7T0_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM): G3DSA:3.20.20.8	21,195	27,672	27,968	32,956	28,792									
Solyc04g080270	Cytochrome c oxidase subunit 3 (AHRD V3.3 *** A0A0B0MIX5_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	155,306	113,532	136,855	144,745	135,212									
Solyc04g080280	Lung seven transmembrane receptor family protein (AHRD V3.3 --* AT5G18520.1)							432,720	311,198	390,693	410,470	393,410									
Solyc04g080290	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G75170.2)		F:GO:0008526: P:G(	F:phosphatidylinositol transporter activity; P:phospholipid transp			PR00180 (PRINTS): IPR001251 (SMA	42,600	60,375	32,417	26,210	30,813									
Solyc04g080300	Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** AT1G19400.3)		F:GO:0004617: P:G(	F:phosphoglycerate	EC:1.1.1.95	Phosphoglycerate de	PTHR42938 (PANTHER): PTHR42938	35,507	27,693	28,648	30,833	29,937									
Solyc04g080310	DNA repair metallo-beta-lactamase family protein (AHRD V3.3 --* AT3G26680.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,060	2,143	0,935	0,895	1,151									
Solyc04g080320	LOW QUALITY:F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,000	0,018	0,000	0,050	0,023									
Solyc04g080330	Peroxidase (AHRD V3.3 *** K4BVB2_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,019	0,050	0,022	0,023									
Solyc04g080340	Cytochrome P450, putative (AHRD V3.3 *** B9R7T9_RICCO)		F:GO:0003824: P:G(	F:catalytic activity; P:tRNA processing; F:FMN binding; F:4 iron			IPR001094 (PRINTS): IPR013785 (G3	27,656	31,996	54,662	52,786	51,555									
Solyc04g080350	RNA-binding domain, putative (AHRD V3.3 *** A0A061GJY5_THECC)		P:GO:0006408	P:snRNA export from nucleus			IPR019385 (PFAM): IPR038092 (G3D	16,717	15,730	15,028	12,521	11,576									
Solyc04g080360	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G19430.3)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	97,959	80,822	70,473	52,899	54,041			-0,387	0,016	-0,411	0,025		down	down
Solyc04g080370	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2QLD6_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM): mobidb-lite (MOB	19,479	16,690	21,969	26,049	24,818									
Solyc04g080380	Leucine carboxyl methyltransferase (AHRD V3.3 *** A0A118K3W6_CYNCS)		F:GO:0018423: P:G(	F:protein C-terminal leucine carboxyl O-methyltransferase activi			IPR007213 (PFAM): IPR011610 (TIGF	0,472	0,273	0,846	1,113	0,851									
Solyc04g080390	plasma membrane fusion protein (AHRD V3.3 *** AT5G42765.1)		C:GO:0009535	C:chloroplast thylakoid membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	42,830	34,062	65,384	74,324	73,313									
Solyc04g080410	Mannose-binding lectin (AHRD V3.3 *-* A0A103XWY0_CYNCS)		F:GO:0030246	F:carbohydrate binding			IPR001229 (SMART): IPR036404 (G3	0,000	0,021	0,000	0,000	0,024									
Solyc04g080420	Mannose-binding lectin (AHRD V3.3 *-* A0A103XWY0_CYNCS)		F:GO:0030246	F:carbohydrate binding			IPR001229 (SMART): IPR001229 (PF	0,586	0,775	0,119	0,117	0,139									
Solyc04g080430	Cytosolic purine 5'-nucleotidase (AHRD V3.3 *** A0A0B0P914_GOSAR)		F:GO:0008253: P:G(	F:5'-nucleotidase ac	EC:3.1.3.5; EC:3.1.3	5'-nucleotidase; Nucl	IPR008380 (PFAM): IPR016695 (PIRS	21,429	26,463	62,101	65,482	61,674									
Solyc04g080435	MYB family transcription factor (AHRD V3.3 *** A0A072VEW4_MEDTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMART): IPR001005 (PF	0,103	0,018	0,000	0,000	0,024									
Solyc04g080440	Maf-like protein (AHRD V3.3 *** AT5G42770.2)		F:GO:0047429	F:nucleoside-tripho	EC:3.6.1.19	Acting on acid anhyd	IPR003697 (PFAM): IPR003697 (PIRS	25,193	24,661	30,930	27,811	29,608									
Solyc04g080450	3-ketoacyl-CoA synthase (AHRD V3.3 *** M0ZWA0_SOLTU)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013747 (PFAM): IPR016039 (G3D	73,017	78,331	147,666	151,747	136,901									
Solyc04g080460	Sugar facilitator protein 4	SFP4	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	4,018	4,653	1,412	1,679	1,811									
Solyc04g080470	DNA glycosylase (AHRD V3.3 *** A0A103XKQ6_CYNCS)		F:GO:0003824: P:G(	F:catalytic activity; P:base-excision repair			IPR003265 (SMART): G3DSA:1.10.16	11,989	14,163	14,204	13,888	12,558									
Solyc04g080480	4-coumarate--CoA ligase-like 4 (AHRD V3.3 *** 4CLL4_ARATH)	4CL-like	F:GO:0003824: P:G(	F:catalytic activity; P:lipid biosynthetic process			G3DSA:3.30.300.30 (GENE3D): G3DS	0,096	0,094	0,025	0,072	0,000									
Solyc04g080490	ZF-HD homeobox protein (AHRD V3.3 *** A0A0B2PTM6_GLYSO)		F:GO:0003677	F:DNA binding			IPR006456 (TIGRI ZF-HD	0,180	0,122	0,000	0,000	0,000									
Solyc04g080500	Myb family transcription factor family protein (AHRD V3.3 *** B9H0R6_POPTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,101	0,150	0,000	0,000	0,000									
Solyc04g080510	CBS domain protein (AHRD V3.3 *** B4G1D2_MAIZE)						IPR000644 (SMART): G3DSA:3.10.58	0,340	0,285	0,148	0,100	0,024									
Solyc04g080530	Pectinesterase (AHRD V3.3 *** K4BVD2_SOLLC)		F:GO:0030599: P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3	0,082	0,057	0,000	0,000	0,024									
Solyc04g080540	DNA polymerase epsilon catalytic subunit A, putative (AHRD V3.3 *** A0A061FCM9_THECC)		P:GO:0009061	P:anaerobic respiration			PTHR33872:SF2 (PANTHER): PTHR3	13,810	8,097	6,447	10,520	11,746			0,858	0,000	0,705	0,013		up	up
Solyc04g080550	Isoflavone reductase-like protein (AHRD V3.3 *** ALL12_OLEEU)	IFR-like	P:GO:0009807: F:G(	P:lignan biosynthetic process; F:oxidoreductase activity, acting			IPR008030 (PFAM): G3DSA:3.40.50.7	3,569	3,356	29,629	39,017	23,755									
Solyc04g080560	LOW QUALITY:Photosystem I assembly protein Ycf4 (AHRD V3.3 --* YCF4_CYCTA)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			PTHR38396 (PANTHER)	0,021	0,000	0,000	0,025	0,071									
Solyc04g080570	Gamma carbonic anhydrase-like protein (AHRD V3.3 *** I3SYK2_MEDTR)						IPR001451 (PFAM): G3DSA:2.160.10	30,637	31,925	21,969	18,280	22,117									
Solyc04g080580	pfkB-like carbohydrate kinase family protein (AHRD V3.3 *** AT1G19600.1)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			IPR011611 (PFAM): IPR029056 (G3D	55,842	46,822	41,814	37,249	40,563									
Solyc04g080590	Proteasome subunit alpha type (AHRD V3.3 *** K4BVD8_SOLLC)		F:GO:0004298: P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000426 (SMART): IPR029055 (G3	60,435	64,268	111,020	103,556	102,107									
Solyc04g080600	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103XYN8_CYNCS)		C:GO:0005737: F:G(	C:cytoplasm; F:clathrin binding; C:vesicle; C:intracellular membr			IPR036869 (G3DSA:1.10.287.GENE3	5,113	8,841	1,992	2,856	2,917									
Solyc04g080610	ornithine carbamoyltransferase		F:GO:0004585: P:G(	F:ornithine carbamo	EC:2.1.3.3	Ornithine carbamoylt	IPR006130 (PRINTS): IPR002292 (PF	29,282	31,879	43,707	41,200	36,991									
Solyc04g080620	Mannan endo-1,4-beta-mannosidase-like protein (AHRD V3.3 *** A0A072V2A7_MEDTR)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	0,021	0,100	0,044	0,047	0,000									
Solyc04g080630	50S ribosomal protein L31 (AHRD V3.3 *** K4BVE2_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002150 (PRINTS): IPR002150 (TI(	36,630	60,186	32,201	31,297	47,557	0,744	0,006	0,560	0,000			up	up	
Solyc04g080640	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072TTD0_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33640 (PANTHER): PTHR33640	0,932	1,699	1,874	2,521	2,944									
Solyc04g080650	LOW QUALITY:Cytochrome P450, putative (AHRD V3.3 *** B9R7Y0_RICCO)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR036396 (G3DSA:1.10.630.GENE3	0,601	0,788	0,025	0,022	0,046									
Solyc04g080660	Carboxyl methyltransferase (AHRD V3.3 *** A0A1B4Z3V0_9ROSA)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM): G3DSA:3.40.50.1	0,000	0,041	0,022	0,025	0,000									
Solyc04g080670	Inositol-pentakisphosphate 2-kinase (AHRD V3.3 *** W9SSZ8_9ROSA)		F:GO:0005524: F:G(	F:ATP binding; F:in(	EC:2.7.1.158	Inositol-pentakisphos	G3DSA:3.30.200.110 (GENE3D): IPR(	19,145	16,491	16,834	15,915	15,429									
Solyc04g080680	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): IPR003959 (PF	0,237	0,210	0,652	0,832	0,779									
Solyc04g080685	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *-* AT4G34580.2)						IPR001251 (SMART): IPR036865 (G3	0,000	0,021	0,000	0,000	0,000									
Solyc04g080690	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *-* AT4G39170.1)						IPR001251 (SMART): IPR036865 (G3	0,000	0,039	0,075	0,125	0,048									
Solyc04g080700	Bifunctional nuclease 1 (AHRD V3.3 *-* BBD1_ARATH)		F:GO:0004518	F:nuclease activity			IPR003729 (PFAM): IPR036104 (G3D	37,133	32,417	93,752	87,856	91,678									
Solyc04g080705	Bifunctional nuclease 1 (AHRD V3.3 *** BBD1_ARATH)		F:GO:0004518: P:G(	F:nuclease activity; P:nucleic acid phosphodiester bond hydroly			PTHR15160:SF3 (PANTHER): PTHR1	36,911	30,000	93,824	81,141	88,639									
Solyc04g080710	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G27660.1)		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	0,681	0,632	0,046	0,050	0,023									
Solyc04g080720	Transferase family protein (AHRD V3.3 *-* B9H4E9_POPTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM): IPR023213 (G3D	0,103	0,115	0,000	0,051	0,047									
Solyc04g080730	mitogen-activated protein kinase 9	mapk9	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	50,555	44,179	36,669	33,364	34,141									
Solyc04g080740	BZIP transcription factor family protein (AHRD V3.3 *** B9H4F3_POPTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	19,202	18,444	23,971	34,147	20,075					0,511	0,042			up
Solyc04g080750	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 *** AT1G35180.1)		C:GO:0016021	C:integral component of membrane			IPR006634 (SMART): IPR006634 (PF	0,397	0,530	0,301	0,170	0,000									
Solyc04g080770	GTP-binding protein, HflX (AHRD V3.3 *** AT5G57960.1)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR006073 (PF	25,596	25,377	50,020	52,307	57,332									
Solyc04g080780	BEL1-like homeodomain protein (AHRD V3.3 *** A0A072V2D2_MEDTR)	bl1	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR001356 (SMAF TALE	0,019	0,041	0,025	0,000	0,000									
Solyc04g080790	BEL1-like homeodomain protein 3, putative (AHRD V3.3 *** A0A061FD76_THECC)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006563 (SMAF TALE	1,561	2,194	2,451	3,778	3,175									

Solyc04g080800	Ribosomal RNA small subunit methyltransferase I (AHRD V3.3 *** A0A0B0MFQ4_GOSAR)		F:GO:0008168	F:methyltransferase activity			IPR014777 (G3DSA:3.40.1010.GENE	7,213	6,426	10,581	11,890	10,782									
Solyc04g080810	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *-* I0IUQ7_SOLLC)		P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	SM00212 (SMART): IPR016170 (G3D	22,021	20,786	49,942	43,846	41,252									
Solyc04g080820	cytokinin oxidase4	CKX4	P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	IPR016170 (G3DSA:3.40.462.GENE3	2,406	2,390	0,118	0,143	0,190									
Solyc04g080830	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 *** AT1G19720.1)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR032867 (PFA	4,893	5,416	3,975	3,197	5,419									
Solyc04g080850	Thioredoxin (AHRD V3.3 *** Q201Z4_9SOLN)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored			PR00421 (PRINTS): IPR005746 (TIGF	148,454	252,999	178,023	155,181	166,397	0,796	0,013					up		
Solyc04g080860	LOW QUALITY:abscisic acid responsive element-binding factor 1 (AHRD V3.3 --* AT1G49720.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	12,313	16,339	32,967	29,717	42,939			0,379	0,037				up	
Solyc04g080870	ATP-dependent protease La (LON) domain protein (AHRD V3.3 *-* AT1G75460.1)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity			mobidb-lite (MOBIDB_LITE): PTHR233	13,186	19,864	33,881	33,013	42,165	0,618	0,028					up		
Solyc04g080880	Cysteine protease family protein (AHRD V3.3 *** B9H4H0_POPTR)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): IPR000668 (SM	17,081	21,040	18,973	16,057	19,160									
Solyc04g080890	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G18210.2)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,192	0,102	0,049	0,022	0,000									
Solyc04g080900	GTPase obg (AHRD V3.3 *** A0A0B0PU27_GOSAR)		F:GO:0005515; F:G(	F:protein binding; F:GTP binding			IPR006073 (PRINTS): IPR006595 (SM	6,595	8,586	5,771	5,935	6,719									
Solyc04g080910	Dehydration responsive element binding transcription factor (AHRD V3.3 *-* W6FFW7_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' ERF	0,416	1,963	0,099	0,252	0,000									
Solyc04g080920	Purple acid phosphatase (AHRD V3.3 *-* K4BVH1_SOLLC)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	1,114	1,562	0,047	0,050	0,047									
Solyc04g080925	Purple acid phosphatase (AHRD V3.3 *-* K4BVH1_SOLLC)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	PTHR22953:SF35 (PANTHER): IPR03	0,309	0,224	0,025	0,025	0,000									
Solyc04g080930	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G42030.1)		F:GO:0005515; C:G(	F:protein binding; C:integral component of peroxisomal membrai			IPR001841 (SMART): IPR001841 (PF	17,293	15,033	17,028	17,977	18,261									
Solyc04g080940	WAT1-related protein (AHRD V3.3 *** M0ZWN9_SOLTU)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	3,844	2,470	0,147	0,073	0,071									
Solyc04g080950	Sec-independent protein translocase protein TatB (AHRD V3.3 *** A0A199UYW9_ANACO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,413	3,850	5,601	5,107	5,199									
Solyc04g080955	DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein (AHRD V3.3 --* AT1G31880.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,022	0,000	0,000									
Solyc04g080960	pre-pro-cysteine proteinase		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): IPR013201 (SM	529,882	396,144	1107,356	907,367	1103,486									
Solyc04g080970	Lateral root primordium protein-related, putative (AHRD V3.3 *** A0A061DFV6_THECC)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:positive regulation of transcription,			IPR006511 (TIGRI SRS	0,397	0,395	0,661	0,310	0,328									
Solyc04g080980	Coatomer subunit alpha (AHRD V3.3 *** K4BVH7_SOLLC)		F:GO:0005198; F:G(	F:structural molecule activity; F:protein binding; P:intracellular p			IPR020472 (PRINTS): IPR001680 (SM	229,468	245,997	237,500	223,018	220,439									
Solyc04g081000	Deficiens	Def	F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN' MIKC_MADS	15,754	25,784	15,582	15,954	17,762	0,736	0,011					up		
Solyc04g081020	Zinc finger, B-box (AHRD V3.3 *** A0A103XBE6_CYNCS)	BBX21	F:GO:0008270	F:zinc ion binding			IPR000315 (SMAF DBB	1,535	1,511	0,563	0,405	0,518									
Solyc04g081030	LTV1, putative (AHRD V3.3 *** A0A061ENH3_THECC)		P:GO:0000056; C:G(	P:ribosomal small subunit export from nucleus; C:nucleus; C:pre			IPR007307 (PFAM): mobidb-lite (MOB	37,882	39,785	36,149	33,490	30,804									
Solyc04g081060	Kinesin-like protein (AHRD V3.3 *** A0A068UGU8_COFCA)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	1,333	1,506	1,260	1,394	1,812									
Solyc04g081070	Hop-interacting protein THI044 (AHRD V3.3 *** G8Z271_SOLLC)	ARC6	P:GO:0010020; C:G(	P:chloroplast fission; C:integral component of chloroplast inner			IPR025344 (PFAM): mobidb-lite (MOB	57,635	57,806	99,991	85,726	93,860									
Solyc04g081080	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BVI7_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): SM00365 (SMAR	0,516	0,323	0,000	0,000	0,000									
Solyc04g081090	V-type proton ATPase proteolipid subunit (AHRD V3.3 *-* A0A0D3DHQ4_BRAOL)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR000245 (PRINTS): IPR011555 (TI(	155,150	146,835	187,859	186,627	180,075									
Solyc04g081100	Lysine-specific histone demethylase 1-1-like protein (AHRD V3.3 *** W9QIE9_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding; F:oxidoreductase activity; P:o			PR00419 (PRINTS): IPR036188 (G3D	54,755	43,568	55,055	55,090	55,928									
Solyc04g081130	LOW QUALITY:glyoxal oxidase-related protein (AHRD V3.3 *** AT1G19900.1)						IPR009880 (PFAM): IPR015202 (PFA	0,000	0,000	0,000	0,025	0,000									
Solyc04g081150	Histone H3 (AHRD V3.3 *** K7VSQ3_MAIZE)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000164 (PRINTS): IPR000164 (SM	28,378	27,712	27,396	22,764	24,297									
Solyc04g081160	Cell growth defect factor 2 (AHRD V3.3 *** B6SQ79_MAIZE)		C:GO:0016021	C:integral component of membrane			IPR039632 (PANTHER): SSF103481 (	8,109	8,588	3,892	2,993	3,969									
Solyc04g081165	wall associated kinase 4 (AHRD V3.3 --* AT1G21210.1)							0,880	0,963	1,044	1,420	1,130									
Solyc04g081170	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN91_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleolus; P:regul			IPR010409 (SMAF BBR-BPC	45,584	45,679	53,604	51,127	50,546									
Solyc04g081190	vsf-1	vsf1	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	25,822	27,270	93,234	95,570	92,026									
Solyc04g081200	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT1G19880.1)		F:GO:0003677	F:DNA binding			IPR000408 (PRINTS): IPR009091 (G3	38,900	46,408	28,711	27,245	30,584									
Solyc04g081210	SUN-like protein 14	SUN14	F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 (GENE3D): IPR00(	127,624	87,843	105,715	91,579	95,209									
Solyc04g081220	Mitochondrial 39S ribosomal protein L53 (AHRD V3.3 *** I6LNS8_HEVBR)						IPR019716 (PFAM): G3DSA:3.40.30.1	5,991	6,788	7,261	6,420	7,007									
Solyc04g081230	TLD-domain containing nucleolar protein (AHRD V3.3 *** AT5G39590.1)						IPR006571 (SMART): IPR006571 (PF	55,403	46,244	60,399	58,232	59,683									
Solyc04g081235	Auxin response factor (AHRD V3.3 *** K4BVK3_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMART): IPR003340 (PF	14,467	18,705	18,618	30,391	23,517					0,708	0,000			up
Solyc04g081250	Small auxin up-regulated RNA51	SAUR51	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	2,637	1,564	3,896	0,844	2,466					-2,192	0,000			down
Solyc04g081260	Filament-plant-like protein (AHRD V3.3 *** A0A072VFI4_MEDTR)						IPR008587 (PFAM): mobidb-lite (MOB	80,244	58,575	14,990	9,596	14,143					-0,642	0,014			down
Solyc04g081270	Small auxin up-regulated RNA52	SAUR52	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF4	1,930	1,736	2,031	1,271	1,453									
Solyc04g081280	5'-3' exoribonuclease 3 (AHRD V3.3 *** AT1G75660.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.13; EC:3.1.1	Acting on ester bonds	IPR001878 (SMART): IPR004859 (PF	48,624	44,833	67,820	73,847	67,706									
Solyc04g081290	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** K4BVK8_SOLLC)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): IPR0(	6,004	10,369	2,153	3,449	3,739									
Solyc04g081300	Endoglucanase (AHRD V3.3 *** K4BVK9_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001701 (PFAM): IPR012341 (G3D	344,385	271,742	70,699	55,234	66,437									
Solyc04g081310	Diphthine synthase, putative (AHRD V3.3 *** B9R875_RICCO)		F:GO:0004164; P:G(	F:diphthine synthas	EC:2.1.1.98	Diphthine synthase	IPR014777 (G3DSA:3.40.1010.GENE	6,897	6,514	7,172	5,898	6,639									
Solyc04g081320	Protein disulfide-isomerase LQY1, chloroplastic (AHRD V3.3 *-* LQY1_ARATH)	SPA	C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			IPR021467 (PFAM): PTHR15852:SF2	8,730	12,861	9,013	9,888	14,965			0,730	0,001				up	
Solyc04g081330	30S ribosomal protein S16, chloroplastic (AHRD V3.3 --* RR16_MORIN)						IPR021467 (PFAM): PTHR35550:SF2	21,706	30,405	15,358	15,623	22,142			0,525	0,003				up	
Solyc04g081340	HVA22-like protein (AHRD V3.3 *** M0ZWH6_SOLTU)		C:GO:0016020	C:membrane			IPR004345 (PFAM): mobidb-lite (MOB	18,093	14,466	29,696	33,665	28,832									
Solyc04g081350	E2F transcription factor (AHRD V3.3 *** G7IE33_MEDTR)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:transcription facto			IPR003316 (SMAF E2F/DP	4,807	8,186	4,942	3,946	4,648									
Solyc04g081360	tRNA (Adenine-N(1)-)-methyltransferase non-catalytic subunit trm6 (AHRD V3.3 *** A0A151U6B3_CAJCA)		P:GO:0030488; C:G(	P:tRNA methylation; C:tRNA (m1A) methyltransferase complex			IPR017423 (PFAM): G3DSA:3.40.50.1	9,686	9,356	11,081	12,589	10,047									
Solyc04g081370	C2H2-like zinc finger protein (AHRD V3.3 *** AT1G75710.1)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.90.228.1 C2H2	6,168	7,072	1,229	1,456	0,913									
Solyc04g081390	WEB family protein (AHRD V3.3 *** A0A0B2SGS1_GLYSO)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			mobidb-lite (MOBIDB_LITE): PTHR320	0,120	0,079	0,000	0,025	0,000									
Solyc04g081400	Phosphotransferase (AHRD V3.3 *** Q4PS96_SOLLC)	hxk4	P:GO:0001678; F:G(	P:cellular glucose h	EC:2.7.1.1	Hexokinase	PR00475 (PRINTS): G3DSA:3.30.420	61,725	68,248	57,537	54,222	54,251									
Solyc04g081410	AP-2 complex subunit sigma (AHRD V3.3 *** AP2S_ARATH)		P:GO:0015031	P:protein transport			G3DSA:3.30.450.60 (GENE3D): IPR0	30,173	31,497	33,245	33,923	28,506									
Solyc04g081420	F10A5.7 (AHRD V3.3 *** Q9LR13_ARATH)						mobidb-lite (MOBIDB_LITE): IPR0403(	44,968	34,946	95,544	112,279	97,946									
Solyc04g081430	Mediator complex, subunit Med7 (AHRD V3.3 *** AT5G03500.6)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR009244 (PFAM): IPR009244 (PAN	14,038	13,649	24,143	23,845	23,905									
Solyc04g081440	beta-fructofuranosidase	fruc	F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetyl	IPR024746 (PFAM): IPR024746 (PAN	265,686	261,623	160,516	163,957	165,748									
Solyc04g081450	Cytomatrix protein-related, putative (AHRD V3.3 *** A0A061FKJ5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,855	3,206	3,678	3,355	3,009									
Solyc04g081460	calcineurin B-like protein 10 (AHRD V3.3 --* AT4G33000.6)		C:GO:0016020	C:membrane			PTHR33306:SF5 (PANTHER): PTHR3	3,681	3,574	3,743	3,059	3,332									
Solyc04g081470	Transcription factor CPC (AHRD V3.3 *-* A0A1D1ZLD7_9ARAE)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	8,836	7,414	6,732	5,961	5,836									
Solyc04g081480	Dihydroxy-acid dehydratase 1 (AHRD V3.3 *** A0A0B0NRA9_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,493	3,413	2,988	3,278	3,425									
Solyc04g081490	beta-tubulin	tub	F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	628,801	566,275	316,910	252,090	334,010									
Solyc04g081500	BRCA1-A complex subunit BRE-like protein (AHRD V3.3 *** AT5G42470.1)		C:GO:0070531; C:G(	C:BRCA1-A complex; C:BRISC complex			IPR010358 (PFAM): IPR010358 (PAN	32,645	29,306	35,995	33,445	33,740									
Solyc04g081510	DUF668 family protein (AHRD V3.3 *** G7J592_MEDTR)						IPR021864 (PFAM): IPR007700 (PFA	17,532	22,775	10,926	8,825	11,093									
Solyc04g081520	SKU5 similar 18 (AHRD V3.3 *** AT1G75790.1)		F:GO:0005507; F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR001117 (PFAM): IPR008972 (G3D	0,592	0,643	0,071	0,073	0,046									
Solyc04g081530	DNAJ-like protein (AHRD V3.3 *** A2TJX6_SOLLC)						IPR001623 (PRINTS): IPR001623 (SM	19,300	25,969	14,875	9,448	14,000									
Solyc04g081540	Kinesin heavy chain isolog (AHRD V3.3 *** A0A0K9PAR0_ZOSMR)						G3DSA:1.10.60.30 (GENE3D): IPR00(	9,303	11,464	19,280	15,966	18,062									
Solyc04g081550	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** B9H4Z3_POPTR)						IPR001938 (PRINTS): IPR001938 (SM	33,801	24,435	7,449	8,706	11,299									
Solyc04g081560	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UXB7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS): IPR001938 (SM	0,338	0,711	0,096	0,022	0,071									
Solyc04g081570	Heat shock protein 90 (AHRD V3.3 *** G9MD87_TOBAC)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS): IPR003594 (SM	489,657	690,518	422,536	438,259	424,344									
Solyc04g081580	RNA helicase DEAD15	DEAD15	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	35,457	39,494	42,353	45,355	43,281									
Solyc04g081590	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BVN8_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	17,312	15,609	19,149	25,707	22,668									
Solyc04g081600	Aldolase superfamily protein (AHRD V3.3 --* AT1G16340.4)							0,281	0,235	0,486	0,432	0,471									
Solyc04g081610	LOW QUALITY:Subtilisin-like protease SBT3.8 (AHRD V3.3 --* SBT38_ARATH)							3,296	3,017	3,539	3,447	3,509									
Solyc04g081700	Ribosomal protein S5/Elongation factor G/III/V family protein (AHRD V3.3 --* AT5G25230.2)							0,000	0,000	0,000	0,025	0,000									
Solyc04g081710	squamosa promoter binding protein-like 14 (AHRD V3.3 --* AT1G20980.1)							0,021	0,000	0,025	0,000	0,000									
Solyc04g081720	LOW QUALITY:Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein (AHRD V3.3 --* AT4G13750.1)							1,534	1,981	2,641	1,974	2,137									
Solyc04g081730	JHL20J20.12 protein, putative (AHRD V3.3 *** A0A061FCM3_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	223,942	288,153	114,387	123,280	115,517									
Solyc04g081740	Glutathione S-transferase family protein (AHRD V3.3 *** AT5G42150.1)	MGST2	F:GO:0005515; F:G(	F:protein binding; F:	EC:5.3.99.3	Prostaglandin-E synt	G3DSA:3.40.30.10 (GENE3D): IPR00	36,527	44,246	65,418	61,407	64,585									
Solyc04g081750	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT1G20110.1)		F:GO:0046872	F:metal ion binding			IPR000306 (SMART): IPR000306 (PF	129,702	127,120	210,832	197,949	183,550									
Solyc04g081755	Lipase, GDSL (AHRD V3.3 *-* A0A103YES1_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,926	0,783	0,974	1,077	1,078									
Solyc04g081760	GDSL esterase/lipase (AHRD V3.3 *-* A0A0B2SN40_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:hydrolase activity, acting			IPR036514 (G3DSA:3.40.50.GENE3D	0,038	0,059	0,050	0,224	0,000									
Solyc04g081770	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SN40_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,061	0,118	0,000	0,000	0,000									
Solyc04g081790	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SN40_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,021	0,039	0,000	0,000	0,000									
Solyc04g081810	Subtilisin-like protease (AHRD V3.3 *** A0A0B2PIS0_GLYSO)		F:GO:0004252; P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR010259 (PF	1,460	2,011	0,329	0,219	0,235									
Solyc04g081820	LA motif RNA-binding domain-containing protein		F:GO:0003723	F:RNA binding			IPR006630 (SMART): IPR006630 (PF	44,477	51,858	53,057	53,756	50,412									
Solyc04g081850	Single hybrid motif superfamily protein (AHRD V3.3 *** AT1G75980.1)						G3DSA:2.40.50.100 (GENE3D): IPR0	8,074	7,452	6,230	6,317	6,150									
Solyc04g081860	Peroxidase (AHRD V3.3 *** K4BVR5_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,040	0,000	0,000	0,000	0,000									
Solyc04g081870	Expansin A11	EXPA11	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	7,335	8,993	0,224	0,139	0,187									
Solyc04g081880	DNA/RNA-binding protein Alba-like protein (AHRD V3.3 *** A0A103Y9U5_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR036882 (G3DSA:3.30.110.GENE3	192,189	219,448	275,824	244,906	243,214									
Solyc04g081890	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FKT7_THECC)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:zinc ion binding; C:inte			IPR001841 (SMART): IPR013083 (G3	27,827	17,710	19,244	41,575	28,052					1,111	0,000			up
Solyc04g081900	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT2G44380.1)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D): IPR01	70,203	72,759	359,229	311,456	276,583									
Solyc04g081910	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9R8F1_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): IPR002048 (SM	25,642	77,584	11,971	19,147	20,492	1,624	0,000	0,772	0,002	0,680	0,003	up	up	up
Solyc04g081920	Pseudouridine synthase family protein (AHRD V3.3 *** AT1G76050.2)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR002942 (SMART): IPR002942 (PF	14,161	20,961	10,824	12,013	12,586									
Solyc04g081930	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9R8F4_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR006620 (SMART): G3DSA:2.60.12	29,335	29,909	40,749	33,349	38,496									
Solyc04g081940	Photosystem I assembly protein Ycf3 (AHRD V3.3 --* YCF3_COFAR)						IPR008011 (PFAM): PTHR13166:SF4	4,173	4,543	3,750	3,069	3,384									
Solyc04g081950	LOW QUALITY:Di-glucose binding protein with Kinesin motor domain-containing protein (AHRD V3.3 --* AT1G72250.4)							0,000	0,043	0,000	0,050	0,000									
Solyc04g081955	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G20300.1)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	0,281	0,333	0,337	0,251	0,306									
Solyc04g081960	LOW QUALITY:Syringolide-induced protein 14-1-1 (AHRD V3.3 *** G7I8D2_MEDTR)						mobidb-lite (MOBIDB_LITE): IPR0387	7,293	17,329	2,507	1,206	2,443									
Solyc04g081970	Thioredoxin (AHRD V3.3 *** A0A103YDW7_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored			G3DSA:3.40.30.10 (GENE3D): IPR01	86,530	165,118	78,742	66,833	110,446	0,959	0,000	0,484	0,041			up	up	
Solyc04g081980	LOW QUALITY:F-Box protein, putative (AHRD V3.3 *-* Q6L3W3_SOLDE)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	2,830	3,100	2,676	2,490	2,071									
Solyc04g081990	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.1)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane; P:tra			IPR001958 (PRINTS): IPR011701 (PF	2,244	1,982	3,111	4,967	3,428									
Solyc04g082000	Phospholipase D (AHRD V3.3 *** K4BVS9_SOLLC)		F:GO:0004630; F:G(	F:phospholipase D	EC:3.1.4.4	Phospholipase D	IPR000008 (SMART): IPR001736 (SM	1,405	2,205	0,626	0,419	0,758									
Solyc04g082010	pre-plastocyanin		F:GO:0005507; F:G(	F:copper ion binding; F:electron transfer activity			IPR001235 (PRINTS): IPR002387 (PF	88,610	287,106	94,368	101,755	225,488	1,724	0,000	1,253	0,000			up	up	
Solyc04g082020	Zim17-type zinc finger protein (AHRD V3.3 *** A0A061FEP0_THECC)		F:GO:0008270	F:zinc ion binding			IPR007853 (PFAM): mobidb-lite (MOB	17,775	17,784	63,381	58,625	63,150									
Solyc04g082030	ornithine decarboxylase	odc	F:GO:0003824; P:G(	F:catalytic activity; P:polyamine biosynthetic process			IPR000183 (PRINTS): IPR002433 (PF	8,491	18,701	5,495	7,049	7,915	1,167	0,000					up		
Solyc04g082040	Mechanosensitive ion channel family protein (AHRD V3.3 *** AT2G17010.1)		C:GO:0016020; P:G(	C:membrane; P:transmembrane transport			IPR016688 (PIRSF): IPR006685 (PFA	23,933	34,518	5,772	6,043	8,704									
Solyc04g082050	Ganglioside-induced differentiation-associated protein 2 (AHRD V3.3 *** A0A199VGA4_ANACO)						IPR001251 (SMART): IPR036865 (G3	0,500	0,744	0,704	0,466	0,566									
Solyc04g082060	F-box domain, cyclin-like protein (AHRD V3.3 *** A0A103YDV2_CYNCS)						IPR005174 (PFAM): G3DSA:1.20.128	12,863	7,900	5,640	6,741	5,715									
Solyc04g082070	tRNA pseudouridine synthase (AHRD V3.3 *** B9H5D6_POPTR)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			G3DSA:3.30.70.580 (GENE3D): IPR0	13,266	17,000	14,504	13,576	15,516									
Solyc04g082090	Alpha-amylase (AHRD V3.3 *** K4BVT6_SOLLC)		F:GO:0004556; F:G(	F:alpha-amylase ac	EC:3.2.1.1	Alpha-amylase	IPR006046 (PRINTS): IPR006047 (SM	36,726	36,035	65,125	65,791	56,552									
Solyc04g082110	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9SR08_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			IPR005512 (PFAM): G3DSA:1.20.58.2	6,396	5,761	1,243	1,406	1,717									
Solyc04g082120	Prolyl oligopeptidase family protein (AHRD V3.3 *** AT1G76140.1)		F:GO:0004252; P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR002470 (PRINTS): IPR001375 (PF	6,146	4,967	21,028	24,924	15,537									
Solyc04g082130	Pseudouridine synthase family protein (AHRD V3.3 *** AT1G20410.1)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			G3DSA:3.30.70.2510 (GENE3D): G3D	16,329	13,754	13,447	10,312	12,194									
Solyc04g082140	pectinesterase		F:GO:0005507; F:G(	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	108,782	241,245	24,339	10,578	21,135	1,173	0,000			-1,202	0,041	up		down
Solyc04g082150	LOW QUALITY:MAP kinase 17 (AHRD V3.3 --* AT2G01450.4)							0,117	0,116	0,225	0,432	0,583									
Solyc04g082160	Ubiquitin family protein (AHRD V3.3 *** D7MTI3_ARALL)		F:GO:0005515	F:protein binding			IPR000626 (SMART): IPR000626 (PF	141,134	118,912	155,340	158,355	154,442									
Solyc04g082170	alcohol dehydrogenase		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): G3DS	0,077	0,039	0,022	0,025	0,069									
Solyc04g082180	alcohol dehydrogenase		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): IPR013154 (PFA	0,019	0,000	0,000	0,000	0,000									
Solyc04g082190	Neutral ceramidase (AHRD V3.3 *** A0A0B2S6C2_GLYSO)		C:GO:0005576; F:G(	C:extracellular regic	EC:3.5.1.23	Ceramidase	IPR038445 (G3DSA:2.60.40.GENE3D	0,000	0,018	0,000	0,000	0,000									
Solyc04g082200	LOW QUALITY:dehydrin	dhn	P:GO:0009415	P:response to water			IPR000167 (PFAM): mobidb-lite (MOB	716,546	1243,759	1148,732	1400,609	1083,979	0,821	0,023					up		
Solyc04g082210	NADH-ubiquinone oxidoreductase chain (AHRD V3.3 *** AT1G20460.1)		C:GO:0016021	C:integral component of membrane			PTHR34936 (PANTHER): PTHR34936	6,367	6,325	7,942	7,121	5,883									
Solyc04g082220	Amino acid transporter, putative (AHRD V3.3 *** B9R8J4_RICCO)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM): PTHR22950 (PAN	0,302	0,800	0,889	0,990	0,709									
Solyc04g082240	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** A0A072VS58_MEDTR)						IPR004320 (PFAM): PTHR33070 (PAN	0,037	0,000	0,022	0,025	0,023									
Solyc04g082250	FtsH-like protein precursor		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): IPR003959 (PF	52,888	89,776	114,781	120,280	165,177	0,790	0,001	0,523	0,001			up	up	
Solyc04g082260	Kinase family protein (AHRD V3.3 *** B9H1Q4_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:3.30.200.20 (GENE3D): IPR0	0,040	0,018	0,072	0,025	0,000									
Solyc04g082270	DUF241 domain protein (DUF241) (AHRD V3.3 *** AT1G76240.1)						IPR004320 (PFAM): PTHR33070 (PAN	0,661	0,611	0,394	0,700	0,349									
Solyc04g082280	At1g76250 (AHRD V3.3 *** Q8GX25_ARATH)		C:GO:0016020	C:membrane			PTHR35112 (PANTHER)	0,021	0,021	0,025	0,072	0,046									
Solyc04g082290	At1g76250 (AHRD V3.3 *-* Q8GX25_ARATH)						mobidb-lite (MOBIDB_LITE): PTHR341	17,002	20,025	6,288	6,824	6,965									
Solyc04g082300	Transducin/WD-like repeat-protein (AHRD V3.3 *** A0A072V4M1_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	30,979	27,731	25,950	24,284	24,834									
Solyc04g082310	TSA: Wollemia nobilis Ref_Wollemi_Transcript_29242_1275 transcribed RNA sequence (AHRD V3.3 *** A0A0C9S3G2_9SPER)						IPR008479 (PFAM): mobidb-lite (MOB	20,975	29,410	38,432	33,471	43,458									
Solyc04g082320	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7RNT7_CAPAN)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	6,470	4,634	6,500	6,562	6,053									
Solyc04g082330	pre-rRNA-processing TSR1-like protein (AHRD V3.3 *** AT1G42440.1)		C:GO:0005634; P:G(	C:nucleus; P:ribosome biogenesis			IPR012948 (SMART): IPR007034 (SM	42,968	43,172	42,947	43,532	38,144									
Solyc04g082340	Carboxypeptidase A6 (AHRD V3.3 *** W9RJ73_9ROSA)		F:GO:0004181; P:G(	F:metallocarboxype	EC:3.4.17	Acting on peptide bor	IPR000834 (SMART): G3DSA:3.40.63	17,679	18,321	16,611	18,178	14,153									
Solyc04g082360	F-box protein (AHRD V3.3 *-* E7CQS0_BRARP)						IPR005174 (PFAM): PTHR44259 (PAN	4,384	4,264	7,140	6,682	7,427									
Solyc04g082370	LOW QUALITY:Kinase interacting (KIP1-like) family protein (AHRD V3.3 --* AT5G58320.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc04g082380	BnaA03g07530D protein (AHRD V3.3 *** A0A078DI26_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,029	1,366	0,612	0,594	0,377									
Solyc04g082390	Dolichol-phosphate mannosyltransferase, putative (AHRD V3.3 *** B9R8M8_RICCO)		F:GO:0016740	F:transferase activity			IPR001173 (PFAM): IPR029044 (G3D	16,950	14,999	25,365	26,988	22,844									
Solyc04g082400	Starch branching enzyme (AHRD V3.3 *** A0A0F7R6Z9_AMAHP)	SBE2	F:GO:0003844; F:G(	F:1,4-alpha-glucan I	EC:2.4.1.18	1,4-alpha-glucan brar	IPR006047 (SMART): G3DSA:3.20.20	80,735	78,438	165,069	148,610	167,019									
Solyc04g082420	BTB/POZ domain-containing protein (AHRD V3.3 *** AT2G30600.6)		F:GO:0005515	F:protein binding			IPR000210 (SMART): IPR000210 (PF	129,459	89,735	140,243	170,158	182,371									

Solyc04g082430	cyclinB2_4	CycB2_4	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	0,446	0,633	0,069	0,025	0,023									
Solyc04g082440	U-box domain-containing 15-like protein (AHRD V3.3 *** A0A0B0PZ68_GOSAR)		F:GO:0004842; F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:cell			IPR000225 (SMART): IPR003613 (SM	0,000	0,059	0,025	0,000	0,000									
Solyc04g082450	integral membrane hemolysin-III-like protein (AHRD V3.3 *-* AT2G45250.1)		P:GO:0006351; C:GC	P:transcription, DNA-templated; C:DRM complex			IPR018737 (PFAM): mobidb-lite (MOB	0,814	1,262	3,524	3,564	2,942									
Solyc04g082460	Catalase 3		F:GO:0004096; P:GC	F:catalase activity;	EC:1.11.1.7; EC:1.1	Peroxidase; Catalase	IPR018028 (PRINTS): IPR011614 (SM	53,016	58,728	293,060	307,692	263,859									
Solyc04g082470	WD40 repeat protein (AHRD V3.3 *** Q1JV04_IPOPU)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	28,510	29,702	41,440	39,513	39,288									
Solyc04g082480	Plant regulator RWP-RK family protein, putative (AHRD V3.3 *** A0A061FD78_THECC)		F:GO:0005515	F:protein binding			IPR000270 (SMAF Nin-like	20,410	18,230	7,553	8,904	11,321			0,579	0,048				up	
Solyc04g082490	Niemann-Pick C1 (AHRD V3.3 *** A0A0B0MTA5_GOSAR)		F:GO:0005319; C:GC	F:lipid transporter activity; C:integral component of membrane			IPR032190 (PFAM): IPR004765 (TIGF	25,996	23,184	14,243	13,522	17,275									
Solyc04g082500	Kinase family protein (AHRD V3.3 *** U5GGQ9_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PIRS	18,318	22,225	6,691	14,825	10,228					1,147	0,000			up
Solyc04g082510	Protein kinase (AHRD V3.3 *** S8D6E4_9LAMI)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	12,613	12,739	73,633	81,306	66,336									
Solyc04g082520	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT4G37420.1)	cwp1	C:GO:0016021; F:GC	C:integral component of membrane; F:transferase activity			IPR008166 (PFAM): PTHR21461 (PAN	0,042	0,271	0,000	0,000	0,023									
Solyc04g082530	Bromodomain-containing protein (AHRD V3.3 *** A0A118K301_CYNCS)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR001487 (SM	9,895	9,837	4,107	6,785	6,657			0,692	0,032	0,721	0,043		up	up
Solyc04g082560	Calcium-binding EF hand family protein (AHRD V3.3 *** B9GPR9_POPTR)		F:GO:0005509; F:GC	F:calcium ion binding; F:protein binding			IPR000261 (SMART): IPR002048 (SM	118,243	106,236	98,818	98,087	101,460									
Solyc04g082565	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT5G43822.1)						IPR029159 (PFAM): IPR038985 (PAN	1,007	1,131	1,247	1,280	1,537									
Solyc04g082570	U-box domain-containing protein 43 (AHRD V3.3 *** A0A0B2RGT2_GLYSO)		F:GO:0004842; F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR000225 (SMART): IPR003613 (SM	0,260	0,425	0,738	0,673	0,541									
Solyc04g082580	F-box/kelch-repeat protein (AHRD V3.3 *** W9RJ33_9ROSA)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR001810 (SM	12,502	8,454	7,031	6,889	6,499									
Solyc04g082590	Protein canopy-1 (AHRD V3.3 *** A0A199UU79_ANACO)		C:GO:0005783; C:GC	C:endoplasmic reticulum; C:integral component of membrane			IPR021852 (PFAM): PTHR31775 (PAN	4,390	4,186	4,774	7,602	6,010					0,676	0,017			up
Solyc04g082600	Protein phosphatase 2C family protein (AHRD V3.3 *** AT2G33700.1)		F:GO:0004722; P:GC	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	7,669	6,050	8,369	9,814	8,528									
Solyc04g082610	glutamate receptor like 3.3	GLR3_3	F:GO:0004970; C:GC	F:ionotropic glutamate receptor activity; C:membrane			PR01176 (PRINTS): IPR001320 (SMA	4,051	2,961	2,344	2,399	2,186									
Solyc04g082620	Kinase, putative (AHRD V3.3 *** B9S6W8_RICCO)		F:GO:0004540; F:GC	F:ribonuclease activity; F:protein kinase activity; F:protein bindi			IPR018997 (SMART): IPR000719 (SM	2,079	1,532	1,817	2,032	2,141									
Solyc04g082630	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4BVZ0_SOLLC)		P:GO:0006006; F:GC	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR020828 (SM	274,238	612,114	137,968	196,296	399,930	1,185	0,000	1,532	0,000			up	up	
Solyc04g082640	Chloroplast inner membrane localized protein (AHRD V3.3 *** Q9C7S3_ARATH)		C:GO:0005739; C:GC	C:mitochondrion; C:chloroplast thylakoid membrane; C:chloropla			mobidb-lite (MOBIDB_LITE): IPR0403	68,536	75,745	74,428	72,893	78,139									
Solyc04g082650	S-acyltransferase (AHRD V3.3 *** K4BVZ2_SOLLC)		C:GO:0005783; C:GC	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	6,819	7,052	8,325	8,039	7,434									
Solyc04g082670	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (AHRD V3.3 *** K4BVZ4_SOLLC)		F:GO:0004579; C:GC	F:dolichyl-diphosph	EC:2.4.1.119	Glycosyltransferases	IPR007676 (PFAM): G3DSA:3.10.50.4	88,892	86,028	102,157	89,206	89,401									
Solyc04g082680	outer envelope pore-like protein (AHRD V3.3 *** AT1G20816.1)		F:GO:0008308; P:GC	F:voltage-gated anion channel activity; P:regulation of anion tra			IPR034575 (PANTHER)	22,780	23,984	25,528	30,694	28,333									
Solyc04g082700	Tonoplast monosaccharide transporter 2	TMT2	C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	52,334	46,176	95,759	91,478	82,018									
Solyc04g082720	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT1G76440.3)		C:GO:0005634; P:GC	C:nucleus; P:positive regulation of DNA demethylation			IPR008978 (G3DSA:2.60.40.GENE3D	20,007	18,575	42,302	41,621	43,411									
Solyc04g082725	zinc finger C3H1 domain protein (AHRD V3.3 --* AT2G39580.2)							0,398	0,260	0,726	0,659	0,759									
Solyc04g082730	HSP20-like chaperones superfamily protein (AHRD V3.3 --* AT1G54850.1)							0,195	0,333	0,137	0,075	0,212									
Solyc04g082740	HSP20-like chaperones superfamily protein (AHRD V3.3 *-* AT1G20870.2)						IPR008978 (G3DSA:2.60.40.GENE3D	3,563	4,464	3,137	2,139	3,815									
Solyc04g082745	DNA-BINDING TRANSCRIPTION FACTOR 2 (AHRD V3.3 --* AT3G18380.3)							0,142	0,220	0,236	0,164	0,282									
Solyc04g082750	3-beta-hydroxy-delta5-steroid dehydrogenase (AHRD V3.3 *** K7WNV1_SOLTU)		F:GO:0003854; P:GC	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	IPR028110 (PFAM): IPR002225 (PFA	9,657	8,634	2,183	1,265	2,043									
Solyc04g082760	SWI/SNF complex subunit SWI3B (AHRD V3.3 *** A0A0B0ME09_GOSAR)		F:GO:0003677; F:GC	F:DNA binding; F:protein binding			IPR001005 (SMART): IPR036388 (G3	24,364	25,787	45,972	45,604	41,629									
Solyc04g082770	RNA-binding protein 24 (AHRD V3.3 *** A0A0B2RNP8_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	53,952	50,066	85,221	81,535	79,954									
Solyc04g082780	Cinnamoyl-CoA reductase family protein (AHRD V3.3 *** B9GPN4_POPTR)	CCR	F:GO:0003824; F:GC	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0	151,384	152,023	235,720	202,819	258,957									
Solyc04g082790	RNA helicase DEAD16	DEAD16	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART): IPR014001 (SM	58,645	59,145	78,243	76,757	74,112									
Solyc04g082800	subtilisin-like protease (AHRD V3.3 *** AT2G33585.1)		C:GO:0005739; C:GC	C:mitochondrion; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR372	10,695	10,840	15,991	12,926	13,379									
Solyc04g082810	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A0K9NWT4_ZOSMR)		F:GO:0003680	F:AT DNA binding			IPR014476 (PIRSF): G3DSA:3.30.133	3,295	3,473	5,998	6,254	5,009									
Solyc04g082825	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** AT1G76510.3)		F:GO:0003677	F:DNA binding			IPR001606 (SMART): IPR036431 (G3	14,288	13,728	27,047	28,324	26,363									
Solyc04g082830	Auxin efflux carrier family protein, putative (AHRD V3.3 *** A0A061FMX0_THECC)		C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): PTHR31651:SF6	12,916	15,541	42,403	47,947	37,265									
Solyc04g082840	B2-type cyclin dependent kinase	cdkb2	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,814	2,255	0,246	0,167	0,283									
Solyc04g082845	FAR1-related sequence 5 (AHRD V3.3 *** AT4G38180.1)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMART): IPR018289 (PF	3,529	2,777	2,943	3,960	3,893									
Solyc04g082860	Glycosyltransferase (AHRD V3.3 *** K4BW12_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR0	0,420	0,417	1,205	1,569	1,271									
Solyc04g082870	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103IBH5_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (TIGF	1,846	2,440	1,891	1,669	1,693									
Solyc04g082880	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (AHRD V3.3 *** PFPA_SOLTU)		F:GO:0003872; F:GC	F:6-phosphofructok	EC:2.7.1.9; EC:2.7.1	Diphosphate--fructos	IPR011183 (PIRSF): G3DSA:3.40.50.	124,211	116,045	182,289	166,045	193,748									
Solyc04g082890	BZIP transcription factor protein (AHRD V3.3 *** B2CM16_SOLCH)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	218,877	216,078	189,046	216,218	188,653									
Solyc04g082900	BUB1-related (AHRD V3.3 *** A0A061FST1_THECC)		F:GO:0005515; P:GC	F:protein binding; P:mitotic spindle assembly checkpoint			IPR013212 (SMART): G3DSA:1.25.40	4,907	6,860	11,303	20,255	11,509					0,844	0,000			up
Solyc04g082910	CP12 domain-containing family protein (AHRD V3.3 *-* B9GPM1_POPTR)		C:GO:0009507; C:GC	C:chloroplast; C:protein-containing complex; P:cellular response			IPR003823 (PFAM): IPR039314 (PAN	14,999	12,834	9,951	9,419	8,505									
Solyc04g082920	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *-* K4BW18_SOLLC)		P:GO:0009765; C:GC	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR029472 (PFA	0,844	0,889	1,072	1,049	1,624									
Solyc04g082930	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1ALX2_SOLTU)		P:GO:0009765; C:GC	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	7,492	11,138	13,563	12,994	18,485									
Solyc04g082940	Cysteine/histidine-rich C1 domain protein (AHRD V3.3 *** G7IA18_MEDTR)						IPR004146 (PFAM): mobidb-lite (MOB	2,649	2,308	4,514	5,236	4,577									
Solyc04g082950	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT2G33570.1)		C:GO:0016021; F:GC	C:integral component of membrane; F:transferase activity, trans			IPR008166 (PFAM): PTHR21461:SF2	9,799	6,858	4,824	5,878	4,383									
Solyc04g082970	electron protein, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT1G43020.1)						IPR025757 (PFAM): IPR006869 (PFA	106,548	39,422	15,805	47,698	16,470	-1,410	0,000			1,594	0,000	down		up
Solyc04g082980	Tetratricopeptide repeat-containing protein (AHRD V3.3 *** D7KTV6_ARALL)		F:GO:0005515; P:GC	F:protein binding; P:RNA catabolic process; C:Ski complex			IPR019734 (SMART): IPR019734 (PF	35,099	36,988	41,908	51,864	50,220									
Solyc04g082990	Tetratricopeptide repeat protein 37 (AHRD V3.3 *-* A0A1D1Y0Z0_9ARAE)		P:GO:0016441; C:GC	P:posttranscriptional gene silencing; C:Ski complex; P:nuclear-t			PTHR34890 (PANTHER)	3,577	3,167	4,813	5,489	4,533									
Solyc04g083000	translocon at the outer envelope membrane of chloroplasts 33 (AHRD V3.3 --* AT1G02280.2)							0,080	0,151	0,090	0,165	0,093									
Solyc04g083010	ABC1-like kinase 3		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM): PTHR10566 (PAN	45,757	54,754	97,324	96,054	120,184									
Solyc04g083140	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,125	1,074	3,752	4,473	7,095									
Solyc04g083150	Cytochrome P450 (AHRD V3.3 *** Q75W19_PANGI)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	12,363	7,716	31,165	29,709	26,407									
Solyc04g083160	Cytochrome P450 (AHRD V3.3 *** A0A0B0P5Q7_GOSAR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	4,861	5,185	0,450	0,486	0,568									
Solyc05g005000	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G10740.4)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	37,635	20,650	8,842	11,315	13,442	-0,840	0,003					down		
Solyc05g005010	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)		C:GO:0016021	C:integral component of membrane			IPR025521 (PFAM): IPR004314 (PFA	2,090	2,663	0,149	0,479	0,354									
Solyc05g005020	Alpha-Glucan Water Dikinase		F:GO:0005524; F:GC	F:ATP binding; F:kinase activity; P:phosphorylation			G3DSA:3.30.470.20 (GENE3D): IPR0	333,741	358,082	425,645	415,947	465,556									
Solyc05g005050	Cysteine-rich receptor-like protein kinase 3 (AHRD V3.3 *-* W9RKP8_9ROSA)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR038408 (G3DSA:3.30.430.GENE3	0,040	0,000	0,000	0,050	0,094									
Solyc05g005060	Kinase, putative (AHRD V3.3 *** B9SPH8_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001245 (PF	0,061	0,226	0,046	0,022	0,165									
Solyc05g005070	Kinase family protein (AHRD V3.3 *** B9HTV7_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	21,684	25,694	3,716	4,651	8,229									
Solyc05g005080	Endo-1,4-beta-glucanase		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012341 (G3DSA:1.50.10.GENE3D	1035,938	842,048	35,495	13,228	29,902					-1,422	0,000			down
Solyc05g005090	Knotted-1 homeobox protein (AHRD V3.3 *** R9R650_9FABA)	tkn3	F:GO:0003677; C:GC	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR005539 (SMAF TALE	0,038	0,078	0,091	0,096	0,048									
Solyc05g005100	Trichome birefringence (AHRD V3.3 *** A0A0K9NN56_ZOSMR)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	25,472	24,210	26,927	24,355	24,933									
Solyc05g005120	F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYNCS)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR006527 (PF	5,317	4,805	11,561	9,489	8,506									
Solyc05g005125	Protein kinase (AHRD V3.3 *-* J9ZZR7_PRUPE)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	1,093	1,225	1,238	1,384	1,324									
Solyc05g005130	Disease resistance protein, putative (AHRD V3.3 *** Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	12,449	10,332	13,015	20,646	15,352					0,665	0,001			up
Solyc05g005140	Leucine-rich repeat receptor-like kinase (AHRD V3.3 *** Q75UP2_IPOBA)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR013210 (PF	8,362	5,068	0,501	0,261	0,398									
Solyc05g005150	Kelch repeat-containing F-box family protein, putative (AHRD V3.3 *** A0A061E7C3_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR015915 (G3	20,941	17,612	3,760	4,473	4,407									
Solyc05g005160	ATP-citrate synthase, putative (AHRD V3.3 *** B9SHC9_RICCO)		F:GO:0005524	F:ATP binding			IPR013650 (PFAM): IPR032263 (PFA	152,116	123,648	64,163	45,881	54,295					-0,481	0,035			down
Solyc05g005170	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A061E6B2_THECC)	PG9	F:GO:0004650; P:GC	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	1,016	2,880	0,675	0,045	0,073									
Solyc05g005180	enoyl-CoA hydratase/isomerase D (AHRD V3.3 *** AT1G60550.1)		F:GO:0008935; P:GC	F:1,4-dihydroxy-2-n	EC:4.1.3.36	1,4-dihydroxy-2-naph	IPR001753 (PFAM): G3DSA:3.90.226	9,790	24,050	5,183	7,725	12,407	1,324	0,000	1,248	0,000			up	up	
Solyc05g005190	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00178 (SMA	218,587	245,097	180,493	158,045	160,166									
Solyc05g005200	Pyrrolidone-carboxylate peptidase (AHRD V3.3 *** W9S1N9_9ROSA)		C:GO:0005829; P:GC	C:cytosol; P:proteol	EC:3.4.19	Acting on peptide bor	IPR000816 (PIRSF): IPR036440 (G3D	41,030	65,651	82,845	86,445	69,969									
Solyc05g005210	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT1G10650.1)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			PF13920 (PFAM): IPR013083 (G3DSA	7,463	9,990	15,788	16,961	13,746									
Solyc05g005230	Plant protein 1589 of Uncharacterized protein function (AHRD V3.3 *** A0A061EE06_THECC)						IPR006476 (PFAM): IPR006476 (TIGF	0,000	0,019	0,000	0,045	0,188									
Solyc05g005240	YABBY gene	INO	P:GO:0007275	P:multicellular organism development			IPR036910 (G3DS YABBY	0,000	0,000	0,100	0,119	0,024									
Solyc05g005250	pantothenate kinase family protein AB211526		F:GO:0004594; F:GC	F:pantothenate kina	EC:2.7.1.33	Pantothenate kinase	IPR004567 (PFAM): G3DSA:3.30.420	28,135	25,495	69,509	67,639	62,741									
Solyc05g005260	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TG49_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid			IPR012442 (PFAM): IPR013103 (PFA	113,251	56,516	22,857	43,210	28,305	-0,977	0,000			0,921	0,000	down		up
Solyc05g005280	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4BW59_SOLLC)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylti	IPR022003 (PFAM): G3DSA:3.90.228	0,101	1,048	2,933	3,860	5,114									
Solyc05g005290	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4BW60_SOLLC)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylti	IPR012317 (PFAM): G3DSA:3.90.228	12,610	33,773	12,775	29,587	21,978	1,444	0,002			1,211	0,000	up		up
Solyc05g005300	LOW QUALITY:bHLH transcription factor 084		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,118	0,386	0,093	0,097	0,094									
Solyc05g005310	NEDD8-specific protease 1 (AHRD V3.3 *** W9SIH8_9ROSA)		P:GO:0006508; F:GC	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM): G3DSA:3.40.395	6,370	5,586	9,005	9,873	8,799									
Solyc05g005320	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7K1C9_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,505	5,713	3,004	3,195	2,497									
Solyc05g005330	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	12,745	15,097	5,763	5,826	10,134			0,803	0,006				up	
Solyc05g005337	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM): IPR009072 (G3D	0,179	0,848	0,319	0,368	0,472									
Solyc05g005340	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT5G63930.2)							0,075	0,043	0,025	0,047	0,023									
Solyc05g005350	Transcription factor (AHRD V3.3 *** A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YB	6,165	5,181	0,075	0,303	0,000									
Solyc05g005360	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YB	2,836	2,441	0,025	0,125	0,023									
Solyc05g005370	Transcription factor (AHRD V3.3 *** A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YB	3,335	2,760	0,025	0,177	0,000									
Solyc05g005380	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	8,226	4,954	0,000	0,150	0,000									
Solyc05g005385	RNA recognition motif (RRM)-containing protein (AHRD V3.3 --* AT5G10800.3)							0,019	0,041	0,000	0,000	0,000									
Solyc05g005390	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	1,465	1,232	0,000	0,000	0,000									
Solyc05g005440	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	4,699	2,793	0,000	0,000	0,023									
Solyc05g005450	LOW QUALITY:Protein SUPPRESSOR OF GENE SILENCING 3 (AHRD V3.3 *-* SGS3_SOLLC)		P:GO:0031047	P:gene silencing by RNA			IPR005381 (PFAM): IPR005380 (PFA	0,058	0,039	0,000	0,000	0,024									
Solyc05g005460	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT2G44370.1)		P:GO:0045454	P:cell redox homeostasis			IPR004146 (PFAM): IPR012336 (PFA	36,135	105,437	24,538	36,317	30,503	1,572	0,000			0,568	0,001	up		up
Solyc05g005470	Nucleoredoxin 1		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D): IPR00	0,061	0,082	0,025	0,025	0,023									
Solyc05g005480	Quinone oxidoreductase-like protein (AHRD V3.3 *** W9RNB1_9ROSA)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.40.50	76,216	111,613	197,853	195,370	330,586			0,738	0,000				up	
Solyc05g005490	carbonic anhydrase	ca1	F:GO:0004089; F:GC	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001765 (SMART): IPR036874 (G3	73,999	86,168	612,308	691,723	591,024									
Solyc05g005510	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103XVT7_CYNCS)						G3DSA:2.40.50.140 (GENE3D): PTHF	28,316	28,176	62,219	60,632	55,754									
Solyc05g005520	LOW QUALITY:Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NN67_ZOSMR)		F:GO:0004864; P:GC	F:protein phosphatase inhibitor activity; P:regulation of signal tr			IPR007062 (PFAM): mobidb-lite (MOB	0,080	0,177	1,112	1,418	1,400									
Solyc05g005540	Polygalacturonase non-catalytic subunit AroGP3 (AHRD V3.3 *** GP3_SOLLC)		C:GO:0005618; P:GC	C:cell wall; P:fruit ripening; C:apoplast; P:cell wall organization			IPR004873 (SMART): IPR004873 (PF	5,731	2,867	0,294	0,175	0,234	-0,962	0,032					down		
Solyc05g005550	Polygalacturonase non-catalytic subunit AroGP2 (AHRD V3.3 *** GP2_SOLLC)		C:GO:0005618; P:GC	C:cell wall; P:fruit ripening; C:apoplast; P:cell wall organization			IPR004873 (SMART): IPR004873 (PF	1002,031	474,796	16,136	7,138	14,133	-1,048	0,000			-1,175	0,000	down		down
Solyc05g005560	polygalacturonase isoenzyme 1 beta subunit	TOMPOLBETA	C:GO:0005618; P:GC	C:cell wall; P:fruit ripening; C:apoplast; P:cell wall organization			IPR004873 (SMART): IPR004873 (PF	4277,221	2331,035	229,974	112,084	240,999	-0,848	0,000			-1,035	0,007	down		down
Solyc05g005570	BURP domain-containing protein (Fragment) (AHRD V1 *--- Q94IC5_9ROSI)		C:GO:0005576	C:extracellular region			IPR004873 (SMART): IPR004873 (PF	13,634	12,969	1,120	0,359	1,569									
Solyc05g005580	DUF936 family protein (AHRD V3.3 *** G7K1E3_MEDTR)						IPR010341 (PFAM): mobidb-lite (MOB	0,197	0,241	0,119	0,241	0,188									
Solyc05g005590	Ribosomal RNA large subunit methyltransferase N (AHRD V3.3 *** A0A0B0PAE8_GOSAR)		F:GO:0008173; P:GC	F:RNA methyltransferase activity; P:tRNA methylation; F:iron-su			IPR013785 (G3DSA:3.20.20.GENE3D	11,359	13,424	21,537	20,551	22,869									
Solyc05g005610	HD domain-containing metal-dependent phosphohydrolase family protein (AHRD V3.3 *** AT5G40270.1)		F:GO:0016787	F:hydrolase activity			IPR003607 (SMART): IPR006674 (PF	1,799	0,958	2,738	2,251	3,177									
Solyc05g005620	RNA-binding 25 (AHRD V3.3 *** A0A0B0MSI7_GOSAR)		F:GO:0003676; P:GC	F:nucleic acid binding; P:mRNA processing			PR01217 (PRINTS): IPR002483 (SMA	189,974	169,565	143,619	149,820	155,297									
Solyc05g005630	Ubiquitin-like-specific protease 1D (AHRD V3.3 *** A0A0B2R587_GLYSO)		P:GO:0006508; F:GC	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:1.10.418.20 (GENE3D): IPR0	16,675	12,490	21,678	21,105	20,914									
Solyc05g005640	methyl-CPG-binding domain 9 (AHRD V3.3 *** AT3G01460.1)		F:GO:0005515	F:protein binding			IPR001965 (SMART): IPR019787 (PF	47,130	49,515	53,202	48,639	50,629									
Solyc05g005650	Methyl-CpG-binding domain-containing protein 9 (AHRD V3.3 *-* A0A1D1Y1M1_9ARAE)		C:GO:0005634	C:nucleus			mobidb-lite (MOBIDB_LITE): PTHR141	18,059	16,230	14,995	15,285	15,276									
Solyc05g005670	U-box domain-containing protein 18 (AHRD V3.3 *** W9RKZ7_9ROSA)		F:GO:0004842; F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR000225 (SMART): IPR003613 (SM	0,730	0,710	0,321	0,025	0,046									
Solyc05g005680	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4BW96_SOLLC)		F:GO:0004553; C:GC	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xylogluco	IPR016455 (PIRSF): IPR000757 (PFA	0,180	0,080	0,783	1,893	1,262					1,279	0,031			up
Solyc05g005685	RNA-binding CRS1 / YhbY (CRM) domain protein (AHRD V3.3 --* AT3G25440.2)							0,040	0,116	0,022	0,050	0,046									
Solyc05g005690	Ribosomal protein S9, putative (AHRD V3.3 *** B9RYF4_RICCO)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014721 (G3DSA:3.30.230.GENE3	81,798	95,917	40,975	35,358	39,538									
Solyc05g005700	aldehyde dehydrogenase family 2 member B7d		F:GO:0016620; P:GC	F:oxidoreductase activity, acting on the aldehyde or oxo group			IPR016163 (G3DSA:3.40.309.GENE3	238,497	155,621	136,755	107,029	136,736									
Solyc05g005710	spermidine synthase	spdsyn	F:GO:0003824; P:GC	F:catalytic activity; P:polyamine metabolic process			IPR030668 (PIRSF): PF01564 (PFAM	358,641	244,626	337,286	260,380	294,056					-0,370	0,027			down
Solyc05g005720	Potassium transporter family protein (AHRD V3.3 *** AT1G60160.1)		F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): IPR003855 (TIGF	112,520	90,831	132,586	134,179	125,040									
Solyc05g005730	RRP15-like protein (AHRD V3.3 *** A0A0B2SG91_GLYSO)		P:GO:0006364	P:rRNA processing			IPR012459 (PFAM): mobidb-lite (MOB	40,986	37,081	32,949	33,471	34,600									
Solyc05g005735	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT4G01130.3)							2,013	2,225	2,246	1,601	1,785									
Solyc05g005740	Potassium transporter (AHRD V3.3 *** M0ZY66_SOLTU)		F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): IPR003855 (TIGF	3,274	4,356	1,115	1,022	1,483									
Solyc05g005750	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S4L7_RICCO)		F:GO:0003824; P:GC	F:catalytic activity; P:trehalose biosynthetic process			IPR003337 (TIGRFAM): IPR023214 ((	53,829	55,839	54,234	63,230	72,125			0,409	0,029				up	
Solyc05g005755	kinesin 3 (AHRD V3.3 --* AT5G54670.3)							0,019	0,043	0,025	0,047	0,000									
Solyc05g005760	NHL repeat-containing family protein (AHRD V3.3 *** B9HJT0_POPTR)		F:GO:0005515	F:protein binding			IPR011042 (G3DSA:2.120.10.GENE3	46,578	35,209	4,208	3,938	4,385									
Solyc05g005770	NHL repeat-containing protein (AHRD V3.3 *** D7KNK1_ARALL)		F:GO:0005515	F:protein binding			IPR011042 (G3DSA:2.120.10.GENE3	14,180	12,618	15,322	16,440	14,273									
Solyc05g005780	AP-1 complex subunit gamma-2 (AHRD V3.3 *** AP1G2_ARATH)		P:GO:0006886; P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR008152 (SMART): IPR011989 (G3	92,436	87,642	90,291	98,025	88,383									
Solyc05g005790	Ring finger protein, putative (AHRD V3.3 *** B9S4M2_RICCO)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	5,261	2,835	5,512	7,474	6,401									
Solyc05g005800	Threonyl-tRNA synthetase (AHRD V3.3 *** AT5G26830.1)		F:GO:0004829; F:GC	F:threonine-tRNA lic	EC:6.1.1.3	Threonine--tRNA liga	IPR002320 (PRINTS): IPR012947 (SM	100,411	95,812	120,838	113,398	120,442									
Solyc05g005810	Serine/threonine-protein kinase WNK-related (AHRD V3.3 *** A0A061E6Z5_THECC)						IPR025610 (PFAM): PTHR13902 (PAN	2,574	2,358	1,326	1,213	1,316									
Solyc05g005820	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** M0ZYA4_SOLTU)		P:GO:0006006; F:GC	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR020828 (SM	0,019	0,041	0,000	0,022	0,096									
Solyc05g005830	WAT1-related protein (AHRD V3.3 *** K4BWB0_SOLLC)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	0,019	0,019	0,022	0,000	0,024									
Solyc05g005840	WAT1-related protein (AHRD V3.3 *** K4BWB1_SOLLC)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			PTHR31218:SF71 (PANTHER): IPR03	0,236	0,275	0,000	0,050	0,023									
Solyc05g005850	WAT1-related protein (AHRD V3.3 *** K4BWB2_SOLLC)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF3	0,021	0,000	0,000	0,000	0,000									
Solyc05g005860	WAT1-related protein (AHRD V3.3 *** K4BWB3_SOLLC)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	5,409	6,069	5,412	7,196	8,483									
Solyc05g005865	Major latex-like protein (AHRD V3.3 *** D2D328_GOSHI)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (SM	10,384	19,642	0,442	2,092	0,000									
Solyc05g005870	nodulin-related MtN21 family protein		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	0,061	0,000	0,000	0,000	0,000									

Solyc05g005873	Ribosomal protein S13 (AHRD V3.3 *** A0A118K2Q9_CYNCS)		F:GO:0003723; F:G	F:RNA binding; F:structural constituent of ribosome; C:ribosome			G3DSA:1.10.8.50 (GENE3D): IPR019		13,522	21,668	17,339	19,396	27,323			0,654	0,000				up	
Solyc05g005877	Protein kinase family protein (AHRD V3.3 *** B2D2G8_BRAOL)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200		0,038	0,083	0,000	0,050	0,048									
Solyc05g005900	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT1G24040.3)						IPR000182 (PFAM): G3DSA:3.40.630		4,070	3,699	3,003	3,388	4,002									
Solyc05g005910	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR		0,493	0,548	0,650	1,742	0,661					1,412	0,003			up
Solyc05g005915	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): IPR000109 (PAN		3,379	1,209	18,014	39,554	15,207	-1,443	0,040			1,133	0,000	down		up
Solyc05g005920	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): IPR000109 (PAN		32,674	30,654	13,268	8,487	11,250									
Solyc05g005930	Glycosyltransferase (AHRD V3.3 *** K4BWC0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR		6,768	11,291	3,209	2,075	3,494	0,765	0,040					up		
Solyc05g005935	Molybdopterin synthase catalytic subunit (AHRD V3.3 --* MOC2B_ORYSI)						mobidb-lite (MOBIDB_LITE)		0,042	0,018	0,000	0,000	0,000									
Solyc05g005940	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR		5,557	2,700	3,936	1,733	3,047					-1,169	0,001			down
Solyc05g005950	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): IPR000109 (PAN		1,240	0,633	0,244	0,092	0,309									
Solyc05g005960	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR		43,263	33,987	8,529	4,898	8,961					-0,800	0,032			down
Solyc05g005970	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125		0,059	0,039	0,000	0,000	0,000									
Solyc05g005980	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125		0,244	0,430	0,025	0,069	0,046									
Solyc05g005990	Major facilitator superfamily protein (AHRD V3.3 *-* AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125		0,346	0,542	0,428	0,730	0,660									
Solyc05g006000	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): PTHR11654:SF1		2,026	1,469	0,386	0,315	0,424									
Solyc05g006010	Major facilitator superfamily protein (AHRD V3.3 *-* AT1G52190.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125		3,515	3,141	3,280	3,689	3,324									
Solyc05g006020	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR006043 (PFAM): PTHR11119 (PAN		2,760	2,968	0,076	0,148	0,188									
Solyc05g006030	D-ribose-binding periplasmic protein (AHRD V3.3 *** AT1G60010.1)						IPR025322 (PFAM): mobidb-lite (MOB		33,009	27,290	20,531	38,386	26,271					0,905	0,000			up
Solyc05g006040	Serine/Threonine-kinase (AHRD V3.3 *-* AT1G10522.2)		P:GO:0010468	P:regulation of gene expression			PTHR35987:SF1 (PANTHER): IPR039		1,035	0,768	0,509	0,890	0,544									
Solyc05g006050	cyclinD1_1	CycD1_1	C:GO:0005634	C:nucleus			IPR013763 (SMART): IPR004367 (SM		8,177	7,682	2,495	2,079	3,313									
Solyc05g006070	RNA-binding family protein, putative isoform 1 (AHRD V3.3 *** A0A061E6U3_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D		4,404	7,320	11,205	10,531	12,053									
Solyc05g006080	Oligosaccharyltransferase complex/magnesium transporter family protein (AHRD V3.3 *** AT4G29870.1)		C:GO:0008250; C:G	C:oligosaccharyltransferase complex; C:integral component of r			IPR021149 (PFAM): mobidb-lite (MOB		37,198	42,936	45,029	45,413	43,988									
Solyc05g006090	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:G	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM): IPR036397 (G3D		0,711	0,836	1,308	1,260	1,323									
Solyc05g006100	RNase H family protein (AHRD V3.3 *** AT1G24090.1)		F:GO:0003676; F:G	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM): IPR007263 (PFA		9,140	8,212	12,154	10,294	10,107									
Solyc05g006120	DNA polymerase lambda (AHRD V3.3 *** DPOLL_ARATH)		F:GO:0003677; F:G	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA po	IPR002008 (PRINTS): IPR022312 (PF		4,430	9,756	7,113	6,201	9,931	1,161	0,005					up		
Solyc05g006130	RNA helicase DEAD17	DEAD17	F:GO:0003676; F:G	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM		7,026	8,053	7,028	6,928	7,646									
Solyc05g006160	Gibberellin-regulated family protein (AHRD V3.3 *** G7LER1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR003854 (PFAM): PTHR23201:SF1		1,400	1,324	0,591	0,877	0,352									
Solyc05g006170	Lycopersicon esculentum Chloroplast Envelope Protein 1		F:GO:0005515	F:protein binding			SM00368 (SMART): IPR032675 (G3D		75,219	76,773	107,837	97,456	115,071									
Solyc05g006200	tRNA (guanine(37)-N1)-methyltransferase (AHRD V3.3 *** K4BWE7_SOLLC)		F:GO:0009019; P:G	F:tRNA (guanine-N1-)-methyltransferase activity; P:tRNA methy			G3DSA:3.30.300.110 (GENE3D): G3D		19,496	17,629	22,488	22,650	23,699									
Solyc05g006210	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RPA4_RICCO)		F:GO:0004553; P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): G3DSA:3.20.20		0,877	1,077	0,290	0,570	0,543									
Solyc05g006215	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103XVT7_CYNCS)						G3DSA:2.40.50.140 (GENE3D): PTHR		18,017	18,852	18,332	19,189	17,271									
Solyc05g006220	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9S2J7_RICCO)		F:GO:0016787	F:hydrolase activity			IPR017439 (PIRSF): IPR011650 (PFA		4,500	19,973	0,996	0,440	1,102	2,175	0,000					up		
Solyc05g006230	Peroxidase (AHRD V3.3 *** K4BWF0_SOLLC)		F:GO:0004601; P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF		0,061	0,000	0,022	0,000	0,023									
Solyc05g006240	Chaperone DnaJ domain protein (AHRD V3.3 *** G7K481_MEDTR)						IPR001623 (PRINTS): IPR001623 (SM		41,821	35,818	34,421	37,026	35,484									
Solyc05g006310	Zinc finger protein, putative (AHRD V3.3 *-* B9RSL7_RICCO)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6	C2H2	0,000	0,000	0,025	0,025	0,000									
Solyc05g006320	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *-* AT3G07170.1)		F:GO:0005515	F:protein binding			IPR001660 (SMART): G3DSA:1.10.15		6,586	6,638	6,295	5,952	5,868									
Solyc05g006323	Sterile alpha motif domain-containing protein (AHRD V3.3 *** A0A103YAP0_CYNCS)		F:GO:0004620	F:phospholipase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit		28,988	27,495	28,027	23,663	25,999									
Solyc05g006330	LOW QUALITY:C3H4 type zinc finger protein (DUF23) (AHRD V3.3 --* AT5G40720.3)								6,281	6,130	5,231	2,910	4,498					-0,846	0,009			down
Solyc05g006340	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061FTT2_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM		13,959	27,818	42,726	23,035	31,841	1,020	0,001	-0,426	0,024	-0,887	0,000	up	down	down
Solyc05g006343	S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61430.8)		F:GO:0003677; C:G	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit		0,061	0,039	0,050	0,000	0,023									
Solyc05g006347	Cinnamoyl-CoA reductase 2 (AHRD V3.3 --* CCR2_ARATH)	CCR							0,021	0,000	0,022	0,000	0,000									
Solyc05g006360	Metalloendoproteinase 1, putative (AHRD V3.3 *** B9S2J2_RICCO)		F:GO:0004222; P:G	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR021190 (PRINTS): IPR006026 (SM		1,761	0,507	0,627	1,695	0,328	-1,770	0,003			1,413	0,011	down		up
Solyc05g006370	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_ORYSA)								0,094	0,043	0,025	0,000	0,000									
Solyc05g006390	LOW QUALITY:CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 *** A0A061FTS5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit		15,627	11,373	6,415	17,193	11,851			0,884	0,008	1,425	0,000		up	up
Solyc05g006400	inositol-1%2C4%2C5-trisphosphate 5-phosphatase (AHRD V3.3 *** AT4G27020.1)						PTHR31354 (PANTHER): PTHR31354		148,197	114,917	214,677	193,185	199,997									
Solyc05g006410	Zinc finger MYND domain-containing protein 15 (AHRD V3.3 *** W9RD84_9ROSA)		F:GO:0046872	F:metal ion binding			G3DSA:3.30.60.180 (GENE3D): IPR0		6,096	4,350	4,503	3,845	4,669									
Solyc05g006420	Two-component response regulator (AHRD V3.3 *** W9S1Y9_9ROSA)	TRR 3	P:GO:0000160	P:phosphorelay signal transduction system			IPR001789 (SMART): IPR001789 (PF		36,435	44,001	13,134	10,537	14,561									
Solyc05g006430	Formin-like protein (AHRD V3.3 *** K4BWH0_SOLLC)		F:GO:0005199; C:G	F:structural constituent of cell wall; C:integral component of mer			IPR015425 (SMART): G3DSA:1.20.58		1,304	0,995	0,580	0,412	0,656									
Solyc05g006440	Symbiotic receptor-like kinase (AHRD V3.3 -** A0A0A6Z6M1_9FABA)		C:GO:0009535; P:G	C:chloroplast thylakoid membrane; P:cytochrome b6f complex a			IPR021562 (PFAM): PTHR35734:SF1		39,029	59,982	27,416	42,009	81,696	0,647	0,011	1,571	0,000	0,618	0,001	up	up	up
Solyc05g006450	Carboxypeptidase (AHRD V3.3 *-* K4BWH2_SOLLC)		F:GO:0004185; P:G	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR029058 (G3DSA:3.40.50.GENE3D		1,012	1,214	0,735	0,579	0,681									
Solyc05g006455	Carboxypeptidase (AHRD V3.3 *-* K4BWH2_SOLLC)		F:GO:0004185; P:G	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF		1,082	0,747	0,672	0,868	0,567									
Solyc05g006460	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S5H2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D		1,369	1,174	1,199	1,479	1,200									
Solyc05g006470	Actin-related protein 2/3 complex subunit 1 (AHRD V3.3 *-* A0A151RYL0_CAJCA)		F:GO:0005515; C:G	F:protein binding; C:Arp2/3 protein complex; P:Arp2/3 complex-r			IPR001680 (SMART): IPR024977 (PF		32,895	32,888	41,208	39,203	36,244									
Solyc05g006490	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *-* G7K5M5_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit		29,854	23,450	51,884	74,424	68,460			0,397	0,009	0,523	0,003		up	up
Solyc05g006510	Hexosyltransferase (AHRD V3.3 *** K4BWH7_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR029044 (G3DSA:3.90.550.GENE3		2,433	1,252	0,362	0,752	1,198									
Solyc05g006520	dehydrogenase AF209924		F:GO:0004739; P:G	F:pyruvate dehydro	EC:1.2.4.1	Pyruvate dehydroger	IPR001017 (PFAM): G3DSA:3.40.50.9		68,374	71,033	103,291	94,245	89,954									
Solyc05g006530	DEAD-box ATP-dependent RNA helicase ISE2 (AHRD V3.3 *** G7K5N2_MEDTR)		F:GO:0003676; F:G	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART): IPR012961 (SM		10,431	12,817	14,589	14,338	17,942									
Solyc05g006540	Paired amphipathic helix SIN3-like protein (AHRD V3.3 *** G7LEQ2_MEDTR)		F:GO:0003714; P:G	F:transcription corepressor activity; P:regulation of transcriptior			IPR013194 (SMART): IPR003822 (PF		0,379	0,217	0,219	0,173	0,187									
Solyc05g006550	Microtubule-associated protein TORTIFOLIA1, putative (AHRD V3.3 *** B9S2H6_RICCO)		C:GO:0005874; F:G	C:microtubule; F:microtubule binding			IPR000357 (PFAM): IPR011989 (G3D		3,096	4,866	0,462	0,417	0,281									
Solyc05g006560	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT1G27200.1)		C:GO:0016021; F:G	C:integral component of membrane; F:transferase activity			IPR008166 (PFAM): PTHR21461:SF1		41,876	24,675	17,933	30,958	26,943	-0,737	0,003	0,583	0,002	0,788	0,000	down	up	up
Solyc05g006570	Receptor-like kinase (AHRD V3.3 *** A0A0K9P790_ZOSMR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200		1,360	1,680	0,168	0,117	0,140									
Solyc05g006580	Mediator of DNA damage checkpoint protein 1 (AHRD V3.3 *** A0A1D1YWN1_9ARAE)		C:GO:0016021	C:integral component of membrane			PTHR36336 (PANTHER)		9,229	7,900	11,056	11,974	10,286									
Solyc05g006590	protein phosphatase 2A catalytic subunit 1	pp2ac1	F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM		32,248	40,701	46,725	44,665	40,866									
Solyc05g006607	Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein (AHRD V3.3 --* AT4G37070.4)								0,019	0,000	0,000	0,049	0,000									
Solyc05g006610	CLAVATA3/ESR (CLE)-related 25-like protein (AHRD V3.3 *** A0A0B0NFL0_GOSAR)		P:GO:0045168	P:cell-cell signaling involved in cell fate commitment			mobidb-lite (MOBIDB_LITE): PTHR342		0,040	0,060	0,000	0,000	0,000									
Solyc05g006620	Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 *** G7LDU5_MEDTR)		F:GO:0005515; P:G	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR003591 (SMA		84,063	60,940	62,049	57,463	59,818									
Solyc05g006630	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT1G27180.8)		F:GO:0005515; P:G	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR003593 (SMA		34,107	27,894	12,936	12,377	14,694									
Solyc05g006640	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IYV6_SOLCH)		F:GO:0000287; F:G	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (TIGF		16,811	38,978	30,195	31,094	31,070	1,238	0,001					up		
Solyc05g006645	Phospholipid-transporting ATPase (AHRD V3.3 *-* K4BWJ0_SOLLC)		F:GO:0000287; F:G	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR032631 (PFAM): PTHR24092:SF8		2,133	4,454	3,735	3,891	4,141									
Solyc05g006650	bHLH transcription factor 036		P:GO:0006355; F:G	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF	bHLH	47,403	34,895	45,757	24,354	40,922					-0,906	0,001			down
Solyc05g006660	CW14 protein (DUF1336) (AHRD V3.3 *** AT1G59650.1)						IPR009769 (PFAM): PTHR31558:SF3		34,961	44,061	49,174	53,204	57,614									
Solyc05g006670	LOW QUALITY:Leucine-rich repeat receptor protein kinase family protein (AHRD V3.3 *** A0A061E5L2_THE		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00365 (SMAR		0,118	0,173	0,140	0,073	0,142									
Solyc05g006680	Galactosyltransferase family protein (AHRD V3.3 *** AT5G62620.1)		P:GO:0006486; F:G	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR001079 (SMART): IPR002659 (PF		12,858	10,672	20,599	18,376	18,205									
Solyc05g006690	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50120.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN		0,409	0,632	1,002	0,697	0,802									
Solyc05g006700	Wall-associated receptor kinase-like 20 (AHRD V3.3 *** A0A061E5G3_THECC)		F:GO:0030247	F:polysaccharide binding			IPR032872 (PFAM): IPR025287 (PFA		1,562	1,719	0,467	0,506	0,282									
Solyc05g006703	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 *** A0A061EDB0_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((		5,788	5,306	4,931	6,343	5,750									
Solyc05g006705	CBL-interacting protein kinase 25 (AHRD V3.3 --* AT5G25110.1)								0,000	0,021	0,000	0,000	0,047									
Solyc05g006710	calcium ATPase 2 (AHRD V3.3 --* AT4G37640.1)						mobidb-lite (MOBIDB_LITE)		0,378	0,474	0,445	0,751	0,543									
Solyc05g006720	HIPL1 protein, putative (AHRD V3.3 *-* B9R921_RICCO)		F:GO:0003824; C:G	F:catalytic activity; C:membrane			IPR011042 (G3DSA:2.120.10.GENE3		0,401	0,420	0,483	0,461	0,402									
Solyc05g006730	Glutathione S-transferase family protein (AHRD V3.3 *-* AT1G10370.1)	GSTU10	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D		0,078	0,163	5,191	8,435	4,927									
Solyc05g006740	Sl Glutathione S-transferase	GSTU11	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:1.20.105		3,562	6,777	1,156	1,151	2,160	0,951	0,017					up		
Solyc05g006760	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G27150.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D		13,824	12,775	13,884	13,589	15,015									
Solyc05g006770	Kinase, putative (AHRD V3.3 *** A0A061E6J7_THECC)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS		10,663	6,006	6,384	5,103	6,269									
Solyc05g006780	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)		F:GO:0003676; F:G	F:nucleic acid binding; F:zinc ion binding			G3DSA:2.80.10.50 (GENE3D): IPR00		48,691	62,644	124,370	100,114	108,133									
Solyc05g006790	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)		F:GO:0003676; F:G	F:nucleic acid binding; F:zinc ion binding			IPR007679 (PFAM): G3DSA:2.80.10.5		0,019	0,018	0,000	0,047	0,047									
Solyc05g006800	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YAN3_CYNCS)		F:GO:0005515; F:G	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR011990 ((		6,291	6,049	13,633	14,409	15,288									
Solyc05g006810	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT1G24340.1)		F:GO:0071949	F:FAD binding			PR00420 (PRINTS): G3DSA:3.40.30.1		3,265	4,466	5,433	5,184	6,078									
Solyc05g006820	DnaJ-like protein (AHRD V3.3 *** Q9SP09_TOBAC)		P:GO:0006457; F:G	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS): IPR001623 (SM		13,207	9,727	14,558	10,170	10,954					-0,512	0,025			down
Solyc05g006830	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)		P:GO:0006662; F:G	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR005746 (PIRS		23,427	18,470	8,664	4,932	5,005			-0,794	0,009				down	
Solyc05g006837	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)								0,000	0,000	0,025	0,022	0,048									
Solyc05g006850	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)		P:GO:0006662; F:G	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR005746 (PIRS		1,370	1,261	1,156	1,473	1,884									
Solyc05g006860	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)		P:GO:0006662; F:G	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR013766 (PFA		0,121	0,158	0,567	0,578	0,967									
Solyc05g006870	Thioredoxin H (AHRD V3.3 *** Q4U0W0_NICAL)		P:GO:0006662; F:G	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR005746 (TIGF		30,929	34,732	10,609	7,655	8,904									
Solyc05g006880	aldehyde dehydrogenase 5F1 (AHRD V3.3 --* AT1G79440.1)								21,655	18,428	12,718	11,333	11,802									
Solyc05g006890	Eukaryotic translation initiation factor 5A (AHRD V3.3 *** K4BWL5_SOLLC)		F:GO:0003746; P:G	F:translation elongation factor activity; P:translational frameshif			IPR020189 (SMART): IPR014722 (G3		10,202	8,921	4,830	5,199	4,865									
Solyc05g006900	glycine-rich protein (AHRD V3.3 *-* AT1G27090.1)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	PTHR37736 (PANTHER)		40,074	32,310	26,934	22,683	24,287									
Solyc05g006910	AMP deaminase (AHRD V3.3 *** A0A061ED95_THECC)		F:GO:0003876; P:G	F:AMP deaminase a	EC:3.5.4.17; EC:3.5.	Adenosine-phosphate	IPR006329 (TIGRFAM): G3DSA:2.30.:		36,988	28,644	46,441	39,593	41,082									
Solyc05g006920	Major facilitator superfamily protein (AHRD V3.3 *** AT1G69860.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR		106,821	79,288	115,200	107,417	111,340									
Solyc05g006930	5'-AMP-activated protein kinase subunit beta-2 (AHRD V3.3 *** A0A151SZL4_CAJCA)						IPR013783 (G3DSA:2.60.40.GENE3D		1,809	2,075	2,284	1,954	2,332									
Solyc05g006940	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT1G27060.1)		F:GO:0003723	F:RNA binding			IPR000408 (PRINTS): IPR009091 (G3		19,980	17,535	44,002	40,351	38,502									
Solyc05g006950	Embryo yellow protein (AHRD V3.3 *** K4BWM1_SOLLC)		P:GO:0006886; C:G	P:intracellular protein transport; C:Golgi transport complex			IPR019335 (PFAM): IPR019335 (PAN		77,589	74,790	101,171	101,361	92,648									
Solyc05g006960	Homeobox transcription factor (AHRD V3.3 *** A0A072UFA2_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3		13,709	13,153	16,941	18,124	15,000									
Solyc05g006970	small multi-drug export protein (AHRD V3.3 *** AT2G02590.1)		C:GO:0009507; C:G	C:chloroplast; C:integral component of membrane			IPR009577 (PFAM): IPR009577 (PAN		1,312	1,945	3,133	3,399	3,261									
Solyc05g006980	Homeobox leucine zipper family protein (AHRD V3.3 *** G7K9R5_MEDTR)		F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN	HD-ZIP	5,188	4,582	6,535	11,087	6,889									
Solyc05g006990	nitrate transporter 1:2 (AHRD V3.3 *** AT1G69850.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): mobidb-lite (MOB		2,323	1,905	1,393	1,154	1,370									
Solyc05g007000	nitrate transporter 1:2 (AHRD V3.3 *** AT1G69850.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR		2,826	2,497	0,351	0,145	0,234									
Solyc05g007010	glyoxal oxidase-related protein (AHRD V3.3 *** AT1G14430.1)						IPR013783 (G3DSA:2.60.40.GENE3D		0,453	0,237	0,240	0,747	0,118									
Solyc05g007020	LOV/LOV protein (AHRD V3.3 *** E3WH16_SOLLC)		C:GO:0005634	C:nucleus			IPR001610 (SMART): IPR000014 (PF		48,961	39,250	83,466	75,528	76,204									
Solyc05g007030	heat-inducible transcription repressor (AHRD V3.3 *** AT3G17900.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit		66,662	55,196	59,816	61,271	59,203									
Solyc05g007040	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G36930.4)								12,495	9,670	0,199	0,780	0,046									
Solyc05g007050	Kinase family protein (AHRD V3.3 *** B9H0D5_POPTR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510		22,255	21,724	15,239	16,208	15,844									
Solyc05g007060	Plant/T7N9-9 protein (AHRD V3.3 *** G7K9S8_MEDTR)						IPR009770 (SMART): G3DSA:3.10.18		95,120	90,877	382,218	377,748	380,159									
Solyc05g007080	Alpha-amylase (AHRD V3.3 *** K4BWN3_SOLLC)		F:GO:0004556; F:G	F:alpha-amylase ac	EC:3.2.1.1	Alpha-amylase	IPR006046 (PRINTS): IPR006047 (SM		269,936	181,946	1089,885	1121,677	1079,279									
Solyc05g007085	Pectate lyase (AHRD V3.3 *** K4BWN4_SOLLC)		F:GO:0030570	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM		0,000	0,059	0,097	0,050	0,188									
Solyc05g007090	zinc knuckle (CCHC-type) family protein (AHRD V3.3 *-* AT5G20220.4)		F:GO:0003676; F:G	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR001878 (PF		3,375	5,416	2,070	1,652	4,914			1,250	0,000				up	
Solyc05g007100	Single-stranded DNA-binding protein WHY1, chloroplastic (AHRD V3.3 *** WHY1_SOLTU)		F:GO:0003697; P:G	F:single-stranded DNA binding; P:regulation of transcription, DN			IPR009044 (G3DS	Whirly	8,400	10,311	8,303	8,616	9,829									
Solyc05g007110	WRKY transcription factor 76	WRKY76	F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF	WRKY	0,021	0,000	0,000	0,000	0,000									
Solyc05g007120	Leucine-rich repeat protein kinase family protein, putative (AHRD V3.3 *** A0A061EAR8_THECC)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR032675 (G3		152,239	99,790	8,609	6,670	8,318									
Solyc05g007130	SUN-like protein 15	SUN15	F:GO:0005515	F:protein binding			IPR000048 (SMART): IPR025064 (PF		20,858	19,120	10,133	10,101	12,068									
Solyc05g007140	Protein kinase (AHRD V3.3 *** Q2HTW4_MEDTR)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PIRS		107,963	72,020	15,721	38,033	29,138			0,886	0,003	1,272	0,000		up	up
Solyc05g007150	UDP-galactose transporter, putative (AHRD V3.3 *** B9S297_RICCO)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM): PTHR10778:SF1		7,366	10,137	9,043	13,919	10,508					0,629	0,009			up
Solyc05g007160	R2R3MYB transcription factor 110	R2R3MYB110	F:GO:0003677	F:DNA binding			IPR001005 (SMAF	MYB	56,529	54,065	10,072	7,561	12,246									
Solyc05g007170	Disease resistance protein, putative (AHRD V3.3 *** Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR021929 (PFA		1,372	1,371	0,321	0,657	0,683									
Solyc05g007180	jasmonic acid 1	ja1	F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN	HD-ZIP	22,921	21,199	1,479	1,390	1,133									
Solyc05g007190	SlSUT2	SUT2	C:GO:0005794; F:G	C:Golgi apparatus; F:sucrose:proton symporter activity; P:respo			PF13347 (PFAM): mobidb-lite (MOBID		31,913	34,781	17,265	16,739	18,147									
Solyc05g007200	RNA recognition motif containing protein (AHRD V3.3 *** K7WP07_SOLTU)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3		30,000	33,085	51,161	40,744	46,452									
Solyc05g007210	BHLH transcription factor (AHRD V3.3 *** C6TBH0_SOYBN)		P:GO:0006355; F:G	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR036638 (G3DS	bHLH	0,019	0,000	0,000	0,000	0,000									
Solyc05g007220	Kelch repeat-containing F-box family protein, putative (AHRD V3.3 *** Q6L3I4_SOLDE)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR006652 (PF		36,425	36,280	61,224	77,254	71,041									
Solyc05g007230	Receptor-like kinase (AHRD V3.3 *** A0A0K9NLV5_ZOSMR)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR003591 (SMA		0,580	0,503	0,000	0,000	0,000									
Solyc05g007240	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-containing protein (AHRD V3.3 --* AT1G09170.8)						mobidb-lite (MOBIDB_LITE): mobidb-lit		33,313	34,092	72,314	54,676	56,143					-0,400	0,039			down
Solyc05g007250	40S ribosomal protein S9, putative (AHRD V3.3 *** Q60CZ2_SOLDE)		F:GO:0003735; P:G	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001912 (SMART): IPR002942 (SM		99,848	126,887	103,258	87,167	88,102									
Solyc05g007260	Ribulose-phosphate 3-epimerase (AHRD V3.3 *** K4BWQ2_SOLLC)	Rpe	F:GO:0004750; P:G	F:ribulose-phosphat	EC:5.1.3.1	Ribulose-phosphate 3	IPR000056 (PFAM): IPR000056 (TIGF		62,334	54,554	94,933	77,718	83,137									
Solyc05g007270	helicase with zinc finger protein (AHRD V3.3 *** AT2G46420.3)						IPR006476 (TIGRFAM): IPR006476 (F		25,791	23,028	20,655	19,405	23,176									
Solyc05g007280	DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein (AHR		F:GO:0005543; C:G	F:phospholipid binding; C:cell cortex; P:cortical protein anchorin			IPR013591 (PFAM): IPR013591 (PRC		4,716	7,119	5,930	6,503	7,444									
Solyc05g007290	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** G7K368_MEDTR)		F:GO:0046872	F:metal ion binding			IPR000408 (PRINTS): IPR000306 (SM		26,623	30,941	27,849	33,026	34,985									
Solyc05g007300	HVA22-like protein (AHRD V3.3 *** K4BWQ6_SOLLC)		P:GO:0009414; C:G	P:response to water deprivation; C:plasmodesma; P:response t			IPR004345 (PFAM): PTHR12300:SF5		0,187	0,082	0,000	0,025	0,023									
Solyc05g007350	Late blight resistance protein, putative (AHRD V3.3 *** Q60CZ7_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA		0,270	0,277	0,265	0,356	0,448									
Solyc05g007360	F-box domain-containing protein (AHRD V3.3 *** A4UV28_SOLTU)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR017451 (TIC		0,021	0,058	0,000	0,000	0,000									
Solyc05g007420	TCP transcription factor 23	TCP23	F:GO:0003700; C:G	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAN	TCP	0,000	0,018	0,000	0,000	0,000									
Solyc05g007430	transmembrane protein (DUF616) (AHRD V3.3 *** AT2G02910.2)		P:GO:0006672; C:G	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): IPR008901 (PAN		5,694	4,592	4,748	4,374	4,362									
Solyc05g007440	Armadillo/beta-catenin-like repeat protein (AHRD V3.3 *** G7LA57_MEDTR)						IPR007205 (PFAM): IPR011989 (G3D		62,441	47,491	62,827	53,148	57,967									

Solyc05g007450	Origin recognition complex, subunit 6 (AHRD V3.3 *** A0A118K386_CYNCS)		F:GO:0003677; C:GO	F:DNA binding; C:nuclear origin of replication recognition comple			IPR008721 (PFAM); G3DSA:1.10.472	2,023	1,852	0,162	0,069	0,167									
Solyc05g007460	sphingoid base hydroxylase 2 (AHRD V3.3 *** AT1G14290.1)		F:GO:0005506; P:GO	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM); PTHR11863:SF9	7,363	9,787	4,067	4,593	4,275									
Solyc05g007470	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G28580.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART); IPR003959 (PF	5,446	40,746	2,319	8,037	16,329	2,927	0,000	2,810	0,000	1,792	0,000	up	up	up
Solyc05g007480	LOW QUALITY:Phytochrome kinase substrate protein, putative (AHRD V3.3 *** G7KDX6_MEDTR)		P:GO:0009638	P:phototropism			IPR039615 (PANTHER); IPR039821 (I	8,981	9,108	3,822	4,761	5,045									
Solyc05g007490	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G26850.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	29,967	44,870	5,334	3,180	4,937									
Solyc05g007500	CAAX amino terminal protease family protein, putative (AHRD V3.3 *** Q60D39_SOLTU)		C:GO:0016020	C:membrane			IPR003675 (PFAM); PTHR43592:SF3	8,857	12,327	11,585	10,557	15,257									
Solyc05g007510	RNA-directed RNA polymerase	rdrp	F:GO:0003676; F:GO	F:nucleic acid bindi	EC:2.7.7.48	RNA-directed RNA po	IPR007855 (PFAM); PTHR23079:SF1	47,848	37,987	37,403	40,000	38,366									
Solyc05g007520	Cold acclimation protein WCOR518, related (AHRD V3.3 *** Q6L3L4_SOLDE)		C:GO:0005576; C:GO	C:extracellular region; C:vesicle; P:regulation of double fertilizat			PR01217 (PRINTS); IPR008502 (PFA	0,000	0,000	0,000	0,000	0,023									
Solyc05g007560	60S ribosomal protein L34 (AHRD V3.3 *** RL34_TOBAC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR008195 (PRINTS); IPR008195 (PF	95,757	114,515	82,357	76,559	76,535									
Solyc05g007570	DUF1666 family protein (AHRD V3.3 *** Q2HVS4_MEDTR)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM); mobidb-lite (MOB	5,040	5,728	6,092	5,249	5,919									
Solyc05g007580	ZF-HD homeobox domain-containing protein (AHRD V3.3 *** A4UV09_SOLTU)		F:GO:0003677	F:DNA binding			IPR006455 (TIGRI ZF-HD	0,482	0,874	0,359	0,470	0,400									
Solyc05g007585	SIN3-like 3 (AHRD V3.3 --* AT1G24190.3)							0,061	0,057	0,000	0,000	0,024									
Solyc05g007590	Isopenicillin N epimerase-like protein (AHRD V3.3 *** G7KWF1_MEDTR)		F:GO:0003824	F:catalytic activity			IPR000192 (PFAM); IPR015421 (G3D	0,057	0,059	0,025	0,025	0,023									
Solyc05g007600	Plastid 50S ribosomal protein L36 (AHRD V3.3 -** RK36_ANEMR)							0,000	0,000	0,000	0,025	0,000									
Solyc05g007610	Late blight resistance protein, putative (AHRD V3.3 *** Q6L421_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	0,042	0,075	0,000	0,069	0,094									
Solyc05g007630	Late blight resistance protein, putative (AHRD V3.3 *** Q6L421_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	0,038	0,074	0,022	0,025	0,024									
Solyc05g007640	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	0,098	0,113	0,025	0,117	0,046									
Solyc05g007650	LOW QUALITY:Clavata3/ESR (CLE) gene family member MtCLE24 (AHRD V3.3 --* G7KF79_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,018	0,000	0,000	0,000									
Solyc05g007670	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT2G02960.6)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART); IPR013083 (G3	22,743	29,130	31,130	28,819	29,187									
Solyc05g007675	GDA1/CD39 nucleoside phosphatase family protein (AHRD V3.3 *** AT2G02970.1)		F:GO:0016787	F:hydrolase activity			IPR000407 (PFAM); G3DSA:3.30.420	70,301	53,467	103,773	100,804	94,428									
Solyc05g007680	LOW QUALITY:Arabinanase/levansucrase/invertase (AHRD V3.3 *** AT1G26761.1)						IPR023296 (G3DSA:2.115.10.GENE3I	5,436	6,956	2,872	2,557	3,648									
Solyc05g007690	MYB-related transcription factor (AHRD V3.3 *** A0A059PRS5_SALMI)	R2R3MYB25	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,077	0,019	0,000	0,000	0,000									
Solyc05g007720	LOW QUALITY:Helicase/SANT-associated, DNA binding protein (AHRD V3.3 --* AT3G24880.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,224	0,276	0,484	0,542	0,351									
Solyc05g007730	Mitochondrial uncoupling protein 3 (AHRD V3.3 *** PUMP3_ARATH)		P:GO:0006839; F:GO	P:mitochondrial transport; F:transmembrane transporter activity			IPR002030 (PRINTS); IPR018108 (PF	8,645	8,371	10,982	9,107	9,682									
Solyc05g007740	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XFB3_CYNCS)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR032867 (PFAM); IPR002885 (TIGF	17,537	17,726	21,692	24,409	22,174									
Solyc05g007750	Cysteine-rich receptor-like protein kinase 40 (AHRD V3.3 --* CRK40_ARATH)							0,000	0,039	0,050	0,070	0,024									
Solyc05g007755	Anaphase-promoting complex subunit 2 (AHRD V3.3 *** W9S0C7_9ROSA)		P:GO:0006511; F:GO	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR016158 (SMART); IPR014786 (SM	8,916	7,315	5,902	6,205	6,835									
Solyc05g007760	LOW QUALITY:SET domain-containing family protein (AHRD V3.3 *** B9HI95_POPTR)		F:GO:0005515	F:protein binding			IPR001214 (SMART); IPR019734 (SM	0,122	0,134	0,000	0,025	0,024									
Solyc05g007770	NAC domain TF	NAC2	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,673	2,709	9,097	20,568	10,717	2,019	0,004			1,179	0,000	up		up
Solyc05g007780	Photosynthetic NDH subcomplex L 2 (AHRD V3.3 *** A0A0F7GYP0_9ROSI)		F:GO:0005509; C:GO	F:calcium ion binding; C:photosystem II oxygen evolving comple			G3DSA:1.20.120.290 (GENE3D); IPR(	1,756	8,149	2,260	4,106	8,014	2,238	0,000	1,810	0,000			up	up	
Solyc05g007790	CASP-like protein (AHRD V3.3 *** K4BWV4_SOLLC)		C:GO:0005886; P:GO	C:plasma membrane; P:cell-cell junction assembly; C:integral cc			IPR006702 (PFAM); IPR006459 (TIGF	0,099	0,213	0,094	0,242	0,420									
Solyc05g007800	Negatively light-regulated protein, putative (AHRD V3.3 *** Q5NRN5_SOLDE)						IPR006760 (PFAM); mobidb-lite (MOB	16,951	14,851	62,731	52,648	49,267									
Solyc05g007810	RNA-binding KH domain-containing protein (AHRD V3.3 *** AT5G15270.3)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR036612 (G3	121,401	111,743	168,443	153,050	166,237									
Solyc05g007820	RING/U-box superfamily protein (AHRD V3.3 *** AT1G14180.1)						IPR013083 (G3DSA:3.30.40.GENE3D	23,169	22,084	28,450	27,469	26,283									
Solyc05g007830	expansin12	EXPA12	C:GO:0005576; P:GO	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS); IPR002963 (PF	9,601	9,486	0,420	1,252	0,791									
Solyc05g007840	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT2G03050.2)		F:GO:0003690; P:GO	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR003690 (SMART); IPR003690 (PF	3,597	3,256	9,886	11,967	8,326									
Solyc05g007850	bacterial spot disease resistance protein 4	bsr4	F:GO:0005515; P:GO	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS); IPR000157 (SMA	3,845	2,454	5,118	5,743	4,640									
Solyc05g007870	R2R3MYB transcription factor 117	R2R3MYB117	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,000	0,182	0,000	0,000	0,047									
Solyc05g007880	Dof zinc finger protein (AHRD V3.3 *** W9S8B0_9ROSA)		F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	8,820	5,138	3,656	4,087	4,383									
Solyc05g007890	Myb family transcription factor APL (AHRD V3.3 *** W9SPH9_9ROSA)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	1,026	1,076	1,353	1,761	1,203									
Solyc05g007900	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061EHX5_THECC)		F:GO:0003824; C:GO	F:catalytic activity; C:cytoplasm; P:protein ubiquitination			PTHR45491 (PANTHER)	9,571	5,629	13,728	13,842	9,197									
Solyc05g007910	50S ribosomal L18-like protein (AHRD V3.3 *** G7KFC6_MEDTR)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.420.100 (GENE3D); IPR(	2,842	2,858	1,870	1,669	2,027									
Solyc05g007930	Beta-1,3-galactosyltransferase-like protein (AHRD V3.3 *** G7KFC0_MEDTR)		P:GO:0006486; F:GO	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR001079 (SMART); IPR001079 (SM	18,060	24,329	11,399	11,827	11,877									
Solyc05g007940	LERNALX L.esculentum ribonuclease lx	rnalx	F:GO:0003723; F:GO	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bond:	IPR001568 (PFAM); IPR036430 (G3D	0,381	0,348	1,811	2,019	1,388									
Solyc05g007950	LERNALE L.esculentum ribonuclease le	rnale	F:GO:0003723; F:GO	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bond:	IPR036430 (G3DSA:3.90.730.GENE3I	0,328	0,412	0,183	0,869	0,492									
Solyc05g007960	O-fucosyltransferase family protein (AHRD V3.3 *** AT2G01480.1)		P:GO:0006004; C:GO	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF); IPR019378 (PFA	27,332	17,474	35,747	35,587	32,445	-0,619	0,025					down		
Solyc05g007970	Phytanoyl-CoA dioxygenase domain protein (AHRD V3.3 *** A0A072UM45_MEDTR)		C:GO:0005886; F:GO	C:plasma membrane	EC:1.14.11; EC:1.14	Acting on paired don	IPR008775 (PFAM); G3DSA:2.60.120	19,864	22,485	33,356	34,829	33,025									
Solyc05g007980	Sulfate transporter, putative (AHRD V3.3 *** B9SJ59_RICCO)		F:GO:0008271; P:GO	F:secondary active sulfate transmembrane transporter activity;			IPR002645 (PFAM); IPR011547 (PFA	0,407	0,493	0,099	0,025	0,024									
Solyc05g007990	Uridine kinase (AHRD V3.3 *** A0A0K9PMG1_ZOSMR)		F:GO:0005524; F:GO	F:ATP binding; F:kinase activity			PR00988 (PRINTS); IPR003593 (SMA	17,311	13,948	22,596	28,253	26,677									
Solyc05g008000	Nudix hydrolase (AHRD V3.3 *** A0A061E9C3_THECC)		F:GO:0016787	F:hydrolase activity			IPR020476 (PRINTS); G3DSA:3.90.79	1,756	1,481	2,175	3,032	2,104									
Solyc05g008015	60S ribosomal protein L31 (AHRD V3.3 *** A0A0A9FFY1_ARUDO)							0,021	0,021	0,000	0,000	0,000									
Solyc05g008020	mitogen-activated protein kinase 15	mapk15	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	0,177	0,060	0,218	0,126	0,046									
Solyc05g008040	ATP-dependent DNA helicase family protein (AHRD V3.3 *** B9HW67_POPTR)		F:GO:0003676; F:GO	F:nucleic acid bindi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR001650 (SMART); IPR014001 (SM	9,840	11,175	7,474	5,932	8,100									
Solyc05g008050	Homeobox associated leucine zipper protein (AHRD V3.3 *** I3SMB9_MEDTR)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003106 (SMAF HD-ZIP	0,294	0,799	0,000	0,000	0,000									
Solyc05g008060	SIPIN4	PIN4	C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM); IPR014024 (TIGF	29,878	33,753	11,856	16,481	15,246									
Solyc05g008070	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR002182 (PFA	0,464	1,574	0,219	0,194	0,353	1,778	0,013					up		
Solyc05g008080	NOD26-like intrinsic protein 4.2	NIP4.2	F:GO:0015267; C:GO	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR000425 (PF	0,059	0,134	0,025	0,022	0,000									
Solyc05g008090	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *-* AT1G70950.1)						IPR027329 (PFAM); mobidb-lite (MOB	36,201	44,716	7,271	7,874	8,633									
Solyc05g008100	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT1G70985.1)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	19,078	14,165	20,841	19,181	19,850									
Solyc05g008110	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --* AT1G23040.3)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	51,798	35,131	275,096	294,644	239,661									
Solyc05g008120	Chaperone DnaJ (AHRD V3.3 *** A0A0B0MDP3_GOSAR)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm			IPR001623 (PRINTS); IPR001623 (SM	2,232	2,432	6,111	4,020	4,475									
Solyc05g008140	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein (AHRD V3.3 --* AT1G16360.4)						mobidb-lite (MOBIDB_LITE); mobidb-lit	10,394	11,381	11,293	10,224	9,952									
Solyc05g008180	quinolinate phoshoribosyltransferase		F:GO:0004514; P:GO	F:nicotinate-nucleot	EC:2.4.2.19	Nicotinate-nucleotide	IPR022412 (PFAM); IPR004393 (TIGF	22,446	20,575	23,187	17,466	22,683					-0,407	0,050			down
Solyc05g008190	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G10530.1)		F:GO:0005515	F:protein binding			IPR012952 (SMART); IPR001680 (SM	26,493	24,046	25,049	23,179	21,707									
Solyc05g008200	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** W9S0D4_9ROSA)		F:GO:0005524; F:GO	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;			IPR002498 (SMART); IPR027409 (G3	262,569	175,639	296,662	329,427	298,673									
Solyc05g008210	Plastid movement impaired protein (AHRD V3.3 *** A0A072VEV4_MEDTR)		C:GO:0005886	C:plasma membrane			IPR025322 (PFAM); PTHR33148 (PAN	5,446	5,618	0,749	0,322	0,751									
Solyc05g008220	Plastid movement impaired protein (AHRD V3.3 *** A0A072VEV4_MEDTR)		C:GO:0005886	C:plasma membrane			IPR025322 (PFAM); PTHR33148 (PAN	0,178	0,965	1,033	1,566	1,448									
Solyc05g008230	U-box domain-containing protein 11 (AHRD V3.3 *** W9RS70_9ROSA)		F:GO:0004842; F:GO	F:ubiquitin-protein transferase activity; F:protein binding; P:prote			IPR000225 (SMART); IPR003613 (SM	79,071	36,928	41,839	32,965	39,601	-1,069	0,000					down		
Solyc05g008235	MYB transcription factor (AHRD V3.3 *** W6JQG2_GENTR)		F:GO:0003677	F:DNA binding			IPR001005 (SMART); G3DSA:1.10.10	0,040	0,000	0,000	0,000	0,000									
Solyc05g008260	Peptidyl serine alpha-galactosyltransferase (AHRD V3.3 *** H3JU07_TOBAC)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity, trans			mobidb-lite (MOBIDB_LITE); mobidb-lit	69,552	55,715	68,524	68,029	64,741									
Solyc05g008270	DUF3326 family protein (AHRD V3.3 *** A0A072VFG1_MEDTR)						IPR021763 (PFAM); PTHR36891:SF1	5,555	7,659	10,770	9,024	13,662									
Solyc05g008280	LOW QUALITY:RNA-binding protein (AHRD V3.3 --* Q941H9_TOBAC)		F:GO:0003676; F:GO	F:nucleic acid bindi	EC:5.2.1.8	Peptidylprolyl isomera	IPR000504 (SMART); IPR000504 (PF	0,126	0,105	0,025	0,000	0,023									
Solyc05g008290	Cupredoxin superfamily protein (AHRD V3.3 *** AT1G23010.1)		F:GO:0005507; F:GO	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR011707 (PFAM); IPR008972 (G3D	130,672	94,591	65,257	43,232	72,247					-0,592	0,003			down
Solyc05g008300	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT1G23000.2)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); IPR0(	2,362	1,753	0,313	0,168	0,189									
Solyc05g008310	Serine/threonine-protein kinase (AHRD V3.3 *** M1D081_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART); IPR000719 (SM	8,286	9,757	5,400	6,058	5,672									
Solyc05g008320	LOW QUALITY:Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7IAT5_MEDTR)		C:GO:0005886; P:GO	C:plasma membrane; P:plant-type secondary cell wall biogenesi			IPR000782 (SMART); IPR036378 (G3	0,330	0,178	0,025	0,025	0,024									
Solyc05g008330	Pentatricopeptide repeat protein (AHRD V3.3 *** D2STE8_GOSHI)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	3,815	4,661	3,470	3,701	3,090									
Solyc05g008340	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061ER80_T		F:GO:0008375; C:GO	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM); PTHR19297 (PAN	7,936	6,763	6,243	5,676	5,725									
Solyc05g008350	ABC transporter family protein (AHRD V3.3 *** A0A097P9S5_HEVBR)	ABCG11	F:GO:0005524; C:GO	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR003439 (PF	37,131	47,725	18,836	18,983	27,134			0,523	0,029				up	
Solyc05g008370	Ribose-5-phosphate isomerase-like protein (AHRD V3.3 *** T2DNB2_PHAVU)	Rpi	F:GO:0004751; P:GO	F:ribose-5-phospha	EC:5.3.1.6	Ribose-5-phosphate	G3DSA:3.40.50.1360 (GENE3D); G3D	22,383	35,598	8,986	9,385	10,446	0,695	0,046					up		
Solyc05g008380	transmembrane protein (AHRD V3.3 *** AT1G71110.1)		C:GO:0016021	C:integral component of membrane			IPR040283 (PANTHER); PTHR31414:	43,914	45,145	48,009	53,720	50,857									
Solyc05g008390	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EGA0_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART); IPR011016 (PF	9,516	9,246	30,176	25,989	29,982									
Solyc05g008400	Repressor of RNA polymerase III transcription (AHRD V3.3 *** K4BX14_SOLLC)		P:GO:0016480	P:negative regulation of transcription by RNA polymerase III			IPR015257 (PFAM); IPR015257 (PIRS	4,501	2,978	5,130	6,181	5,807									
Solyc05g008420	Tetratricopeptide repeat protein 5 (AHRD V3.3 *** A0A0B2PGQ7_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	9,843	6,595	5,532	6,755	6,778									
Solyc05g008430	ALG-2 interacting protein X (AHRD V3.3 *** A0A0B2PBQ1_GLYSO)		F:GO:0005515	F:protein binding			IPR004328 (SMART); IPR038499 (G3	143,970	177,418	89,123	100,974	102,481									
Solyc05g008440	Sarcoplasmic reticulum histidine-rich calcium-binding protein (AHRD V3.3 *-* B6TJG2_MAIZE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	105,336	92,047	61,853	58,954	61,084									
Solyc05g008450	FAD/NAD(P)-binding oxidoreductase (AHRD V3.3 *** AT1G15140.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			PR00410 (PRINTS); IPR039261 (G3D	127,001	165,272	344,089	335,627	349,088									
Solyc05g008460	ATP synthase subunit beta (AHRD V3.3 *** A0A0V0IJL8_SOLCH)		C:GO:0000275; F:GO	C:mitochondrial pro	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR005722 (TIG	373,096	401,197	530,386	486,462	509,278									
Solyc05g008480	Histone chaperone (AHRD V3.3 *** A9TVI5_PHYPA)		C:GO:0005634; P:GO	C:nucleus; P:chromatin assembly or disassembly			IPR036747 (G3DSA:2.60.40.GENE3D	2,624	2,528	1,616	1,599	1,195									
Solyc05g008485	hydroxysteroid dehydrogenase 2 (AHRD V3.3 --* AT3G47350.3)							0,021	0,041	0,050	0,075	0,024									
Solyc05g008490	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT2G02690.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,043	0,000	0,076	0,000									
Solyc05g008500	Protein DETOXIFICATION (AHRD V3.3 *** K4BX24_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); PTHR11206 (PAN	0,078	0,101	0,025	0,000	0,047									
Solyc05g008510	Protein DETOXIFICATION (AHRD V3.3 *** K4BX25_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); IPR002528 (TIGF	6,867	11,214	20,883	30,006	21,691					0,528	0,013			up
Solyc05g008520	cyclin-D1-binding protein (AHRD V3.3 *** AT1G22970.1)		P:GO:0051726	P:regulation of cell cycle			G3DSA:1.20.1410.10 (GENE3D); PF1	20,972	19,930	35,678	34,603	30,177									
Solyc05g008530	Sec-independent translocase protein TatC (AHRD V3.3 *** A0A0B0PM57_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR002033 (PRINTS); IPR002033 (PF	29,888	32,859	45,549	54,691	53,696									
Solyc05g008540	Origin recognition complex subunit 4 (AHRD V3.3 *** K4BX28_SOLLC)		C:GO:0000808; F:GO	C:origin recognition complex; F:DNA binding; F:ATP binding; C:n			IPR003959 (PFAM); G3DSA:3.40.50.3	2,083	1,847	1,737	0,882	1,722									
Solyc05g008560	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SJZ3_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	10,984	8,757	11,069	13,207	11,205									
Solyc05g008565	Retinoblastoma-related protein (AHRD V3.3 --* RBR_VITVI)							3,782	3,542	4,241	4,749	4,793									
Solyc05g008580	Phosphatidylserine synthase 2 (AHRD V3.3 *** W8TFN0_TOBAC)		P:GO:0006659	P:phosphatidylserine biosynthetic process			IPR004277 (PFAM); PTHR15362 (PAN	12,883	13,502	22,231	23,698	19,411									
Solyc05g008590	plant viral-response family protein (DUF716) (AHRD V3.3 *** AT5G13890.3)		C:GO:0016021	C:integral component of membrane			IPR006904 (PFAM); PTHR16007:SF1	14,246	15,398	24,337	21,957	22,385									
Solyc05g008595	Cytochrome P450 superfamily protein (AHRD V3.3 --* AT3G53130.1)							0,752	1,299	1,437	1,222	1,293									
Solyc05g008600	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4BX34_SOLLC)	ddtfr6a	F:GO:0004332; P:GO	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	483,288	455,529	608,717	515,814	538,568									
Solyc05g008610	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G18210.2)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR006620 (SMART); G3DSA:2.60.12	33,416	26,577	43,182	38,568	38,151									
Solyc05g008620	DNA replication complex GINS protein psf3 (AHRD V3.3 *** A0A061FM87_THECC)		C:GO:0005634; P:GO	C:nucleus; P:DNA replication; C:integral component of membran			IPR021151 (PFAM); IPR038437 (G3D	1,445	1,355	0,235	0,095	0,189									
Solyc05g008630	G-type lectin S-receptor-like Serine/Threonine-kinase (AHRD V3.3 --* AT1G11340.3)							4,726	4,063	6,907	6,687	6,857									
Solyc05g008633	Poly(A) polymerase (AHRD V3.3 *** A0A0B2QVW5_GLYSO)		F:GO:0003723; F:GO	F:RNA binding; F:pc	EC:2.7.7.19	Polynucleotide aden	IPR014492 (PIRSF); IPR007012 (PFA	55,196	46,251	99,883	99,361	94,219									
Solyc05g008637	Carotenoid cleavage dioxygenase 8 (AHRD V3.3 --* A0A061GRL5_THECC)							6,788	5,626	10,791	10,944	9,831									
Solyc05g008640	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G80400.1)		C:GO:0016020; F:GO	C:membrane; F:ligase activity			IPR001841 (SMART); IPR001841 (PF	0,558	0,718	7,299	7,370	4,683									
Solyc05g008650	LOW QUALITY:Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			G3DSA:3.40.50.300 (GENE3D); PTHR	0,037	0,000	0,075	0,099	0,000									
Solyc05g008660	LOW QUALITY:UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT5G05880.1)		F:GO:0043531	F:ADP binding				0,000	0,000	0,000	0,095	0,000									
Solyc05g008670	Zinc finger transcription factor 36	C3H36	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	0,040	0,154	0,022	0,000	0,048									
Solyc05g008690	LOW QUALITY:NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q6_9SOLN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc05g008710	LOW QUALITY:Myzus persicae-induced lipase 1 (AHRD V3.3 --* AT5G14180.1)							0,000	0,000	0,000	0,000	0,023									
Solyc05g008720	LOW QUALITY:EIN3-binding F-box protein 1 (AHRD V3.3 *-* Q2PQJ0_SOLLC)							0,000	0,000	0,000	0,000	0,024									
Solyc05g008730	F-box protein (AHRD V3.3 *-* S4T6I7_CAPAN)		F:GO:0004842; C:GO	F:ubiquitin-protein transferase activity; C:SCF ubiquitin ligase cc			IPR006553 (SMART); IPR032675 (G3	0,019	0,000	0,025	0,048	0,000									
Solyc05g008740	LOW QUALITY:RNA-dependent RNA polymerase (AHRD V3.3 *-* M1C692_SOLTU)		P:GO:0016070; F:GO	P:RNA metabolic process; F:transferase activity; P:gene silencing by RNA; P:regulation of gene expres				0,000	0,000	0,000	0,025	0,000									
Solyc05g008750	Stigma/style cell cycle inhibitor 1 (AHRD V3.3 *** F8QMT1_TOBAC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	6,602	7,057	14,539	13,441	11,510									
Solyc05g008770	Bidirectional amino acid transporter 1 (AHRD V3.3 *-* A0A061E5W5_THECC)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1740.10 (GENE3D); IPR(	14,798	14,345	6,870	5,507	7,994									
Solyc05g008780	PROTON PUMP INTERACTOR 1 family protein (AHRD V3.3 *-* U5GXF2_POPTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	120,194	106,858	67,799	76,683	71,459									
Solyc05g008790	Ceramide kinase (AHRD V3.3 *** A0A151RG30_CAJCA)		F:GO:0003951	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR001206 (PFAM); G3DSA:2.60.200	21,389	18,465	34,590	31,982	32,939									
Solyc05g008800	Lipid phosphate phosphatase 2 family protein (AHRD V3.3 --* B9HWC6_POPTR)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	5,564	5,041	3,663	3,738	3,956									
Solyc05g008805	Lipid phosphate phosphatase-like protein (AHRD V3.3 *** A0A072VR60_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000326 (SMART); IPR000326 (PF	12,300	9,482	8,523	8,493	8,136									
Solyc05g008815	Lipid phosphate phosphatase-like protein (AHRD V3.3 *** A0A072U232_MEDTR)		F:GO:0008195; C:GO	F:phosphatidate ph	EC:3.1.3.4	Phosphatidate phosp	IPR000326 (SMART); IPR000326 (PF	82,327	83,672	19,313	24,259	26,390									
Solyc05g008820	Lipid phosphate phosphatase-like protein (AHRD V3.3 *** A0A072U232_MEDTR)		F:GO:0008195; C:GO	F:phosphatidate ph	EC:3.1.3.4	Phosphatidate phosp	IPR000326 (SMART); IPR000326 (PF	3,044	5,937	2,960	3,420	4,732									
Solyc05g008830	Octicosapeptide/Phox/Bem1p family protein (AHRD V3.3 *** AT2G01190.1)		F:GO:0005515	F:protein binding			IPR000270 (SMART); IPR000270 (PF	122,236	98,994	86,706	77,538	80,988									
Solyc05g008840	RING/U-box superfamily protein (AHRD V3.3 *** AT1G73760.1)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,061	0,062	0,000	0,000	0,000									
Solyc05g008860	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BX60_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART); IPR000719 (SM	11,631	12,629	10,656	9,920	10,232									
Solyc05g008870	Nucleotidylyl transferase superfamily protein (AHRD V3.3 *** AT2G01220.2)		F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process			IPR036653 (G3DSA:3.90.950.GENE3I	25,466	24,316	46,868	43,923	47,062									
Solyc05g008880	LOW QUALITY:proline transporter 2 (AHRD V3.3 --* AT3G55740.3)		C:GO:0016021	C:integral component of membrane			PTHR37199:SF2 (PANTHER); PTHR3	0,021	0,000	0,000	0,000	0,000									
Solyc05g008890	Reticulon-like protein (AHRD V3.3 *** K4BX63_SOLLC)		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM); PTHR10994 (PAN	0,059	0,101	0,050	0,000	0,024									
Solyc05g008895	Lipid transfer protein (AHRD V3.3 *** I0IK55_9MYRT)		P:GO:0006869	P:lipid transport			G3DSA:1.10.110.10 (GENE3D); IPR0	0,570	0,587	0,046	0,022	0,000									
Solyc05g008900	Fiber protein Fb34 (AHRD V3.3 *** A0A072VR88_MEDTR)		C:GO:0005886; C:GO	C:plasma membrane; C:integral component of membrane			IPR009606 (PFAM); PTHR31769:SF3	30,179	27,427	9,225	7,103	9,909									
Solyc05g008910	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *-* AT5G38200.1)		F:GO:0016787	F:hydrolase activity			IPR011697 (PFAM); IPR029062 (G3D	0,121	0,256	0,044	0,122	0,024									
Solyc05g008920	DUF789 family protein (AHRD V3.3 *** G7KMK8_MEDTR)						IPR008507 (PFAM); mobidb-lite (MOB	59,443	41,404	224,689	213,837	211,997									
Solyc05g008930	Protein kinase family protein (AHRD V3.3 *** AT5G38210.2)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	11,671	14,027	23,097	24,277	22,891									
Solyc05g008940	Kinase family protein (AHRD V3.3 *** D7KAJ2_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	3,110	9,000	3,294	3,198	4,925	1,553	0,001					up		
Solyc05g008950	Kinase family protein (AHRD V3.3 *** D7KAJ2_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	0,582	0,820	0,383	0,344	0,449									
Solyc05g008960	Kinase family protein (AHRD V3.3 *** D7KAJ2_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	3,492	6,056	1,505	1,376	1,525									
Solyc05g008970	Protein kinase family protein (AHRD V3.3 *-* AT5G38210.2)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	0,836	1,020	0,284	0,552	0,497									
Solyc05g008980	Kinase family protein (AHRD V3.3 *** D7KAJ2_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	1,168	6,317	0,364	0,464	0,923	2,454	0,000					up		
Solyc05g008990	Kinase family protein (AHRD V3.3 *** D7KAJ2_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR032872 (PF	0,759	1,497	0,065	0,075	0,354									

Solyc05g009000	Receptor-like protein kinase (AHRD V3.3 *** D3G6F0_CAPAN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR032872 (PFAM); G3DSA:3.30.200	5,012	9,845	0,979	1,345	1,836									
Solyc05g009010	Protein kinase family protein (AHRD V3.3 *-* AT5G38210.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	14,902	28,049	2,660	5,791	5,952			1,154	0,002	1,116	0,004		up	up
Solyc05g009020	Mitochondrial substrate carrier family protein (AHRD V3.3 *** B9HJ54_POPTR)		F:GO:0022857; P:GC	F:transmembrane transporter activity; P:transmembrane transpc	IPR002067 (PRINTS); IPR023395 (G3	7,897	6,362	7,448	7,664	7,255									
Solyc05g009030	3-isopropylmalate dehydrogenase (AHRD V3.3 *** K4BX77_SOLLC)		F:GO:0003862; P:GC	F:3-isopropylmalate EC:1.1.1.85 3-isopropylmalate de	IPR024084 (SMART); G3DSA:3.40.71	44,991	55,977	92,665	84,926	85,771									
Solyc05g009040	Receptor-like protein kinase (AHRD V3.3 *** D3G6F0_CAPAN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	0,352	0,758	0,542	0,560	0,878									
Solyc05g009050	Receptor-like protein kinase (AHRD V3.3 *** D3G6F0_CAPAN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:3.30.20	4,407	8,401	2,266	2,156	2,493	0,958	0,005					up		
Solyc05g009070	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G68410.4)		F:GO:0004722; P:GC	F:protein serine/thr EC:3.1.3.16 Protein-serine/threon	IPR001932 (SMART); IPR001932 (SM	83,550	100,440	35,459	42,891	56,871			0,678	0,002				up	
Solyc05g009080	Polyketide cyclase/dehydrase and lipid transporter (AHRD V3.3 *** G7LFP8_MEDTR)				IPR023393 (G3DSA:3.30.530.GENE3I	15,051	12,565	10,505	11,815	14,012									
Solyc05g009090	Receptor-like protein kinase (AHRD V3.3 *** D3G6F0_CAPAN)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	0,021	0,000	0,072	0,022	0,000									
Solyc05g009100	LRR receptor-like kinase (AHRD V3.3 *** G7IC91_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	G3DSA:1.10.510.10 (GENE3D); IPR0	1,073	1,298	0,165	0,190	0,256									
Solyc05g009120	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT1G68390.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM); PTHR31042:SF7	0,726	1,356	12,453	18,593	10,641									
Solyc05g009130	core-2/i-branching beta-1,6-n-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT1G10880.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM); PTHR31042 (PAN	0,863	0,721	0,919	0,971	0,852									
Solyc05g009140	Metallo-beta-lactamase superfamily protein (AHRD V3.3 *** A0A072VR93_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR001279 (SMART); IPR001279 (PF	16,593	15,251	39,523	40,873	35,959									
Solyc05g009150	zinc finger protein-like protein (AHRD V3.3 *** AT3G18290.1)		F:GO:0008270	F:zinc ion binding	IPR001841 (SMART); IPR008913 (PF	51,685	41,945	38,778	44,301	46,214									
Solyc05g009160	Chaperone protein dnaJ 15 (AHRD V3.3 *** DNJ15_ARATH)				IPR001623 (PRINTS); IPR001623 (SM	26,787	26,080	32,320	34,540	29,271									
Solyc05g009170	Zinc finger family protein (AHRD V3.3 *** B9HWF8_POPTR)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.6 C2H2	0,604	4,418	0,690	0,489	0,307	2,884	0,000					up		
Solyc05g009180	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HWF8_POPTR)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.60 (GENE3D); mobic	0,572	0,518	0,072	0,025	0,000									
Solyc05g009190	chlorophyll a/b-binding protein	cab4a	F:GO:0004817; F:GC	F:cysteine-tRNA lig EC:6.1.1.16 Cysteine--tRNA ligas	IPR024909 (PRINTS); IPR014729 (G3	56,236	59,884	47,202	46,742	50,001									
Solyc05g009200	DUF1639 family protein (AHRD V3.3 *** G7IC98_MEDTR)				IPR012438 (PFAM); PTHR33130 (PAN	0,232	0,039	0,000	0,025	0,000									
Solyc05g009210	LOW QUALITY:membrane-associated kinase regulator (AHRD V3.3 *** AT1G68330.1)		F:GO:0004674; P:GC	F:protein serine/thr EC:2.7.11 Transferring phospho	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,495	0,834	0,044	0,141	0,047									
Solyc05g009220	Glutamine--tRNA ligase (AHRD V3.3 *** SYQ_LUPLU)		F:GO:0004819; F:GC	F:glutamine-tRNA lic EC:6.1.1.18 Glutamine--tRNA liga	IPR000924 (PRIN bHLH	102,638	92,821	113,256	103,119	106,578									
Solyc05g009230	Myb domain protein (AHRD V3.3 *** K7PMP7_HEVBR)	R2R3MYB116	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,102	0,261	0,234	0,342	0,140									
Solyc05g009240	DUF639 family protein (AHRD V3.3 *** G7L0J4_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR006927 (PFAM); PTHR31860:SF5	4,190	5,401	3,521	5,331	3,852									
Solyc05g009250	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RLP9_9ROSA)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (SMAF ERF	0,871	0,986	1,309	1,046	1,111									
Solyc05g009260	Protein TRANSPORT INHIBITOR RESPONSE 1 (AHRD V3.3 *-* TIR1_ARATH)		P:GO:0007275; P:GC	P:multicellular organism development; P:cellular protein metabol	IPR032675 (G3DSA:3.80.10.GENE3D	1,394	1,756	0,647	0,432	0,802									
Solyc05g009270	3-ketoacyl-CoA synthase (AHRD V3.3 *** M9Z390_GOSRA)		P:GO:0006633; C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a	IPR016039 (G3DSA:3.40.47.GENE3D	2,907	4,766	0,384	1,052	0,657									
Solyc05g009280	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1B5V3_SOLTU)		P:GO:0006633; C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a	IPR013747 (PFAM); IPR013601 (PFA	0,000	0,000	0,166	0,323	0,119									
Solyc05g009290	Protein FLX-like 3 (AHRD V3.3 *** A0A199UZ70_ANACO)				mobidb-lite (MOBIDB_LITE); mobidb-lit	44,175	41,435	75,193	67,497	64,545									
Solyc05g009300	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT2G29180.1)		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:integral component of men	mobidb-lite (MOBIDB_LITE); PTHR367	23,933	25,694	10,280	13,606	19,803			0,941	0,000				up	
Solyc05g009310	CONSTANS-like zinc finger protein (AHRD V3.3 *** I1LEW9_SOYBN)	BBX15	F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding	IPR000315 (SMAF CO-like	3,450	2,679	0,500	0,262	1,646									
Solyc05g009320	LOB domain-containing protein, putative (AHRD V3.3 *** B9T058_RICCO)				IPR004883 (PFAN LBD	9,043	8,275	0,535	0,591	0,662									
Solyc05g009330	Fiber protein Fb34 (AHRD V3.3 *** G7JX88_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR009606 (PFAM); PTHR31769 (PAN	24,656	22,838	6,155	3,630	5,204									
Solyc05g009340	LOW QUALITY:BnaC02g18280D protein (AHRD V3.3 *-* A0A078CZZ8_BRANA)					0,063	0,410	0,193	0,149	0,211									
Solyc05g009350	Zinc finger transcription factor 37	C3H37	F:GO:0046872	F:metal ion binding	IPR000571 (SMAF C3H	72,717	40,364	23,078	18,823	20,633	-0,822	0,000					down		
Solyc05g009360	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)				mobidb-lite (MOBIDB_LITE); PTHR333	18,911	34,355	94,171	76,632	71,540	0,887	0,003					up		
Solyc05g009370	50S ribosomal protein L15 (AHRD V3.3 *** A0A072VRA4_MEDTR)		F:GO:0003735; P:GC	F:structural constituent of ribosome; P:translation; C:large ribos	IPR005749 (TIGRFAM); IPR021131 (F	16,388	31,974	83,071	81,216	89,254	0,991	0,000					up		
Solyc05g009380	lyrate		F:GO:0003676; P:GC	F:nucleic acid binding; P:multicellular organism development	G3DSA:3.30.160.60 (GENE3D); mobic	1,684	0,740	0,479	0,466	0,635									
Solyc05g009390	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G77420.1)		C:GO:0016020	C:membrane	IPR000073 (PRINTS); IPR029058 (G3	9,968	27,223	20,055	15,954	19,044	1,475	0,000					up		
Solyc05g009400	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HJ37_POPTR)		F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR011990 (G3D	1,698	2,573	1,440	1,399	1,267									
Solyc05g009405	transcription factor (AHRD V3.3 --* AT4G26170.1)					0,141	0,265	0,138	0,072	0,143									
Solyc05g009410	Adenylate isopentenyltransferase (AHRD V3.3 *** I0IUP6_SOLLC)		P:GO:0008033	P:tRNA processing	G3DSA:1.10.287.890 (GENE3D); IPR(	1,263	1,404	0,258	0,316	0,400									
Solyc05g009420	Transmembrane protein, putative (AHRD V3.3 *** G7K1J5_MEDTR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); PTHR367	39,008	73,434	122,671	127,953	92,179	0,937	0,042					up		
Solyc05g009430	Nuclease S1 (AHRD V3.3 *** A0A0B0MLZ3_GOSAR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:endonuclease activity; P:DNA catabolis	IPR008947 (G3DSA:1.10.575.GENE3I	1,298	1,013	1,882	3,832	2,244					1,027	0,004			up
Solyc05g009440	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061E5Z1_THECC)		P:GO:0030001; F:GC	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D); G3DS	0,224	0,539	0,022	0,025	0,024									
Solyc05g009450	Solanum lycopersicum Cytokinin Response Factor 10		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	16,697	17,076	6,668	8,971	9,682									
Solyc05g009460	Conserved peptide upstream open reading frame 53 (AHRD V3.3 --* B3H7G6_ARATH)					3,068	2,165	1,308	1,995	2,185									
Solyc05g009470	Alpha-glucosidase (AHRD V3.3 *** Q9LEC9_SOLTU)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:2.60.40.1760 (GENE3D); IPR(	142,682	111,796	49,236	51,265	56,726									
Solyc05g009480	LOW QUALITY:NIM1-interacting 2 (AHRD V3.3 -** AT3G25882.1)		P:GO:0010112	P:regulation of systemic acquired resistance	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,387	0,022	0,098	0,094									
Solyc05g009490	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT2G27120.3)					0,349	0,302	0,172	0,291	0,330									
Solyc05g009500	Major facilitator superfamily protein (AHRD V3.3 *** AT1G68570.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM); PTHR11654:SF1	1,168	1,690	0,498	1,250	0,842									
Solyc05g009520	LOW QUALITY:BnaA06g07410D protein (AHRD V3.3 *** A0A078E7A2_BRANA)				PTHR34539:SF1 (PANTHER); PTHR3	2,467	4,477	6,545	10,495	6,950									
Solyc05g009530	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4BXC		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR001078 (PFAM); IPR004167 (PFA	34,723	40,931	53,377	62,352	58,968									
Solyc05g009540	Protein kinase-like protein (AHRD V3.3 *** Q8RWN3_ARATH)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	67,746	57,549	56,348	61,810	57,878									
Solyc05g009545	Cysteine proteinases superfamily protein (AHRD V3.3 --* AT1G22080.2)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,046	0,000	0,000									
Solyc05g009550	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061ECG5_THECC)		P:GO:0015031	P:protein transport	G3DSA:1.20.1260.60 (GENE3D); IPR(	557,719	499,260	92,017	122,564	165,007									
Solyc05g009560	Homologous-pairing protein 2 homolog (AHRD V3.3 *** HOP2_ARATH)		P:GO:0007131	P:reciprocal meiotic recombination	PF18517 (PFAM); IPR036388 (G3DS/	2,384	3,316	2,319	1,586	1,607									
Solyc05g009570	30S ribosomal protein 3 (AHRD V3.3 *** W9SB90_9ROSA)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038447 (G3DSA:1.20.58.GENE3D	2,623	5,762	1,302	2,968	3,995	1,164	0,007	1,609	0,000	1,190	0,002	up	up	up
Solyc05g009590	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G18420.1)		P:GO:0015743	P:malate transport	IPR020966 (PFAM); PTHR31086 (PAN	0,000	0,117	0,000	0,000	0,000									
Solyc05g009600	Serine/threonine protein phosphatase 2a regulatory subunit A, putative (AHRD V3.3 *** B9ST19_RICCO)		F:GO:0005515	F:protein binding	IPR011989 (G3DSA:1.25.10.GENE3D	197,426	187,636	217,957	211,592	213,814									
Solyc05g009610	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EB00_THECC)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	6,427	13,231	3,882	4,996	3,817									
Solyc05g009620	Protein PLANT CADMIUM RESISTANCE 2 (AHRD V3.3 *** A0A1D1Y359_9ARAE)		C:GO:0016021	C:integral component of membrane	IPR006461 (PFAM); IPR006461 (TIGF	0,019	0,000	0,025	0,022	0,000									
Solyc05g009630	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); PF18052 (PFAM)	20,263	32,334	17,263	19,163	20,138	0,699	0,023					up		
Solyc05g009650	Plant regulator RWP-RK family protein (AHRD V3.3 --* A0A072W053_MEDTR)				mobidb-lite (MOBIDB_LITE); PTHR349	0,000	0,043	0,000	0,025	0,000									
Solyc05g009660	Transcription factor PERIANTHIA-like protein (AHRD V3.3 *** A0A0B0NQX8_GOSAR)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMAF bZIP	0,446	0,268	0,143	0,342	0,142									
Solyc05g009670	Plasma-membrane choline transporter family protein (AHRD V3.3 *** AT1G25500.2)		C:GO:0016021	C:integral component of membrane	IPR007603 (PFAM); mobidb-lite (MOB	7,128	7,545	2,472	3,356	4,212									
Solyc05g009680	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G25510.1)		F:GO:0004190; P:GC	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR032799 (PFAM); IPR021109 (G3D	29,941	26,724	8,019	10,824	11,090									
Solyc05g009690	GDT1-like protein 5 (AHRD V3.3 *** A0A0B2P885_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR001727 (PFAM); PTHR12608:SF1	80,825	96,711	73,062	75,036	71,955									
Solyc05g009700	Amino acid transporter, putative (AHRD V3.3 *** B9ST31_RICCO)		P:GO:0003333; C:GC	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM); PTHR22950:SF3	2,915	4,099	7,330	5,947	7,014									
Solyc05g009710	Mediator of RNA polymerase II transcription subunit 25 (AHRD V3.3 *-* A0A0B0PNK0_GOSAR)				IPR021419 (PFAM); mobidb-lite (MOB	13,194	9,621	13,156	14,310	12,724									
Solyc05g009720	Two-component response regulator (AHRD V3.3 *** W9RG69_9ROSA)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6C G2-like	6,178	3,550	3,667	3,713	3,224									
Solyc05g009730	LOW QUALITY:Serine/Threonine-kinase ATM-like protein (AHRD V3.3 --* AT3G48190.3)				mobidb-lite (MOBIDB_LITE)	0,138	0,075	0,122	0,342	0,165									
Solyc05g009740	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT5G48620.6)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR002182 (PFA	5,434	9,264	7,135	8,754	7,458									
Solyc05g009750	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q8_SOLLC)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); G3DSA:3.40.50.3	0,441	0,412	0,116	0,353	0,094									
Solyc05g009760	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q8_SOLLC)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	4,413	7,893	2,021	3,620	4,032	0,861	0,036	0,978	0,005			up	up	
Solyc05g009780	Methionine aminopeptidase 1 (AHRD V3.3 *** A0A0K9NZD6_ZOSMR)		F:GO:0004177; P:GC	F:aminopeptidase a EC:3.4.11 Acting on peptide bor	IPR001714 (PRINTS); G3DSA:3.90.23	15,914	22,940	21,385	17,690	28,726			0,423	0,020				up	
Solyc05g009790	AP2/B3 transcription factor family protein (AHRD V3.3 *** AT1G25560.1)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR003340 (SMAF RAV	3,833	15,411	3,541	5,809	3,839	2,029	0,000					up		
Solyc05g009800	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** A0A0K9Q2Y3_ZOSMR)		C:GO:0005768; C:GC	C:endosome; C:vacuole; C:trans-Golgi network; C:plasma meml	G3DSA:2.60.120.430 (GENE3D); IPR(	30,070	27,913	80,469	86,808	74,197									
Solyc05g009820	Hexosyltransferase (AHRD V3.3 *** K4BXF6_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups	IPR002495 (PFAM); IPR029044 (G3D	29,667	17,836	2,528	2,409	4,125	-0,705	0,048					down		
Solyc05g009840	NAC domain-containing protein (AHRD V3.3 *** A0A060A661_BOENI)	NAC044	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAN NAC	50,073	63,349	26,194	25,887	29,478									
Solyc05g009850	GC-rich sequence DNA-binding factor-like protein (AHRD V3.3 *** AT5G08550.1)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; C:nu	IPR022783 (PFAM); mobidb-lite (MOB	56,273	50,251	61,616	58,592	59,181									
Solyc05g009860	Leucoanthocyanidin reductase (AHRD V3.3 *-* J7M947_9ERIC)		F:GO:0016491	F:oxidoreductase activity	G3DSA:3.40.50.720 (GENE3D); IPR0(	2,239	1,720	0,068	0,025	0,023									
Solyc05g009870	Transmembrane Fragile-X-F-associated protein (AHRD V3.3 *** AT1G68820.4)		C:GO:0016021	C:integral component of membrane	PF13920 (PFAM); IPR013083 (G3DS/	7,866	5,380	31,784	38,118	27,117									
Solyc05g009875	Transmembrane Fragile-X-F-associated protein (AHRD V3.3 *-* AT1G68820.4)		C:GO:0016021	C:integral component of membrane	IPR019396 (PFAM); PTHR10044 (PAN	2,748	2,101	13,276	16,579	10,719									
Solyc05g009880	bHLH transcription factor 038	bHLH038	P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	3,036	2,333	0,075	0,025	0,167									
Solyc05g009890	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G25700.1)		F:GO:0004190; P:GC	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR001461 (PRINTS); IPR021109 (G3	1,273	2,896	0,000	0,095	0,047									
Solyc05g009910	Coiled-coil domain-containing protein, putative (AHRD V3.3 *** B9SEI0_RICCO)				IPR007590 (PFAM); PTHR12111:SF2	37,707	41,755	91,638	83,583	82,230									
Solyc05g009920	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G26090.1)				PF17886 (PFAM); IPR008978 (G3DS/	1,429	1,650	2,658	2,883	3,420									
Solyc05g009930	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT3G25690.6)		C:GO:0009707	C:chloroplast outer membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	84,969	90,208	76,096	71,255	99,868			0,389	0,024				up	
Solyc05g009940	oxidoreductase/transition metal ion-binding protein (AHRD V3.3 *-* AT5G52410.3)		C:GO:0009941; C:GC	C:chloroplast envelope; C:integral component of membrane	PTHR33740:SF1 (PANTHER); PTHR3	22,222	20,416	31,193	33,228	31,957									
Solyc05g009950	Cytochrome b561 (AHRD V3.3 *** A0A151S1S0_CAJCA)		C:GO:0009941; C:GC	C:chloroplast envelope; C:integral component of membrane; F:c	IPR006593 (SMART); G3DSA:1.20.12	16,572	11,595	2,332	1,281	1,998									
Solyc05g009970	Glycerol kinase (AHRD V3.3 *** A0A0B0MNH3_GOSAR)		F:GO:0016301; P:GC	F:kinase activity; P:phosphorylation	mobidb-lite (MOBIDB_LITE); mobidb-lit	26,450	23,629	25,084	20,854	21,591									
Solyc05g009980	Decapping 5 (AHRD V3.3 *** A0A061EB44_THECC)		C:GO:0000932; F:GC	C:P-body; F:mRNA binding; C:cytosol; P:positive regulation of c	IPR025609 (SMART); IPR019050 (SM	385,385	293,143	348,855	323,934	335,605									
Solyc05g009990	Leucine-rich repeat family protein (AHRD V3.3 *** A0A061ECS2_THECC)		F:GO:0005515	F:protein binding	PR00019 (PRINTS); IPR032675 (G3D	0,548	0,992	0,112	0,073	0,094									
Solyc05g010000	LOW QUALITY:Protein IDA (AHRD V3.3 *** A0A0B2RXU6_GLYSO)		P:GO:0010227	P:floral organ abscission	mobidb-lite (MOBIDB_LITE); IPR0396	0,000	0,018	0,000	0,000	0,000									
Solyc05g010030	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT3G25640.2)				IPR006460 (PFAM); IPR006460 (TIGF	2,171	2,729	0,093	0,051	0,165									
Solyc05g010040	homeodomain GLABROUS 2 (AHRD V3.3 --* AT1G05230.9)		F:GO:0016787	F:hydrolase activity	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc05g010050	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G26120.1)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	8,279	7,236	6,063	6,372	6,355									
Solyc05g010060	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A072TS35_MEDTR)		C:GO:0005802; C:GC	C:trans-Golgi network; C:plasma membrane; F:phosphate ion tra	IPR004331 (PFAM); mobidb-lite (MOB	0,654	0,505	0,047	0,000	0,046									
Solyc05g010070	DNL-type zinc finger protein (AHRD V3.3 *** W9R2L6_9ROSA)		F:GO:0008270	F:zinc ion binding	IPR007853 (PFAM); PTHR20922:SF1	1,056	1,027	0,984	1,266	1,108									
Solyc05g010080	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT1G62970.1)		F:GO:0005199	F:structural constituent of cell wall	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,884	0,496	0,508	0,683	0,688									
Solyc05g010100	Cytidine/deoxycytidylate deaminase family protein (AHRD V3.3 *** B9HIU1_POPTR)		P:GO:0002100; F:GC	P:tRNA wobble ade EC:3.5.4.4 Adenosine deaminas	IPR002125 (PFAM); G3DSA:3.40.140	62,081	54,244	73,431	75,642	75,575									
Solyc05g010120	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IZF0_SOLCH)		F:GO:0000287; F:GC	F:magnesium ion bi EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	PR00119 (PRINTS); PF13246 (PFAM)	48,391	46,401	22,848	26,259	33,883			0,564	0,009				up	
Solyc05g010130	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G25597.1)		C:GO:0016021	C:integral component of membrane	PTHR33264 (PANTHER); PTHR33264	0,058	0,059	0,068	0,050	0,120									
Solyc05g010140	Receptor protein kinase (AHRD V3.3 *-* T2C4B6_BRAJU)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	PR01217 (PRINTS); IPR000719 (SMA	45,578	37,248	33,881	34,397	32,628									
Solyc05g010150	HD domain-containing protein 2 (AHRD V3.3 *** A0A1D1XLV3_9ARAE)		F:GO:0002953	F:5'-deoxynucleotidase activity	IPR003607 (SMART); IPR006674 (PF	8,234	8,174	10,927	10,763	9,971									
Solyc05g010160	Importin, putative (AHRD V3.3 *** B9RLA7_RICCO)		P:GO:0006886; F:GC	P:intracellular protein transport; F:Ran GTPase binding	IPR001494 (SMART); IPR001494 (PF	62,610	54,340	36,296	32,923	32,594									
Solyc05g010180	Carotenoid isomerase (AHRD V3.3 *** A0A077EPD5_TOBAC)	CRTISO-Like 1	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process	IPR036188 (G3DSA:3.50.50.GENE3D	16,117	24,086	28,409	30,741	56,388	0,605	0,025	0,986	0,000			up	up	
Solyc05g010200	LOW QUALITY:L-ascorbate oxidase (AHRD V3.3 --* Q9ZR61_CUCME)				mobidb-lite (MOBIDB_LITE)	0,077	0,292	0,000	0,000	0,000									
Solyc05g010220	LOW QUALITY:F-box protein (AHRD V3.3 *** W9SM54_9ROSA)		F:GO:0005515	F:protein binding	IPR001810 (SMART); G3DSA:1.20.12	0,019	0,021	0,000	0,000	0,000									
Solyc05g010240	Chaperonin-60 beta subunit (AHRD V3.3 *** P93570_SOLTU)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; P:protein refolding	IPR001844 (PRINTS); IPR002423 (PF	3,620	4,838	3,375	1,750	4,287									
Solyc05g010260	6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *** M1CCQ2_SC	6PGD2	F:GO:0004616; P:GC	F:phosphogluconate EC:1.1.1.44 Phosphogluconate de	IPR006183 (PRINTS); IPR006114 (SM	74,467	80,094	103,879	86,468	94,526									
Solyc05g010270	LOW QUALITY:piezo-type mechanosensitive ion channel component (AHRD V3.3 --* AT2G48060.3)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,215	0,189	0,050	0,101	0,117									
Solyc05g010280	LAG1 longevity assurance-like protein (AHRD V3.3 *** AT1G13580.3)		C:GO:0016021	C:integral component of membrane	IPR006634 (SMART); IPR006634 (PF	17,586	17,366	25,726	25,451	24,802									
Solyc05g010290	trigger factor (AHRD V3.3 *** AT3G25545.1)		C:GO:0005783; P:GC	C:endoplasmic reticulum; P:proteasome assembly	IPR016565 (PFAM); PTHR37227 (PAN	10,061	8,892	13,750	17,635	14,842									
Solyc05g010300	DNA-directed RNA polymerase family protein (AHRD V3.3 *** AT2G15430.1)		F:GO:0003899; P:GC	F:DNA-directed 5'-3 EC:2.7.7.6 DNA-directed RNA pc	IPR011263 (SMART); IPR011263 (PF	25,539	25,599	34,640	32,885	32,504									
Solyc05g010310	Chalcone-flavonone isomerase family protein (AHRD V3.3 *** K4BXK4_SOLLC)	CHI	F:GO:0016872	F:intramolecular lyase activity	IPR016087 (PFAM); IPR016088 (G3D	0,000	0,018	0,000	0,000	0,023									
Solyc05g010320	Chalcone-flavonone isomerase family protein (AHRD V3.3 *** K4BXK5_SOLLC)	CHI	F:GO:0016872	F:intramolecular lyase activity	IPR016087 (PFAM); IPR016088 (G3D	23,827	20,331	4,827	4,537	4,657									
Solyc05g010330	Peroxidase (AHRD V3.3 *** K4BXK6_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,155	0,018	0,162	0,242	0,212									
Solyc05g010340	Uridine kinase (AHRD V3.3 *** A0A0K9NRI5_ZOSMR)		F:GO:0005524; F:GC	F:ATP binding; F:kinase activity	PR00988 (PRINTS); IPR006083 (PFA	3,822	4,652	22,278	28,952	20,139									
Solyc05g010350	F-box/RNI-like superfamily protein (AHRD V3.3 *** A0A061E967_THECC)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	3,060	2,980	2,166	2,119	2,287									
Solyc05g010390	LOW QUALITY:Glycosyl hydrolase superfamily protein (AHRD V3.3 --* AT1G45191.1)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane; F:transmembrane transporter activity; P:transmembra		0,000	0,021	0,000	0,000	0,023									
Solyc05g010400	NSP-interacting kinase 1 (AHRD V3.3 *** AT5G16000.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART); IPR013210 (PF	10,467	7,607	1,704	1,311	1,418									
Solyc05g010420	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 *** DCAM_SOLCI)		F:GO:0004014; P:GC	F:adenosylmethioni EC:4.1.1.5 Adenosylmethionine	IPR001985 (PIRSF); IPR001985 (TIGI	1613,077	1827,151	8868,071	10611,554	8369,520									
Solyc05g010423	S-adenosylmethionine decarboxylase uORF (AHRD V3.3 *-* Q6RUQ6_DAUCA)		F:GO:0004014; P:GC	F:adenosylmethioni EC:4.1.1.5 Adenosylmethionine	IPR012511 (PFAM); PTHR35727 (PAN	210,439	227,850	1032,438	1267,532	970,460									
Solyc05g010427	aminoalcoholphosphotransferase (AHRD V3.3 *-* AT3G25585.6)		P:GO:0008654; C:GC	P:phospholipid biosynthetic process; C:membrane; C:integral cc	IPR014472 (PANTHER); PTHR10414:	11,794	12,480	13,265	14,924	13,942									
Solyc05g010440	aminoalcoholphosphotransferase (AHRD V3.3 *-* AT3G25585.4)		F:GO:0004142; F:GC	F:diacylglycerol chc EC:2.7.8.1; EC:2.7.8 Ethanolaminephosph	IPR014472 (PANTHER); PTHR10414:	9,656	9,609	10,984	10,651	11,037									
Solyc05g010450	LOW QUALITY:micronuclear linker histone polyprotein-like protein (AHRD V3.3 *-* AT3G25590.1)				PTHR34197 (PANTHER); PTHR34197	19,985	19,072	14,208	18,627	13,642									
Solyc05g010470	Transducin family protein (AHRD V3.3 *** B9I9Y8_POPTR)		F:GO:0005515; C:GC	F:protein binding; C:nucleolus; P:rRNA processing	IPR020472 (PRINTS); IPR001680 (SM	28,231	29,650	25,598	22,578	21,673									
Solyc05g010475	DUF1262 family protein (AHRD V3.3 *** A0A072UEA2_MEDTR)				IPR010683 (PFAM); PTHR31050 (PAN	0,000	0,000	0,025	0,000	0,000									
Solyc05g010515	BTB/POZ domain-containing protein (AHRD V3.3 --* AT1G55760.1)					0,116	0,122	0,075	0,048	0,095									
Solyc05g010517	BZip transcription factor (AHRD V3.3 *** Q9AT29_PHAVU)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (SMART); IPR004827 (PF	0,864	0,532	1,414	3,827	2,003					1,414	0,001			up
Solyc05g010530	Protein kinase family protein (AHRD V3.3 *-* AT5G38210.2)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); PIRSF000654 (	19,919	24,035	9,552	9,604	11,628									
Solyc05g010550	LOW QUALITY:1-acyl-sn-glycerol-3-phosphate acyltransferase 2 (AHRD V3.3 --* LPAT2_ARATH)		F:GO:0005509; C:GC	F:calcium ion binding; C:membrane; C:integral component of membrane		0,102	0,330	0,025	0,000	0,024									
Solyc05g010565	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 -** A7KHC0_MEDTR)				PS51257 (PROSITE_PROFILES)	0,160	0,608	0,000	0,000	0,000									
Solyc05g010570	Transcription initiation factor TFIID subunit 11 (AHRD V3.3 *** A0A0B0NA85_GOSAR)		C:GO:0005634; P:GC	C:nucleus; P:transcription initiation from RNA polymerase II proi	IPR009072 (G3DSA:1.10.20.GENE3D	23,549	19,568	29,556	31,010	30,492									
Solyc05g010580	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 --* A7KH83_MEDTR)				PS51257 (PROSITE_PROFILES)	4,176	4,205	0,000	0,000	0,000									
Solyc05g010583	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 -** G7JBC9_MEDTR)					1,216	2,172	0,000	0,000	0,000									
Solyc05g010585	Defensin-like (DEFL) family protein (AHRD V3.3 -** AT2G04046.1)					0,000	0,058	0,000	0,000	0,000									
Solyc05g010590	WPP domain-interacting tail-anchored protein 1 (AHRD V3.3 *** A0A1D1YXK4_9ARAE)		C:GO:0016021; P:GC	C:integral component of membrane; P:regulation of establishme	mobidb-lite (MOBIDB_LITE); IPR0399	5,227	9,605	5,590	6,165	7,100	0,902	0,014					up		
Solyc05g010600	Unknown protein (AHRD V3.3)					0,000	0,021	0,000	0,000	0,000									
Solyc05g010610	bHLH transcription factor 039		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	7,268	6,670	6,210	5,474	5,979									

Solyc05g010620	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HWT0_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM); IPR002885 (F	3,072	2,893	1,945	2,181	2,190									
Solyc05g010630	LOW QUALITY:Redox-regulatory protein FAM213A-like protein (AHRD V3.3 *-* A0A0B2R8Q7_GLYSO)		P:GO:0055114	P:oxidation-reduction process			IPR032801 (PFAM); IPR032801 (PAN	0,059	0,172	0,047	0,000	0,000									
Solyc05g010640	LOW QUALITY:Redox-regulatory protein FAM213A (AHRD V3.3 *** A0A1D1Y8W1_9ARAE)		P:GO:0055114	P:oxidation-reduction process			PTHR28630:SF13 (PANTHER); IPR03	0,935	1,204	0,708	0,735	0,682									
Solyc05g010645	DNA-directed RNA polymerase subunit (AHRD V3.3 --* Q9LNK0_ARATH)							0,019	0,000	0,000	0,000	0,000									
Solyc05g010650	U box domain-containing protein (AHRD V3.3 *-* A0A103YA23_CYNCS)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR003613 (SMART); IPR000225 (SM	1,445	1,064	0,000	0,000	0,023									
Solyc05g010660	DNA-directed RNA polymerase (AHRD V3.3 *** K4BXN8_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p	IPR029262 (SMART); G3DSA:3.30.70	27,720	22,324	24,899	25,270	24,404									
Solyc05g010670	Heat shock family protein (AHRD V3.3 *** B9HWT4_POPTR)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			G3DSA:3.30.230.80 (GENE3D); IPR0:	403,657	519,963	824,971	802,204	856,663									
Solyc05g010680	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G30380.2)		F:GO:0016787	F:hydrolase activity			IPR022742 (PFAM); IPR029058 (G3D	0,159	0,417	0,025	0,000	0,024									
Solyc05g010710	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XX62_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); G3D	12,977	14,616	1,182	0,827	1,059									
Solyc05g010720	Enoyl-CoA hydratase/isomerase family protein (AHRD V3.3 *** B9HTL0_POPTR)		F:GO:0003824	F:catalytic activity			G3DSA:3.90.226.10 (GENE3D); IPR0(	2,003	1,283	1,453	1,495	1,907									
Solyc05g010730	N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein (AHRD V3.3 *-* AT3G58130.2)		F:GO:0000225; P:G(	F:N-acetylglucosam	EC:3.5.1.89	N-acetylglucosaminyl	IPR003737 (PANTHER); IPR039516 (I	0,000	0,000	0,025	0,025	0,023									
Solyc05g010750	Myosin heavy chain-related (AHRD V3.3 *-* A0A061GI21_THECC)		C:GO:0016021	C:integral component of membrane			PTHR34360 (PANTHER); PTHR34360	0,484	0,303	0,340	0,338	0,448									
Solyc05g010760	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT3G22250.1)							0,595	0,445	0,813	0,757	0,847									
Solyc05g010770	Pre-mRNA splicing Prp18-interacting factor (AHRD V3.3 --* AT4G37120.1)						mobidb-lite (MOBIDB_LITE)	2,147	2,153	1,647	1,409	1,531									
Solyc05g010775	CDK-activating kinase 1AT (AHRD V3.3 --* AT4G28980.3)							1,218	1,167	0,833	0,738	0,610									
Solyc05g010780	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HWT8_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	5,294	5,198	4,319	4,258	3,652									
Solyc05g010790	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9RLG0_RICCO)						PTHR24015 (PANTHER); PTHR24015	1,252	1,406	0,824	0,750	1,018									
Solyc05g010800	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9RLG1_RICCO)		P:GO:0006284; F:G(	P:base-excision re	EC:3.2.2.21; EC:3.2.	DNA-3-methyladenine	G3DSA:1.10.340.30 (GENE3D); IPR0(	0,019	0,000	0,000	0,000	0,000									
Solyc05g010810	Phosphatidylinositol 4-kinase (AHRD V3.3 *** J3R305_GOSBA)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR000403 (PFAM); mobidb-lite (MOB	293,747	163,699	808,189	691,107	624,194	-0,816	0,002					down		
Solyc05g011810	bHLH transcription factor 040		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	13,382	11,676	12,378	11,324	10,854									
Solyc05g011820	Prolyl oligopeptidase family protein (AHRD V3.3 *** AT1G69020.2)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bo	IPR002470 (PRINTS); G3DSA:2.130.1	3,045	2,644	0,669	1,238	1,199									
Solyc05g011825	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 --* A0A1D1YIL4_9ARAE)							0,000	0,000	0,000	0,022	0,023									
Solyc05g011830	18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *-* AT2G03810.7)		P:GO:0009786	P:regulation of asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	22,224	16,483	57,450	77,322	58,603					0,432	0,014			up
Solyc05g011840	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein (AHRD V3.3 --* AT4G14350.4)							0,042	0,000	0,022	0,047	0,000									
Solyc05g011850	Sulfotransferase (AHRD V3.3 *** K4BXQ8_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,080	0,000	0,022	0,047	0,000									
Solyc05g011860	Sulfotransferase (AHRD V3.3 *** K4BXQ9_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,078	0,019	0,000	0,000	0,071									
Solyc05g011870	Sulfotransferase (AHRD V3.3 *** K4BXR0_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM); G3DSA:3.40.50.3	0,211	0,134	0,000	0,000	0,000									
Solyc05g011880	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** A0A072UHY2_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR010237 (TIGRFAM); IPR010237 (F	0,021	0,000	0,000	0,000	0,000									
Solyc05g011890	Sulfotransferase (AHRD V3.3 *** K4BXR2_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM); G3DSA:3.40.50.3	8,487	6,897	14,905	9,102	6,495			-1,202	0,000	-0,711	0,039		down	down
Solyc05g011900	Sulfotransferase (AHRD V3.3 *** K4BXR3_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,482	0,209	0,000	0,000	0,000									
Solyc05g011920	ACT domain-containing protein (AHRD V3.3 *** A0A118JXJ7_CYNCS)		P:GO:0009735	P:response to cytokinin			G3DSA:3.30.70.260 (GENE3D); IPR0(	6,367	14,300	6,417	5,247	5,670	1,192	0,001					up		
Solyc05g011930	Chaperone DnaJ-domain containing protein (AHRD V3.3 *-* Q8RWZ0_ARATH)						IPR036869 (G3DSA:1.10.287.GENE3I	15,829	16,227	14,684	14,445	13,823									
Solyc05g011950	Chaperone DnaJ-domain containing protein (AHRD V3.3 *-* Q8RWZ0_ARATH)		C:GO:0016021	C:integral component of membrane			IPR036869 (G3DSA:1.10.287.GENE3I	0,040	0,019	0,000	0,022	0,000									
Solyc05g011960	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103YBW3_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR036869 (G3DSA:1.10.287.GENE3I	6,046	9,730	8,632	16,965	12,388					0,978	0,000			up
Solyc05g011970	Cytochrome P450 (AHRD V3.3 *** A0A103XV52_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	12,698	22,489	16,307	30,797	24,456					0,922	0,000			up
Solyc05g011980	Photosystem II reaction center protein M (AHRD V3.3 --* PSBM_PHYPA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR039926 (PANTHER); PTHR33333:	150,310	152,500	75,702	52,336	61,614					-0,530	0,001			down
Solyc05g011990	Nucleolar 14 (AHRD V3.3 *** A0A0B0NLB8_GOSAR)		C:GO:0032040	C:small-subunit processome			IPR007276 (PFAM); mobidb-lite (MOB	23,507	23,866	26,472	24,839	21,226									
Solyc05g012000	Adenine nucleotide alpha hydrolases-like superfamily protein, putative (AHRD V3.3 *** A0A061FX93_THECC)						IPR014729 (G3DSA:3.40.50.GENE3D	0,578	0,555	0,072	0,000	0,000									
Solyc05g012010	RING/U-box superfamily protein (AHRD V3.3 *** AT5G15790.5)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART); IPR013083 (G3	8,008	7,101	21,072	24,944	19,485									
Solyc05g012020	Ontology_term=GO:0003700,GO:0046982	RIN	F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN1 MIKC_MADS	2,688	2,245	395,946	486,023	338,544									
Solyc05g012030	LOW QUALITY:Protein BIG GRAIN 1-like E (AHRD V3.3 *** BIG1E_ARATH)		P:GO:0009734	P:auxin-activated signaling pathway			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,259	0,373	0,022	0,000	0,000									
Solyc05g012040	Squamosa promoter binding protein 6b		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR004333 (PFAM SBP	6,047	6,865	13,832	15,974	13,909									
Solyc05g012045	Mov34/MPN/PAD-1 family protein (AHRD V3.3 --* AT3G06820.3)							0,063	0,184	0,193	0,218	0,094									
Solyc05g012050	CRABS CLAW b	CRCb	P:GO:0007275	P:multicellular organism development			IPR006780 (PFAM YABBY	0,000	0,000	0,022	0,000	0,024									
Solyc05g012060	Histone-lysine N-methyltransferase ATX1, putative isoform 2 (AHRD V3.3 *-* A0A061E9H7_THECC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:negative regulation of cell popula			G3DSA:3.30.160.360 (GENE3D); IPR(	5,508	4,171	3,613	2,669	3,571									
Solyc05g012070	UDP-glucose:protein transglucosylase-like protein	UPTG1	F:GO:0016866; P:G(	F:intramolecular transferase activity; P:plant-type cell wall orgar			IPR037595 (PFAM); IPR004901 (PIRS	62,906	73,813	65,912	61,112	56,522									
Solyc05g012080	cytochrome b5 isoform B		C:GO:0016021; F:G(	C:integral component of membrane; F:heme binding; F:metal ior			IPR001199 (PRINTS); IPR001199 (SM	4,593	6,749	7,828	7,171	7,249									
Solyc05g012090	Dihydropterin pyrophosphokinase-dihydropteroate synthase (AHRD V3.3 *** C5IXL4_SOLLC)		F:GO:0003848; F:G(	F:2-amino-4-hydrox	EC:2.5.1.15; EC:2.7.	Dihydropteroate synt	IPR000550 (PFAM); IPR000489 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc05g012100	Fructokinase-like protein 2 (AHRD V3.3 *** D9IWP0_NICBE)		C:GO:0000427; P:G(	C:plastid-encoded p	EC:2.7.1.4; EC:2.7.1	Fructokinase; Hexoki	IPR029056 (G3DSA:3.40.1190.GENE:	16,177	19,105	62,089	60,808	62,316									
Solyc05g012110	6-phosphogluconolactonase, putative (AHRD V3.3 *** B9REC3_RICCO)	PGLS	P:GO:0005975; P:G(	P:carbohydrate met	EC:3.1.1.31; EC:3.1.	6-phosphogluconolac	IPR006148 (PFAM); G3DSA:3.40.50.1	32,363	25,069	27,460	26,386	29,665									
Solyc05g012120	Ribosome maturation factor RimP (AHRD V3.3 *** A0A0B2RDN8_GLYSO)		P:GO:0042274	P:ribosomal small subunit biogenesis			PTHR34544 (PANTHER); PTHR34544	5,169	5,726	8,178	7,341	7,624									
Solyc05g012130	Ser/Thr protein kinase (AHRD V3.3 *** B3GK00_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	50,058	44,351	60,932	59,787	58,359									
Solyc05g012140	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061GZ24_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	30,634	22,693	33,065	22,143	27,971					-0,575	0,000			down
Solyc05g012150	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial (AHRD V3.3 *** K4BXT8_SOLLC)		C:GO:0005743; P:G(	C:mitochondrial inner membrane; P:ubiquinone biosynthetic proc			IPR007715 (PFAM); IPR027540 (PTH	6,731	6,388	11,915	10,322	10,396									
Solyc05g012160	SPIRAL1-like1 (AHRD V3.3 *** AT1G26355.1)		P:GO:0043622	P:cortical microtubule organization			mobidb-lite (MOBIDB_LITE); mobidb-lit	147,541	150,512	112,620	93,580	102,164									
Solyc05g012170	Ferredoxin--NADP reductase, root isozyme 2, chloroplastic (AHRD V3.3 --* FNRR2_ARATH)							0,000	0,039	0,000	0,000	0,000									
Solyc05g012172	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G40910.9)							0,000	0,021	0,000	0,000	0,000									
Solyc05g012174	Defensin protein (AHRD V3.3 --* A0A0S4LZC9_VIGRA)							0,021	0,039	0,000	0,000	0,000									
Solyc05g012176	low-molecular-weight cysteine-rich 35 (AHRD V3.3 -** AT2G22121.1)							0,040	0,076	0,000	0,000	0,000									
Solyc05g012180	methyl esterase 13 (AHRD V3.3 *** AT1G26360.1)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM); IPR029058 (G3D	0,000	0,274	0,022	0,118	0,235									
Solyc05g012190	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART); IPR003959 (PF.	13,512	11,425	9,296	7,741	9,560									
Solyc05g012200	Asparagine synthetase, putative (AHRD V3.3 *** B9REC9_RICCO)		F:GO:0004066; P:G(	F:asparagine synth	EC:6.3.5.4	Asparagine synthase	IPR001962 (PFAM); IPR017932 (PFA	10,073	11,890	11,397	11,565	11,559									
Solyc05g012210	Ninja-family protein AFP1-like protein (AHRD V3.3 *** V5KZR9_SOLNI)		P:GO:0007165	P:signal transduction			IPR032308 (PFAM); IPR032310 (PFA	1,615	6,161	0,489	0,941	0,915	1,947	0,001					up		
Solyc05g012220	Magnesium transporter MRS2-like protein (AHRD V3.3 *** G7ZYX9_MEDTR)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:2.40.128.330 (GENE3D); IPR(	5,852	5,249	5,956	6,878	6,464									
Solyc05g012230	Protein POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND REDISTRIBUTION (AHRD V3.3 --*		P:GO:0008356	P:asymmetric cell division			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,266	2,650	3,177	3,549	4,273									
Solyc05g012240	Nuclear transport factor 2 family protein with RNA binding domain, putative isoform 2 (AHRD V3.3 *** A0A06		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR002075 (PF.	0,526	1,072	1,178	0,531	1,501									
Solyc05g012250	Purple acid phosphatase (AHRD V3.3 --* A0A0V0INC4_SOLCH)							1,965	2,038	2,411	2,069	1,932									
Solyc05g012253	cysteine-rich receptor-like protein kinase 17 (AHRD V3.3 --* AT4G23250.3)							0,376	0,580	0,570	0,465	0,423									
Solyc05g012257	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RV44_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,498	1,847	1,947	2,032	1,594									
Solyc05g012260	Purple acid phosphatase (AHRD V3.3 *** A0A0V0IMQ9_SOLCH)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR015914 (PFAM); IPR004843 (PFA	59,334	52,640	76,567	73,349	71,253									
Solyc05g012270	Argininosuccinate synthase (AHRD V3.3 *** K4BXV0_SOLLC)		F:GO:0004055; F:G(	F:argininosuccinate	EC:6.3.4.5	Argininosuccinate sy	IPR001518 (PFAM); IPR014729 (G3D	41,055	46,071	161,255	149,748	154,453									
Solyc05g012280	Wall-associated receptor kinase-like 20 (AHRD V3.3 *** A0A0B0NFE1_GOSAR)		F:GO:0030247	F:polysaccharide binding			IPR025287 (PFAM); IPR032872 (PFA	0,119	0,253	0,000	0,050	0,023									
Solyc05g012290	UPF0420 protein C16orf58 like (AHRD V3.3 *** A0A0B2P340_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR006968 (PFAM); IPR006968 (PAN	23,369	18,761	5,730	5,899	5,745									
Solyc05g012310	WD repeat-containing protein (AHRD V3.3 *** A0A0K9P960_ZOSMR)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	4,010	4,411	6,009	6,059	5,753									
Solyc05g012320	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G63010.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR001680 (PF.	0,658	0,694	0,308	0,241	0,165									
Solyc05g012330	Ureide permease (AHRD V3.3 *-* A0A124SG70_CYNCS)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR009834 (PFAM); IPR030189 (PAN	12,686	11,889	11,383	13,968	13,140									
Solyc05g012340	SPFH domain/band 7 family protein (AHRD V3.3 *** G7JHI5_MEDTR)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:ubiquitin-dependent ERAD pathway;			IPR001107 (SMART); IPR001107 (PF.	24,063	24,474	22,911	23,647	23,983									
Solyc05g012350	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G13820.1)		F:GO:0016620; F:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR000073 (PRINTS); IPR029058 (G3	0,172	0,154	0,141	0,048	0,000									
Solyc05g012360	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G13820.1)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS); IPR000073 (PF	0,861	1,192	0,557	0,534	0,330									
Solyc05g012370	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G13820.1)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS); IPR000073 (PF	3,810	5,844	2,008	2,316	3,408									
Solyc05g012380	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** A0A0B2R8X2_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR012946 (SMART); IPR012946 (PF.	3,965	3,733	0,792	0,507	1,037									
Solyc05g012390	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K383_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	29,537	29,013	45,110	41,733	41,596									
Solyc05g012400	Chromatin modification-related protein EAF7 (AHRD V3.3 *** A0A1D1ZI31_9ARAE)		P:GO:0006355; C:G(	P:regulation of transcription, DNA-templated; C:H4/H2A histone			IPR012423 (PFAM); IPR012423 (PAN	21,371	19,620	18,901	17,524	16,619									
Solyc05g012410	Chromatin modification-related protein EAF7 (AHRD V3.3 *** A0A1D1ZI31_9ARAE)		P:GO:0006355; C:G(	P:regulation of transcription, DNA-templated; C:H4/H2A histone			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,085	0,698	0,000	0,000	0,000									
Solyc05g012420	14-3-3 protein, putative (AHRD V3.3 *** B9REF4_RICCO)		F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS); IPR023410 (SM	0,019	0,000	0,000	0,000	0,000									
Solyc05g012430	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR001611 (PFA	0,059	0,081	0,025	0,050	0,047									
Solyc05g012440	cytochrome c oxidase assembly protein CtaG / Cox11 family (AHRD V3.3 *** AT1G02410.3)		F:GO:0005507	F:copper ion binding			IPR007533 (PFAM); IPR023471 (G3D	9,217	9,856	10,281	10,968	11,761									
Solyc05g012450	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G78240.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	52,238	37,550	83,983	101,045	86,714									
Solyc05g012460	Cobalamin biosynthesis CobW-like protein (AHRD V3.3 *** AT1G26520.1)						IPR011629 (SMART); IPR036627 (G3	13,776	11,960	18,951	16,932	17,821									
Solyc05g012480	Mitochondrial processing peptidase (AHRD V3.3 *** Q41445_SOLTU)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			IPR007863 (PFAM); IPR011765 (PFA	57,960	62,297	138,070	136,255	126,754									
Solyc05g012490	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HID5_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,042	0,037	0,050	0,050	0,046									
Solyc05g012500	WRKY transcription factor 57	WRKY57	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	51,392	56,420	46,394	54,538	48,701									
Solyc05g012510	Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** K4BXX3_SOLLC)		P:GO:0005975; F:G(	P:carbohydrate met	EC:2.4.1.1	Glycogen phosphoryl	IPR000811 (PIRSF); G3DSA:3.40.50.:	220,964	288,123	41,127	38,709	87,645			1,087	0,000				up	
Solyc05g012520	SNAP25 like protein SNAP33 (AHRD V3.3 *** A0A0B2SW23_GLYSO)		C:GO:0005886	C:plasma membrane			IPR000727 (SMART); G3DSA:1.20.5.1	0,101	0,060	0,096	0,025	0,023									
Solyc05g012530	LOW QUALITY:POZ/BTB containin G-protein 1 (AHRD V3.3 --* AT3G61600.2)							0,540	0,581	0,000	0,000	0,000									
Solyc05g012540	Heparanase, putative (AHRD V3.3 *** B9RCW6_RICCO)		C:GO:0016020; F:G(	C:membrane; F:hydrolase activity, acting on glycosyl bonds			G3DSA:3.20.20.80 (GENE3D); IPR00!	0,040	0,096	0,143	0,168	0,093									
Solyc05g012550	Remorin family protein (AHRD V3.3 *-* AT5G61280.2)		F:GO:0003677; F:G(	F:DNA binding; F:tra	EC:3.6.1.15	Nucleoside-triphosph	IPR005516 (PFAM); mobidb-lite (MOB	0,196	0,276	0,197	0,145	0,118									
Solyc05g012560	ripening regulated protein (DDTFR7)	ddtfr7	C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity; F:metal ioi			IPR001841 (SMART); IPR013083 (G3	37,518	24,426	32,814	35,479	31,023	-0,591	0,018					down		
Solyc05g012570	LOW QUALITY:Nodulin-related protein 1, putative (AHRD V3.3 *-* A0A061EHK7_THECC)		P:GO:0009408; P:G(	P:response to heat; P:regulation of abscisic acid biosynthetic p			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,098	0,563	0,093	0,022	0,023									
Solyc05g012580	cation/H+ exchanger 19 (AHRD V3.3 --* AT3G17630.2)							278,663	293,366	71,681	49,524	67,011					-0,531	0,001			down
Solyc05g012590	Ankyrin repeat family protein (AHRD V3.3 *** AT2G03430.1)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS); IPR002110 (SM	20,612	22,645	21,200	16,350	17,195									
Solyc05g012600	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 --* AT3G59570.3)						PTHR36730 (PANTHER)	4,934	10,079	4,300	4,713	9,866	1,057	0,031	1,185	0,000			up	up	
Solyc05g012610	appr-1-p processing enzyme family protein (AHRD V3.3 *** AT1G69340.2)						IPR001251 (SMART); IPR002589 (SM	50,990	41,304	73,238	72,316	68,040									
Solyc05g012620	uvrB/uvrC motif-containing protein (AHRD V3.3 *** AT2G03390.4)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR011722 (SMART); IPR001943 (PF.	28,448	37,434	36,227	38,815	48,884			0,429	0,005				up	
Solyc05g012630	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061EBM2_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	1,245	2,079	1,107	1,460	1,202									
Solyc05g012640	T-box transcription factor, putative (DUF863) (AHRD V3.3 *** AT1G69360.1)						IPR008581 (PFAM); mobidb-lite (MOB	34,150	27,245	21,676	23,037	23,985									
Solyc05g012650	T-box transcription factor, putative (DUF863) (AHRD V3.3 *** AT1G69360.1)						IPR008581 (PFAM); mobidb-lite (MOB	29,009	23,119	21,596	20,958	25,277									
Solyc05g012660	Glycosyltransferase, putative (AHRD V3.3 *** B9RCX8_RICCO)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM); IPR007657 (PAN	0,176	0,389	0,409	1,313	0,967									
Solyc05g012670	Glycosyltransferase (AHRD V3.3 *** K4DC82_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR(	4,622	5,319	0,473	0,665	1,107									
Solyc05g012680	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT2G03350.1)						IPR007493 (PFAM); IPR036758 (G3D	6,821	6,431	0,941	1,185	1,411									
Solyc05g012690	Sporulation RMD1 (AHRD V3.3 *** A0A0B0MRY3_GOSAR)		C:GO:0005739; P:G(	C:mitochondrion; P:regulation of root meristem growth; P:regula			IPR003734 (PFAM); PTHR16255:SF9	16,631	19,100	33,595	37,863	30,984									
Solyc05g012700	integral membrane family protein (AHRD V3.3 *** AT1G28140.1)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane			IPR019275 (PFAM); PTHR36716:SF2	28,098	30,264	64,110	68,101	73,328									
Solyc05g012710	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* A0A061EA43_THI	MinE	F:GO:0005515; P:G(	F:protein binding; P:regulation of division septum assembly			IPR001680 (SMART); IPR015943 (G3	8,613	11,368	19,848	21,055	21,511									
Solyc05g012720	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061EA43_THECC)		F:GO:0005515	F:protein binding			IPR001680 (SMART); IPR015943 (G3	0,969	1,015	0,899	1,333	1,126									
Solyc05g012740	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0005515; F:G(	F:protein binding; F:ADP binding			PR00364 (PRINTS); IPR021929 (PFA	0,000	0,000	0,000	0,000	0,071									
Solyc05g012770	WRKY transcription factor 4	WRKY4	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	4,980	10,862	18,389	21,147	18,608	1,147	0,004					up		
Solyc05g012780	DUF1336 family protein (DUF1336) (AHRD V3.3 *** AT3G29180.3)						IPR009769 (PFAM); PTHR31558:SF1	1,559	1,502	0,351	0,661	0,777									
Solyc05g012790	S-acyltransferase (AHRD V3.3 *** K4BY01_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM); mobidb-lite (MOB	11,645	11,067	2,106	1,797	1,896									
Solyc05g012800	LOW QUALITY:UDP-N-acetylmuramoylalanine--D-glutamate ligase (AHRD V3.3 *** A0A0B0MT50_GOSAR)		F:GO:0005524; C:G(	F:ATP binding; C:cy	EC:6.3.2.9	UDP-N-acetylmuram	IPR013221 (PFAM); G3DSA:3.40.50.7	11,006	11,208	6,155	5,045	6,881									
Solyc05g012805	transmembrane protein (AHRD V3.3 *** AT3G11810.1)		C:GO:0016020	C:membrane			PTHR33133 (PANTHER); PTHR33133	21,815	19,811	10,533	11,898	14,085									
Solyc05g012820	transmembrane protein (AHRD V3.3 *** AT3G11810.1)		C:GO:0016021	C:integral component of membrane			PTHR33133 (PANTHER); PTHR33133	6,985	5,579	14,945	13,511	13,141									
Solyc05g012823	Nucleotide-diphospho-sugar transferase family protein (AHRD V3.3 --* AT1G70630.5)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,080	0,082	0,050	0,000	0,048									
Solyc05g012840	LOW QUALITY:TCP transcription factor 1 (AHRD V3.3 *** G3BGU2_SOLLC)						IPR017887 (PFAM TCP	0,038	0,037	0,022	0,000	0,023									
Solyc05g012850	transmembrane protein (AHRD V3.3 *** AT3G11810.1)		C:GO:0016021	C:integral component of membrane			PTHR33133:SF7 (PANTHER); PTHR3:	34,972	29,279	20,341	23,793	27,509			0,433	0,034				up	
Solyc05g012870	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072UY68_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33133:SF1 (PANTHER); PTHR3:	0,094	0,059	0,025	0,000	0,000									
Solyc05g012900	JJH-R-like protein		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR021929 (PFA	0,485	2,775	0,577	0,797	1,297	2,524	0,000					up		
Solyc05g012910	NBS-LRR resistance protein-like protein (AHRD V3.3 *-* A1Y9Q6_9SOLN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); G3DSA:3.40.50.3	0,000	0,055	0,072	0,143	0,234									
Solyc05g012915	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,019	0,047	0,000	0,046									
Solyc05g012920	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RL03_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (TIGF	8,680	10,503	7,992	8,211	7,277									
Solyc05g012940	ribonuclease H2 subunit B (AHRD V3.3 *** AT4G20325.1)		C:GO:0032299	C:ribonuclease H2 complex			PF17745 (PFAM); IPR019024 (PFAM)	2,304	2,416	13,136	16,996	10,764									
Solyc05g012950	Sulfotransferase (AHRD V3.3 *** K4BY19_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,237	0,298	1,341	2,115	1,110									
Solyc05g012970	Sulfotransferase (AHRD V3.3 *** K4BY19_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,000	0,000	0,022	0,000	0,000									
Solyc05g013030	26S proteasome non-ATPase regulatory subunit-like protein (AHRD V3.3 *** G7I549_MEDTR)		F:GO:0005198; P:G(	F:structural molecule activity; P:ubiquitin-dependent protein cata			SM00753 (SMART); IPR000717 (SMA	96,233	96,282	124,218	121,393	115,929									
Solyc05g013040	Pattern formation EMB30-like protein (AHRD V3.3 *** A0A0B0NVB0_GOSAR)		F:GO:0005086; P:G(	F:ARF guanyl-nucleotide exchange factor activity; P:regulation (			IPR000904 (SMART); IPR000904 (PF.	32,821	29,442	98,327	98,052	82,776									
Solyc05g013050	Vesicle transport v-SNARE protein (AHRD V3.3 *** A0A0K0XR08_TOBAC)		F:GO:0005484; C:G(	F:SNAP receptor activity; C:Golgi apparatus; P:intracellular prot			IPR000727 (SMART); G3DSA:1.20.5.1	29,434	25,260	39,847	39,755	36,883									
Solyc05g013060	plant/protein (AHRD V3.3 *** AT1G13990.1)						mobidb-lite (MOBIDB_LITE); PTHR371	6,025	5,569	29,721	28,577	28,017									
Solyc05g013070	Protein kinase, putative (AHRD V3.3 *** B9S913_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PRINTS); IPR002110 (SM	64,059	88,923	99,846	102,290	90,783									
Solyc05g013120	LOW QUALITY:Ninja-family protein AFP1 (AHRD V3.3 --* AFP1_ARATH)							4,495	3,804	1,008	1,719	1,831									
Solyc05g013130	Transmembrane emp24 domain-containing protein 10 (AHRD V3.3 *** W9SPK8_9ROSA)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR009038 (SMART); IPR009038 (PF.	23,435	26,518	18,128	13,375	17,889									
Solyc05g013140	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G14020.1)		C:GO:0005737; P:G(	C:cytoplasm; P:fucose metabolic process; C:integral componen			G3DSA:3.40.50.11350 (GENE3D); IPF	1,804	1,508	1,422	1,035	1,108									
Solyc05g013150	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic (AHRD \		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.127	[Ribulose-bisphospha	IPR001214 (SMART); IPR001214 (PF.	3,477	6,105	1,506	1,975	3,055			1,007	0,008				up	

Solyc05g013160	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic (AHRD \		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.127	[Ribulose-bisphospha	IPR001214 (SMART): IPR011192 (PIF	11,674	17,390	28,568	35,333	43,325			0,597	0,002				up	
Solyc05g013170	GCK domain-containing protein (AHRD V3.3 *-* AT1G14060.1)		F:GO:0003746; P:G(	F:translation elongation factor activity; P:translational elongatio			SM01227 (SMART): IPR012891 (PFAI	9,906	11,862	12,304	11,587	9,475									
Solyc05g013180	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A193CD86_9ERIC)		C:GO:0016021	C:integral component of membrane			IPR004342 (PFAM): IPR004331 (PFAI	5,825	4,727	3,462	4,902	4,595									
Solyc05g013190	Ribosomal protein L32 (AHRD V3.3 *** K7VPA9_SOLTU)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR002677 (TIGRFAM): IPR002677 (F	2,070	2,471	1,263	1,780	1,647									
Solyc05g013200	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HY03_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	4,322	4,156	3,802	3,805	3,882									
Solyc05g013203	Ribonuclease (AHRD V3.3 *** Q41722_ZINVI)		F:GO:0003723; F:G(	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bonds	IPR036430 (G3DSA:3.90.730.GENE3I	0,021	0,081	0,000	0,095	0,070									
Solyc05g013205	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 --* A0A0B2RFB6_GLYSO)							0,021	0,000	0,000	0,000	0,000									
Solyc05g013210	S-like ribonuclease (AHRD V3.3 *** B9X1G4_DIOMU)		F:GO:0003723; F:G(	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bonds	IPR036430 (G3DSA:3.90.730.GENE3I	0,080	0,059	0,025	0,047	0,024									
Solyc05g013240	DUF538 family protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G55265.1)		C:GO:0016021	C:integral component of membrane			IPR036758 (G3DSA:2.30.240.GENE3I	9,020	9,164	7,030	6,387	5,763									
Solyc05g013250	F-box/RNI-like superfamily protein (AHRD V3.3 --* AT3G26922.2)							0,299	0,644	0,216	0,197	0,139									
Solyc05g013260	Disease resistance protein, putative (AHRD V3.3 *-* Q6L432_SOLDE)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFAI	10,204	7,694	2,787	3,235	2,878									
Solyc05g013270	Protein kinase (AHRD V3.3 *** Q40234_SOLPI)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,021	0,021	0,022	0,000	0,024									
Solyc05g013280	Pseudomonas resistance		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	16,719	15,735	9,729	10,022	11,881									
Solyc05g013300	Pseudomonas syringae pv tomato resis.	Pto	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	15,701	12,104	9,109	9,256	11,503									
Solyc05g013310	protein kinase family protein (AHRD V3.3 *-* AT5G54380.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	5,736	3,563	2,681	2,488	3,632									
Solyc05g013320	serine/threonine protein kinase Pto		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	12,362	12,559	7,873	7,637	9,082									
Solyc05g013330	zinc finger (Ran-binding) family protein (AHRD V3.3 --* AT2G17975.2)							0,238	0,337	0,415	0,582	0,495									
Solyc05g013340	AP-1 complex subunit mu-1 (AHRD V3.3 *** A0A1D1ZCP5_9ARAE)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS): IPR001392 (PII	92,667	87,027	106,603	109,147	99,933									
Solyc05g013370	LOW QUALITY:MADS-box transcription factor family protein, putative (AHRD V3.3 *-* A0A061DIN1_THECC		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR036879 (G3DS M-type_MADS	0,115	0,098	0,050	0,175	0,071									
Solyc05g013380	Alanine aminotransferase 2 (AHRD V3.3 *** A0A151TGW4_CAJCA)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR004839 (PFAM): IPR015422 (G3D	90,001	119,251	42,559	39,128	68,636			0,686	0,000				up	
Solyc05g013390	Protein Ycf2 (AHRD V3.3 --* A0A0F6T355_9ROSI)							6,526	5,514	5,315	4,549	4,793									
Solyc05g013400	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GR61_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	29,247	24,646	21,650	24,160	25,564									
Solyc05g013410	F-box family protein (AHRD V3.3 *** AT1G70590.1)		F:GO:0005515	F:protein binding			IPR006597 (SMART): IPR011990 (G3	7,724	8,288	3,839	3,984	4,445									
Solyc05g013420	LOW QUALITY:myb-like transcription factor family protein (AHRD V3.3 *-* AT5G61620.1)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,114	0,041	0,000	0,022	0,023									
Solyc05g013430	LOW QUALITY:myb-like transcription factor family protein (AHRD V3.3 *-* AT5G61620.1)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,117	0,059	0,022	0,051	0,023									
Solyc05g013435	LOW QUALITY:LINE-1 reverse transcriptase (AHRD V3.3 --* A0A1D1ZAL7_9ARAE)						IPR026960 (PFAM)	0,063	0,101	0,192	0,200	0,236									
Solyc05g013440	Amine oxidase (AHRD V3.3 *** K4BY65_SOLLC)		F:GO:0005507; F:G(	F:copper ion bindin(	EC:1.4.3.21	Primary-amine oxida:	G3DSA:3.10.450.40 (GENE3D): G3DS	121,423	114,540	161,601	147,972	174,102									
Solyc05g013450	Protein DETOXIFICATION (AHRD V3.3 *** K4BY66_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp(			IPR002528 (PFAM): IPR002528 (TIGF	2,197	4,815	1,188	1,226	2,834									
Solyc05g013460	Protein DETOXIFICATION (AHRD V3.3 *** K4BY67_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp(			IPR002528 (PFAM): IPR002528 (TIGF	16,216	15,878	10,404	9,090	10,543									
Solyc05g013470	Protein DETOXIFICATION (AHRD V3.3 *** K4BY68_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp(			IPR002528 (TIGRFAM): IPR002528 (F	0,040	0,019	0,025	0,076	0,048									
Solyc05g013480	Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *** A0A061E7M0_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	70,920	61,506	135,162	124,999	130,869									
Solyc05g013490	Cyclin-related family protein (AHRD V3.3 *** B9HLR1_POPTR)						IPR031937 (PFAM): mobidb-lite (MOB	83,908	66,462	93,007	94,958	92,039									
Solyc05g013495	DUF4228 domain protein (AHRD V3.3 *-* A0A072VDE1_MEDTR)						IPR025322 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,000	0,023									
Solyc05g013500	Glycosyltransferase (AHRD V3.3 *** A0A0R0ITQ1_SOYBN)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity			IPR005069 (PFAM): IPR025322 (PFAI	1,078	0,995	0,261	0,389	0,283									
Solyc05g013510	Phosphate transporter (AHRD V3.3 *** K4BY72_SOLLC)		F:GO:0005315; P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph			IPR001204 (PFAM): PTHR11101:SF8	26,115	30,682	61,025	53,822	70,473									
Solyc05g013530	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *** A0A0K9NT10_ZOSMR)		F:GO:0005515	F:protein binding			IPR000270 (SMART): IPR000270 (PF.	4,953	3,496	11,234	20,261	13,612					0,853	0,002			up
Solyc05g013540	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RN47_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,038	0,000	0,265	0,263	0,164									
Solyc05g013560	serine-rich protein-like protein (AHRD V3.3 *-* AT5G55980.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,380	0,816	0,168	0,142	0,329									
Solyc05g013570	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT1G67900.6)						G3DSA:3.30.710.10 (GENE3D): IPR0	9,156	11,835	2,798	1,674	1,725									
Solyc05g013580	Beta-1,4-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061E8J3_THECC)		F:GO:0003830; P:G(	F:beta-1,4-mannos	EC:2.4.1.144	Beta-1,4-mannosyl-g	IPR006813 (PFAM): PTHR12224:SF4	47,163	26,561	31,146	52,949	38,528	-0,802	0,001			0,767	0,000	down		up
Solyc05g013620	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 --* A0A151U3Z8_CAJCA)		C:GO:0000943; F:G(	C:retrotransposon nucleocapsid; F:nucleic acid binding; P:DNA			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,136	0,509	1,080	1,454	1,085									
Solyc05g013630	LOW QUALITY:CP-interacting protein-L (AHRD V3.3 *** A0A0K0PWY1_CAPAN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,496	8,161	17,529	16,012	12,546									
Solyc05g013640	DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 --* AT1G24575.1)							0,000	0,037	0,050	0,022	0,024									
Solyc05g013650	LOW QUALITY:lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.		C:GO:0016021	C:integral component of membrane			IPR007877 (PFAM): PTHR31210:SF1	0,019	0,077	0,000	0,000	0,000									
Solyc05g013660	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		C:GO:0016021	C:integral component of membrane			IPR007877 (PFAM): PTHR31210:SF3	12,100	10,500	7,121	5,882	7,194									
Solyc05g013670	chloroplast sensor kinase (AHRD V3.3 *** AT1G67840.1)		F:GO:0004673; C:G(	F:protein histidine k	EC:2.7.13.3	Histidine kinase	IPR036890 (G3DSA:3.30.565.GENE3I	10,166	12,132	11,715	13,345	17,325			0,561	0,013				up	
Solyc05g013680	GDSL esterase/lipase (AHRD V3.3 *** W9RN10_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,291	0,375	0,044	0,073	0,024									
Solyc05g013690	GDSL esterase/lipase family (AHRD V3.3 *** A0A151TAB7_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	2,319	6,429	0,000	0,025	0,116									
Solyc05g013700	Eukaryotic translation initiation factor 4B family protein (AHRD V3.3 *** B9HTR6_POPTR)		F:GO:0003743	F:translation initiation factor activity			IPR010433 (PFAM): mobidb-lite (MOB	73,988	66,063	87,649	85,907	82,121									
Solyc05g013710	Quinolinate synthase A (AHRD V3.3 *-* W9RJG8_9ROSA)		F:GO:0008047; C:G(	F:enzyme activator activity; C:chloroplast; P:positive regulation			G3DSA:3.90.1010.10 (GENE3D): IPR(	0,870	0,683	2,422	3,241	3,188									
Solyc05g013720	Alpha-galactosidase (AHRD V3.3 *** K4BY93_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR002241 (PRINTS): PF17801 (PFAI	102,575	109,985	119,702	103,150	122,327									
Solyc05g013730	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G26370.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; P:fucose metabolic proces			IPR019378 (PFAM): IPR024709 (PIRS	44,628	43,632	50,008	45,864	43,917									
Solyc05g013740	Coilin-like protein (AHRD V3.3 *-* U6BQ51_NICBE)						IPR031722 (PFAM): mobidb-lite (MOB	52,531	42,698	38,039	37,416	36,906									
Solyc05g013750	Dual specificity phosphatase (AHRD V3.3 *** A0A124SD30_CYNCS)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR007123 (PF.	10,896	23,734	8,137	7,405	12,736									
Solyc05g013760	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,079	0,081	0,000	0,000	0,072									
Solyc05g013773	PK12 protein kinase (AHRD V3.3 *** O49967_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	20,971	20,719	24,657	22,091	23,069									
Solyc05g013777	Serine/threonine-protein kinase AFC2 (AHRD V3.3 *-* W9RKJ5_9ROSA)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	mobidb-lite (MOBIDB_LITE): mobidb-lit	5,318	5,219	6,138	6,040	6,458									
Solyc05g013780	Myosin heavy chain, putative (AHRD V3.3 *** A0A072TT98_MEDTR)		C:GO:0043229; P:G(	C:intracellular organelle; P:late endosome to vacuole transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	42,057	39,770	32,398	33,715	29,585									
Solyc05g013790	Nucleoporin GLE1 (AHRD V3.3 *** W9RMY7_9ROSA)		C:GO:0005643; P:G(	C:nuclear pore; P:poly(A)+ mRNA export from nucleus			IPR012476 (PFAM): IPR038506 (G3D	25,417	23,671	29,424	28,049	29,116									
Solyc05g013795	50S ribosomal protein L33, chloroplastic (AHRD V3.3 -** RK33_BUXMI)							0,362	0,357	0,183	0,145	0,235									
Solyc05g013810	Glycosyl hydrolase family 5 protein (AHRD V3.3 *** D7KPG3_ARALL)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	2,774	5,252	13,619	18,697	17,167									
Solyc05g013820	Proteasome subunit beta type (AHRD V3.3 *** A0A0V0HT89_SOLCH)		F:GO:0004298; C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000243 (PRINTS): IPR029055 (G3	23,829	27,155	47,613	49,193	43,663									
Solyc05g013850	Sieve element occlusion c (AHRD V3.3 *** E2FKK0_9SOLN)		P:GO:0010088	P:phloem development			IPR027944 (PFAM): IPR027942 (PFAI	14,602	22,842	2,130	2,756	4,060									
Solyc05g013860	sieve element occlusion protein (AHRD V3.3 *** AT1G67790.1)		P:GO:0010088	P:phloem development			IPR027942 (PFAM): IPR027944 (PFAI	0,434	0,349	0,069	0,097	0,190									
Solyc05g013870	Sieve element occlusion c (AHRD V3.3 *** E2FKK0_9SOLN)		P:GO:0010088	P:phloem development			IPR027942 (PFAM): IPR027944 (PFAI	20,759	25,794	11,287	20,636	22,727			1,005	0,000	0,872	0,000		up	up
Solyc05g013880	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061E701_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	0,835	0,847	0,025	0,076	0,047									
Solyc05g013920	Cysteine protease, putative (AHRD V3.3 *** B9RMS9_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): IPR013201 (SM	27,268	24,130	25,296	25,041	21,127									
Solyc05g013930	RNA-binding family protein (AHRD V3.3 *** B9HLD5_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	1,392	0,800	0,000	0,000	0,000									
Solyc05g013940	Actin-related family protein (AHRD V3.3 *** B9HTF8_POPTR)		F:GO:0005524; C:G(	F:ATP binding; C:Arp2/3 protein complex; P:Arp2/3 complex-me(			IPR004000 (SMART): IPR004000 (PF.	29,272	22,623	33,868	36,982	31,509									
Solyc05g013950	LOW QUALITY:Dehydroascorbate reductase-like protein (AHRD V3.3 *-* Q3HS01	DHAR1	P:GO:0010731; F:G(	P:protein glutathion	EC:1.8.5.1	Glutathione dehydroc	G3DSA:1.20.1050.10 (GENE3D): PTH	0,021	0,000	0,025	0,000	0,000									
Solyc05g013960	Oxysterol-binding protein, putative (AHRD V3.3 *** B9RMS3_RICCO)		C:GO:0005829; F:G(	C:cytosol; F:sterol transporter activity; P:sterol transport; C:me			IPR001849 (SMART): G3DSA:2.40.16	66,885	56,869	72,479	68,474	67,213									
Solyc05g013970	RNA binding protein, putative (AHRD V3.3 *-* B9RMS1_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	12,178	17,716	14,316	13,903	13,813									
Solyc05g013980	phospholipase-like protein (PEARLI 4) with TRAF-like domain protein (AHRD V3.3 --* AT3G58270.3)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PS51257 (PROSITE_PROFILES)	0,143	0,139	0,000	0,047	0,070									
Solyc05g013990	T-complex protein 1 (AHRD V3.3 *** B9HTF6_POPTR)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR027410 (G3	200,416	185,312	310,715	284,448	277,311									
Solyc05g014000	Pectate lyase (AHRD V3.3 *** M1AQF5_SOLTU)		F:GO:0030570; P:G(	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	241,287	146,756	2,179	0,266	1,025					-2,982	0,000			down
Solyc05g014030	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT3G26100.6)						IPR000408 (PRINTS): IPR009091 (G3	84,833	70,737	119,250	106,058	107,911									
Solyc05g014040	LOW QUALITY:WRKY transcription factor 70	WRKY70	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,000	0,039	0,000	0,000	0,000									
Solyc05g014050	Inner membrane protein (AHRD V3.3 *** S8C850_9LAMI)		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase acti			IPR028055 (TIGRFAM): IPR001708 (F	29,428	34,257	58,860	62,125	59,038									
Solyc05g014085	F-box family protein (AHRD V3.3 *-* B9HK48_POPTR)						PTHR31790 (PANTHER)	9,617	6,545	5,735	7,367	7,377									
Solyc05g014090	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G19540.1)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	0,063	0,124	0,000	0,000	0,000									
Solyc05g014100	F-box family protein (AHRD V3.3 --* AT3G06240.1)						IPR006527 (PFAM): PTHR10992:SF9	32,478	23,033	19,501	22,023	20,841									
Solyc05g014110	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G47590.1)						IPR029058 (G3DSA:3.40.50.GENE3D	23,622	19,148	15,726	16,696	16,601									
Solyc05g014120	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	13,863	7,524	85,628	96,552	71,619	-0,855	0,041					down		
Solyc05g014130	COP1-interacting protein 4 (AHRD V3.3 *-* AT5G37190.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	16,544	17,246	14,901	12,780	11,665									
Solyc05g014140	beta-ketoacyl reductase 1 (AHRD V3.3 *-* AT1G67730.1)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane; F			G3DSA:3.40.50.720 (GENE3D): PTHF	0,520	0,425	0,025	0,025	0,047									
Solyc05g014150	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT3G55290.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS): IPR002347 (PF	0,396	0,353	0,000	0,045	0,047									
Solyc05g014155	Regulator of G-protein signaling (AHRD V3.3 *-* A0A077ET31_CAPAN)		F:GO:0004930; F:G(	F:G protein-coupled receptor activity; F:GTPase activator activity; C:nucleus; C:plasma membrane; P:G				3,614	3,450	1,747	1,879	2,401									
Solyc05g014160	REGULATOR OF G-PROTEIN SIGNALING 1 (AHRD V3.3 *-* AT3G26090.2)		F:GO:0004930; F:G(	F:G protein-coupled receptor activity; F:GTPase activator activ			IPR016137 (SMART): IPR016137 (PF.	3,587	2,946	2,004	1,935	2,144									
Solyc05g014163	REGULATOR OF G-PROTEIN SIGNALING 1 (AHRD V3.3 --* AT3G26090.1)		F:GO:0004930; F:G(	F:G protein-coupled receptor activity; F:GTPase activator activity; C:nucleus; C:plasma membrane; P:G				0,279	0,137	0,276	0,275	0,189									
Solyc05g014165	REGULATOR OF G-PROTEIN SIGNALING 1 (AHRD V3.3 *-* AT3G26090.1)		F:GO:0004930; F:G(	F:G protein-coupled receptor activity; F:GTPase activator activity; C:nucleus; C:plasma membrane; P:G				0,042	0,018	0,025	0,022	0,047									
Solyc05g014170	Regulator of G-protein signaling 1 (AHRD V3.3 --* A0A192GRN3_9ROSA)		F:GO:0004930; F:G(	F:G protein-coupled receptor activity; F:GTPase activator activity; C:nucleus; C:plasma membrane; P:G				0,641	0,564	0,486	0,463	0,351									
Solyc05g014190	CAAX amino terminal protease family protein (AHRD V3.3 *** AT3G26085.4)		C:GO:0016020	C:membrane			IPR003675 (PFAM): PTHR43592:SF7	0,830	1,823	0,933	2,098	3,222			1,766	0,000	1,160	0,014		up	up
Solyc05g014200	TGN-related, localized SYP41 interacting protein (AHRD V3.3 *** AT1G24460.1)		P:GO:0007034; P:G(	P:vacuolar transport; P:response to salt stress; P:circumnutatio			mobidb-lite (MOBIDB_LITE): PTHR131	57,280	44,855	42,707	48,378	46,328									
Solyc05g014210	GDSL esterase/lipase (AHRD V3.3 *** A0A0K9PUT3_ZOSMR)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,140	0,097	0,000	0,050	0,023									
Solyc05g014230	RING finger protein (AHRD V3.3 *** A0A0B0MVX3_GOSAR)						IPR001841 (SMART): IPR013083 (G3	0,254	0,284	0,119	0,145	0,023									
Solyc05g014240	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT1G67720.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR000719 (PF.	20,335	17,061	13,281	15,184	16,503									
Solyc05g014250	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EEU1_THECC)						IPR001841 (SMART): PF13920 (PFAM	5,092	3,465	2,694	2,798	3,785									
Solyc05g014260	Two-component response regulator (AHRD V3.3 *** W9RKG5_9ROSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding; F:D			IPR001789 (SMAF ARR-B	19,037	18,811	8,089	9,579	11,361									
Solyc05g014270	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *** A0A072U7R9_MEDTR)						IPR027329 (PFAM): mobidb-lite (MOB	0,180	0,387	0,049	0,072	0,071									
Solyc05g014280	small heat shock protein 1	Hsp25.7B					IPR002068 (PFAM): IPR008978 (G3D	2,106	3,095	82,244	74,137	95,345									
Solyc05g014300	LOW QUALITY:NAC domain containing protein 5 (AHRD V3.3 --* AT1G02250.1)							0,101	0,197	0,631	0,821	0,585									
Solyc05g014310	multidrug resistance protein (AHRD V3.3 *** AT1G67700.5)		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	mobidb-lite (MOBIDB_LITE): mobidb-lit	20,846	42,876	34,081	39,770	48,998	1,067	0,000	0,522	0,006			up	up	
Solyc05g014320	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G27320.2)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): PTHR23024:SF2	19,853	6,592	12,225	21,779	14,183	-1,566	0,000			0,838	0,000	down		up
Solyc05g014340	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9HTC9_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR011989 (G3DSA:1.25.10.GENE3D	14,241	19,235	18,746	19,443	17,040									
Solyc05g014360	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT2G29370.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,336	0,879	1,684	1,097	1,409									
Solyc05g014370	Mitotic spindle checkpoint protein MAD2 (AHRD V3.3 *** A0A151QV91_CAJCA)		P:GO:0007094	P:mitotic spindle assembly checkpoint			IPR036570 (G3DSA:3.30.900.GENE3I	3,305	2,686	7,305	6,354	5,035									
Solyc05g014390	ABC subfamily C transporter (AHRD V3.3 *** A0A077RXF4_WHEAT)	ABCC21	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	95,165	48,865	521,248	526,589	445,392	-0,933	0,002					down		
Solyc05g014400	RecQ-mediated genome instability protein 1 (AHRD V3.3 *** A0A151RRF7_CAJCA)		F:GO:0000166; C:G(	F:nucleotide binding; C:RecQ helicase-Topo III complex			IPR032199 (PFAM): mobidb-lite (MOB	4,007	4,229	1,607	1,293	1,409									
Solyc05g014410	RecQ-mediated genome instability protein 1 (AHRD V3.3 *-* RMI1_ARATH)		F:GO:0000166; C:G(	F:nucleotide binding; C:RecQ helicase-Topo III complex			IPR033472 (SMART): IPR013894 (PF.	1,668	1,808	0,719	0,646	0,796									
Solyc05g014420	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** A0A0K9NVB9_ZOSMR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF.	0,000	0,019	0,000	0,000	0,000									
Solyc05g014470	glyceraldehyde 3-phosphate dehydrogenase	gapdh	P:GO:0006006; F:G(	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR020828 (SM	958,039	991,928	630,596	527,500	586,588									
Solyc05g014485	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** A0A0B5GNJ2_BOMCI)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			G3DSA:3.30.360.10 (GENE3D): IPR0	2,880	3,037	1,525	1,602	2,163									
Solyc05g014490	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RMN2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFAI	6,000	6,252	6,460	7,192	6,324									
Solyc05g014500	ABC transporter family protein (AHRD V3.3 *-* B9GJX7_POPTR)	ABCC22	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	3,002	2,946	2,907	3,200	2,831									
Solyc05g014510	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9RMN1_RICCO)		F:GO:0005515	F:protein binding			IPR002110 (SMART): PF13637 (PFAM	11,014	11,671	1,639	2,248	2,932									
Solyc05g014540	DNA polymerase alpha subunit B (AHRD V3.3 *** K4BYH3_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA p(	IPR016722 (PIRSF): IPR007185 (PFA	8,979	6,828	4,015	3,391	3,621									
Solyc05g014550	LOW QUALITY:TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 *** A0A0I		C:GO:0016021	C:integral component of membrane			IPR006634 (SMART): PTHR31766:SF	0,214	0,338	0,479	1,024	0,707									
Solyc05g014560	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G24360.1)		F:GO:0004316; P:G(	F:3-oxoacyl-[acyl-c	EC:2.3.1.85; EC:1.1.	Fatty-acid synthase;	IPR002347 (PRINTS): IPR002347 (PF	1,753	1,274	0,146	0,116	0,141									
Solyc05g014570	LOW QUALITY:MYB family transcription factor (AHRD V3.3 -** A0A072VEW4_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): IPR00	0,019	0,000	0,000	0,000	0,000									
Solyc05g014590	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT5G57150.1)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	0,344	0,178	0,447	1,480	0,903									
Solyc05g014630	PPR superfamily protein (AHRD V3.3 --* AT4G31070.2)							0,920	0,958	0,898	0,822	0,636									
Solyc05g014633	LOW QUALITY:UPF0496 protein (AHRD V3.3 *-* A0A061E8F5_THECC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR007749 (PFAM): PTHR31113:SF3	0,040	0,039	0,025	0,050	0,046									
Solyc05g014640	RUN and FYVE domain-containing protein 2 (AHRD V3.3 *** A0A0B0N071_GOSAR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	31,185	30,914	18,087	19,866	18,321									
Solyc05g014652	Lojap-related protein (AHRD V3.3 *** A0A061E8Z3_THECC)		C:GO:0005739; P:G(	C:mitochondrion; P:negative regulation of translation; F:ribosom			PF02410 (PFAM): G3DSA:3.30.460.1(	7,634	8,710	5,193	4,691	4,453									
Solyc05g014690	RNA helicase DEAH-box14	DEAH14	F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR001650 (SMART): IPR014001 (SM	4,223	3,992	0,981	0,867	1,035									
Solyc05g014700	Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** AT1G67600.1)		C:GO:0016021	C:integral component of membrane			IPR003832 (PFAM): IPR003832 (PAN	0,157	0,190	0,000	0,000	0,024									
Solyc05g014710	Remorin family protein (AHRD V3.3 *** A0A061E752_THECC)						IPR005516 (PFAM): mobidb-lite (MOB	1,516	1,942	0,097	0,025	0,046									
Solyc05g014720	DNA topoisomerase (AHRD V3.3 *** A0A022PYK0_ERYGU)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:5.99.1.2	DNA topoisomerase	IPR013497 (PRINTS): IPR003601 (SM	5,095	4,474	1,330	0,991	1,246									
Solyc05g014760	Kinase family protein (AHRD V3.3 *** B9HTA6_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	522,420	464,056	319,906	474,740	416,289					0,572	0,004			up
Solyc05g014765	glutamate receptor 3.5 (AHRD V3.3 --* AT2G32390.5)							2,368	2,260	1,531	3,074	2,197					1,008	0,025			up
Solyc05g014790	Lipoxygenase (AHRD V3.3 *** A0A0V0IV84_SOLCH)	LOX11	F:GO:0005515; F:G(	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR013819 (PRINTS): IPR001246 (PF	67,078	60,821	83,355	80,471	83,478									
Solyc05g014820	Histone H2A (AHRD V3.3 *** K4BYK0_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR002119 (SM	0,000	0,018	0,000	0,000	0,000									
Solyc05g014830	Histone H2A (AHRD V3.3 *-* K4BYK1_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRIN NF-YC	0,000	0,000	0,025	0,000	0,000									
Solyc05g014895	Histone H2A (AHRD V3.3 *** K4BYJ8_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR002119 (SM	0,019	0,000	0,000	0,000	0,000									
Solyc05g014970	Urease (AHRD V3.3 *** K4BYL5_SOLLC)		F:GO:0009039; F:G(	F:urease activity; F	EC:3.5.1.5	Urease	IPR005848 (PRINTS): IPR011612 (PF	47,139	46,151	45,628	46,535	47,543									
Solyc05g014980	Adenylate kinase (AHRD V3.3 *** B7FN18_MEDTR)		F:GO:0004017; F:G(	F:adenylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS): G3DSA:3.40.5C	13,317	15,368	16,799	17,687	17,672									
Solyc05g015000	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR032675 (G3	0,000	0,019	0,000	0,000	0,000									
Solyc05g015035	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9GU68_POPTR)		F:GO:0003677	F:DNA binding			IPR001356 (SMART): G3DSA:1.10.10	0,000	0,000	0,025	0,000	0,000									
Solyc05g015040	RNA helicase DEAH-box 15	DEAH15	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR011545 (PF.	7,262	5,694	7,413	7,856	8,218									
Solyc05g015043	ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RMI9_RICCO)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR007502 (SMART): G3DSA:1.20.12	3,036	2,511	3,577	3,609	3,864									
Solyc05g015047	ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RMI9_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, vi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR011709 (PFAM): PTHR18934:SF1	10,828	9,374	12,215	11,255	10,035									

Solyc05g015050	nucleolar protein gar2-like protein (AHRD V3.3 *** AT2G42320.2)		P:GO:0006913; P:GC	P:nucleocytoplasmic transport; P:nuclear pore organization; F:s		IPR019448 (PFAM): mobidb-lite (MOB	76,397	61,338	39,335	39,150	36,244									
Solyc05g015060	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding		IPR003593 (SMART): IPR025753 (PF	0,063	0,231	0,044	0,125	0,000									
Solyc05g015070	U-box domain-containing family protein (AHRD V3.3 *** B9HT95_POPTR)		F:GO:0004842; F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:prot		IPR003613 (SMART): IPR000225 (SM	0,040	0,043	0,000	0,000	0,070									
Solyc05g015150	Receptor-like kinase (AHRD V3.3 *** G7KTA0_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		IPR000719 (SMART): G3DSA:1.10.51	19,649	14,142	15,597	12,982	13,684									
Solyc05g015210	Transforming growth factor-beta receptor-associated protein 1-like protein (AHRD V3.3 *** W9QP08_9ROS/		F:GO:0005515; P:GC	F:protein binding; P:intracellular protein transport; P:vesicle-mec		IPR001180 (PFAM): IPR019453 (PFA	22,346	21,753	18,377	18,499	19,552									
Solyc05g015220	Mannosyl-oligosaccharide glucosidase (AHRD V3.3 *** W9S315_9ROSA)		F:GO:0004573; P:GC	F:mannosyl-oligosa EC:3.2.1.16	Mannosyl-oligosacch	IPR031335 (PFAM): IPR038518 (G3D	45,030	41,543	52,598	50,158	51,825									
Solyc05g015230	LOW QUALITY:Glutathione S-transferase family protein (AHRD V3.3 --* AT3G62760.1)						0,000	0,000	0,025	0,022	0,071									
Solyc05g015250	Mannosyl-oligosaccharide glucosidase, putative (AHRD V3.3 *-* B9RMG4_RICCO)		F:GO:0004573; P:GC	F:mannosyl-oligosa EC:3.2.1.16	Mannosyl-oligosacch	IPR038518 (G3DSA:2.70.98.GENE3D	3,660	3,203	4,389	3,865	4,304									
Solyc05g015300	BURP domain protein RD22 (AHRD V3.3 *** RD22_ARATH)		C:GO:0016020	C:membrane		IPR004873 (SMART): IPR004873 (PF	0,000	0,000	0,000	0,000	0,023									
Solyc05g015310	Minichromosome maintenance (MCM2/3/5) family protein (AHRD V3.3 *** AT1G67440.2)		F:GO:0003924; F:GC	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.10.40.50 (GENE3D): IPR00	16,002	14,515	33,816	25,712	27,431									
Solyc05g015320	microtubule-associated protein 65-8 (AHRD V3.3 *** AT1G27920.1)		P:GO:0000226; F:GC	P:microtubule cytoskeleton organization; F:microtubule binding		G3DSA:1.20.58.1520 (GENE3D): PF0	0,220	0,498	0,000	0,073	0,142									
Solyc05g015350	Cytochrome P450 (AHRD V3.3 *** A0A103XVZ6_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc		IPR001128 (PRINTS): IPR002401 (PF	0,000	0,000	0,075	0,050	0,024									
Solyc05g015370	LOW QUALITY:HORMA domain-containing 1 (AHRD V3.3 *-* A0A0B0NC02_GOSAR)		C:GO:0016020	C:membrane		IPR036570 (G3DSA:3.30.900.GENE3	5,298	1,662	155,501	154,012	89,716			-0,796	0,001				down	
Solyc05g015390	Rubber elongation factor protein (AHRD V3.3 *** A0A072TUR8_MEDTR)		C:GO:0005773; C:GC	C:vacuole; C:endoplasmic reticulum; C:lipid droplet; P:pollen dev		IPR008802 (PFAM): IPR008802 (PAN	672,274	451,162	738,855	636,998	669,496									
Solyc05g015410	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 --* Q2R0Q5_ORYSJ)					IPR029480 (PFAM): PTHR10775 (PAN	1,839	1,381	3,167	4,393	5,474									
Solyc05g015415	ureidoglycolate amidohydrolase (AHRD V3.3 --* AT5G43600.1)						1,010	0,664	1,566	2,002	1,085									
Solyc05g015420	HCP family protein with MYND-type zinc finger protein (AHRD V3.3 *** A0A072U431_MEDTR)		F:GO:0005515	F:protein binding		IPR002893 (PFAM): G3DSA:3.30.60.1	19,864	28,382	28,517	20,799	21,539									
Solyc05g015433	kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing protein (AHRD V3.3 --* AT2G35050.2)						3,754	3,912	2,538	2,701	2,634									
Solyc05g015460	F-box family protein (AHRD V3.3 --* AT5G07610.1)						0,266	1,524	1,851	2,587	2,477									
Solyc05g015470	LOW QUALITY:chaperone protein dnaJ-like protein (AHRD V3.3 *** AT5G43260.1)					PTHR34687:SF1 (PANTHER): PTHR3	9,042	10,032	14,329	17,948	17,275									
Solyc05g015480	Molybdenum cofactor sulfurase (AHRD V3.3 *** A0A1D1Y5S2_9ARAE)		F:GO:0003824	F:catalytic activity		PTHR14237:SF33 (PANTHER): PTHR	3,891	2,534	5,933	4,924	4,341									
Solyc05g015490	Lipid transfer protein (AHRD V3.3 *** A0A0M3SGG1_GOSAR)		C:GO:0016021	C:integral component of membrane		IPR016140 (SMART): G3DSA:1.10.11	5,343	7,206	14,580	15,174	13,254									
Solyc05g015500	Ran BP2/NZF zinc finger-like superfamily protein		F:GO:0003729	F:mRNA binding		IPR001876 (SMART): G3DSA:4.10.10	253,480	241,704	214,680	208,446	204,609									
Solyc05g015510	Squamosa promoter-binding protein 10		F:GO:0003677; C:GC	F:DNA binding; C:nucleus		IPR004333 (PFAN SBP	53,548	35,186	51,006	56,276	63,004									
Solyc05g015520	F-box family protein (AHRD V3.3 *** B8Y9B5_PONTR)		F:GO:0005515	F:protein binding		IPR001810 (SMART): IPR015915 (G3	36,785	33,230	133,816	115,673	113,956									
Solyc05g015530	Stress associated endoplasmic reticulum protein, putative (AHRD V3.3 *** B9RMD3_RICCO)		C:GO:0005783	C:endoplasmic reticulum		IPR010580 (PFAM): PTHR15601:SF5	59,041	68,910	78,659	86,086	74,785									
Solyc05g015535	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G34310.5)						0,019	0,098	0,047	0,145	0,095									
Solyc05g015550	Nuclear transcription factor Y protein (AHRD V3.3 *** I3TAW1_MEDTR)		F:GO:0046982	F:protein heterodimerization activity		PR00615 (PRINTS NF-YB	3,839	2,760	0,642	1,243	0,942									
Solyc05g015553	BTB/POZ/Kelch-associated protein (AHRD V3.3 --* AT4G01160.2)						0,281	0,181	0,577	0,694	0,401									
Solyc05g015580	LOW QUALITY:YDG/SRA domain-containing protein (AHRD V3.3 --* AT5G47160.3)						0,122	0,100	0,000	0,000	0,000									
Solyc05g015610	Histidine kinase CHK3 (AHRD V3.3 *** A0A0A1WDG8_NICAT)		F:GO:0000155; P:GC	F:phosphorelay ser EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR003594 (SM	87,681	55,542	99,883	116,183	108,935	-0,631	0,037					down		
Solyc05g015630	Nuclear transport factor 2 (AHRD V3.3 *** NTF2_ARATH)		C:GO:0005737; P:GC	C:cytoplasm; P:protein import into nucleus; C:nuclear pore centi		IPR002075 (PFAM): G3DSA:3.10.450	13,021	10,893	11,048	10,702	9,903									
Solyc05g015640	Ciliary neurotrophic factor (AHRD V3.3 *** A0A0B0PI91_GOSAR)		C:GO:0005768; C:GC	C:endosome; C:trans-Golgi network; C:integral component of m		PTHR35280 (PANTHER)	0,040	0,000	0,000	0,025	0,000									
Solyc05g015650	Calmodulin-binding transcription activator (AHRD V3.3 *** Q8S389_BRANA)		F:GO:0003677; F:GC	F:DNA binding; F:protein binding		IPR000048 (SMAF CAMTA	47,223	42,633	43,925	42,586	46,510									
Solyc05g015656	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SDM1_CAJCA)					IPR019557 (PFAM): mobidb-lite (MOB	0,115	0,078	0,072	0,092	0,282									
Solyc05g015700	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT3G48660.1)		C:GO:0016021	C:integral component of membrane		IPR021775 (PFAM): PTHR33128:SF9	0,384	0,244	0,181	0,430	0,165									
Solyc05g015710	transmembrane protein (AHRD V3.3 *** AT1G27290.2)		C:GO:0016021	C:integral component of membrane		PTHR34781:SF2 (PANTHER): PTHR3	18,256	21,304	24,780	26,395	23,358									
Solyc05g015720	MADS-box transcription factor (AHRD V3.3 *** F1T119_9ERIC)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR002487 (PFAM): PTHR11945:SF2	4,501	3,831	2,110	2,062	1,652									
Solyc05g015725	beta-amylase 2 (AHRD V3.3 --* AT4G00490.1)						1,554	0,879	1,113	0,862	0,944									
Solyc05g015750	SEPALLATA3	sep3	F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I		IPR002100 (PRIN MIKC_MADS	206,614	208,104	213,537	184,716	203,721									
Solyc05g015800	Alcohol acyl transferase (AHRD V3.3 *** Q6QLX4_SOLLC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3	0,057	0,142	0,076	0,000	0,024									
Solyc05g015820	BZIP transcription factor (AHRD V3.3 *** G7KUQ5_MEDTR)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane		IPR012458 (PFAM): mobidb-lite (MOB	24,015	24,832	37,889	39,054	38,084									
Solyc05g015840	Squamosa promoter binding protein 13		F:GO:0003677; C:GC	F:DNA binding; C:nucleus		IPR036893 (G3DS SBP	9,843	15,597	5,134	6,807	8,514									
Solyc05g015850	WRKY transcription factor 75	WRKY75	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of transc		IPR003657 (SMAF WRKY	0,060	0,250	2,040	4,742	3,645					1,215	0,028			up
Solyc05g015860	dihydrosphingosine phosphate lyase (AHRD V3.3 *** AT1G27980.1)		F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR015421 (G3DSA:3.40.640.GENE3	38,408	31,687	82,102	87,400	78,845									
Solyc05g015861	dihydrosphingosine phosphate lyase (AHRD V3.3 *-* AT1G27980.1)		F:GO:0003824	F:catalytic activity		IPR015422 (G3DSA:3.90.1150.GENE	23,202	19,471	51,421	52,863	48,466									
Solyc05g015862	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)		F:GO:0008194; F:GC	F:UDP-glycosyltransferase activity; F:transferase activity, trans		G3DSA:3.40.50.2000 (GENE3D): PTH	0,000	0,019	0,000	0,000	0,000									
Solyc05g015870	LOW QUALITY:F-box associated ubiquitination effector family protein (AHRD V3.3 --* AT4G22390.2)						0,019	0,000	0,000	0,000	0,024									
Solyc05g015880	regulator of nonsense transcript protein (AHRD V3.3 *** AT5G14090.1)		P:GO:0009630; P:GC	P:gravitropism; P:regulation of auxin polar transport		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,000	0,000	0,049	0,024									
Solyc05g015890	transmembrane protein (AHRD V3.3 *** AT1G27990.1)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	1,244	1,719	2,012	3,301	1,274									
Solyc05g015900	LOW QUALITY:Protein TIC 214 (AHRD V3.3 --* TI214_CALFG)					mobidb-lite (MOBIDB_LITE)	0,000	0,018	0,000	0,000	0,000									
Solyc05g015920	GYF domain-containing protein (AHRD V3.3 *** AT1G27430.1)		F:GO:0005515	F:protein binding		IPR003169 (SMART): IPR035445 (G3	89,722	79,297	93,462	87,097	90,808									
Solyc05g015930	GYF domain-containing protein (AHRD V3.3 *** AT1G27430.1)		F:GO:0005515	F:protein binding		IPR003169 (SMART): IPR035445 (G3	128,320	108,429	128,575	125,088	122,104									
Solyc05g015940	hydroxysteroid dehydrogenase 1 (AHRD V3.3 *-* AT5G50700.1)		C:GO:0016020	C:membrane			0,295	0,099	0,000	0,073	0,046									
Solyc05g015950	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** K4BYW1_SOLLC)		F:GO:0004345; P:GC	F:glucose-6-phosph EC:1.1.1.49	Glucose-6-phosphate	IPR001282 (PRINTS): IPR001282 (TI(	31,288	32,508	71,214	79,092	64,826									
Solyc05g015980	Gap junction beta-4 protein isoform 1 (AHRD V3.3 *** A0A061E410_THECC)					PTHR36068 (PANTHER)	12,500	12,612	7,118	9,317	8,131									
Solyc05g015990	LOW QUALITY:serine carboxypeptidase-like 43 (AHRD V3.3 --* AT2G12480.4)						0,000	0,021	0,000	0,000	0,000									
Solyc05g016005	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_OLTVI)						0,019	0,059	0,250	0,047	0,257									
Solyc05g016020	TBP-associated factor 11 (AHRD V3.3 --* AT4G20280.1)						0,000	0,021	0,000	0,399	0,023									
Solyc05g016030	S-acyltransferase (AHRD V3.3 *** K4BYW8_SOLLC)		C:GO:0005783; C:GC	C:endoplasmic retic EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	23,582	25,683	19,260	21,487	21,862									
Solyc05g016060	cysteine-rich/transmembrane domain A-like protein (AHRD V3.3 *** AT2G32190.1)		C:GO:0005886; C:GC	C:plasma membrane; C:integral component of membrane		IPR028144 (PFAM): PTHR31568:SF1	88,597	103,661	32,110	40,206	47,544									
Solyc05g016070	TOPLESS-related 1 (AHRD V3.3 *-* AT1G80490.3)		F:GO:0005515; P:GC	F:protein binding; P:regulation of transcription, DNA-templated		IPR001680 (SMART): IPR015943 (G3	0,019	0,019	0,025	0,050	0,071									
Solyc05g016090	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)					IPR019557 (PFAM): mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc05g016120	Photosystem II protein D1 (AHRD V3.3 *-* PSBA_BARVE)		C:GO:0009522; P:GC	C:photosystem I; P:photosynthetic electron transport in photosy		IPR003359 (PFAM): IPR000484 (PFA	1,401	2,030	2,951	5,556	8,264			1,484	0,016				up	
Solyc05g016130	LOW QUALITY:Photosystem I assembly protein Ycf3 (AHRD V3.3 *-* YCF3_SOLTU)		F:GO:0005515	F:protein binding		IPR019734 (SMART): IPR011990 (G3	0,000	0,000	0,000	0,000	0,023									
Solyc05g016180	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *-* AT5G38200.3)		P:GO:0006541; F:GC	P:glutamine metabolic process; F:hydrolase activity			1,755	1,724	1,600	1,667	1,505									
Solyc05g016190	Heavy metal-associated domain, HMA (AHRD V3.3 *** A0A103YA56_CYNCS)		P:GO:0030001; F:GC	P:metal ion transport; F:metal ion binding		PTHR22814:SF144 (PANTHER): PTHF	0,491	0,101	0,025	0,000	0,000									
Solyc05g016230	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein (AHRD V3.3 *** W9QZP3_9ROSA)		P:GO:0006281	P:DNA repair		IPR001357 (SMART): IPR001965 (SM	19,497	19,288	32,600	31,399	31,708									
Solyc05g016240	Topoisomerase II-associated protein PAT1 (AHRD V3.3 *** AT3G22270.1)		P:GO:0000290	P:deadenylation-dependent decapping of nuclear-transcribed ml		mobidb-lite (MOBIDB_LITE): mobidb-lit	98,742	90,342	140,615	153,287	150,045									
Solyc05g016250	OTU domain-containing (AHRD V3.3 *** A0A0B0PSP5_GOSAR)		F:GO:0004843; C:GC	F:thiol-dependent ul EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.80 (GENE3D): IPR00	13,881	13,044	12,118	11,142	10,627									
Solyc05g016253	Mitochondrial import inner membrane translocase subunit TIM14 (AHRD V3.3 *** A0A0B2PXU1_GLYSO)		C:GO:0001405; F:GC	C:PAM complex, Tim23 associated import motor; F:ATPase acti		IPR036869 (G3DSA:1.10.287.GENE3	0,733	0,999	0,225	0,511	0,614									
Solyc05g016257	myosin (AHRD V3.3 *-* AT4G33200.3)		F:GO:0005488	F:binding			0,135	0,337	0,075	0,148	0,095									
Solyc05g016260	myosin (AHRD V3.3 *-* AT5G20470.1)		F:GO:0003774; F:GC	F:motor activity; F:/ EC:3.6.1.15	Nucleoside-triphosphate phosphatase		1,119	1,264	0,658	1,095	0,422									
Solyc05g016310	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G59080.1)		F:GO:0004190; P:GC	F:aspartic-type end EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	7,485	5,591	7,354	18,572	15,826			1,102	0,000	1,337	0,000		up	up
Solyc05g016320	Exostosin family protein (AHRD V3.3 *** A0A072VBU5_MEDTR)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc		IPR004263 (PFAM): mobidb-lite (MOB	0,098	0,117	0,025	0,025	0,000									
Solyc05g016330	Cytochrome P450 (AHRD V3.3 *** W9R369_9ROSA)	CYP97B3	F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc		IPR001128 (PRINTS): IPR002401 (PF	19,873	23,903	19,720	17,615	23,149									
Solyc05g016370	Unknown protein (AHRD V3.3)						0,202	0,349	0,240	0,344	0,140									
Solyc05g016380	Rhomboid-like protein (AHRD V3.3 *-* I3SPB7_MEDTR)		C:GO:0016020	C:membrane		PTHR44836 (PANTHER): SSF144091	1,532	1,232	1,011	0,881	1,177									
Solyc05g016390	Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 *-* AT1G79480.2)		F:GO:0016874	F:ligase activity		IPR012946 (SMART): IPR012946 (PF	6,359	5,641	3,410	3,698	4,843									
Solyc05g016410	Casein kinase family protein (AHRD V3.3 *** B9HDX8_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR000719 (PF	113,552	99,509	116,669	104,301	107,112									
Solyc05g016440	Mediator of RNA polymerase II transcription subunit 23 (AHRD V3.3 *** MED23_ARATH)					IPR021629 (PFAM): mobidb-lite (MOB	38,861	36,062	44,903	53,203	48,035									
Solyc05g016460	Mediator of RNA polymerase II transcription subunit 23-like protein (AHRD V3.3 *** A0A0U2SQG6_REHGL)					mobidb-lite (MOBIDB_LITE): mobidb-lit	17,815	13,491	19,072	24,189	21,667									
Solyc05g016600	LOW QUALITY:LA RNA-binding protein (AHRD V3.3 --* AT5G21160.3)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			0,170	1,417	0,148	0,525	0,069									
Solyc05g016620	Ankyrin repeat-containing protein (AHRD V3.3 *-* W9R9C7_9ROSA)		C:GO:0016020	C:membrane		PTHR45037 (PANTHER): IPR036770	0,021	0,036	0,000	0,022	0,000									
Solyc05g016690	Nudix hydrolase (AHRD V3.3 *** A0A061GGI6_THECC)		F:GO:0016787	F:hydrolase activity		IPR020476 (PRINTS): IPR003293 (PF	0,000	0,018	0,000	0,025	0,024									
Solyc05g016710	Run and tbc1 domain containing 3, plant, putative isoform 2 (AHRD V3.3 --* A0A061ETJ4_THECC)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,217	0,281	0,119	0,098	0,070									
Solyc05g016720	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 --* AT1G05670.3)						0,058	0,036	0,000	0,000	0,000									
Solyc05g017745	transcriptional factor B3 family protein (AHRD V3.3 --* AT4G31690.1)		F:GO:0003677	F:DNA binding		IPR003340 (PROSITE_PROFILES): II	0,173	0,122	0,000	0,000	0,000									
Solyc05g017760	Acetoacetyl-CoA thiolase (AHRD V3.3 *** F5CLC4_CATRO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR002155 (PIRSF): IPR020616 (PFA	89,833	91,696	93,101	80,537	86,951									
Solyc05g017785	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD V3.3 --* AT1G11100.5)					mobidb-lite (MOBIDB_LITE)	1,808	2,383	1,772	1,451	1,550									
Solyc05g017790	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G44870.2)						1,132	1,594	1,057	1,281	1,274									
Solyc05g017830	Stomatal closure-related actin-binding protein 1 (AHRD V3.3 *-* SCAB1_ARATH)		F:GO:0003779; P:GC	F:actin binding; P:actin filament organization; P:regulation of sto		IPR032009 (PFAM): IPR039640 (PAN	0,000	0,000	0,025	0,000	0,000									
Solyc05g017840	Plant cadmium resistance 10-like protein (AHRD V3.3 *-* A0A0B0N332_GOSAR)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,522	0,611	0,381	0,500	0,450									
Solyc05g017843	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 *-* K4B581_SOLLC)		F:GO:0000166; F:GC	F:nucleotide binding; F:protein kinase activity; C:membrane; P:c		IPR001480 (PFAM): IPR036426 (G3D	0,040	0,060	0,025	0,146	0,095									
Solyc05g017860	Protein VAC14 like (AHRD V3.3 *** A0A0B2Q990_GLYSO)		P:GO:0006661; C:GC	P:phosphatidylinositol biosynthetic process; C:PAS complex		IPR021841 (PFAM): IPR011989 (G3D	28,716	26,852	34,883	40,119	36,823									
Solyc05g017893	THO complex subunit 2 (AHRD V3.3 *** A0A0B2QJL2_GLYSO)		C:GO:0000347; P:GC	C:THO complex; P:mRNA processing; P:mRNA export from nucl		IPR032302 (PFAM): IPR021418 (PFA	74,445	67,215	77,781	83,811	80,684									
Solyc05g017900	Drug/metabolite transporter (AHRD V3.3 *** A0A124SG72_CYNCS)		C:GO:0016021	C:integral component of membrane		IPR000620 (PFAM): PTHR42920 (PAN	4,830	3,918	6,955	6,271	6,007									
Solyc05g017910	LOW QUALITY:myrosinase-binding protein 2 (AHRD V3.3 --* AT1G52030.3)					IPR025558 (PFAM): PTHR34427 (PAN	1,387	2,371	1,180	1,233	0,895									
Solyc05g017915	LOW QUALITY:armadillo repeat kinesin 3 (AHRD V3.3 --* AT1G12430.2)					IPR025558 (PFAM): PTHR34427 (PAN	2,804	6,599	1,626	2,781	2,708	1,254	0,001					up		
Solyc05g017930	LOW QUALITY:Potassium channel (AHRD V3.3 *-* Q9LEG6_SOLLC)		F:GO:0005216; P:GC	F:ion channel activity; P:ion transport; C:membrane; P:transmer		IPR005821 (PFAM): PTHR10217:SF5	0,122	0,166	0,099	0,147	0,095									
Solyc05g017940	Drug/metabolite transporter (AHRD V3.3 *-* A0A124SG72_CYNCS)		C:GO:0016021	C:integral component of membrane		IPR000620 (PFAM): PTHR42920 (PAN	1,633	1,053	1,592	1,358	1,510									
Solyc05g017950	anion:sodium symporter		C:GO:0016020	C:membrane		IPR038770 (G3DSA:1.20.1530.GENE	87,101	159,594	103,281	124,280	170,267	0,900	0,000	0,717	0,000			up	up	
Solyc05g017970	Alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic (AHRD V3.3 --* PHSL_IPOBA)						0,201	0,238	0,100	0,145	0,306									
Solyc05g017980	Microtubule-associated protein 70-2 (AHRD V3.3 *** A0A0B2QPG9_GLYSO)		P:GO:0007010; F:GC	P:cytoskeleton organization; F:microtubule binding		IPR009768 (PFAM): mobidb-lite (MOB	104,483	89,715	51,117	46,570	48,864									
Solyc05g017990	TRNA/rRNA methyltransferase family protein (AHRD V3.3 *** A0A061GMB9_THECC)		F:GO:0003723; P:GC	F:RNA binding; P:RNA processing; F:RNA methyltransferase ac		IPR013123 (SMART): IPR029064 (G3	40,479	52,042	70,350	72,257	74,653									
Solyc05g018033	ATP-dependent RNA helicase Dhx29 (AHRD V3.3 --* M7Y6K4_TRIUA)						0,056	0,039	0,000	0,000	0,000									
Solyc05g018050	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G60080.1)		F:GO:0003824; P:GC	F:catalytic activity; P:cellular protein metabolic process		IPR001841 (SMART): IPR001841 (PF	0,736	2,379	0,770	0,863	1,052									
Solyc05g018060	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT3G06880.2)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,050	0,000									
Solyc05g018120	Transcription initiation factor TFIID subunit 11 (AHRD V3.3 *** A0A0B0NA85_GOSAR)		C:GO:0005634; P:GC	C:nucleus; P:transcription initiation from RNA polymerase II proi		IPR009072 (G3DSA:1.10.20.GENE3D	13,222	12,471	17,673	16,536	18,434									
Solyc05g018125	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G35190.2)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process		IPR027443 (G3DSA:2.60.120.GENE3	0,785	0,839	0,775	0,772	1,037									
Solyc05g018130	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G35190.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process		PR00682 (PRINTS): IPR026992 (PFA	1,463	1,735	4,680	3,584	4,501									
Solyc05g018150	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT5G19680.1)		F:GO:0005515	F:protein binding		PR00019 (PRINTS): IPR003591 (SMA	25,318	25,922	52,113	52,225	50,510									
Solyc05g018180	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *** A0A103YM25_CYNCS)					PF05664 (PFAM): IPR008528 (PANTH	39,115	34,582	27,209	29,744	29,937									
Solyc05g018200	LOW QUALITY:NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT4G23430.4)						0,019	0,021	0,000	0,000	0,000									
Solyc05g018210	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GMG4_THECC)					IPR029058 (G3DSA:3.40.50.GENE3D	69,473	61,452	69,919	62,129	63,695									
Solyc05g018220	LOW QUALITY:Agamous-like MADS-box protein AGL9 homolog (AHRD V3.3 --* AGL9_SINAL)						0,078	0,019	0,044	0,094	0,118									
Solyc05g018230	Sugar transporter protein 12	STP12	C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport		IPR003663 (PRINTS): IPR003663 (TI(	0,235	0,178	0,096	0,116	0,237									
Solyc05g018233	CRS2-associated factor 1, chloroplastic (AHRD V3.3 *** A0A0K9PK33_ZOSMR)		F:GO:0003723	F:RNA binding		IPR001890 (SMART): IPR001890 (PF	26,114	28,688	93,672	84,974	95,447									
Solyc05g018300	Phosphatase 2c, putative isoform 1 (AHRD V3.3 *** A0A061GUC7_THECC)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		PR00103 (PRINTS): IPR001932 (SMA	41,468	48,864	52,651	51,810	51,626									
Solyc05g018310	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GMH2_THECC)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane; F:ligase activ		IPR001841 (SMART): IPR001841 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc05g018320	arabinogalactan		P:GO:0007165	P:signal transduction		IPR032308 (PFAM): mobidb-lite (MOB	38,059	44,458	45,082	44,259	43,156									
Solyc05g018330	RNA-binding protein-like protein (AHRD V3.3 *-* AT4G28990.2)		F:GO:0003723; C:GC	F:RNA binding; C:nucleus; P:regulation of transcription, DNA-ter		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,047	0,075	0,000									
Solyc05g018340	TATA-binding protein-associated factor 2N (AHRD V3.3 *** W9S109_9ROSA)		F:GO:0003723; P:GC	F:RNA binding; P:regulation of transcription, DNA-templated		IPR001876 (SMART): G3DSA:4.10.10	34,455	41,590	46,748	45,912	44,467									
Solyc05g018350	Transcription factor, putative (AHRD V3.3 *** B9SQC7_RICCO)		C:GO:0005634; F:GC	C:nucleus; F:sequence-specific DNA binding; F:transcription rec		PF13837 (PFAM): Trihelix	14,751	14,268	25,935	25,067	19,594									
Solyc05g018370	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 --* A0A072UFM0_MEDTR)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane		mobidb-lite (MOBIDB_LITE)	4,475	5,170	0,000	0,000	0,000									
Solyc05g018390	Vernalization insensitive 3-like protein (AHRD V3.3 *** A0A0B0P442_GOSAR)		F:GO:0005515	F:protein binding		IPR013783 (G3DSA:2.60.40.GENE3D	17,887	19,491	24,410	26,973	23,631									
Solyc05g018395	Proteasome subunit alpha type (AHRD V3.3 --* A0A0V0HRW3_SOLCH)					PS51257 (PROSITE_PROFILES)	0,114	0,118	0,000	0,025	0,000									
Solyc05g018410	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** G7L901_MEDTR)		F:GO:0003860	F:3-hydroxyisobutyı EC:3.1.2.4	3-hydroxyisobutyryl-(	IPR032259 (PFAM): G3DSA:3.90.226	74,138	71,086	86,260	79,072	80,324									
Solyc05g018436	ZF-HD homeobox protein family (AHRD V3.3 --* A0A151R0E9_CAJCA)					IPR006456 (PFAM): IPR006456 (PRC	0,000	0,021	0,000	0,000	0,000									
Solyc05g018480	Histone H2A (AHRD V3.3 --* K4BYK5_SOLLC)					mobidb-lite (MOBIDB_LITE)	0,000	0,229	0,000	0,000	0,000									
Solyc05g018490	Copper ion-binding protein, putative (AHRD V3.3 *** G7JBR2_MEDTR)		F:GO:0003743; P:GC	F:translation initiation factor activity; P:translational initiation		mobidb-lite (MOBIDB_LITE): mobidb-lit	57,447	57,825	72,966	65,796	66,638									
Solyc05g018500	Protein OBERON 3-like protein (AHRD V3.3 *** A0A0B0MD36_GOSAR)		C:GO:0005634; P:GC	C:nucleus; P:root meristem specification; P:maintenance of roo		IPR004082 (PRINTS): IPR032535 (PF	28,090	37,674	13,530	13,636	15,806									
Solyc05g018510	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *** G7JU55_MED_ABCG36		F:GO:0005524; C:GC	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR029481 (PF	140,898	94,659	2,240	2,653	2,774									
Solyc05g018520	NADH-cytochrome b5 reductase (AHRD V3.3 *** K4BZA6_SOLLC)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process		IPR001834 (PRINTS): IPR001709 (PF	63,728	59,365	106,850	92,743	103,729									
Solyc05g018560	LOW QUALITY:Serine/Threonine kinase family catalytic domain protein (AHRD V3.3 --* AT1G18390.2)						0,145	0,059	0,000	0,000	0,023									
Solyc05g018570	26S protease regulatory subunit, putative (AHRD V3.3 *** B9STQ0_RICCO)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata		IPR003593 (SMART): PF17862 (PFAM	81,101	77,881	106,748	106,229	100,140									
Solyc05g018590	26S protease regulatory subunit, putative (AHRD V3.3 *** B9STQ0_RICCO)		F:GO:0005524; C:GC	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata		IPR003593 (SMART): IPR032501 (PF	73,262	74,528	90,824	88,429	87,105									
Solyc05g018600	Actin-related protein (AHRD V3.3 *** A0A103XN71_CYNCS)		C:GO:0005634; P:GC	C:nucleus; P:chromatin remodeling		IPR004000 (SMART): IPR004000 (PF	14,020	13,226	16,964	13,827	15,794									
Solyc05g018610	DnaJ-like protein (AHRD V3.3 *** Q8VZB6_ARATH)		C:GO:0005789; P:GC	C:endoplasmic reticulum membrane; P:ubiquitin-dependent ERA		IPR001623 (PRINTS): IPR001623 (SM	34,815	44,609	51,572	53,009	48,908									
Solyc05g018615	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G63860.1)		F:GO:0009881; P:GC	F:photoreceptor activity; P:response to UV-B; F:protein homodi		IPR000408 (PRINTS): IPR000408 (PF	63,056	77,451	89,165	74,813	94,608									
Solyc05g018630	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *-* AT5G63860.1)		F:GO:0009881; P:GC	F:photoreceptor activity; P:response to UV-B; F:protein homodi		IPR000408 (PFAM): IPR009091 (G3D	0,019	0,019	0,097	0,000	0,047									

Solyc05g018640	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 --* AT5G63860.1)		F:GO:0009881; P:GC	F:photoreceptor activity; P:response to UV-B; F:protein homodimerization activity			0,105	0,080	0,212	0,072	0,118									
Solyc05g018650	Ferrochelatase (AHRD V3.3 *** K4BZB9_SOLLC)	FC	F:GO:0004325; P:GC	F:ferrochelatase ac EC:4.99.1.1	Protoporphyrin ferroc	IPR001015 (TIGRFAM): IPR001015 (F	88,055	102,725	113,318	114,330	135,413									
Solyc05g018653	Ferrochelatase (AHRD V3.3 *-* K4BZB9_SOLLC)	FC	F:GO:0004325; P:GC	F:ferrochelatase ac EC:4.99.1.1	Protoporphyrin ferroc	IPR001015 (PFAM): G3DSA:3.40.50.1	17,785	18,495	22,740	23,475	26,879									
Solyc05g018660	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151S0S9_CAJCA)					IPR019557 (PFAM): PTHR44194 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc05g018700	Protein disulfide-isomerase (AHRD V3.3 *** Q6IV17_IPOBA)		P:GO:0045454	P:cell redox homeostasis		PR00421 (PRINTS): G3DSA:3.40.30.1	153,992	109,909	110,681	82,648	92,498									
Solyc05g018730	calcium uniporter-like protein (DUF607) (AHRD V3.3 --* AT1G09575.2)					mobidb-lite (MOBIDB_LITE)	1,003	0,975	0,444	0,551	0,446									
Solyc05g018750	Cell wall protein AWA1 isoform 1 (AHRD V3.3 *** A0A061DLI6_THECC)		F:GO:0005515	F:protein binding		IPR009719 (PFAM): mobidb-lite (MOB	57,662	48,214	30,670	29,113	30,687									
Solyc05g018760	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DMB3_THECC)		C:GO:0016021; F:GC	C:integral component of membrane; F:ligase activity		IPR001841 (SMART): IPR013083 (G3	11,762	14,384	34,441	28,229	23,068			-0,580	0,002				down	
Solyc05g018770	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G29840.1)					IPR029058 (G3DSA:3.40.50.GENE3D	0,397	0,302	0,346	0,388	0,331									
Solyc05g018793	transmembrane protein (AHRD V3.3 *-* AT2G07674.2)		C:GO:0005739; C:GC	C:mitochondrion; C:membrane		PTHR35289 (PANTHER): PD020792 (	0,019	0,000	0,050	0,022	0,024									
Solyc05g018810	Nucleosome assembly protein 1-1 (AHRD V3.3 *** NAP1A_TOBAC)		C:GO:0005634; P:GC	C:nucleus; P:nucleosome assembly		IPR002164 (PFAM): G3DSA:3.30.112	334,852	288,468	385,773	294,090	295,055			-0,390	0,015	-0,388	0,021		down	down
Solyc05g018820	LOW QUALITY:cotton fiber protein (AHRD V3.3 *-* AT5G56980.1)		C:GO:0016021	C:integral component of membrane		IPR008480 (PFAM): IPR025520 (PFA	1,918	0,721	1,463	1,911	1,308	-1,382	0,041					down		
Solyc05g018850	LOW QUALITY:NAC domain containing protein 82 (AHRD V3.3 --* AT5G09330.5)						1,379	0,929	6,951	4,983	8,553									
Solyc05g018870	Transmembrane 9 superfamily member (AHRD V3.3 *** K4BZE1_SOLLC)		C:GO:0016021	C:integral component of membrane		IPR004240 (PFAM): IPR004240 (PAN	0,726	0,817	1,060	1,048	0,779									
Solyc05g018875	Transmembrane 9 superfamily member (AHRD V3.3 *-* K4BZE1_SOLLC)		C:GO:0016021	C:integral component of membrane		IPR004240 (PFAM): PTHR10766:SF8	0,302	0,177	0,168	0,192	0,262									
Solyc05g018880	Lysine-specific histone demethylase 1 like 1 (AHRD V3.3 *-* A0A0B2PY52_GLYSO)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process		IPR002937 (PFAM): G3DSA:3.90.660	1,368	1,780	0,075	0,101	0,118									
Solyc05g018890	LOW QUALITY:histone H2A deubiquitinase (DUF3755) (AHRD V3.3 --* AT3G07565.4)						1,011	0,716	0,208	0,460	0,303									
Solyc05g018920	Kinase, putative (AHRD V3.3 *-* B9SF98_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:3.30.200.20 (GENE3D): IPR0	0,000	0,000	0,000	0,000	0,024									
Solyc05g018930	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *-* A0A072TZ02_MEDTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR002902 (PFAM): IPR038408 (G3D	0,368	0,142	0,025	0,119	0,000									
Solyc05g019980	trichome birefringence-like protein (DUF828) (AHRD V3.3 *-* AT3G06080.2)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane; F:O-acε		IPR025846 (PFAM): IPR029962 (PAN	0,000	0,018	0,000	0,000	0,000									
Solyc05g019985	ZF-HD homeobox protein (AHRD V3.3 *-* A0A1D1Y306_9ARAE)		C:GO:0005634; P:GC	C:nucleus; P:floral meristem determinacy; P:plant-type ovary de		IPR006456 (PFAM): mobidb-lite (MOB	0,000	0,039	0,025	0,000	0,000									
Solyc05g020010	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_VITVI)		C:GO:0009522; P:GC	C:photosystem I; P:photosynthesis; C:integral component of me		IPR001280 (PFAM): IPR036408 (G3D	0,000	0,186	0,075	0,225	0,236									
Solyc05g020020	CONSTANS-like zinc finger protein (AHRD V3.3 *** A0A023GS52_SOYBN)	BBX8	F:GO:0008270	F:zinc ion binding		IPR000315 (SMAF CO-like	30,191	26,891	20,877	18,547	21,385									
Solyc05g021073	Glycosyltransferase (AHRD V3.3 *-* K4AWL3_SOLLC)		C:GO:0043231; F:GC	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl		G3DSA:3.40.50.2000 (GENE3D): PTH	0,019	0,000	0,000	0,000	0,024									
Solyc05g021090	NAC domain protein, (AHRD V3.3 *** A0A061FA31_THECC)	NAC046	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated		IPR003441 (PFAM NAC	0,019	0,021	0,025	0,048	0,023									
Solyc05g021100	Pleckstrin-like (PH) domain protein (AHRD V3.3 *** G7K3B9_MEDTR)		F:GO:0004674; C:GC	F:protein serine/thr EC:2.7.11	Transferring phospho	IPR011993 (G3DSA:2.30.29.GENE3D	22,754	20,703	29,276	33,757	29,530									
Solyc05g021105	Pleckstrin-like (PH) domain protein (AHRD V3.3 *-* G7K3B9_MEDTR)		F:GO:0004674; C:GC	F:protein serine/thr EC:2.7.11	Transferring phosphorus-containing groups		0,038	0,000	0,025	0,000	0,024									
Solyc05g021110	Pleckstrin-like (PH) domain protein (AHRD V3.3 *-* G7K3B9_MEDTR)		F:GO:0004674; C:GC	F:protein serine/thr EC:2.7.11	Transferring phosphorus-containing groups		0,000	0,000	0,025	0,072	0,073									
Solyc05g021140	LOW QUALITY:Nbs-lrr resistance protein, putative (AHRD V3.3 *-* A0A061FM42_THECC)		F:GO:0043531	F:ADP binding		IPR002182 (PFAM): PTHR23155:SF8	0,000	0,018	0,000	0,000	0,000									
Solyc05g021145	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT1G77340.1)					mobidb-lite (MOBIDB_LITE)	1,969	1,354	0,671	0,658	0,753									
Solyc05g021160	LOW QUALITY:phosphoribosylanthranilate isomerase 1 (AHRD V3.3 --* AT1G07780.9)						0,000	0,018	0,000	0,000	0,000									
Solyc05g021190	LOW QUALITY:Photosystem II D2 protein (AHRD V3.3 *-* PSBD_PLETE)		P:GO:0009772; F:GC	P:photosynthetic electron transport in photosystem II; F:electro		IPR036854 (G3DSA:1.20.85.GENE3D	0,096	0,098	0,125	0,125	0,094									
Solyc05g021370	Lectin alpha chain (AHRD V3.3 --* LECA_DIOGU)						0,000	0,000	0,072	0,000	0,000									
Solyc05g021390	Cytochrome P450 (AHRD V3.3 *** A0A161ABB0_OCIBA)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR001128 (PRINTS): IPR002401 (PF	0,000	0,000	0,069	0,047	0,093									
Solyc05g021500	Cystathionine beta-lyase (AHRD V3.3 *-* Q9MT31_SOLTU)		F:GO:0003824; F:GC	F:catalytic activity; F:cystathionine beta-lyase activity; C:chloroplast; C:plastid; F:lyase activity; F:pyrid			0,743	0,776	0,239	0,076	0,304									
Solyc05g021520	LOW QUALITY:protein dimerization (AHRD V3.3 --* AT5G45610.2)						0,116	0,081	0,125	0,072	0,165									
Solyc05g021530	Alcohol dehydrogenase (AHRD V3.3 --* Q4LAW8_CAPCH)						7,310	6,396	4,585	4,101	4,047									
Solyc05g021535	calmodulin-binding transcription activator (AHRD V3.3 --* AT3G16940.3)		F:GO:0003677	F:DNA binding		IPR005559 (PFAM)	5,586	5,562	3,077	3,587	2,989									
Solyc05g021540	Alcohol dehydrogenase (AHRD V3.3 *-* Q4LAW8_CAPCH)		F:GO:0003979; F:GC	F:UDP-glucose 6-dehydrogenase activity; F:alcohol dehydrogenase (NAD) activity; F:zinc ion binding; F			3,801	2,782	1,715	1,886	1,746									
Solyc05g021550	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7M8Q0_ARALL)						6,180	5,234	3,069	3,317	3,340									
Solyc05g021555	Alcohol dehydrogenase (AHRD V3.3 *** Q4LAW8_CAPCH)		F:GO:0016491	F:oxidoreductase activity		PTHR43880:SF22 (PANTHER): PTHR	4,332	2,709	1,345	2,222	1,577									
Solyc05g021570	Alcohol dehydrogenase (AHRD V3.3 *-* ADH_FRAAN)		F:GO:0004024; C:GC	F:alcohol dehydrog EC:1.1.1.284; EC:1.	S-(hydroxymethyl)glu	G3DSA:3.90.180.10 (GENE3D): PTHR	2,014	1,466	0,796	1,173	1,084									
Solyc05g021580	Serine/threonine-protein kinase TOR (AHRD V3.3 *-* TOR_ARATH)		F:GO:0000166; F:GC	F:nucleotide binding; F:protein serine/threonine kinase activity; F:ATP binding; P:protein phosphorylatio			2,638	1,519	1,022	1,528	1,390									
Solyc05g023600	Sister-chromatide cohesion protein 3 (AHRD V3.3 --* D7LHE4_ARALL)						0,000	0,000	0,000	0,000	0,024									
Solyc05g023660	LOW QUALITY:Transposase (AHRD V3.3 *-* F8UTT6_SOLDE)		F:GO:0003677; F:GC	F:DNA binding; F:transposase activity; P:transposition, DNA-me		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,000	0,000	0,000									
Solyc05g023680	RING-finger E3 ubiquitin ligase, putative (AHRD V3.3 *** A0A072VDM7_MEDTR)		C:GO:0005720; P:GC	C:nuclear heterochromatin; P:maintenance of DNA methylation;		IPR001841 (SMART): IPR003105 (SM	6,883	7,805	0,810	0,646	0,891									
Solyc05g023700	LOW QUALITY:4-alpha-glucanotransferase (AHRD V3.3 --* K3ZRU9_SETIT)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,183	0,158	0,072	0,048	0,141									
Solyc05g023710	Nucleolar complex protein 2 isoform 2 (AHRD V3.3 *** A0A061FUS6_THECC)					IPR005343 (PFAM): mobidb-lite (MOB	17,498	17,790	21,672	23,966	22,308									
Solyc05g023715	Protein TIC 22, chloroplastic (AHRD V3.3 --* A0A0B2PF70_GLYSO)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,260	0,182	0,243	0,406	0,451									
Solyc05g023720	Cytochrome f (AHRD V3.3 *** CYF_SOLTU)		F:GO:0005506; F:GC	F:iron ion binding; F:electron transfer activity; P:photosynthesis		IPR002325 (PRINTS): IPR024094 (PF	0,038	0,232	0,187	0,598	0,209									
Solyc05g023730	LOW QUALITY:50S ribosomal protein L2, chloroplastic (AHRD V3.3 *-* RK2_SOLBU)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation		IPR002171 (SMART): IPR022666 (PF	0,590	1,716	0,421	0,576	0,425									
Solyc05g023740	Arabidopsis mei2-like protein	aml1	F:GO:0003676	F:nucleic acid binding		IPR000504 (SMART): IPR007201 (PF	148,763	117,309	116,947	118,342	117,385									
Solyc05g023750	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *** G5DWI4_SILLA)		F:GO:0005096; F:GC	F:GTPase activator activity; F:protein binding; C:cytoplasm		IPR001164 (PRINTS): IPR001164 (SM	132,442	99,081	87,423	75,918	84,026									
Solyc05g023760	Receptor like protein kinase SOL2 (AHRD V3.3 *** F8WS95_SOLPE)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:3.30.200.20 (GENE3D): G3DS	2,802	2,939	1,964	1,701	2,589									
Solyc05g023763	coiled-coil protein (AHRD V3.3 *-* AT5G23700.3)		P:GO:0000911	P:cytokinesis by cell plate formation		mobidb-lite (MOBIDB_LITE): PTHR317	7,162	6,212	4,266	4,378	4,845									
Solyc05g023767	coiled-coil protein (AHRD V3.3 *-* AT3G48860.1)		P:GO:0000911	P:cytokinesis by cell plate formation		IPR040321 (PANTHER): PTHR31762:	12,630	10,443	7,151	6,279	7,828									
Solyc05g023770	coiled-coil protein (AHRD V3.3 *** AT3G48860.2)		P:GO:0000911	P:cytokinesis by cell plate formation		mobidb-lite (MOBIDB_LITE): mobidb-lit	18,309	14,701	10,422	9,239	10,016									
Solyc05g023775	NADH-quinone oxidoreductase protein (AHRD V3.3 *-* A0A072V639_MEDTR)					mobidb-lite (MOBIDB_LITE)	0,019	0,018	0,125	0,075	0,000									
Solyc05g023800	Ran protein/TC4 protein 1	RAN1	F:GO:0003924; F:GC	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	IPR002041 (PRINTS): SM00174 (SMA	242,874	237,828	417,366	395,902	377,756									
Solyc05g023820	LOW QUALITY:Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT3G48800.1)		F:GO:0005515	F:protein binding		IPR001660 (SMART): IPR001660 (PF	25,099	29,867	23,690	22,886	23,498									
Solyc05g023830	LOW QUALITY:Malate dehydrogenase [NADP], chloroplastic (AHRD V3.3 --* MDHP_MAIZE)					mobidb-lite (MOBIDB_LITE)	1,316	0,530	1,406	1,512	1,326									
Solyc05g023833	1-deoxy-D-xylulose 5-phosphate synthase 1 (AHRD V3.3 --* AT3G21500.3)						0,096	0,746	0,145	0,814	0,614									
Solyc05g023845	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 --* AT5G10100.2)						0,770	0,609	0,270	0,268	0,332									
Solyc05g023900	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YG29_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding		IPR002885 (PFAM): IPR032867 (PFA	3,146	2,520	2,875	3,314	3,086									
Solyc05g023990	LOW QUALITY:Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT1G09970.2)		F:GO:0004674; F:GC	F:protein serine/thr EC:2.7.11	Transferring phosphorus-containing groups		0,080	0,073	0,050	0,000	0,165									
Solyc05g024000	LOW QUALITY:PRF (AHRD V3.3 *-* Q96485_SOLLC)		F:GO:0043531	F:ADP binding			0,000	0,000	0,025	0,000	0,000									
Solyc05g024010	Zinc finger protein CONSTANS-LIKE 14 (AHRD V3.3 *** B9GMQ8_POPTR)	BBX12	F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding		IPR000315 (SMAF CO-like	24,172	23,830	26,298	23,912	24,124									
Solyc05g024020	LOW QUALITY:DnaK family protein (AHRD V3.3 *-* A0A072UMK6_MEDTR)					IPR032795 (PFAM): PTHR37897 (PAN	0,134	0,101	0,126	0,022	0,046									
Solyc05g024050	LOW QUALITY:17.0 kDa class II heat shock protein (AHRD V3.3 --* HSP23_MAIZE)						0,019	0,116	0,025	0,025	0,024									
Solyc05g024055	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *-* A0A0B0PVB3_GOSAR)		P:GO:0010228; P:GC	P:vegetative to reproductive phase transition of meristem; P:his		PTHR10742:SF260 (PANTHER): PTHF	0,019	0,021	0,022	0,000	0,024									
Solyc05g024060	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *-* A0A0B0PVB3_GOSAR)		F:GO:0003677; F:GC	F:DNA binding; F:oxidoreductase activity; P:oxidation-reduction process			0,061	0,061	0,000	0,025	0,000									
Solyc05g024120	Vacuolar protein sorting-associated protein 33-like protein (AHRD V3.3 *-* W9RWW6_9ROSA)		C:GO:0005829; P:GC	C:cytosol; P:vesicle docking involved in exocytosis; C:plant-type vacuole membrane; P:vesicle-mediate			5,300	9,905	6,174	6,720	7,250	0,924	0,017					up		
Solyc05g024160	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** B6T6H3_MAIZE)		F:GO:0004739; P:GC	F:pyruvate dehydro EC:1.2.4.1	Pyruvate dehydroger	IPR005475 (SMART): IPR009014 (G3	5,401	5,562	4,288	3,517	2,943									
Solyc05g024190	Chlorophyll synthase (AHRD V3.3 --* C3W4Q2_TOBAC)	CHLG	C:GO:0009507; C:GC	C:chloroplast; C:chloroplast thylakoid; P:chlorophyll biosynthetic process; C:membrane; C:integral comp			0,948	0,386	0,285	0,322	0,211									
Solyc05g024200	Kinesin-like protein KIN-5C (AHRD V3.3 --* KN5C_ARATH)						0,042	0,138	0,000	0,050	0,000									
Solyc05g024230	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *-* A0A0V0IM90_SOLCH)		F:GO:0003677; F:GC	F:DNA binding; F:DI EC:2.7.1.11	6-phosphofructokinas	PTHR31194:SF42 (PANTHER): PTHR:	0,276	0,452	0,170	0,122	5,688									
Solyc05g024240	Enoyl CoA hydratase/isomerase (AHRD V3.3 *** A0A0K9NXW3_ZOSMR)		F:GO:0003824	F:catalytic activity		IPR001753 (PFAM): G3DSA:3.90.226	22,675	22,638	46,502	41,061	47,412									
Solyc05g024245	Enoyl CoA hydratase/isomerase (AHRD V3.3 *** A0A0K9NXW3_ZOSMR)		F:GO:0003824	F:catalytic activity		IPR014748 (G3DSA:1.10.12.GENE3D	11,031	11,822	20,897	18,799	22,276									
Solyc05g024260	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BZR4_SOLLC)		C:GO:0016021	C:integral component of membrane		IPR004316 (PFAM): G3DSA:1.20.128	22,461	21,865	242,170	200,275	197,996									
Solyc05g024290	Protein kinase superfamily protein (AHRD V3.3 *** AT5G13160.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (PFAM): PIRSF000615 (P	55,255	63,287	60,931	52,510	58,966									
Solyc05g024340	Exocyst subunit exo70 family protein (AHRD V3.3 *** A0A072UIK5_MEDTR)		C:GO:0000145; P:GC	C:exocyst; P:exocytosis		IPR004140 (PFAM): G3DSA:1.20.128	0,000	0,019	0,000	0,000	0,000									
Solyc05g024360	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* A0A072U6R9_MEDTR)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction		IPR000157 (PFAM): IPR035897 (G3D	0,061	0,101	0,000	0,076	0,000									
Solyc05g024370	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT5G17680.2)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:3.40.50.3	0,040	0,094	0,044	0,149	0,024									
Solyc05g024373	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G46450.3)		P:GO:0007165; F:GC	P:signal transduction; F:ADP binding		PTHR11017:SF200 (PANTHER): PTHI	0,019	0,000	0,025	0,000	0,000									
Solyc05g024377	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* A0A072UXW1_MEDTR)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction		IPR000157 (PFAM): IPR035897 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc05g024380	LOW QUALITY:magnesium transporter 2 (AHRD V3.3 --* AT1G16010.3)						0,121	0,021	0,025	0,098	0,047									
Solyc05g024390	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)					IPR019557 (PFAM): PTHR44194 (PAN	0,019	0,000	0,000	0,050	0,000									
Solyc05g024400	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT1G51910.1)						0,000	0,000	0,000	0,000	0,024									
Solyc05g024410	Na+/H+ exchanger 8 (AHRD V3.3 --* AT1G14660.2)						0,606	1,020	0,763	0,788	0,774									
Solyc05g024415	Galactose oxidase/kelch repeat protein (AHRD V3.3 *** G7IH11_MEDTR)		F:GO:0005515	F:protein binding		IPR015915 (G3DSA:2.120.10.GENE3	76,334	82,509	185,143	160,090	176,070									
Solyc05g024420	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT1G13570.2)						0,000	0,019	0,000	0,050	0,000									
Solyc05g024430	transmembrane protein (AHRD V3.3 *** AT4G13500.1)		C:GO:0009507; C:GC	C:chloroplast; C:integral component of membrane		PTHR36343 (PANTHER)	11,541	20,254	5,801	7,115	13,016	0,838	0,002	1,157	0,000			up	up	
Solyc05g024480	LOW QUALITY:50S ribosomal protein L2, chloroplastic (AHRD V3.3 --* RK2_DAUCA)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus		mobidb-lite (MOBIDB_LITE): PTHR319	0,000	0,019	0,000	0,000	0,000									
Solyc05g025500	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SWK2_RICCO)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR012946 (SMART): IPR000490 (PF	14,803	15,243	7,251	7,554	9,131									
Solyc05g025510	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT5G08560.3)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR006595 (SM	145,314	121,982	102,305	106,779	104,339									
Solyc05g025520	calmodulin-binding protein-like protein (AHRD V3.3 --* AT5G10660.3)					mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,025	0,000									
Solyc05g025550	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT4G10840.2)					mobidb-lite (MOBIDB_LITE)	0,000	0,039	0,000	0,000	0,000									
Solyc05g025560	LOW QUALITY:Cytochrome c oxidase subunit 1 (AHRD V3.3 *-* B4XVS9_9ROSI)		F:GO:0004129; P:GC	F:cytochrome-c oxi EC:1.9.3.1	Cytochrome-c oxidas	IPR036927 (G3DSA:1.20.210.GENE3	0,021	0,021	0,025	0,050	0,024									
Solyc05g025580	LOW QUALITY:N-glycosylase/DNA lyase OGG1 (AHRD V3.3 --* OGG1_ARATH)						0,378	0,337	0,636	0,717	0,329									
Solyc05g025590	Replication protein A DNA-binding subunit (AHRD V3.3 *** A0A1D1YP03_9ARAE)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D		IPR004365 (PFAM): G3DSA:2.40.50.1	7,567	7,298	9,424	9,629	9,095									
Solyc05g025620	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT3G47560.4)					PTHR42886:SF14 (PANTHER): PTHR	0,197	0,135	0,195	0,075	0,094									
Solyc05g025630	WD-repeat protein, putative (AHRD V3.3 *-* B9SP08_RICCO)		F:GO:0005515	F:protein binding		IPR015943 (G3DSA:2.130.10.GENE3	0,059	0,039	0,000	0,000	0,024									
Solyc05g025635	WD-repeat protein, putative (AHRD V3.3 *** B9SP08_RICCO)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR015943 (G3	0,042	0,122	0,022	0,025	0,000									
Solyc05g025650	DNA-directed RNA polymerase III subunit RPC4, putative (AHRD V3.3 *** A0A061GKB3_THECC)		F:GO:0003677; F:GC	F:DNA binding; F:DI EC:2.7.7.6	DNA-directed RNA pc	IPR007811 (PFAM): IPR007811 (PAN	8,355	7,796	14,178	11,380	11,941									
Solyc05g025670	Respiratory burst oxidase, putative (AHRD V3.3 *-* B9RR53_RICCO)		F:GO:0004601; F:GC	F:peroxidase activi EC:1.6.3.1; EC:1.11.	NAD(P)H oxidase (H2O2-forming); Peroxidase		0,117	0,147	0,172	0,293	0,352									
Solyc05g025680	Respiratory burst oxidase, putative (AHRD V3.3 *-* B9RR53_RICCO)		C:GO:0016020; F:GC	C:membrane; F:oxidoreductase activity; P:oxidation-reduction p		IPR000778 (PRINTS): IPR013121 (PF	0,754	1,216	3,332	5,448	2,687									
Solyc05g025683	Respiratory burst oxidase, putative (AHRD V3.3 *-* B9RR53_RICCO)		F:GO:0004601; F:GC	F:peroxidase activi EC:1.11.1.7	Peroxidase	IPR013130 (PFAM): PTHR11972 (PAN	0,703	0,829	1,757	3,855	2,359					1,132	0,022			up
Solyc05g025687	Respiratory burst oxidase, putative (AHRD V3.3 *-* B9RR53_RICCO)		F:GO:0004601; F:GC	F:peroxidase activi EC:1.11.1.7	Peroxidase	G3DSA:1.10.238.10 (GENE3D): IPR0	0,372	0,685	1,268	2,504	1,201					0,995	0,026			up
Solyc05g025710	60S ribosomal protein L23 (AHRD V3.3 *-* RL23_ARATH)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation		IPR036853 (G3DSA:2.40.150.GENE3	0,000	0,000	0,000	0,048	0,000									
Solyc05g025720	LOW QUALITY:ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 --* A0A0B0PT61_GOSAI		C:GO:0016020	C:membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,021	0,000	0,000	0,000									
Solyc05g025730	LOW QUALITY:Endoglucanase (AHRD V3.3 *** K4BZW1_SOLLC)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR012341 (G3DSA:1.50.10.GENE3D	0,591	0,839	0,267	0,318	0,519									
Solyc05g025740	SH3 domain-containing protein (AHRD V3.3 *** AT2G07360.1)		F:GO:0005515	F:protein binding		IPR001452 (SMART): IPR001452 (PF	60,451	59,037	63,886	63,571	61,968									
Solyc05g025750	SH3 domain-containing protein (AHRD V3.3 *-* AT2G07360.2)		C:GO:0005634; C:GC	C:nucleus; C:cytosol; C:plasma membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	13,679	11,122	14,469	14,625	13,314									
Solyc05g025790	Potassium channel (AHRD V3.3 *-* Q9SSV3_NICPA)		F:GO:0005249; C:GC	F:voltage-gated potassium channel activity; C:integral compone		PTHR10217 (PANTHER): PTHR10217	1,009	1,348	0,778	1,067	1,271									
Solyc05g025800	LOW QUALITY:receptor like protein 38 (AHRD V3.3 --* AT3G23120.1)						0,057	0,236	0,000	0,074	0,071									
Solyc05g025810	Adipocyte plasma membrane-associated protein, putative (AHRD V3.3 *** B9RR90_RICCO)		P:GO:0009058; F:GC	P:biosynthetic proc EC:4.3.3.2	Strictosidine synthas	IPR018119 (PFAM): IPR011042 (G3D	7,335	7,385	1,869	2,308	3,619			0,934	0,036				up	
Solyc05g025820	Kinase family protein (AHRD V3.3 *-* U5GAR5_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR001245 (PFAM): G3DSA:3.30.200	0,264	0,435	0,264	0,171	0,164									
Solyc05g025870	Carboxypeptidase A6 (AHRD V3.3 --* A0A0B2RNE2_GLYSO)		F:GO:0004181; C:GC	F:metallocarboxype EC:3.4.17	Acting on peptide bonds (peptidases)		0,976	0,677	0,622	0,630	0,753									
Solyc05g025890	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT2G06025.6)					G3DSA:3.40.630.30 (GENE3D): IPR0	0,019	0,101	0,000	0,000	0,023									
Solyc05g025900	Damaged dna-binding 2, putative isoform 1 (AHRD V3.3 *** A0A061GKJ3_THECC)					mobidb-lite (MOBIDB_LITE): mobidb-lit	39,458	42,882	44,038	41,986	40,556									
Solyc05g025905	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *-* K4BBV6_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			4,406	4,385	2,656	2,582	2,742									
Solyc05g025910	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *-* K4BBV6_SOLLC)		F:GO:0004373; F:GC	F:glycogen (starch) EC:2.4.1.21; EC:2.4.	Starch synthase; Glycogen(starch) synthase		0,098	0,140	0,025	0,047	0,072									
Solyc05g025957	Histone H2A (AHRD V3.3 --* M1DGY7_SOLTU)					IPR032454 (PFAM)	0,000	0,000	0,049	0,025	0,000									
Solyc05g025980	Histone H2A (AHRD V3.3 *** M1DI90_SOLTU)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimei		IPR002119 (PRINTS): IPR002119 (SM	0,000	0,000	0,000	0,048	0,023									
Solyc05g026045	40S ribosomal protein S28 (AHRD V3.3 *-* W9SEX7_9ROSA)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation		IPR000289 (PFAM): G3DSA:2.40.50.1	0,457	0,259	0,211	0,221	0,469									
Solyc05g026050	Vacuolar protein sorting-associated protein 32 homolog 1 (AHRD V3.3 *** VP321_ARATH)		P:GO:0007034	P:vacuolar transport		IPR005024 (PFAM): G3DSA:1.10.287	47,068	56,560	52,944	67,328	59,691									
Solyc05g026060	Glycine-rich protein (AHRD V3.3 *-* D7M4B5_ARALL)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): PTHR315	7,015	5,275	8,564	8,160	7,163									
Solyc05g026080	glycine-rich protein (AHRD V3.3 *** AT4G32920.3)		C:GO:0016021	C:integral component of membrane		PTHR31513:SF8 (PANTHER): PTHR3	22,439	21,607	26,874	29,912	27,422									
Solyc05g026090	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151R878_CAJCA)					IPR019557 (PFAM): PTHR44194 (PAN	0,021	0,019	0,000	0,000	0,024									
Solyc05g026130	AP-1 complex subunit sigma-like protein (AHRD V3.3 *** G7L0L8_MEDTR)		P:GO:0015031	P:protein transport		G3DSA:3.30.450.60 (GENE3D): IPR0	18,381	21,525	23,149	20,359	20,311									
Solyc05g026140	UPF0420 C16orf58-like protein (AHRD V3.3 *** A0A072U484_MEDTR)		C:GO:0005739; P:GC	C:mitochondrion; P:auxin polar transport; C:chloroplast envelo		IPR006968 (PFAM): PTHR12770:SF5	12,132	13,403	11,091	9,952	12,902									
Solyc05g026157	mitochondrial processing peptidase alpha subunit (AHRD V3.3 *-* AT3G16480.1)		F:GO:0004222; P:GC	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	G3DSA:3.30.830.10 (GENE3D): PTHR	0,019	0,000	0,000	0,000	0,000									
Solyc05g026180	NAC domain protein (AHRD V3.3 *** S5R947_9ROSA)	NAC047	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated		IPR003441 (PFAM NAC	0,981	1,318	0,291	0,514	0,613									
Solyc05g026223	ankyrin repeat protein (AHRD V3.3 --* AT1G73350.7)						2,838	1,954	2,137	1,903	2,123									
Solyc05g026227	30S ribosomal protein S11 (AHRD V3.3 *-* A0A0K9PCU6_ZOSMR)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation		IPR036967 (G3DSA:3.30.420.GENE3	3,234	2,346	2,166	2,734	2,637									
Solyc05g026240	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9Q1P6_ZOSMR)		F:GO:0005515	F:protein binding		IPR013210 (PFAM): IPR001611 (PFA	31,800	25,515	1,582	1,038	1,181									
Solyc05g026250	LOW QUALITY:PHD finger protein ALFIN-LIKE 4 (AHRD V3.3 --* ALFL4_ORYSJ)						0,199	0,573	0,668	0,657	0,648									
Solyc05g026260	LOW QUALITY:Histone H1 (AHRD V3.3 --* A0A0B0P577_GOSAR)		C:GO:0000786; F:GC	C:nucleosome; F:double-stranded DNA binding; F:protein bindin		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,041	0,000	0,000	0,000									
Solyc05g026310	Derlin (AHRD V3.3 *** A0A0V0HZ18_SOLCH),Pfam:PF04511		C:GO:0005789; C:GC	C:endoplasmic reticulum membrane; C:integral component of me		IPR007599 (PFAM): mobidb-lite (MOB	26,294	23,494	49,748	54,209	46,756									
Solyc05g026330	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** A2PZD5_IPONI)		F:GO:0008171	F:O-methyltransferase activity		IPR002935 (PFAM): G3DSA:3.40.50.1	0,000	0,019	0,000	0,000	0,000									
Solyc05g026335	Unknown protein (AHRD V3.3)						0,019	0,019	0,000	0,000	0,000									

Solyc05g026350	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** A2PZD5_IPONI)		F:GO:0008171	F:O-methyltransferase activity			IPR002935 (PFAM): G3DSA:3.40.50.1	0,000	0,039	0,000	0,000	0,000									
Solyc05g026360	Pollen-specific SF21-like protein (AHRD V3.3 *** G7LJK8_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,452	0,380	0,381	0,488	0,516									
Solyc05g026370	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	0,227	0,361	0,022	0,000	0,000									
Solyc05g026373	K(+) efflux antiporter (AHRD V3.3 *-* A0A0K9NUN8_ZOSMR)		F:GO:0015299: C:G(	F:solute:proton antiporter activity; C:integral component of mem			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,884	0,615	0,964	1,065	0,921									
Solyc05g026377	K(+) efflux antiporter (AHRD V3.3 *-* A0A0K9NUN8_ZOSMR)		P:GO:0006812: F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	2,356	2,467	1,922	1,821	1,515									
Solyc05g026380	K(+) efflux antiporter (AHRD V3.3 *-* A0A0K9NUN8_ZOSMR)		P:GO:0006812: F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	9,012	7,326	6,034	6,938	6,859									
Solyc05g026385	K(+) efflux antiporter (AHRD V3.3 --* A0A0K9Q146_ZOSMR)		F:GO:0015299: C:G(	F:solute:proton antiporter activity; C:integral component of membrane; P:proton transmembrane transpo				5,696	4,359	3,417	4,348	4,423									
Solyc05g026420	Ferritin-2, chloroplastic (AHRD V3.3 --* FRI2_SOYBN)							1,288	1,331	2,004	1,456	1,651									
Solyc05g026460	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT3G59000.2)							0,200	0,520	0,372	0,271	0,473									
Solyc05g026470	transcriptional corepressor LEUNIG (AHRD V3.3 *-* AT4G32551.1)		F:GO:0005515	F:protein binding			IPR006594 (PFAM): PTHR44376 (PAN	0,038	0,095	0,050	0,076	0,095									
Solyc05g026480	transcriptional corepressor LEUNIG (AHRD V3.3 *-* AT4G32551.2)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	0,037	0,136	0,047	0,050	0,117									
Solyc05g026490	Phosphomannomutase/phosphoglucomutase (AHRD V3.3 *** A0A0B2PFJ1_GLYSO)		P:GO:0005975: F:G(	P:carbohydrate metabolic process; F:intramolecular transferase			IPR005841 (PRINTS): IPR005844 (PF	0,019	0,076	0,000	0,000	0,023									
Solyc05g026500	LOW QUALITY:Phenylalanine ammonia-lyase (AHRD V3.3 --* PAL1_SOLLC)	PAL						0,642	0,525	0,393	0,487	0,520									
Solyc05g026510	Sister-chromatide cohesion protein 3 (AHRD V3.3 *** D7LHE4_ARALL)						IPR013721 (PFAM): mobidb-lite (MOB	88,278	80,369	105,852	113,506	108,527									
Solyc05g026517	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc05g026520	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,021	0,021	0,000	0,025	0,000									
Solyc05g026540	Transmembrane protein (AHRD V3.3 *** A0A0B0N2J4_GOSAR)		C:GO:0005634: C:G(	C:nucleus; C:vacuolar membrane; C:endoplasmic reticulum; C:G			IPR019308 (PFAM): mobidb-lite (MOB	121,407	135,745	131,587	128,732	118,957									
Solyc05g026550	NADH dehydrogenase-like complex L (AHRD V3.3 *** A0A0F7CYX9_9ROSI)		F:GO:0016655: P:G(	F:oxidoreductase activity, acting on NAD(P)H, quinone or simila			IPR019654 (PFAM): IPR019654 (PAN	7,757	13,807	4,938	6,937	12,181	0,859	0,022	1,293	0,000			up	up	
Solyc05g026560	ARM repeat superfamily protein (AHRD V3.3 *** AT1G23180.1)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	48,037	55,047	69,409	60,537	76,186									
Solyc05g026570	Chlororespiratory reduction 3 (AHRD V3.3 *** A0A0F7CZ71_9ROSI)		C:GO:0009535: P:G(	C:chloroplast thylakoid membrane; P:photosynthetic electron tra			IPR038931 (PANTHER)	4,793	9,480	1,333	3,020	5,896	1,008	0,010	2,140	0,000	1,185	0,006	up	up	up
Solyc05g031600	tryptophan aminotransferase related 2 (AHRD V3.3 *** AT4G24670.2)		F:GO:0016846	F:carbon-sulfur lyase activity			IPR015422 (G3DSA:3.90.1150.GENE	0,102	0,417	0,071	0,070	0,213									
Solyc05g032620	LOW QUALITY:multimeric translocon complex in the outer envelope membrane 132 (AHRD V3.3 --* AT2G16640.3)						mobidb-lite (MOBIDB_LITE)	3,851	2,714	0,875	0,873	1,175									
Solyc05g032630	LOW QUALITY:aldehyde dehydrogenase 3H1 (AHRD V3.3 --* AT1G44170.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,214	0,061	0,246	0,000	0,373									
Solyc05g032640	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT5G50915.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,134	0,122	0,000	0,000	0,000									
Solyc05g032650	Zinc finger transcription factor 38	C3H38	F:GO:0046872	F:metal ion binding			IPR006768 (PFAM): IPR040194 (PAN	0,000	0,000	0,000	0,049	0,000									
Solyc05g032660	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT4G13250.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	15,505	27,188	14,005	15,471	26,024	0,837	0,001	0,890	0,000			up	up	
Solyc05g032670	26S proteasome non-ATPase regulatory subunit 3 (AHRD V3.3 -** A0A0A9QZE4_ARUDO)						mobidb-lite (MOBIDB_LITE)	18,398	15,825	14,249	15,857	12,602									
Solyc05g032680	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *-* A0A072TX02_MEDTR)		F:GO:0003860	F:3-hydroxyisobutyı	EC:3.1.2.4	3-hydroxyisobutyryl-(	IPR032259 (PFAM): G3DSA:3.90.226	4,507	3,272	1,237	1,367	1,272									
Solyc05g032700	Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 *-* A0A151SRU5_CAJCA)						PTHR45245 (PANTHER)	0,282	0,434	0,137	0,099	0,024									
Solyc05g032710	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072TX02_MEDTR)		F:GO:0003860	F:3-hydroxyisobutyı	EC:3.1.2.4	3-hydroxyisobutyryl-(	IPR032259 (PFAM): G3DSA:3.90.226	4,810	4,642	1,509	2,075	1,313									
Solyc05g032750	EEIG1/EHBP1 protein amino-terminal domain protein (AHRD V3.3 *** A0A072V6S3_MEDTR)		P:GO:0009902	P:chloroplast relocation			IPR018392 (SMART): IPR019448 (PF	48,099	44,317	57,260	49,880	48,870									
Solyc05g032760	PHD finger alfin-like protein (AHRD V3.3 *-* A0A072VES1_MEDTR)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR001965 (SMART): IPR013083 (G3	3,481	3,628	1,900	2,280	2,400									
Solyc05g032770	PHD finger alfin-like protein (AHRD V3.3 *** A0A072VDQ0_MEDTR)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR021998 (PFAM): mobidb-lite (MOB	4,072	4,675	2,963	3,175	3,830									
Solyc05g032780	LOW QUALITY:TCP transcription factor 1 (AHRD V3.3 *** G3BGU2_SOLLC)						IPR017887 (PFAM): TCP	0,000	0,019	0,025	0,000	0,000									
Solyc05g032850	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *** AT3G13460.4)		F:GO:0003723	F:RNA binding			IPR007275 (PFAM): G3DSA:3.10.590	48,566	42,074	61,280	58,263	57,641									
Solyc05g032880	50S ribosomal protein L9 (AHRD V3.3 *** A0A0B2PT62_GLYSO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR020070 (PFAM): IPR036935 (G3D	22,148	21,003	25,692	22,861	25,177									
Solyc05g039940	LOW QUALITY:Glucan endo-1,3-beta-glucosidase, acidic isoform GL161 (AHRD V3.3 --* E13K_TOBAC)						mobidb-lite (MOBIDB_LITE)	2,689	1,736	1,256	1,132	1,086									
Solyc05g039950	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	1,464	0,801	0,772	0,523	0,586									
Solyc05g039960	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 *-* A0A061EBN2_THECC)						PTHR13833:SF41 (PANTHER): PTHR	0,000	0,018	0,000	0,000	0,000									
Solyc05g039990	Mannose-binding lectin superfamily protein (AHRD V3.3 --* AT3G16470.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,921	4,434	3,948	3,058	3,358									
Solyc05g040020	Vps51/Vps67 family (components of vesicular transport) protein (AHRD V3.3 --* AT5G16300.4)							0,040	0,000	0,000	0,000	0,000									
Solyc05g040040	F-box family protein (AHRD V3.3 *** AT5G48170.1)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	0,021	0,021	0,000	0,000	0,000									
Solyc05g040050	DnaJ domain-containing protein (AHRD V3.3 *** A0A103YK36_CYNCS)						IPR001623 (PRINTS): IPR001623 (SM	16,541	20,728	13,995	14,394	15,734									
Solyc05g040055	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT1G27180.8)						mobidb-lite (MOBIDB_LITE): PTHR331	0,897	1,307	0,122	0,240	0,235									
Solyc05g040100	Membrin (AHRD V3.3 *** A0A0V0HLU2_SOLCH)		F:GO:0005484: C:G(	F:SNAP receptor activity; C:Golgi apparatus; P:vesicle-mediate			IPR027027 (PIRSF): PTHR21230:SF1	3,035	3,127	2,028	1,417	1,739									
Solyc05g041110	Protein kinase superfamily protein (AHRD V3.3 *-* AT3G56760.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,021	0,000	0,000	0,000	0,000									
Solyc05g041140	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9HHI8_POPTR)		F:GO:0005504: P:G(	F:fatty acid binding; P:systemic acquired resistance			IPR016140 (PFAM): G3DSA:1.10.110	0,000	0,000	0,025	0,000	0,000									
Solyc05g041200	4-hydroxyphenylpyruvate dioxygenase (AHRD V3.3 *** K4C0A1_SOLLC)	HPPD2	F:GO:0003868: P:G(	F:4-hydroxyphenylp	EC:1.13.11; EC:1.13	Acting on single donc	IPR004360 (PFAM): IPR005956 (TIGF	63,219	47,704	198,390	197,440	196,290									
Solyc05g041230	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_STAPU)		C:GO:0009521: P:G(	C:photosystem; P:photosynthetic electron transport chain; F:ch			IPR000932 (PFAM): PTHR33180:SF4	0,000	0,021	0,000	0,000	0,023									
Solyc05g041240	LOW QUALITY:Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *-* A0A103XZP5_CYNCS)						PF05664 (PFAM): PTHR31280:SF15 (	0,021	0,000	0,000	0,000	0,000									
Solyc05g041340	Ankyrin repeat-containing-like protein (AHRD V3.3 *-* A0A061GL73_THECC)		C:GO:0016020	C:membrane			IPR036770 (G3DSA:1.25.40.GENE3D	0,000	0,018	0,000	0,000	0,024									
Solyc05g041360	Maturase K (AHRD V3.3 *-* MATK_SOLLC)		P:GO:0006397: C:G(	P:mRNA processing; C:chloroplast			IPR024942 (PFAM): IPR002866 (PAN	0,081	0,268	0,000	0,250	0,093									
Solyc05g041390	LOW QUALITY:TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 -** AT4G10360.3)							0,997	1,271	0,646	1,043	1,009									
Solyc05g041420	MAP kinase kinase kinase 36	MAPKKK36	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	15,263	14,074	23,427	24,620	20,039									
Solyc05g041430	PTB domain engulfment adapter (AHRD V3.3 *** AT2G04790.2)						PTHR36342 (PANTHER)	8,376	9,322	4,412	4,805	8,100			0,874	0,002				up	
Solyc05g041440	Ankyrin repeat-containing-like protein (AHRD V3.3 *** A0A061GL73_THECC)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR029472 (PF	4,973	4,525	0,209	0,195	0,237									
Solyc05g041500	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT5G11290.2)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc05g041530	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G25770.3)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity			IPR001375 (PFAM): IPR029058 (G3D	20,740	25,901	6,889	5,879	11,366			0,718	0,007				up	
Solyc05g041540	Carboxypeptidase (AHRD V3.3 *** K4C0D5_SOLLC)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	1,758	2,595	0,471	0,669	1,005									
Solyc05g041570	Polyprotein (AHRD V3.3 *-* Q94KV0_ARATH)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane				0,021	0,000	0,000	0,000	0,000									
Solyc05g041590	Ankyrin repeat-containing-like protein (AHRD V3.3 *** A0A061GL73_THECC)		C:GO:0016021	C:integral component of membrane			IPR036770 (G3DSA:1.25.40.GENE3D	0,019	0,000	0,000	0,025	0,000									
Solyc05g041623	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 *-* AT3G56760.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PTHF	0,000	0,018	0,000	0,000	0,000									
Solyc05g041627	QWRF motif protein (DUF566) (AHRD V3.3 --* AT2G24070.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,025	0,000									
Solyc05g041680	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLBU)		F:GO:0005524: C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,000	0,023									
Solyc05g041693	At3g48690-like protein (AHRD V3.3 --* D9ZTP9_ARALL)							0,042	0,099	0,050	0,022	0,024									
Solyc05g041700	LOW QUALITY:Auxin efflux carrier component (AHRD V3.3 --* M0S2X6_MUSAM)							1,176	2,617	1,039	1,216	1,081									
Solyc05g041750	LOW QUALITY:Proline-rich receptor-like protein kinase PERK10 (AHRD V3.3 --* PEK10_ARATH)							0,059	0,211	0,118	0,201	0,238									
Solyc05g041770	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	0,839	0,941	0,551	0,519	0,686									
Solyc05g041780	CDPK-related protein kinase (AHRD V3.3 --* CRK_DAUCA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,335	0,461	0,244	0,292	0,187									
Solyc05g041850	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_SCHNE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,362	0,073	0,118	0,337	0,211									
Solyc05g041860	N-acetyltransferase (AHRD V3.3 *** B6TRH8_MAIZE)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			G3DSA:3.40.630.30 (GENE3D): IPR0	16,129	15,370	17,855	14,586	16,734									
Solyc05g041910	Auxin induced-like protein (AHRD V3.3 *** A0A0K9P8V5_ZOSMR)		C:GO:0016021: P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART): IPR005018 (PF	207,095	577,829	105,736	118,630	120,009	1,500	0,016					up		
Solyc05g041920	Ribonuclease 3 family protein (AHRD V3.3 *** B9GTV4_POPTR)		F:GO:0004525: P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	IPR000999 (SMART): IPR000999 (PF	0,000	0,021	0,047	0,022	0,000									
Solyc05g041995	SIN3-like 3 (AHRD V3.3 --* AT1G24190.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc05g042030	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein (AHRD V3.3 *** AT4G		F:GO:0003682	F:chromatin binding			IPR001025 (SMART): IPR001965 (SM	51,549	51,616	48,716	49,287	50,103									
Solyc05g042040	UBA/UBX domain protein (AHRD V3.3 *** AT4G22150.1)		F:GO:0005515	F:protein binding			IPR001012 (SMART): IPR012989 (SM	6,376	9,300	4,878	5,001	6,259									
Solyc05g042050	Nodulin MtN21/EamA-like transporter family protein (AHRD V3.3 *-* A0A072UZA3_MEDTR)		C:GO:0016020	C:membrane				1,599	1,374	1,272	1,612	1,106									
Solyc05g042055	Nodulin MtN21 /EamA-like transporter family protein (AHRD V3.3 *-* AT2G05755.1)		C:GO:0016021	C:integral component of membrane			PTHR22911 (PANTHER): PTHR22911	5,973	5,522	5,787	7,060	5,773									
Solyc05g042070	1-phosphatidylinositol-4-phosphate 5-kinase 3 (AHRD V3.3 --* AT2G26420.3)							5,127	5,015	5,379	6,050	6,198									
Solyc05g042090	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* Q9SBC3_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,000	0,000	0,022	0,000	0,000									
Solyc05g042120	embryo defective 1381 (AHRD V3.3 *** AT2G31340.1)						PTHR36017 (PANTHER): IPR027417 (	19,513	18,206	18,299	16,915	19,190									
Solyc05g042122	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 *-* G8A1X8_MEDTR)						IPR025558 (PFAM): mobidb-lite (MOB	1,522	1,189	0,808	0,878	0,916									
Solyc05g042150	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *-* A0A0B2PAA1_GLYSC		C:GO:0005829: P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			IPR008545 (PFAM): PTHR32054:SF2	0,019	0,039	0,090	0,000	0,023									
Solyc05g042170	LOW QUALITY:cell cycle checkpoint control protein family (AHRD V3.3 --* AT3G05480.3)						mobidb-lite (MOBIDB_LITE)	0,040	0,039	0,094	0,050	0,047									
Solyc05g042180	LOW QUALITY:Poly(RC)-binding protein, putative (AHRD V3.3 *-* B9SPR0_RICCO)		F:GO:0003723	F:RNA binding			IPR004088 (PFAM): IPR036612 (G3D	0,179	0,096	0,025	0,050	0,000									
Solyc05g043217	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* A0A061ERC8_THECC)							0,160	0,162	0,000	0,101	0,095									
Solyc05g043232	Zinc finger CCCH domain-containing protein (AHRD V3.3 *-* A0A0K9PNZ2_ZOSMR)		F:GO:0046872	F:metal ion binding			PTHR14493 (PANTHER): PTHR14493	0,037	0,064	0,000	0,025	0,000									
Solyc05g043240	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_CHLAT)							0,105	0,075	0,000	0,050	0,023									
Solyc05g043330	GDSL esterase/lipase (AHRD V3.3 *** W9STE9_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	9,551	5,939	0,797	1,447	1,032									
Solyc05g043353	Centromere/kinetochore protein (ZW10), putative (AHRD V3.3 *** A0A061DLQ5_THECC)		P:GO:0000278: C:G(	P:mitotic cell cycle; C:chromosome, centromeric region; C:nucle			G3DSA:1.10.357.150 (GENE3D): IPR(	19,380	18,846	22,760	25,334	22,823									
Solyc05g043357	LOW QUALITY:ATP synthase subunit alpha, chloroplastic (AHRD V3.3 --* ATPA_PELHO)		F:GO:0004040: C:G(	F:amidase activity; C:membrane; C:integral component of memt			IPR026960 (PFAM)	0,000	0,000	0,025	0,000	0,000									
Solyc05g043380	phosphatidylinositol 4-kinase gamma-like protein (AHRD V3.3 --* AT3G56600.2)							0,000	0,000	0,022	0,000	0,000									
Solyc05g043390	Pseudouridine-5'-phosphate glycosidase (AHRD V3.3 --* M7YM69_TRIUA)							1,865	1,311	1,070	0,650	0,917									
Solyc05g043400	LOW QUALITY:Alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic (AHRD V3.3 --* PHSL_IPOBA)							0,061	0,076	0,051	0,000	0,047									
Solyc05g043410	LOW QUALITY:BTB/POZ domain-containing protein At5g60050 (AHRD V3.3 --* Y5600_ARATH)							0,081	0,019	0,025	0,092	0,094									
Solyc05g043420	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,139	0,181	0,096	0,070	0,047									
Solyc05g043425	Protein translocase subunit SecA (AHRD V3.3 --* W1P303_AMBTC)		F:GO:0016787	F:hydrolase activity			IPR002925 (PFAM): IPR029058 (G3D	83,590	73,353	106,676	78,542	94,453					-0,438	0,007			down
Solyc05g043430	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G32520.2)		F:GO:0016787	F:hydrolase activity			IPR002925 (PFAM): IPR029058 (G3D	160,517	134,594	204,853	155,945	191,513					-0,390	0,011			down
Solyc05g044470	B-cell receptor-associated 31-like protein (AHRD V3.3 *-* AT5G42570.1)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte			PTHR12701:SF13 (PANTHER): IPR00	1,890	1,614	3,379	3,774	3,655									
Solyc05g044480	RNA helicase DEAH-box16	DEAH16	F:GO:0005524	F:ATP binding			IPR001650 (SMART): IPR014001 (SM	32,900	26,359	13,549	11,930	16,021									
Solyc05g044490	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,019	0,073	0,000	0,025	0,072									
Solyc05g044510	RNA helicase DEAH-box17	DEAH17	F:GO:0005524: F:G(	F:ATP binding; F:metal ion binding			IPR001650 (SMART): IPR014001 (SM	0,019	0,021	0,000	0,000	0,000									
Solyc05g044530	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SHP6_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAN	0,000	0,041	0,000	0,000	0,000									
Solyc05g044570	LOW QUALITY:Helicase protein with RING/U-box domain-containing protein (AHRD V3.3 *-* AT1G05120.1)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	0,021	0,021	0,000	0,000	0,000									
Solyc05g044580	Actin-like ATPase superfamily protein (AHRD V3.3 --* AT1G80460.2)							4,656	3,735	7,504	8,017	6,331									
Solyc05g044585	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q7XET1_ORYSJ)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): mobidb-lite (MOB	0,880	1,212	1,088	0,941	1,176									
Solyc05g044590	LOW QUALITY:histone acetyltransferase of the MYST family 2 (AHRD V3.3 --* AT5G09740.1)							0,160	0,160	0,096	0,120	0,142									
Solyc05g044600	Glutamate--tRNA ligase, chloroplastic/mitochondrial (AHRD V3.3 --* SYE_TOBAC)							1,357	1,329	0,987	1,048	1,275									
Solyc05g044610	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *-* AT4G00800.2)		C:GO:0005623: P:G(	C:cell; P:intracellular protein transport; P:vesicle-mediated trans			mobidb-lite (MOBIDB_LITE): PTHR126	79,982	65,813	85,554	95,349	90,926									
Solyc05g044615	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT4G00800.1)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	71,373	50,394	61,762	79,430	72,120									
Solyc05g044620	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (AHRD V3.3 -** AT1G19020.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	11,265	10,768	10,457	10,402	10,578									
Solyc05g044630	NifU-like protein 3 (AHRD V3.3 *-* W9RHZ6_9ROSA)		F:GO:0005506: P:G(	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl			IPR001075 (PFAM): IPR034904 (G3D	11,102	17,634	12,080	12,292	20,223	0,695	0,015	0,739	0,000			up	up	
Solyc05g045650	glutamate receptor-like3.4	GLR3_4	F:GO:0004930: F:G(	F:G protein-coupled receptor activity; F:ionotropic glutamate rec			IPR000337 (PRINTS): IPR001320 (SM	3,592	4,366	1,629	2,173	2,163									
Solyc05g045660	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT3G21700.1)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	0,021	0,041	0,000	0,000	0,000									
Solyc05g045670	Glucose-6-phosphate/phosphate-translocator (AHRD V3.3 *** O64911_SOLTU)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR004696 (TIGRFAM): IPR004853 (F	40,295	47,537	0,180	0,000	0,095									
Solyc05g045705	CTD small phosphatase-like protein 2, putative (AHRD V3.3 *** A0A061F6J6_THECC)		P:GO:0010089	P:xylem development			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,762	1,080	0,460	0,364	0,189									
Solyc05g045730	LOW QUALITY:transcriptional regulator EFH1-like protein (AHRD V3.3 --* AT1G28630.5)		C:GO:0005739	C:mitochondrion				0,021	0,021	0,099	0,069	0,072									
Solyc05g045740	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT		C:GO:0005739: C:G(	C:mitochondrion; C:integral component of membrane				0,038	0,059	0,050	0,047	0,023									
Solyc05g045750	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_CERME)		C:GO:0005739: P:G(	C:mitochondrion; P:mRNA processing			mobidb-lite (MOBIDB_LITE)	0,000	0,019	0,025	0,000	0,000									
Solyc05g045790	Cytochrome c oxidase subunit 2 (AHRD V3.3 *** K4C0R2_SOLLC)		F:GO:0004129: F:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR002429 (PFAM): IPR036257 (G3D	0,040	0,043	0,099	0,225	0,047									
Solyc05g045880	LOW QUALITY:WRKY transcription factor 66	WRKY66	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,000	0,019	0,000	0,000	0,000									
Solyc05g045910	Ribosomal protein S3 (AHRD V3.3 *-* I3NTU1_9SOLA)		F:GO:0003723: F:G(	F:RNA binding; F:structural constituent of ribosome; C:mitochon			PTHR35928 (PANTHER)	0,000	0,000	0,025	0,000	0,000									
Solyc05g045927	WRKY family transcription factor (AHRD V3.3 *-* AT4G01250.1)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMART): IPR036576 (G3	0,000	0,077	0,000	0,000	0,000									
Solyc05g045950	Protein phosphatase 2A regulatory subunit A (AHRD V3.3 *-* C0L8B0_BETPN)		C:GO:0000159: F:G(	C:protein phosphat:	EC:3.1.3.16	Protein-serine/threor	IPR011989 (G3DSA:1.25.10.GENE3D	0,021	0,021	0,000	0,022	0,024									
Solyc05g046030	Peroxidase (AHRD V3.3 *** K4C0T6_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc05g046085	pentatricopeptide (PPR) repeat-containing protein (AHRD V3.3 --* AT2G17033.4)							0,140	0,204	0,025	0,000	0,024									
Solyc05g046110	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)		F:GO:0008375: C:G(	F:acetylglucosaminyltransferase activity; C:integral component			IPR006740 (PFAM): G3DSA:3.90.550	0,382	0,767	0,074	0,076	0,023									
Solyc05g046120	Formin-like protein (AHRD V3.3 *** K4C0U5_SOLLC)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): IPR015425 (SMA	2,742	2,252	7,038	5,983	7,213									
Solyc05g046130	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769:SF4	1,575	1,812	0,632	0,584	0,375									
Solyc05g046140	Major latex-like protein (AHRD V3.3 *** Q9AXU0_PRUPE)		P:GO:0006952	P:defense response			IPR000916 (SMART): IPR000916 (PF	0,000	0,184	0,025	0,049	0,023									
Solyc05g046180	LOW QUALITY:Alcohol dehydrogenase 2 (AHRD V3.3 --* ADH2_SOLLC)						mobidb-lite (MOBIDB_LITE): PTHR375	0,098	0,183	0,318	0,626	0,728									
Solyc05g046190	LOW QUALITY:1-phosphatidylinositol-4-phosphate 5-kinase 3 (AHRD V3.3 --* AT2G26420.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,022	0,000	0,046									
Solyc05g046240	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)						PTHR33088:SF18 (PANTHER): PTHR:	0,019	0,000	0,022	0,000	0,024									
Solyc05g046270	Protein Ycf2 (AHRD V3.3 --* YCF2_OENGL)						PTHR35318:SF2 (PANTHER): PTHR3	1,894	0,914	1,509	1,495	1,289									
Solyc05g046280	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XBJ8_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,119	2,175	2,362	2,893	2,967									
Solyc05g046283	Alcohol dehydrogenase, putative (AHRD V3.3 --* B9RHN6_RICCO)							0,337	0,120	0,264	0,047	0,210									
Solyc05g046285	H -ATPase 1 (AHRD V3.3 --* AT2G18960.3)							0,384	0,123	0,336	0,145	0,165									
Solyc05g046287	At2g11520-like protein (AHRD V3.3 -** B3SKN4_ARALL)							0,718	0,633	0,583	0,687	0,401									
Solyc05g046290	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4C0W2_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucc	IPR008264 (PRINTS): IPR016455 (PII	0,042	0,082	0,097	0,294	0,214									
Solyc05g046295	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9IAP0_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,038	0,019	0,000	0,000	0,000									
Solyc05g046300	Ethanolamine-phosphate cytidylyltransferase (AHRD V3.3 *** A0A0B2NXA1_GLYSO)		F:GO:0003824: P:G(	F:catalytic activity; P:biosynthetic process			IPR004821 (PFAM): IPR014729 (G3D	43,246	42,025	43,386	40,494	40,598									

Solyc05g046310	N-acetyl-gamma-glutamyl-phosphate reductase (AHRD V3.3 *** A0A1D1YQR0_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	21,645	11,978	51,046	56,359	45,604	-0,827	0,030					down		
Solyc05g046320	Small auxin up-regulated RNA55	SAUR55	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): mobidb-lite (MOB	1,245	1,984	0,352	0,191	0,353									
Solyc05g046330	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (AHRD V3.3 *** A0A0B2PTB3_GL		P:GO:0006487; C:G(	P:protein N-linked glycosylation; C:oligosaccharyltransferase cc			IPR008814 (PFAM): IPR008814 (PAN	72,128	72,310	65,686	65,379	65,414									
Solyc05g046340	Phosphomannomutase (AHRD V3.3 *** K4C0W7_SOLLC)		F:GO:0004615; C:G(	F:phosphomannomu	EC:5.4.2.8	Phosphomannomutas	IPR006379 (TIGRFAM): IPR023214 ((	0,019	0,118	0,409	0,862	0,426									
Solyc05g046360	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)		P:GO:0006402; C:G(	P:mRNA catabolic process; C:CCR4-NOT complex			PF04078 (PFAM): IPR011989 (G3DS/	0,159	0,316	0,046	0,193	0,094									
Solyc05g046380	LOW QUALITY:Yellow stripe-like transporter 6 (AHRD V3.3 --* T1Q4F6_ARAHY)		C:GO:0005886; C:G(	C:plasma membrane; C:membrane; C:integral component of mei			PTHR31645 (PANTHER): PTHR31645	0,000	0,000	0,000	0,048	0,000									
Solyc05g046390	neuronal acetylcholine receptor subunit alpha-5 (AHRD V3.3 *** AT2G31490.1)		C:GO:0005747; C:G(	C:mitochondrial respiratory chain complex I; C:integral compone			PTHR35479:SF2 (PANTHER): PTHR3!	81,760	89,526	117,321	96,095	104,938									
Solyc05g047390	Mitochondrial import receptor subunit TOM7-1 (AHRD V3.3 *** TOM7A_SOLTU)		C:GO:0005742; P:G(	C:mitochondrial outer membrane translocase complex; P:proteir			IPR012621 (PFAM): PTHR34944:SF2	37,138	39,499	37,717	35,570	35,940									
Solyc05g047420	Exosome complex component rrp45 (AHRD V3.3 *** W9RTK1_9ROSA)		C:GO:0000178; P:G(	C:exosome (RNase complex); P:RNA processing			IPR015847 (PFAM): IPR027408 (G3D	30,307	22,619	23,626	23,520	21,247									
Solyc05g047440	LOW QUALITY:Ycf1 protein (AHRD V3.3 *-* ATCG01130.1)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM): IPR008896 (PAN	0,037	0,064	0,025	0,025	0,070									
Solyc05g047450	Methyl-CpG-binding domain protein (AHRD V3.3 *** A0A072UCD8_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; F:zinc ion binding			IPR001739 (SMART): IPR011124 (PF.	31,758	32,717	55,284	49,799	48,467									
Solyc05g047460	Auxin Response Factor 7B	ARF7B	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF ARF	47,058	39,010	45,632	49,976	45,084									
Solyc05g047490	lipid-binding serum glycoprotein family protein (AHRD V3.3 --* AT3G20270.3)							0,363	0,214	0,000	0,000	0,000									
Solyc05g047510	Sulfotransferase (AHRD V3.3 *** K4C0Y5_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D): IPR0(	1,809	1,038	0,000	0,000	0,000									
Solyc05g047520	ATP-dependent RNA helicase DOB1 (AHRD V3.3 *** A0A0K9PZL4_ZOSMR)		F:GO:0003723; F:G(	F:RNA binding; F:RI	EC:3.6.1.15	Nucleoside-triphosph	IPR012961 (SMART): IPR014001 (SM	60,662	49,151	61,038	62,044	62,584									
Solyc05g047530	trans-cinnamate 4-monooxygenase	C4H	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,573	1,107	3,728	2,060	4,092									
Solyc05g047540	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GYI5_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,469	2,457	1,018	1,696	2,272									
Solyc05g047550	Kinase (AHRD V3.3 *** D7LHK4_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR014729 (G3	0,493	0,348	0,122	0,198	0,281									
Solyc05g047560	LOW QUALITY:Glycosyltransferase, putative (AHRD V3.3 *** B9S3B5_RICCO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity			IPR001296 (PFAM): G3DSA:3.40.50.2	0,226	0,264	0,025	0,025	0,188									
Solyc05g047580	Terpene cyclase/mutase family member (AHRD V3.3 *** O82141_PANGI)		F:GO:0016866	F:intramolecular transferase activity			G3DSA:1.50.10.20 (GENE3D): IPR01!	0,661	0,629	0,022	0,025	0,023									
Solyc05g047590	Sl Pectinesterase		F:GO:0004857; F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR012334 (G3	21,176	19,175	0,233	0,094	0,210									
Solyc05g047600	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0I757_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	26,123	15,302	16,064	16,926	17,731									
Solyc05g047610	S-acyltransferase (AHRD V3.3 *-* M1B2H3_SOLTU)		C:GO:0016021; F:G(	C:integral compone	EC:2.3.1.225	Protein S-acyltransfe	PTHR22883 (PANTHER): PTHR22883	2,561	3,112	3,193	2,401	2,912									
Solyc05g047615	SHI-related sequence 6 (AHRD V3.3 --* AT3G54430.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,000	0,000	0,000									
Solyc05g047620	LOW QUALITY:Movement protein (AHRD V3.3 *-* A0A151UGG0_CAJCA)		P:GO:0016032; C:G(	P:viral process; C:host cell junction; C:host cell plasmodesma; F			IPR028919 (PFAM): PTHR33054:SF1!	0,063	0,076	0,075	0,025	0,000									
Solyc05g047640	S-acyltransferase (AHRD V3.3 *** K4C0Z7_SOLLC)		C:GO:0016021; F:G(	C:integral compone	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883:SF9	6,402	6,653	6,758	7,833	6,901									
Solyc05g047670	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,019	0,025	0,101	0,094									
Solyc05g047680	Cytochrome P450 (AHRD V3.3 *** F4YF83_9APIA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	1,285	1,254	0,169	0,169	0,189									
Solyc05g047690	Histone deacetylase complex subunit SAP18 (AHRD V3.3 *** SAP18_ARATH)						G3DSA:3.10.20.550 (GENE3D): IPR0'	28,173	30,161	47,029	47,718	45,889									
Solyc05g047700	NBS-LRR resistance protein-like protein (AHRD V3.3 *-* A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding				1,399	1,139	0,996	0,782	0,852									
Solyc05g047710	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G61050.2)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:lipid binding			IPR000008 (SMART): IPR035892 (G3	0,692	0,648	0,171	0,526	0,234									
Solyc05g048750	coiled-coil protein (AHRD V3.3 *-* AT2G45520.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	84,218	71,599	59,115	53,612	53,375									
Solyc05g048760	phosphomannomutase	pmm	F:GO:0004615; C:G(	F:phosphomannomu	EC:5.4.2.8	Phosphomannomutas	IPR023214 (G3DSA:3.40.50.GENE3D	41,034	42,060	51,682	53,310	51,437									
Solyc05g048770	Isoaspartyl peptidase/L-asparaginase (AHRD V3.3 *** A0A072TN67_MEDTR)		F:GO:0004298	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000246 (PFAM): G3DSA:3.60.20.3	7,448	5,490	7,709	6,889	7,973									
Solyc05g048780	Ripening related protein family (AHRD V3.3 *** A0A072TZD6_MEDTR)						IPR036908 (G3DSA:2.40.40.GENE3D	0,021	0,000	0,068	0,025	0,210									
Solyc05g048790	Ripening related protein family (AHRD V3.3 *** G7L460_MEDTR)						IPR036908 (G3DSA:2.40.40.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc05g048800	Protein O-glucosyltransferase 1 (AHRD V3.3 *-* A0A0B0N3M8_GOSAR)		C:GO:0016021; F:G(	C:integral component of membrane; F:glucosyltransferase activi			IPR006598 (SMART): IPR006598 (PF.	0,000	0,058	0,000	0,000	0,000									
Solyc05g048810	Adenosine-deaminase family protein (AHRD V3.3 *** B9I8G9_POPTR)		F:GO:0003723; F:G(	F:RNA binding; F:ac	EC:3.5.4.4	Adenosine deaminas	IPR002466 (SMART): IPR002466 (PF.	68,666	61,731	55,160	53,193	54,526									
Solyc05g048820	Remorin (AHRD V3.3 *** A0A0B2NVY4_GLYSO)						IPR005518 (PFAM): IPR005516 (PFA	0,000	0,018	0,000	0,000	0,000									
Solyc05g048830	MYB-related transcription factor (AHRD V3.3 *** A0A059PRS4_SALMI)	R2R3MYB17	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	1,234	1,851	0,190	0,508	0,424									
Solyc05g048850	RNA helicase DEAD18	DEAD18	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART): IPR014001 (SM	13,502	14,471	21,561	22,656	20,150									
Solyc05g048860	DEAD-box ATP-dependent RNA helicase 8 (AHRD V3.3 *-* A0A0B0MGL8_GOSAR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	3,721	2,694	4,374	4,515	4,613									
Solyc05g049880	MACPF domain-containing CAD1-like protein (AHRD V3.3 *** A0A0B0MZU8_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,923	1,064	0,647	0,696	0,872									
Solyc05g049900	Bestrophin/UPF0187 (AHRD V3.3 *** A0A103XUR8_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR021134 (PFAM): IPR024701 (PIRS	14,596	12,098	11,957	12,017	12,774									
Solyc05g049910	F-box family protein (AHRD V3.3 --* AT5G50220.1)							0,000	0,039	0,000	0,000	0,000									
Solyc05g049940	RESTRICTED TEV MOVEMENT 3 (AHRD V3.3 --* AT3G58350.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,392	2,657	3,515	2,987	3,202									
Solyc05g049950	Small nuclear ribonucleoprotein-associated protein (AHRD V3.3 *** K4C128_SOLLC)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus			PR01217 (PRINTS): IPR001163 (SMA	70,856	73,827	64,989	58,801	57,452									
Solyc05g049960	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** A0A103XI63_CYNCS)		F:GO:0003677	F:DNA binding			IPR001606 (SMART): SM01014 (SMA	14,501	12,429	21,658	22,453	19,365									
Solyc05g049970	mitogen-activated protein kinase 6	mapk6	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	10,576	13,340	14,765	13,476	15,546									
Solyc05g049980	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G61490.4)	PG55-1	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3I	19,377	23,499	20,954	31,465	25,828					0,587	0,008			up
Solyc05g049990	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A072TW71_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): mobic	19,985	22,575	2,111	1,686	4,100									
Solyc05g050000	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G51130.1)		F:GO:0008168	F:methyltransferase activity			IPR010675 (PFAM): PF06325 (PFAM)	4,314	4,209	12,839	25,178	16,101					0,976	0,002			up
Solyc05g050010	1-aminocyclopropane-1-carboxylic acid synthase-4	ACS4	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			PR00753 (PRINTS): IPR004839 (PFA	1,608	0,589	56,413	91,215	39,221	-1,405	0,038			0,696	0,003	down		up
Solyc05g050015	LOW QUALITY:60S ribosomal protein L3 (AHRD V3.3 *-* RL3_ORYSJ)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000597 (PFAM)	0,000	0,083	0,022	0,050	0,023									
Solyc05g050020	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G01270.1)		F:GO:0016874; F:G(	F:ligase activity; F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	9,400	6,741	8,301	9,203	9,481									
Solyc05g050040	WRKY transcription factor 62	WRKY62	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			PTHR31282 (PAN' WRKY	0,000	0,019	0,025	0,000	0,024									
Solyc05g050050	WRKY transcription factor 63	WRKY63	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,040	0,116	0,000	0,000	0,000									
Solyc05g050060	WRKY transcription factor 64	WRKY64	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,019	0,000	0,000	0,000	0,000									
Solyc05g050090	Fatty acid/sphingolipid desaturase (AHRD V3.3 *** AT2G46210.1)		P:GO:0006629; C:G(	P:lipid metabolic process; C:integral component of membrane; F			IPR001199 (SMART): IPR005804 (PF.	0,099	0,124	0,000	0,025	0,023									
Solyc05g050110	DUF2358 family protein (DUF2358) (AHRD V3.3 *** AT2G46220.1)						IPR018790 (PFAM): IPR018790 (PAN	4,306	10,261	2,132	3,605	6,252	1,279	0,001	1,541	0,000			up	up	
Solyc05g050120	cytosolic NADP-malic enzyme	me2	F:GO:0004471; F:G(	F:malate dehydroge	EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS): IPR012301 (SM	234,861	389,549	174,857	206,165	236,626	0,756	0,004	0,433	0,033			up	up	
Solyc05g050130	Acidic endochitinase (AHRD V3.3 *** CHIA_TOBAC)		P:GO:0005975	P:carbohydrate metabolic process			IPR001223 (PFAM): G3DSA:3.20.20.8	0,980	4,361	3,313	4,528	5,348	2,174	0,007					up		
Solyc05g050200	Eukaryotic translation initiation factor 1A (AHRD V3.3 *** IF1A_ONOVI)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			IPR001253 (SMART): IPR006196 (PF.	160,067	171,219	246,211	213,117	211,104									
Solyc05g050210	GDSL esterase/lipase family (AHRD V3.3 *** A0A151QZV0_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	2,026	3,004	0,882	1,734	0,824									
Solyc05g050220	TAF-3 (AHRD V3.3 *** Q40587_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	4,740	3,421	9,324	11,078	10,547									
Solyc05g050230	Ubiquitin conjugating enzyme E2 (AHRD V3.3 *** A5YVL3_ADICA)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART): IPR016135 (G3D	140,745	156,825	225,421	223,691	210,143									
Solyc05g050240	Plastid division protein PDV1 (AHRD V3.3 *-* A0A199W2F8_ANACO)		P:GO:0010020	P:chloroplast fission			IPR038939 (PANTHER): PTHR33600::	0,098	0,139	0,000	0,000	0,000									
Solyc05g050280	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:			IPR004993 (PFAM): IPR031110 (PTH	40,918	38,050	45,677	52,640	41,873									
Solyc05g050320	Glycosyl hydrolase superfamily protein (AHRD V3.3 *** AT4G01040.2)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:chitin binding; C:integral c			G3DSA:3.20.20.80 (GENE3D): mobidt	4,927	3,619	4,276	6,725	5,896					0,654	0,036			up
Solyc05g050325	Chitinase domain-containing 1 (AHRD V3.3 *** A0A0B0P1B6_GOSAR)		P:GO:0005975	P:carbohydrate metabolic process			IPR029070 (G3DSA:3.10.50.GENE3D	5,859	6,391	7,492	10,414	9,071									
Solyc05g050330	WRKY transcription factor 60	WRKY60	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	3,747	3,047	5,116	5,814	5,477									
Solyc05g050340	WRKY transcription factor 58	WRKY58	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	2,257	23,267	2,035	4,417	5,891	3,389	0,000	1,519	0,000	1,110	0,002	up	up	up
Solyc05g050350	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART): G3DSA:1.10.28	0,061	0,694	0,050	0,094	0,117									
Solyc05g050360	cyclic nucleotide gated channel 1 (AHRD V3.3 *** AT5G53130.1)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART): G3DSA:1.10.28	0,222	1,610	0,047	0,364	0,283									
Solyc05g050380	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART): IPR005821 (PF.	3,219	29,431	0,841	3,052	6,806	3,213	0,000	2,994	0,000	1,840	0,000	up	up	up
Solyc05g050390	beclin 1	atg6	P:GO:0006914	P:autophagy			IPR040455 (PFAM): PF17675 (PFAM)	48,818	40,133	58,188	58,307	54,681									
Solyc05g050400	RNA-binding domain CCCH-type zinc finger protein (AHRD V3.3 *-* A0A072UWB6_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	0,094	0,037	0,000	0,025	0,023									
Solyc05g050430	LOW QUALITY:NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR036388 (G3D	0,197	0,193	0,140	0,318	0,282									
Solyc05g050438	RNA-binding domain CCCH-type zinc finger protein (AHRD V3.3 *-* A0A072UWB6_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	0,057	0,043	0,000	0,000	0,070									
Solyc05g050480	LOW QUALITY:Arsenical pump-driving ATPase (AHRD V3.3 *** K4C181_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,000	0,000	0,000	0,022	0,000									
Solyc05g050490	ATPase ASNA1 homolog (AHRD V3.3 *** M1A9Y0_SOLTU)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR025723 (PFAM): IPR016300 (TIGF	0,374	0,353	0,194	0,289	0,402									
Solyc05g050500	LOW QUALITY:ATP synthase delta chain, putative (AHRD V3.3 *** B9SBC4_RICCO)		P:GO:0015986; F:G(	P:ATP synthesis co	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR026015 (G3DSA:1.10.520.GENE3I	33,072	56,330	23,751	32,214	44,479	0,795	0,000	0,902	0,000	0,442	0,009	up	up	up
Solyc05g050510	Protein yippee-like (AHRD V3.3 *** K4C183_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:metal ion binding			IPR004910 (PFAM): PTHR13848:SF8	0,084	0,079	0,093	0,170	0,023									
Solyc05g050520	NC domain-containing protein-like protein (AHRD V3.3 *** AT4G00905.1)		F:GO:0010181	F:FMN binding			IPR012349 (G3DSA:2.30.110.GENE3I	0,581	0,466	0,166	0,095	0,164									
Solyc05g050530	Pyridoxamine 5'-phosphate oxidase family protein (AHRD V3.3 *** AT2G46580.1)		F:GO:0004733; P:G(	F:pyridoxamine-pho	EC:1.4.3.5	Pyridoxal 5'-phospha	IPR024624 (PFAM): IPR012349 (G3D	1,404	0,929	0,624	0,603	0,961									
Solyc05g050540	Laccase (AHRD V3.3 *** B9SBE5_RICCO)		F:GO:0005507; P:G(	F:copper ion bindin	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR011707 (PFAM): IPR017761 (TIGF	0,927	1,138	0,312	0,265	0,164									
Solyc05g050550	DUF688 family protein (AHRD V3.3 *** A0A072U4Q9_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR343	0,570	0,584	0,022	0,000	0,023									
Solyc05g050560	Basic helix-loop-helix (BHLH) family transcription factor (AHRD V3.3 *** A0A0K9PZ13_ZOSMR)		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	6,253	17,278	9,616	7,562	8,882	1,493	0,000					up		
Solyc05g050570	Molybdopterin biosynthesis CNX3-like protein (AHRD V3.3 *** A0A0B0MZX3_GOSAR)		P:GO:0006777	P:Mo-molybdopterin cofactor biosynthetic process			IPR023045 (TIGRFAM): IPR036522 ((	1,676	2,184	3,649	2,814	2,857									
Solyc05g050580	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4C190_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal			IPR008974 (G3DSA:2.60.210.GENE3I	27,983	24,328	40,161	31,021	32,370									
Solyc05g050590	Phosphatidylinositol 3-and 4-kinase family protein (AHRD V3.3 *** D7LEK1_ARALL)		F:GO:0005515	F:protein binding			IPR000626 (SMART): G3DSA:3.10.20	0,100	0,159	0,025	0,000	0,000									
Solyc05g050600	dynamin-like protein (AHRD V3.3 *** AT5G42080.4)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR001401 (SM	80,492	76,337	91,466	92,155	83,662									
Solyc05g050630	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G01320.3)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13424 (PFAM	32,538	38,307	11,228	13,464	24,720			1,133	0,000				up	
Solyc05g050680	Casein kinase II subunit beta (AHRD V3.3 *** M1A9X4_SOLTU)		C:GO:0005956; F:G(	C:protein kinase CK2 complex; F:protein kinase regulator activi			IPR000704 (PRINTS): IPR000704 (SM	42,017	44,105	61,709	59,802	52,966									
Solyc05g050690	UvrB/UvrC domain protein (DUF3506) (AHRD V3.3 --* AT4G33630.3)							0,021	0,000	0,000	0,000	0,000									
Solyc05g050695	Transmembrane Fragile-X-F-associated protein (AHRD V3.3 --* AT1G68820.2)							0,077	0,018	0,050	0,072	0,046									
Solyc05g050700	LOW QUALITY:Leucine-rich repeat protein (AHRD V3.3 *** A0A0A6ZKK7_PETHY)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR032675 (G3D	0,451	0,537	0,309	0,223	0,284									
Solyc05g050710	Lecithin-cholesterol acyltransferase-like 1 (AHRD V3.3 *** A0A0B2SJV8_GLYSO)		P:GO:0006629; F:G(	P:lipid metabolic process; F:O-acyltransferase activity			IPR003386 (PFAM): PTHR11440 (PAI	7,994	7,637	3,675	4,882	6,756			0,872	0,001				up	
Solyc05g050720	Preprotein translocase subunit SECE1 (AHRD V3.3 *** A0A1D1Z4R7_9ARAE)		P:GO:0006605; C:G(	P:protein targeting; C:membrane			IPR001901 (PFAM): PTHR37247 (PAI	5,791	5,535	6,927	7,723	7,169									
Solyc05g050730	Stigma-specific protein Stig1 (AHRD V3.3 *** A0A103Y3M1_CYNCS)		C:GO:0016020	C:membrane			IPR006969 (PFAM): IPR006969 (PAN	0,000	0,000	0,075	0,049	0,000									
Solyc05g050735	30S ribosomal protein S2, chloroplastic (AHRD V3.3 --* RR2_MARPO)						mobidb-lite (MOBIDB_LITE)	0,360	0,232	0,221	0,458	0,426									
Solyc05g050740	DegV domain-containing protein (AHRD V3.3 *-* A0A0B0NRK7_GOSAR)						PTHR36376 (PANTHER)	5,015	4,600	7,479	10,654	8,881									
Solyc05g050760	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,198	0,144	0,218	0,241	0,117									
Solyc05g050770	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): G3DSA:3.40.5(	6,614	14,777	7,141	8,183	14,769	1,187	0,004	1,042	0,000			up	up	
Solyc05g050780	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc05g050800	phosphoglycerate mutase family protein		P:GO:0016311; F:G(	P:dephosphorylation; F:phosphatase activity			IPR012398 (PIRSF): IPR029033 (G3D	225,962	486,027	39,615	39,795	55,863									
Solyc05g050805	DnaJ protein (AHRD V3.3 *-* A0A199V6W4_ANACO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS): IPR001623 (SM	0,084	0,165	0,000	0,095	0,215									
Solyc05g050810	DnaJ protein (AHRD V3.3 *-* A0A199V3N0_ANACO)		P:GO:0006457; F:G(	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS): IPR001623 (SM	0,140	0,506	0,025	0,120	0,164									
Solyc05g050820	DNAJ (AHRD V3.3 *** A0A061DUH3_THECC)		P:GO:0006457; F:G(	P:protein folding; F:unfolded protein binding			G3DSA:2.60.260.20 (GENE3D): G3DS	1,128	5,948	0,955	1,408	1,479	2,407	0,000					up		
Solyc05g050830	Ethylene-responsive transcription factor4		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; C:nuc			PTHR31985:SF77 ERF	7,498	5,720	2,680	1,300	1,767					-1,024	0,010			down
Solyc05g050840	Kinesin-like protein (AHRD V3.3 --* A0A061FG77_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	87,730	105,850	116,331	110,635	103,003									
Solyc05g050850	Bifunctional 6(G)-fructosyltransferase/2,1-fructan:2,1-fructan 1-fructosyltransferase (AHRD V3.3 --* GFT_ALLCE)							20,987	19,849	12,557	9,807	10,754									
Solyc05g050870	Peroxidase (AHRD V3.3 *** K4C1C0_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,076	0,000	0,025	0,000									
Solyc05g050890	Peroxidase (AHRD V3.3 *** K4C1C1_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,061	0,019	0,000	0,022	0,024									
Solyc05g050900	Spindle and kinetochore-associated protein 1 homolog (AHRD V3.3 *** SKA1_ARATH)		P:GO:0007059; F:G(	P:chromosome segregation; F:microtubule binding; P:cell divisic			IPR009829 (PFAM): G3DSA:1.10.10.1	5,655	3,435	2,391	1,775	2,366									
Solyc05g050910	Flavin-containing monooxygenase (AHRD V3.3 *** K4C1C3_SOLLC)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.	Flavin-containing mo	IPR000960 (PRINTS): IPR036188 (G3	9,573	7,599	9,646	8,057	8,746									
Solyc05g050920	Flavin-containing monooxygenase (AHRD V3.3 *** K4C1C4_SOLLC)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.	Flavin-containing mo	IPR000960 (PRINTS): IPR000960 (PII	11,505	11,995	4,146	3,999	5,212									
Solyc05g050930	LOW QUALITY:DUF641 family protein (DUF641) (AHRD V3.3 *** AT3G60680.1)		P:GO:0009639; P:G(	P:response to red or far red light; P:negative gravitropism			IPR006943 (PFAM): PTHR31161:SF3	19,898	20,994	21,702	24,582	20,389									
Solyc05g050935	cDNA, clone: J075106H20, full insert sequence (AHRD V3.3 --* B7F975_ORYSJ)		P:GO:0002949; F:G(	P:tRNA threonylcarl	EC:3.4.24; EC:2.3.1.	Acting on peptide bonds (peptidases); N(6)-L-threonylcarbam		1,944	1,902	2,484	2,364	2,715									
Solyc05g050940	glycoprotease 1 (AHRD V3.3 *** AT2G45270.1)		P:GO:0002949; F:G(	P:tRNA threonylcarl	EC:3.4.24	Acting on peptide bor	IPR017861 (PRINTS): G3DSA:3.30.42	12,228	12,117	17,050	17,124	18,598									
Solyc05g050960	DNA repair RAD51-like protein (AHRD V3.3 *** A0A0B0M9S0_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:A'	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR016467 (PIRSF): IPR013632 (PFA	1,342	1,337	1,462	0,995	0,939									
Solyc05g050970	Transketolase (AHRD V3.3 *** AT2G45290.2)		F:GO:0004802	F:transketolase act	EC:2.2.1.1	Transketolase	IPR005475 (SMART): IPR005475 (PF.	90,074	105,479	231,372	227,415	233,870									
Solyc05g050980	3-phosphoshikimate 1-carboxyvinyltransferase (AHRD V3.3 *** K4C1D0_SOLLC)	EPSPS1	F:GO:0003866; P:G(	F:3-phosphoshikima	EC:2.5.1.19	3-phosphoshikimate	IPR036968 (G3DSA:3.65.10.GENE3D	29,564	35,306	29,029	29,822	32,509									
Solyc05g050990	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE3-like1	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			PR01713 (PRINTS): G3DSA:3.40.50.7	3,463	3,291	4,732	5,398	5,514									
Solyc05g051000	40S ribosomal protein S13 (AHRD V3.3 *** RS13_SOYBN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000589 (SMART): IPR012606 (SM	34,249	40,619	38,954	36,059	38,247									
Solyc05g051010	Dihydroflavonol 4-reductase-like protein (AHRD V3.3 *** G7JDF6_MEDTR)	DFR	F:GO:0003854; P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D): IPR0(	6,749	6,619	0,332	0,215	0,139									
Solyc05g051030	Cornichon family protein (AHRD V3.3 *** AT1G12390.1)		P:GO:0016192	P:vesicle-mediated transport			IPR003377 (SMART): IPR003377 (PF	37,202	24,683	27,749	25,195	23,178	-0,565	0,045					down		
Solyc05g051040	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61180.1)		C:GO:0005774; C:G(	C:vacuolar membrane; C:integral component of membrane; F:lic			IPR001841 (SMART): IPR013083 (G3	28,837	28,607	27,885	29,094	25,217									
Solyc05g051050	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	34,920	29,814	30,560	29,999	27,281									
Solyc05g051060	Homeodomain-like superfamily protein (AHRD V3.3 *** AT5G16560.1)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6C G2-like	13,417	9,341	5,801	5,984	6,571									
Solyc05g051070	Pre-mRNA-splicing factor ISY1-like protein (AHRD V3.3 *** A0A0K9NV93_ZOSMR)		P:GO:0000350	P:generation of catalytic spliceosome for second transesterifica			IPR029012 (G3DSA:1.10.287.GENE3I	20,780	20,170	24,301	24,770	24,060									
Solyc05g051080	LOW QUALITY:B3 domain-containing protein family (AHRD V3.3 --* A0A151R9R2_CAJCA)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			PTHR36264 (PANTHER)	0,042	0,330	0,050	0,000	0,000									
Solyc05g051100	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *-* A0A0B0PVB3_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:oxidoreductase activity; P:oxidation-reduction process				0,000	0,039	0,000	0,000	0,000									
Solyc05g051140	protein FLOWERING locus D-like protein (AHRD V3.3 --* AT3G10390.4)							0,019	0,019	0,000	0,000	0,000									
Solyc05g051180	Ethylene-responsive transcription factor (AHRD V3.3 *** G7JJR7_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,000	0,037	0,068	0,000	0,000									
Solyc05g051200	ethylene-responsive factor 1	ERF.C1	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,692	0,897	2,698	2,032	1,765									
Solyc05g051210	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT3G27230.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	0,232	0,078	0,191	0,171	0,165									
Solyc05g051220	Potassium channel TORK1 (AHRD V3.3 *** Q5NT78_TOBAC)		F:GO:0005249; F:G(	F:voltage-gated potassium channel activity; F:protein binding; P			IPR003938 (PRINTS): IPR000595 (SM	14,102	4,933	12,135	13,493	15,704	-1,484	0,000					down		
Solyc05g051230	Adenylyltransferase and sulfurtransferase MOCS3 (AHRD V3.3 *-* A0A078EZM7_BRANA)		F:GO:0008641	F:ubiquitin-like modifier activating enzyme activity			IPR000594 (PFAM): IPR000594 (PFA	82,829	72,629	57,442	53,654	57,674									
Solyc05g051240	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G66180.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032861 (PF	96,078	43,019	31,828	95,140	64,409	-1,135	0,000	1,013	0,001	1,580	0,000	down	up	up
Solyc05g051250	Glutamine synthetase (AHRD V3.3 *** A0A0V0I3I3_SOLCH)		F:GO:0004356; P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetase	IPR008146 (SMART): IPR008147 (PF.	0,424	0,937	0,022	0,072	0,070									

Solyc05g051260	Endo-1,4-beta-xylanase (AHRD V3.3 *** A0A151U7N8_CAJCA)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001000 (SMART); IPR001000 (PF	13,818	83,414	0,414	0,072	1,106	2,618	0,028					up		
Solyc05g051270	Cysteine-rich repeat secretory protein 60 (AHRD V3.3 *** A0A061EEI8_THECC)		C:GO:0009506; C:GO	C:plasmodesma; C:integral component of membrane	IPR038408 (G3DSA:3.30.430.GENE3	0,448	0,394	0,493	0,506	0,541									
Solyc05g051280	Lipase class 3 family protein / putative calmodulin-binding heat-shock protein (AHRD V3.3 *** F4K8L2_ARAT		P:GO:0016042	P:lipid catabolic process	IPR005592 (PFAM); IPR002921 (PFA	18,613	15,813	11,588	11,294	12,031									
Solyc05g051290	HMG-Y-related A (AHRD V3.3 *** A0A0B0M969_GOSAR)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem	IPR017956 (PRINTS); IPR000116 (PF	4,889	6,963	2,687	2,573	2,499									
Solyc05g051310	LOW QUALITY:Ethylene-responsive transcription factor 5 (AHRD V3.3 *-* ERF5_NICSY)		P:GO:0009725; P:GO	P:response to hormone; P:regulation of cellular metabolic process		0,080	0,271	0,072	0,072	0,142									
Solyc05g051330	DNA-binding storekeeper protein-related transcriptional regulator, putative (AHRD V3.3 *** A0A061EFY6_TH		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR007592 (PFAM GeBP	5,435	4,420	6,605	5,860	6,438									
Solyc05g051340	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H373_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	9,739	6,755	8,434	9,854	9,977									
Solyc05g051350	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09910.1)		F:GO:0003824; P:GO	F:catalytic activity; P:carbohydrate metabolic process; F:carbol	IPR029413 (PFAM); IPR029411 (PFA	0,021	0,000	0,025	0,050	0,071									
Solyc05g051370	Transcription initiation factor TFIID subunit 8 (AHRD V3.3 *** A0A0B0P5F6_GOSAR)		F:GO:0046982	F:protein heterodimerization activity	IPR009072 (G3DSA:1.10.20.GENE3D	10,402	8,445	9,475	10,075	9,964									
Solyc05g051380	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7JWC7_MEDTR)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN AP2	2,025	1,993	0,099	0,327	0,023									
Solyc05g051390	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** AT1G09720.1)		F:GO:0003779	F:actin binding	IPR011684 (PFAM); mobidb-lite (MOB	0,061	0,019	0,000	0,000	0,000									
Solyc05g051400	Mitochondrial carrier protein (AHRD V3.3 *** A0A0K9PSM6_ZOSMR)		F:GO:0022857; P:GO	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS); IPR018108 (PF	170,436	142,646	21,984	34,289	31,855					0,641	0,001			up
Solyc05g051410	cyclinD4_2	CycD4_2	C:GO:0005634	C:nucleus	IPR004367 (SMART); IPR013763 (SM	1,087	1,522	0,225	0,148	0,306									
Solyc05g051420	ZF-HD homeobox protein family (AHRD V3.3 *** A0A151TGZ5_CAJCA)		F:GO:0003677	F:DNA binding	IPR006456 (TIGRI ZF-HD	0,056	0,037	0,000	0,025	0,000									
Solyc05g051425	dihydrofolate reductase (AHRD V3.3 *** AT4G24380.1)				IPR005645 (PFAM); IPR029058 (G3D	0,000	0,000	0,514	0,250	0,611									
Solyc05g051430	dihydrofolate reductase (AHRD V3.3 *** AT4G24380.1)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc05g051440	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G65340.1)				IPR006460 (TIGRFAM); IPR006460 (F	0,000	0,021	0,022	0,000	0,000									
Solyc05g051460	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072TTL6_MEDTR)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of transc	IPR000047 (PRIN HD-ZIP	2,372	3,297	0,524	0,509	0,283									
Solyc05g051480	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_PELHO)					0,953	1,142	0,491	0,363	0,329									
Solyc05g051490	LMBR1-like membrane protein (AHRD V3.3 *** AT5G65290.1)		C:GO:0016021	C:integral component of membrane	IPR006876 (PFAM); mobidb-lite (MOB	28,293	32,959	41,639	41,943	40,866									
Solyc05g051500	WEB family protein, chloroplastic (AHRD V3.3 *-* A0A199V6Z9_ANACO)				mobidb-lite (MOBIDB_LITE); mobidb-lit	1,106	2,114	1,038	1,650	1,410									
Solyc05g051510	Prohibitin (AHRD V3.3 *** O04361_TOBAC)		C:GO:0016020	C:membrane	IPR000163 (PRINTS); IPR001107 (SM	3,197	3,950	6,820	6,866	7,015									
Solyc05g051515	Histone H3 (AHRD V3.3 *** K7VSQ3_MAIZE)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS); IPR000164 (SM	53,083	51,458	70,935	70,124	67,727									
Solyc05g051520	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G22400.1)		F:GO:0016428	F:tRNA (cytosine-5-)-methyltransferase activity	IPR023267 (PRINTS); IPR023270 (PF	39,880	32,862	23,785	23,165	24,612									
Solyc05g051530	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	ABCG12	F:GO:0005524; C:GO	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0	0,387	1,381	0,071	0,025	0,117									
Solyc05g051550	MYB-related transcription factor (AHRD V3.3 *** A0A059PRU0_SALMI)	R2R3MYB92	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,019	0,019	0,025	0,000	0,047									
Solyc05g051560	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G64970.1)		F:GO:0022857; P:GO	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS); IPR023395 (G3	9,618	7,366	4,520	3,273	2,782			-0,703	0,034				down	
Solyc05g051570	Ras-related protein (AHRD V3.3 *** W9QNC0_9ROSA)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS); SM00173 (SMAR	56,647	60,018	42,188	38,529	42,593									
Solyc05g051580	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G10250.2)		F:GO:0005515	F:protein binding	IPR000210 (SMART); IPR027356 (PF	1,357	2,526	0,025	0,000	0,070									
Solyc05g051583	F-box family protein, putative (AHRD V3.3 *** A0A061FZW6_THECC)		F:GO:0005515	F:protein binding	IPR017451 (TIGRFAM); IPR001810 (F	0,081	0,181	0,000	0,170	0,141									
Solyc05g051590	Nucleotide-sugar transporter family protein (AHRD V3.3 *** A0A061DIM9_THECC)		C:GO:0000139; F:GO	C:Golgi membrane; F:pyrimidine nucleotide-sugar transmembrar	IPR007271 (PFAM); IPR007271 (PIRS	16,865	14,649	22,244	24,159	22,827									
Solyc05g051610	Kinase family protein (AHRD V3.3 *** D7MGJ0_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ubiquitin-protein transferase activity	IPR000719 (SMART); IPR003613 (SM	0,097	0,103	0,000	0,022	0,024									
Solyc05g051620	DNA-directed RNA polymerase III subunit RPC4 (AHRD V3.3 *** A0A0B0P813_GOSAR)		F:GO:0003677; F:GO	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA po	IPR007811 (PFAM); mobidb-lite (MOB	4,807	6,267	4,954	4,136	5,044									
Solyc05g051630	RFT1-like protein (AHRD V3.3 *** A0A103Y8L2_CYNCS)		F:GO:0005319; P:GO	F:lipid transporter activity; P:lipid transport; C:integral componer	IPR007594 (PFAM); IPR007594 (PAN	9,064	6,900	7,098	8,320	8,342									
Solyc05g051640	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C1J5_SOLLC)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR003591 (SMART); IPR000719 (SM	3,172	1,900	0,196	0,073	0,094									
Solyc05g051650	QWRF motif protein (DUF566) (AHRD V3.3 *** AT4G25190.1)		C:GO:0005737; C:GO	C:cytoplasm; C:centrosome; C:nuclear microtubule; P:centrosor	IPR007573 (PFAM); mobidb-lite (MOB	0,000	0,036	0,000	0,000	0,000									
Solyc05g051660	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	34,590	33,726	9,490	15,573	16,360			0,784	0,001	0,718	0,009		up	up
Solyc05g051670	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM); IPR029058 (G3D	0,097	0,116	0,075	0,047	0,094									
Solyc05g051680	Structural maintenance of chromosomes family protein (AHRD V3.3 *** D7M0L2_ARALL)		P:GO:0000724; F:GO	P:double-strand break repair via homologous recombination; F:r	IPR003395 (PFAM); G3DSA:3.40.50.3	33,123	30,194	23,450	21,857	21,145									
Solyc05g051690	Cell number regulator 6 (AHRD V3.3 *** A0A0B0MIM9_GOSAR)		C:GO:0016021	C:integral component of membrane	IPR006461 (TIGRFAM); IPR006461 (F	9,975	11,459	12,926	12,104	10,942									
Solyc05g051700	Iron-sulfur cluster assembly protein IscA (AHRD V3.3 *** G7LBB6_MEDTR)		F:GO:0005198; F:GO	F:structural molecule activity; F:iron-sulfur cluster binding; P:pro	IPR016092 (TIGRFAM); IPR035903 ((	29,621	33,474	110,427	118,118	116,709									
Solyc05g051710	RPM1-interacting protein 4 (RIN4) family protein (AHRD V3.3 *** G7LBA7_MEDTR)				IPR008700 (PFAM); mobidb-lite (MOB	0,512	0,863	1,518	2,348	1,680									
Solyc05g051720	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS); IPR011905 (TI(	0,059	0,000	0,000	0,000	0,000									
Solyc05g051730	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR011905 (TIGRFAM); IPR002109 (F	0,000	0,000	0,000	0,022	0,000									
Solyc05g051740	Prosystemin (AHRD V3.3 --* O48857_SOLNI)				mobidb-lite (MOBIDB_LITE)	0,521	0,275	0,025	0,047	0,047									
Solyc05g051750	TOMPRORNA_prosystemin		F:GO:0005179; C:GO	F:hormone activity; C:cytoplasm; P:regulation of signaling recer	IPR009966 (PFAM); mobidb-lite (MOB	45,157	37,420	22,549	27,650	26,677									
Solyc05g051760	MIZU-KUSSEI-like protein (Protein of unknown function%2C DUF617) (AHRD V3.3 *** AT2G21990.1)				IPR006460 (PFAM); IPR006460 (TIGF	0,223	0,200	0,126	0,025	0,070									
Solyc05g051770	transmembrane protein (AHRD V3.3 *** AT5G09995.2)		C:GO:0016021	C:integral component of membrane	PTHR33825:SF5 (PANTHER); PTHR3:	11,389	12,491	11,498	11,175	13,598									
Solyc05g051780	Gamma-glutamyltranspeptidase family protein (AHRD V3.3 *** B9H594_POPTR)		P:GO:0006751; F:GO	P:glutathione catab EC:3.4.19; EC:3.4.19 Acting on peptide bor	PR01210 (PRINTS); G3DSA:3.60.20.4	22,497	15,258	18,008	16,737	16,827									
Solyc05g051790	DNA-directed RNA polymerase II (AHRD V3.3 *** G7K102_MEDTR)		F:GO:0003677; F:GO	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA po	IPR000783 (PFAM); IPR005571 (PFA	41,524	37,940	36,531	36,555	34,750									
Solyc05g051800	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT2G22120.2)		F:GO:0008270	F:zinc ion binding	IPR011016 (SMART); IPR011016 (PF	5,131	6,280	5,129	5,834	4,831									
Solyc05g051820	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** G7LAE8_MEDTR)		P:GO:0030001; F:GO	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D); IPR0(	0,000	0,018	0,000	0,025	0,023									
Solyc05g051840	Trafficking protein particle complex subunit 12 (AHRD V3.3 *** W9QL80_9ROSA)		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR011990 (G3	18,399	21,957	27,921	23,939	23,716									
Solyc05g051850	putative myo-inositol-1-phosphatase	ins1p	F:GO:0004512; P:GO	F:inositol-3-phosph EC:5.5.1.4 Inositol-3-phosphate	IPR002587 (PFAM); IPR013021 (PFA	156,607	141,562	441,406	198,873	373,617					-1,147	0,007			down
Solyc05g051860	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT1G78020.1)				IPR007650 (PFAM); PTHR33059:SF4	0,061	0,101	0,075	0,025	0,094									
Solyc05g051870	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *** A0A103XBC9_CYNCS),Pfam:PF01190		C:GO:0005615	C:extracellular space	PF01190 (PFAM); PTHR31614 (PANT	1,302	1,024	0,259	0,320	0,377									
Solyc05g051880	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4C1L9_SOLLC)		F:GO:0003824; P:GO	F:catalytic activity; P:trehalose biosynthetic process	IPR006379 (TIGRFAM); IPR003337 (F	0,164	0,060	0,000	0,000	0,000									
Solyc05g051900	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM); G3DSA:1.20.125	4,163	5,879	5,319	9,422	10,109			0,920	0,001	0,824	0,002		up	up
Solyc05g051910	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D); G3D	0,000	0,000	0,050	0,092	0,046									
Solyc05g051920	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM); G3DSA:1.20.125	0,777	0,629	0,520	0,460	0,872									
Solyc05g051930	LOW QUALITY:Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D); IPR(	0,000	0,021	0,000	0,025	0,000									
Solyc05g051940	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D); G3D	0,097	0,021	0,075	0,000	0,000									
Solyc05g051960	LOW QUALITY:Major facilitator superfamily transporter (AHRD V3.3 *-* A0A0K0KFR2_CARHR)		C:GO:0016021; P:GO	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D); mob	0,434	0,414	0,627	0,265	0,469									
Solyc05g051970	N-lysine methyltransferase (AHRD V3.3 *** AT1G78150.2)				IPR025131 (PFAM); mobidb-lite (MOB	1,166	1,532	0,998	0,545	0,919									
Solyc05g051990	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 --* AT4G38540.1)					5,467	4,465	6,873	6,187	5,995									
Solyc05g051994	RNA-binding family protein (AHRD V3.3 *-* B9I063_POPTR)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM); IPR012677 (G3D	7,921	6,439	9,295	9,823	8,598									
Solyc05g051996	E3 ubiquitin-protein ligase ORTHRUS 2 (AHRD V3.3 --* A0A0B2SRL7_GLYSO)					0,152	0,196	0,072	0,000	0,095									
Solyc05g052010	RNA-binding family protein (AHRD V3.3 --* A0A061F8S2_THECC)					7,146	7,025	8,891	9,517	9,061									
Solyc05g052020	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G51180.2)		P:GO:0044255	P:cellular lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	31,190	28,252	36,372	37,000	37,493									
Solyc05g052030	ethylene response factor 4	ERF.B3	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	5,489	10,994	6,015	4,107	3,615									
Solyc05g052040	Ethylene-responsive transcription factor (AHRD V3.3 *** M4WYH8_GOSHI)	ERF.B1	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	171,018	50,585	36,743	126,094	44,443	-1,733	0,000			1,784	0,000	down		up
Solyc05g052050	DNA-binding protein Pti4	ERF.A3	F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	18,755	53,320	28,694	23,259	15,816	1,531	0,000	-0,860	0,002			up	down	
Solyc05g052070	small GTP-binding protein C	rab1c	F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS); SM00176 (SMAR	35,282	37,379	46,335	53,793	48,280									
Solyc05g052080	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT5G07490.1)		C:GO:0016021	C:integral component of membrane	PTHR34189 (PANTHER); PTHR34189	0,000	0,021	0,000	0,000	0,000									
Solyc05g052100	Glutamate dehydrogenase (AHRD V3.3 *** K4C1P1_SOLLC)		P:GO:0006520; F:GO	P:cellular amino acid metabolic process; F:oxidoreductase activ	IPR006095 (PRINTS); IPR006096 (SM	17,238	22,856	13,891	11,801	15,547									
Solyc05g052130	metacaspase 1 (AHRD V3.3 *** AT1G02170.1),Pfam:PF00656		F:GO:0004197; P:GO	F:cysteine-type enc EC:3.4.22 Acting on peptide bor	PF00656 (PFAM); G3DSA:3.40.50.12(	0,484	0,545	0,309	0,145	0,517									
Solyc05g052140	ATP synthase epsilon chain (AHRD V3.3 *** A0A0K9P5X2_ZOSMR)		P:GO:0015986; C:GO	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR036771 (G3DSA:2.60.15.GENE3D	0,322	0,347	0,900	0,464	0,708									
Solyc05g052150	ATP synthase subunit delta, mitochondrial		P:GO:0015986; C:GO	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR020546 (PFAM); IPR036771 (G3D	57,303	60,506	102,374	91,406	97,988									
Solyc05g052160	Translocase of chloroplast (AHRD V3.3 *** K4C1P7_SOLLC)		F:GO:0005525; P:GO	F:GTP binding; P:intracellular protein transport; C:chloroplast ou	IPR005688 (TIGRFAM); IPR006703 (F	28,092	25,124	26,794	28,169	28,254									
Solyc05g052170	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT4G19985.6)		F:GO:0004343; P:GO	F:glucosamine 6-ph EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	PTHR13355:SF12 (PANTHER); IPR03	10,290	7,821	11,524	11,750	11,722									
Solyc05g052180	Eukaryotic translation initiation factor 1A (AHRD V3.3 --* IF1A_ONOVI)		F:GO:0003743; P:GO	F:translation initiation factor activity; P:translational initiation	IPR001253 (SMART); G3DSA:2.40.50	5,579	4,900	5,946	5,274	4,586									
Solyc05g052190	Transcription elongation factor TFIIS (AHRD V3.3 *** RDO2_ARATH)		C:GO:0005634	C:nucleus	IPR003617 (SMART); IPR017923 (PF	12,103	7,954	16,367	17,433	14,772									
Solyc05g052200	Protein kinase (AHRD V3.3 *** A0A0K9NZM3_ZOSMR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D); IPR0	79,249	68,000	66,193	70,160	68,753									
Solyc05g052210	transmembrane protein (AHRD V3.3 *-* AT3G51580.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	21,036	17,858	27,371	27,952	26,108									
Solyc05g052220	U-box protein (AHRD V3.3 *-* A0A072V2F3_MEDTR)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR013083 (G3DSA:3.30.40.GENE3D	18,414	16,159	30,493	24,936	26,309									
Solyc05g052230	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT5G64320.1)					0,021	0,021	0,000	0,000	0,000									
Solyc05g052240	Chalcone-flavonone isomerase family protein (AHRD V3.3 *** A0A0V0H4Z0_SOLCI CHI		F:GO:0016872	F:intramolecular lyase activity	IPR016088 (G3DSA:3.50.70.GENE3D	22,851	26,474	156,343	208,162	171,778									
Solyc05g052260	appr-1-p processing enzyme family protein (AHRD V3.3 *** AT2G40600.1)				IPR002589 (SMART); G3DSA:3.40.22	37,961	37,202	71,350	77,089	74,210									
Solyc05g052270	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IJQ5_SOLCH)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); IPR004041 (PF	54,429	37,370	65,563	60,790	57,019									
Solyc05g052280	Peroxidase (AHRD V3.3 *** K4C1Q9_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,579	2,345	1,653	1,532	2,212									
Solyc05g052290	BTB/POZ domain-containing protein (AHRD V3.3 *-* W9QXG0_9ROSA)		F:GO:0005515	F:protein binding	IPR000210 (SMART); G3DSA:1.25.40	0,000	0,000	0,000	0,022	0,000									
Solyc05g052300	Amino acid transporter family protein (AHRD V3.3 *** B9HYI5_POPTR)		P:GO:0003333; F:GO	P:amino acid transmembrane transport; F:amino acid transmem	IPR013057 (PFAM); PTHR22950 (PAN	0,263	0,654	0,324	0,480	0,748									
Solyc05g052310	Alpha-soluble NSF attachment (AHRD V3.3 *** A0A0B0PIV9_GOSAR)		F:GO:0005515; P:GO	F:protein binding; P:intracellular protein transport	IPR000744 (PRINTS); IPR019734 (SM	49,213	48,502	61,666	61,929	58,977									
Solyc05g052320	LOW QUALITY:Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NPK0_ZOSMR)		P:GO:0006812; F:GO	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR038770 (G3DSA:1.20.1530.GENE	0,397	0,662	0,271	0,189	0,330									
Solyc05g052340	Laccase (AHRD V3.3 *** K4C1R5_SOLLC)		F:GO:0005507; P:GO	F:copper ion binding; P:oxidation-reduction process	IPR001117 (PFAM); IPR008972 (G3D	0,096	0,099	0,025	0,025	0,047									
Solyc05g052350	Receptor-like kinase (AHRD V3.3 *** C0SW26_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART); IPR032675 (G3	13,118	8,767	5,830	6,959	7,323									
Solyc05g052355	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 --* NU4C_ACOAM)					0,117	0,185	0,312	0,318	0,213									
Solyc05g052360	Laccase (AHRD V3.3 *-* M1CLA2_SOLTU)		F:GO:0005507	F:copper ion binding	IPR008972 (G3DSA:2.60.40.GENE3D	0,115	0,249	0,389	0,579	0,469									
Solyc05g052370	Laccase (AHRD V3.3 *** M1CL08_SOLTU)		F:GO:0005507; F:GO	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red	IPR008972 (G3DSA:2.60.40.GENE3D	0,283	0,336	0,894	0,842	0,775									
Solyc05g052390	Laccase (AHRD V3.3 *** B9HSI6_POPTR)		F:GO:0005507; P:GO	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR011707 (PFAM); IPR008972 (G3D	9,636	11,499	0,644	1,239	1,715									
Solyc05g052410	Dehydration responsive element binding protein (AHRD V3.3 *** Q8GZF2_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	4,061	3,916	21,206	22,996	17,419									
Solyc05g052420	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)		F:GO:0004864; C:GO	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR023393 (G3DSA:3.30.530.GENE3	0,061	0,167	0,074	0,000	0,047									
Solyc05g052430	Trichome birefringence-like protein (AHRD V3.3 *-* G7K771_MEDTR)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR026057 (PFAM); IPR025846 (PFA	0,000	0,018	0,000	0,025	0,024									
Solyc05g052450	Trichome birefringence-like protein (AHRD V3.3 *** G7K771_MEDTR)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR025846 (PFAM); IPR026057 (PFA	0,822	1,632	1,912	2,636	2,312									
Solyc05g052460	Leucine-rich repeat and IQ domain-containing protein 3, putative isoform 3 (AHRD V3.3 *** A0A061FM07_TI		C:GO:0016021	C:integral component of membrane	IPR018939 (PFAM); PTHR15071:SF0	0,390	0,336	0,385	0,469	0,496									
Solyc05g052470	Ferritin (AHRD V3.3 *** K4C1S8_SOLLC)		P:GO:0006826; P:GO	P:iron ion transport; P:cellular iron ion homeostasis; F:ferric iror	IPR012347 (G3DSA:1.20.1260.GENE	58,267	48,840	98,627	83,024	84,067									
Solyc05g052480	Multiple inositol polyphosphate phosphatase 1 (AHRD V3.3 *** A0A0B2R9V9_GLYSO)		F:GO:0003993; P:GO	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR029033 (G3DSA:3.40.50.GENE3D	9,794	9,890	17,136	19,246	16,557									
Solyc05g052490	GDA1/CD39 nucleoside phosphatase family protein (AHRD V3.3 *** AT4G19180.3)		F:GO:0016787	F:hydrolase activity	G3DSA:3.30.420.150 (GENE3D); IPR(	0,119	0,140	0,190	0,416	0,189									
Solyc05g052500	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G40280.1)		F:GO:0008168	F:methyltransferase activity	G3DSA:3.40.50.150 (GENE3D); IPR0(	19,477	17,572	7,284	7,173	6,972									
Solyc05g052510	Clathrin heavy chain (AHRD V3.3 *** K4C1T2_SOLLC)		F:GO:0005198; P:GO	F:structural molecule activity; P:intracellular protein transport; P	IPR000547 (SMART); IPR016025 (G3	547,285	467,688	560,561	604,056	559,479									
Solyc05g052520	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G07160.1)		F:GO:0004722; P:GO	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART); IPR036457 (G3	34,695	19,450	33,432	54,316	27,099					0,704	0,002			up
Solyc05g052530	Endoglucanase (AHRD V3.3 *** M1CLA9_SOLTU)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001701 (PFAM); IPR012341 (G3D	0,000	0,019	0,000	0,000	0,000									
Solyc05g052540	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G55990.1)		P:GO:0050826	P:response to freezing	IPR026057 (PFAM); IPR025846 (PFA	0,289	0,147	0,148	0,149	0,142									
Solyc05g052550	CCCH-type zinc-finger protein (AHRD V3.3 *-* A0A0X8ZWW6_PETHY)		F:GO:0046872	F:metal ion binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	374,706	126,733	67,194	260,532	137,580	-1,541	0,000	1,031	0,000	1,957	0,000	down	up	up
Solyc05g052560	LOW QUALITY:Pectinacetylesterase family protein (AHRD V3.3 --* AT2G46930.1)					292,256	93,857	50,041	201,432	100,176	-1,616	0,000	0,998	0,000	2,010	0,000	down	up	up
Solyc05g052570	Zinc finger transcription factor 39	C3H39	F:GO:0005515; F:GO	F:protein binding; F:metal ion binding	IPR002110 (SMART); IPR000571 (SM	774,252	237,167	136,073	547,586	268,700	-1,684	0,000	0,979	0,001	2,010	0,000	down	up	up
Solyc05g052580	CTD small phosphatase-like protein (AHRD V3.3 *** W9S4E3_9ROSA)		F:GO:0016791	F:phosphatase activity	IPR004274 (SMART); IPR023214 (G3	25,210	25,496	25,890	27,809	27,116									
Solyc05g052590	Serine/threonine-protein kinase (AHRD V3.3 *** W0TR71_ACAMN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:3.30.20	2,105	2,779	1,584	0,802	1,223									
Solyc05g052600	Sedoheptulose-1,7-bisphosphatase (AHRD V3.3 *** G7JAP0_MEDTR)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:phosphatase activity	IPR023079 (PRINTS); IPR033391 (PF	99,496	186,159	67,098	77,921	148,111	0,931	0,001	1,139	0,000			up	up	
Solyc05g052610	Myb family transcription factor family protein (AHRD V3.3 *** B9HT09_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	28,133	28,105	20,841	22,527	21,178									
Solyc05g052620	Coronatine-insensitive 1	Coi1	F:GO:0004842; F:GO	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	G3DSA:1.20.1280.50 (GENE3D); PF1	37,904	28,486	80,741	70,677	66,675									
Solyc05g052630	flocculation protein (AHRD V3.3 *** AT2G39950.9)				mobidb-lite (MOBIDB_LITE); mobidb-lit	209,009	165,314	238,751	223,240	218,609									
Solyc05g052640	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT2G39970.1)		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	37,906	35,994	51,649	49,277	44,810									
Solyc05g052650	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* V5PZN5_9CARY)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3	0,850	2,523	0,162	0,167	0,048	1,577	0,004					up		
Solyc05g052660	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic (AHRD V3.3 --* DXR_ORYSJ)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,912	3,128	0,097	0,117	0,023	1,791	0,002					up		
Solyc05g052670	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT2G39980.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3	0,061	0,340	0,928	1,828	0,210									
Solyc05g052680	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT2G39980.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3	0,641	1,757	16,102	12,837	6,542			-1,302	0,000				down	
Solyc05g052690	Eukaryotic translation initiation factor 3 subunit F (AHRD V3.3 *** K4C1V0_SOLLC)		F:GO:0003743; F:GO	F:translation initiation factor activity; F:protein binding; C:eukary	IPR000555 (SMART); IPR000555 (PF	18,123	18,291	19,645	17,002	18,487									
Solyc05g052700	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G47080.1)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	6,027	7,754	8,787	8,293	8,353									
Solyc05g052710	30S ribosomal protein S31 (AHRD V3.3 *** A0A0K9P6K0_ZOSMR),Pfam:PF17067		C:GO:0005840	C:ribosome	IPR030826 (TIGRFAM); IPR030826 (F	12,003	17,143	13,268	13,821	20,291			0,608	0,004				up	
Solyc05g052715	ATP binding protein, putative (AHRD V3.3 *** B9SLM8_RICCO)				mobidb-lite (MOBIDB_LITE); mobidb-lit	16,375	17,477	41,140	48,082	41,620									
Solyc05g052720	Pleckstrin homology domain-containing protein 1 (AHRD V3.3 *** M7ZGC3_TRIUA)		P:GO:0001881; C:GO	P:receptor recycling; C:early endosome; C:trans-Golgi network;	IPR001849 (SMART); IPR011993 (G3	49,387	43,378	44,494	41,176	38,143									
Solyc05g052750	Alpha/beta hydrolase related protein (AHRD V3.3 *** A0A061FLN1_THECC)		C:GO:0016021	C:integral component of membrane	IPR019498 (PFAM); PTHR34953 (PAN	9,293	12,245	3,871	5,148	6,455									
Solyc05g052760	Phosphoinositide phospholipase C (AHRD V3.3 *** O49952_SOLTU)		F:GO:0004435; P:GO	F:phosphatidylinositi EC:3.1.4.11; EC:3.1. Phosphoinositide pho	IPR001192 (PRINTS); IPR001711 (SM	165,492	129,340	159,022	148,969	150,255									
Solyc05g052780	Pollen-specific protein SF3, putative (AHRD V3.3 *** B9SWP2_RICCO)		F:GO:0046872	F:metal ion binding	IPR001781 (SMART); IPR001781 (PF	66,033	68,278	50,077	45,970	45,089									
Solyc05g052790	nucleotide-sugar transporter family protein		C:GO:0005794; F:GO	C:Golgi apparatus; F:pyrimidine nucleotide-sugar transmembran	IPR004853 (PFAM); PTHR44010 (PAN	39,289	47,454	21,991	26,048	28,210									
Solyc05g052800	60S ribosomal protein L35a (AHRD V3.3 *** B6VC50_VERFO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038661 (G3DSA:2.40.10.GENE3D	252,524	277,073	144,134	145,446	151,879									
Solyc05g052810	60S ribosomal protein L35a (AHRD V3.3 *** B6VC50_VERFO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038661 (G3DSA:2.40.10.GENE3D	37,152	43,676	34,237	30,698	29,906									
Solyc05g052820	proline transporter 3	prot3	P:GO:0003333; C:GO	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM); PTHR22950 (PAN	3,751	3,202	1,116	0,788	1,380									
Solyc05g052840	Tubulin folding cofactor C (AHRD V3.3 *** M4MD06_GOSAR)		P:GO:0000902; P:GO	P:cell morphogenesis; P:post-chaperonin tubulin folding pathway	IPR006599 (SMART); IPR012945 (PF	8,157	8,071	3,704	3,166	2,997									
Solyc05g052850	R2R3MYB transcription factor 109	R2R3MYB109	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	3,957	2,887	3,812	3,085	3,441									

Solyc05g052860	Lipase (AHRD V3.3 *** G7JAK3_MEDTR)						IPR006873 (PFAM): mobidb-lite (MOB	0,180	0,194	0,688	0,416	0,354									
Solyc05g052870	Glycosyltransferase (AHRD V3.3 *** A0A068J5Q3_PANGI)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	2,530	4,295	3,833	4,023	3,471									
Solyc05g052890	Cytochrome f (AHRD V3.3 --* CYF_PINTH)		P:GO:0006979	P:response to oxidative stress			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,018	0,000	0,000	0,024									
Solyc05g052900	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	0,040	0,096	0,025	0,074	0,023									
Solyc05g052910	Protein DA1-related 1 (AHRD V3.3 *** DAR1_ARATH)		F:GO:0043130; F:G(	F:ubiquitin binding; F:metal ion binding			IPR001781 (SMART): IPR022087 (PF.	14,145	12,815	5,176	5,087	5,940									
Solyc05g052920	Folylpolyglutamate synthase (AHRD V3.3 *** K4C1X2_SOLLC)		F:GO:0004326; F:G(	F:tetrahydrofolylpol	EC:6.3.2.17	Tetrahydrofolate syn	IPR001645 (TIGRFAM): IPR013221 (F	62,873	70,840	68,833	69,710	69,632									
Solyc05g052930	Protein YIPF (AHRD V3.3 *** K4C1X3_SOLLC)		C:GO:0005794; C:G(	C:Golgi apparatus; C:membrane; P:vesicle-mediated transport			IPR006977 (PFAM): mobidb-lite (MOB	11,189	12,932	11,340	10,625	10,307									
Solyc05g052940	CASP-like protein (AHRD V3.3 *** K4C1X4_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021:SF0	2,124	1,676	1,038	1,017	1,041									
Solyc05g052950	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT3G55580.1)		C:GO:0005634; P:G(	C:nucleus; P:cold acclimation; F:histone binding; P:cellular resp			IPR000408 (PRINTS): PF13540 (PFAI	1,307	0,986	3,293	2,876	2,552									
Solyc05g052960	BTB-POZ and MATH domain protein (AHRD V3.3 *** B9VXZ7_CAPAN)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR002083 (PF.	26,910	26,794	40,040	40,464	36,109									
Solyc05g052970	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G39750.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	83,024	72,579	67,966	58,150	59,727									
Solyc05g052980	Protein phosphatase 2C (AHRD V3.3 *** Q8RVG0_TOBAC)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	207,787	120,948	181,107	302,458	222,131	-0,754	0,008			0,742	0,000	down		up
Solyc05g052990	maternal effect embryo arrest 60 (AHRD V3.3 *** AT5G05950.1)		C:GO:0016021	C:integral component of membrane			PTHR33430 (PANTHER): PTHR33430	9,688	8,762	5,125	4,001	5,189									
Solyc05g053000	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072V017_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	0,560	0,598	0,690	0,487	0,807									
Solyc05g053010	Lectin receptor kinase (AHRD V3.3 *** A0A0K1U259_NICBE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	5,438	6,218	1,689	2,051	2,379									
Solyc05g053020	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UY44_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS): IPR001938 (SM	3,006	1,529	0,749	0,657	0,422									
Solyc05g053030	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7KGS4_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART): PTHR15486 (PA	2,277	2,283	0,118	0,049	0,432									
Solyc05g053040	RING/U-box superfamily protein (AHRD V3.3 *** AT3G55530.1)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:ubiquitin-dependent prote			IPR001841 (SMART): IPR001841 (PF.	40,128	31,167	51,862	42,704	45,643									
Solyc05g053050	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 *** AT5G02220.1)		P:GO:0032875	P:regulation of DNA endoreduplication			IPR040389 (PANTHER): PTHR33142:	0,019	0,059	0,050	0,049	0,000									
Solyc05g053070	Dehydrin family protein, expressed (AHRD V3.3 *-* Q40711_ORYSJ)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,519	0,473	0,143	0,145	0,144									
Solyc05g053080	LOW QUALITY:endomembrane-type CA-ATPase 4 (AHRD V3.3 --* AT1G07670.2)							1,504	3,027	0,497	0,490	0,519									
Solyc05g053090	Transcription factor GRAS (AHRD V3.3 *** A0A103Y9C7_CYNCS)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM_GRAS	17,437	28,395	29,180	32,682	32,957	0,729	0,034					up		
Solyc05g053100	Dihydrolipoyl dehydrogenase (AHRD V3.3 *** W9QVW5_9ROSA)		F:GO:0009055; P:G(	F:electron transfer activity; P:cell redox homeostasis; F:flavin a			PR00411 (PRINTS): PR00368 (PRINT	14,307	34,614	9,575	13,771	26,728	1,303	0,000	1,474	0,000			up	up	
Solyc05g053110	Oligopeptide transporter, putative (AHRD V3.3 *** B9T1I2_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (TIGRFAM): IPR004813 (F	0,019	0,059	0,000	0,050	0,047									
Solyc05g053120	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,551	0,715	0,000	0,051	0,000									
Solyc05g053130	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7KYK1_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	37,814	32,059	45,003	46,085	42,668									
Solyc05g053140	26S proteasome regulatory subunit family protein (AHRD V3.3 *** B9MU88_POPTR)		F:GO:0005198; C:G(	F:structural molecule activity; C:nucleus; C:cytosol; P:ubiquitin-(			IPR000717 (SMART): SM00753 (SMA	25,100	27,269	27,281	31,859	27,072									
Solyc05g053160	AWPM-19-like membrane family protein (AHRD V3.3 *** B9HSV5_POPTR)		C:GO:0016021	C:integral component of membrane			IPR008390 (PFAM): IPR008390 (PAN	1,025	2,041	0,840	1,761	0,209									
Solyc05g053180	ABC-2 and Plant PDR ABC-type transporter family protein (AHRD V3.3 --* AT4G15233.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,348	0,000	0,022	0,118									
Solyc05g053190	tRNA pseudouridine synthase (AHRD V3.3 *** K4C1Z9_SOLLC)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR020097 (PFAM): G3DSA:3.30.70.5	8,293	8,885	13,210	12,420	13,401									
Solyc05g053200	Mutator-like transposase-like protein (AHRD V3.3 *** Q9FI74_ARATH)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR000270 (SMART): IPR006564 (SM	5,454	4,446	3,804	3,322	3,724									
Solyc05g053210	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C201_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.31	117,426	107,265	378,269	406,574	398,295									
Solyc05g053220	rRNA-processing protein fcf2 (AHRD V3.3 *** A0A1D1XWZ0_9ARAE)						IPR014810 (PFAM): mobidb-lite (MOB	10,354	11,348	10,368	9,209	9,262									
Solyc05g053230	Protein kinase superfamily protein (AHRD V3.3 *** AT3G62220.3)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	39,380	47,451	37,115	35,855	36,977									
Solyc05g053240	Squamosa promoter binding protein12b		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR036770 (G3DS_SBP	118,415	115,359	62,191	55,310	62,372									
Solyc05g053250	DNL-type zinc finger protein (AHRD V3.3 *** A0A151SE20_CAJCA)		F:GO:0008270	F:zinc ion binding			IPR007853 (PFAM): IPR024158 (PAN	6,215	7,226	10,796	12,231	12,637									
Solyc05g053255	CTP synthase family protein (AHRD V3.3 --* AT4G02120.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,264	0,475	0,488	0,363	0,376									
Solyc05g053260	DNA (Cytosine-5)-methyltransferase DRM2 (AHRD V3.3 *** A0A0B2R7N7_GLYSO)		P:GO:0006306	P:DNA methylation			mobidb-lite (MOBIDB_LITE): PTHR230	19,484	15,070	20,494	20,632	18,878									
Solyc05g053270	DNA (Cytosine-5-)-methyltransferase (AHRD V3.3 *-* A0A0K9PLU1_ZOSMR)		P:GO:0006306	P:DNA methylation			G3DSA:3.40.50.150 (GENE3D): PTHF	1,806	1,539	2,259	1,872	2,007									
Solyc05g053280	Galactosyltransferase family protein (AHRD V3.3 *** AT3G06440.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR001079 (SMART): IPR001079 (PF.	32,133	21,785	44,151	43,983	42,333									
Solyc05g053290	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G62260.2)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	48,940	38,852	35,940	101,683	43,707					1,503	0,000			up
Solyc05g053300	dihydrolipoamide dehydrogenase precursor		F:GO:0004148; F:G(	F:dihydrolipoyl dehy	EC:1.8.1.4	Dihydrolipoyl dehydrc	PR00368 (PRINTS): PR00411 (PRINT	85,849	94,928	216,560	213,843	201,407									
Solyc05g053310	Stress responsive A/B barrel domain protein (AHRD V3.3 *** G7JS72_MEDTR)		P:GO:0009865	P:pollen tube adhesion			IPR013097 (SMART): G3DSA:3.30.70	36,382	37,546	20,920	16,760	19,561									
Solyc05g053320	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TVZ8		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR001878 (PF.	1,956	2,404	1,351	0,872	1,011									
Solyc05g053330	MYB transcription factor (AHRD V3.3 *** Q39550_CRAPL)	R2R3MYB112	F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB	0,000	0,000	0,462	0,720	0,780									
Solyc05g053340	gibberellin 2-oxidase 1	ga2ox-1	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR005123 (PFA	0,135	0,531	0,025	0,000	0,000									
Solyc05g053350	Desiccation-related protein PCC13-62 (AHRD V3.3 *** A0A0B2QYX9_GLYSO),Pfam:PF13668						PF13668 (PFAM): PTHR31694 (PANT	5,594	14,602	0,905	3,092	0,328									
Solyc05g053360	transmembrane protein (AHRD V3.3 *** AT1G02380.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR341	28,850	34,118	25,801	21,264	24,984									
Solyc05g053370	Zinc/iron transporter, putative (AHRD V3.3 *** B9RL85_RICCO)		F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM): IPR003689 (F	3,454	3,632	1,527	1,486	2,054									
Solyc05g053380	WRKY transcription factor 48	WRKY48	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF_WRKY	0,376	0,322	0,147	0,095	0,118									
Solyc05g053390	Prefoldin subunit 3 (AHRD V3.3 *** K4C219_SOLLC)		P:GO:0006457; C:G(	P:protein folding; C:prefoldin complex			IPR009053 (G3DSA:1.10.287.GENE3	28,866	30,068	27,812	24,182	25,000									
Solyc05g053400	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	1,783	1,025	1,619	1,315	1,527									
Solyc05g053410	phytochrome B2	PHYB2	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR001294 (PRINTS): IPR003018 (SM	22,264	62,043	30,388	69,708	100,044	1,507	0,000	1,715	0,000	1,200	0,000	up	up	up
Solyc05g053420	LOW QUALITY:GRAS family transcription factor, putative (AHRD V3.3 *** A0A061E	GRAS					IPR005202 (PFAM_GRAS	0,040	0,000	0,025	0,150	0,023									
Solyc05g053430	DNA-directed RNA polymerase subunit (AHRD V3.3 *** K4C223_SOLLC)		F:GO:0003676; P:G(	F:nucleic acid binding; P:transcription, DNA-templated; P:mRNA			IPR001529 (SMART): IPR001222 (SM	4,337	3,189	3,830	3,365	3,009									
Solyc05g053440	60S ribosomal protein L29, putative (AHRD V3.3 *** B9RZN1_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002673 (PFAM): mobidb-lite (MOB	162,828	182,798	101,522	87,419	87,870									
Solyc05g053460	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT3G17080.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM): PTHR31232:SF5	0,038	0,268	0,000	0,000	0,000									
Solyc05g053470	Chaperonin CPN60, mitochondrial (AHRD V3.3 *** CH60A_ARATH)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR002423 (PF	143,559	139,465	286,738	264,377	266,046									
Solyc05g053480	hydroxyethylthiazole kinase family protein (AHRD V3.3 *** AT3G24030.1)		F:GO:0004417; P:G(	F:hydroxyethylthiaz	EC:2.7.1.5	Hydroxyethylthiazole	IPR000417 (PRINTS): IPR029056 (G3	4,166	3,701	8,869	8,355	8,213									
Solyc05g053490	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein, putative (AHRD V3.3 *** A0A06		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): mobidb-lite (MOB	7,699	4,980	14,681	17,530	14,118									
Solyc05g053500	GATA transcription factor, putative (AHRD V3.3 *** B9RWP4_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMAF_GATA	0,515	0,319	0,172	0,146	0,211									
Solyc05g053510	DNA-directed RNA polymerase II (AHRD V3.3 *** G7K102_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR036710 (G3DSA:3.40.1340.GENE	0,040	0,018	0,022	0,000	0,000									
Solyc05g053520	DNA polymerase delta subunit 4 family (AHRD V3.3 *** D7KJU8_ARALL)		C:GO:0005634; P:G(	C:nucleus; P:DNA replication			IPR007218 (PFAM): mobidb-lite (MOB	0,042	0,158	0,090	0,050	0,047									
Solyc05g053530	9-cis-epoxycarotenoid dioxygenase, putative (AHRD V3.3 *** B9RWM0_RICCO)		F:GO:0016702; P:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR004294 (PFAM): mobidb-lite (MOB	0,021	0,021	0,000	0,025	0,000									
Solyc05g053540	Dihydroxy-acid dehydratase (AHRD V3.3 *** A0A1D1YZH9_9ARAE)		F:GO:0004160; P:G(	F:dihydroxy-acid de	EC:4.2.1.9	Dihydroxy-acid dehy(	IPR004404 (TIGRFAM): IPR000581 (F	84,000	76,460	231,770	237,752	254,678									
Solyc05g053550	chalcone synthase 2	CHS-2	P:GO:0009058; F:G(	P:biosynthetic process; F:transferase activity, transferring acyl			IPR012328 (PFAM): IPR016039 (G3D	809,579	467,404	1317,373	1235,822	1267,706	-0,766	0,003					down		
Solyc05g053570	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG37	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013581 (PF.	0,889	0,953	1,016	1,288	1,429									
Solyc05g053580	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT3G27960.3)							0,040	0,021	0,025	0,075	0,069									
Solyc05g053590	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG38	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	47,894	34,789	37,974	44,078	43,926									
Solyc05g053600	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG39	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR029481 (PF.	10,496	49,777	22,110	38,545	35,008	2,262	0,022	0,660	0,013	0,802	0,000	up	up	up
Solyc05g053610	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG40	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	0,544	1,778	15,129	13,553	12,856									
Solyc05g053620	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)						IPR025886 (PFAM): PTHR32278:SF2	92,454	146,475	43,973	51,868	45,375	0,691	0,035					up		
Solyc05g053630	LOW QUALITY:Clavata3/ESR (CLE) gene family member MtCLE06 (AHRD V3.3 --* G7L1C0_MEDTR)							1,678	0,650	0,000	0,050	0,000									
Solyc05g053640	LOW QUALITY:Clavata3/ESR (CLE) gene family member MtCLE06 (AHRD V3.3 --* G7L1C0_MEDTR)							5,851	1,612	0,000	0,025	0,000									
Solyc05g053650	26S proteasome non-ATPase regulatory subunit 1 (AHRD V3.3 *** A0A151T358_CAJCA)		C:GO:0000502; F:G(	C:proteasome complex; F:enzyme regulator activity; P:regulatio			PF13646 (PFAM): IPR016642 (PIRSF	97,715	95,274	137,322	137,253	129,139									
Solyc05g053670	60S ribosomal protein L13a-like protein (AHRD V3.3 *** Q3HRW1_SOLTU)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR036899 (G3DSA:3.90.1180.GENE	212,747	220,359	183,423	159,832	164,597									
Solyc05g053680	Pectinesterase (AHRD V3.3 *** K4C248_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM): IPR012334 (G3D	0,351	0,190	0,000	0,000	0,023									
Solyc05g053690	Ubiquitin carboxyl-terminal hydrolase 2 (AHRD V3.3 *** A0A0B2QQX6_GLYSO)		F:GO:0008270; P:G(	F:zinc ion binding; F	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001607 (SMART): IPR013083 (G3	1,090	1,570	0,650	0,827	0,799									
Solyc05g053710	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G13730.1)						IPR000195 (SMART): IPR000195 (PF.	23,111	20,315	25,906	25,712	28,685									
Solyc05g053715	Serinc-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 --* AT1G16180.2)							1,492	2,308	1,239	1,040	1,055									
Solyc05g053720	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G04910.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; P:fucose metabolic proces			IPR019378 (PFAM): IPR024709 (PIRS	30,645	34,328	23,552	23,538	22,241									
Solyc05g053730	stress response NST1-like protein (AHRD V3.3 *** AT5G49210.2)						mobidb-lite (MOBIDB_LITE): PTHR364	20,361	21,239	23,302	19,634	22,693									
Solyc05g053740	Alkaline ceramidase 3 (AHRD V3.3 *** A0A0B0NPT2_GOSAR)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra			IPR008901 (PFAM): PTHR12956:SF5	3,134	2,724	3,398	4,071	2,912									
Solyc05g053760	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SYM1_RICCO)		C:GO:0009507; P:G(	C:chloroplast; P:chaperone-mediated protein folding			IPR001623 (PRINTS): IPR001623 (SM	8,336	13,430	18,290	24,604	16,001	0,712	0,037					up		
Solyc05g053770	Electron transport complex protein rnfC, putative isoform 1 (AHRD V3.3 *-* A0A061EJK1_THECC)		F:GO:0004386	F:helicase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	38,419	29,734	38,368	33,212	34,185									
Solyc05g053780	RNA binding protein-like protein (AHRD V3.3 *** Q3HVL3_SOLTU)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	201,484	203,174	260,608	268,495	252,514									
Solyc05g053790	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE6-like	C:GO:0016021	C:integral component of membrane			PR01713 (PRINTS): G3DSA:3.90.25.1	0,061	0,037	0,099	0,101	0,142									
Solyc05g053800	DNA repair protein RAD50 (AHRD V3.3 *** RAD50_ARATH)		P:GO:0000723; P:G(	P:telomere mainten	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	80,724	66,731	102,520	106,088	105,633									
Solyc05g053810	Serine hydroxymethyltransferase (AHRD V3.3 *** M1BAA6_SOLTU)		F:GO:0004372; P:G(	F:glycine hydroxyme	EC:2.1.2.1	Glycine hydroxymeth	IPR001085 (PIRSF): IPR015422 (G3D	393,827	399,256	146,809	136,126	145,668									
Solyc05g053820	Glycosyltransferase (AHRD V3.3 *** K4DHN1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	22,778	24,409	42,421	44,816	41,835									
Solyc05g053830	Protein transport protein sec23, putative (AHRD V3.3 *** B9RRN0_RICCO)		P:GO:0006886; F:G(	P:intracellular protein transport; F:zinc ion binding; C:COPII vesi			IPR006896 (PFAM): G3DSA:2.30.30.3	166,014	172,604	158,719	164,124	155,095									
Solyc05g053835	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G04240.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13424 (PFAM	184,828	236,025	248,936	243,575	246,709									
Solyc05g053850	protein SELF PRUNING 5G		F:GO:0008429; P:G(	F:phosphatidylethanolamine binding; P:regulation of flower deve			IPR036610 (G3DSA:3.90.280.GENE3	0,101	0,107	0,098	0,139	0,047									
Solyc05g053860	Organic cation/carnitine transporter (AHRD V3.3 *** A0A072TPM4_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	68,688	30,904	13,117	3,467	10,745	-1,120	0,002			-1,916	0,000	down		down
Solyc05g053870	E3 ubiquitin-protein ligase RGLG2 (AHRD V3.3 *** A0A151QXI5_CAJCA)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): IPR002035 (SM	21,775	24,084	3,549	3,527	4,173									
Solyc05g053880	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 --* B9TA05_RICCO)						IPR032704 (PFAM): G3DSA:3.40.50.3	4,770	5,664	3,781	3,037	2,824									
Solyc05g053890	Glycosyltransferase (AHRD V3.3 *** K4C268_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	2,269	1,881	0,799	0,782	0,849									
Solyc05g053900	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G05840.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	8,942	6,280	10,803	10,929	9,175									
Solyc05g053930	Protein kinase (AHRD V3.3 *** A3RI54_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	37,792	62,907	6,773	6,735	8,679									
Solyc05g053940	Ras-related GTP binding protein (AHRD V3.3 *** A1E0Y0_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	53,119	54,501	71,897	79,798	66,892									
Solyc05g053950	DUF1365 family protein (AHRD V3.3 *** AT1G30130.3)		C:GO:0016021	C:integral component of membrane			IPR010775 (PFAM): IPR010775 (PAN	13,485	15,038	27,359	27,131	29,117									
Solyc05g053960	Extensin-like protein (AHRD V3.3 *** O49946_SOLTU)							0,462	0,669	0,771	0,668	0,803									
Solyc05g053965	Amino acid transporter, putative (AHRD V3.3 *** B9S8W8_RICCO)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM): PTHR22950 (PAI	0,140	0,182	0,125	0,099	0,142									
Solyc05g053990	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	20,105	16,702	21,335	22,362	21,645									
Solyc05g054000	NBS-LRR resistance protein-like protein (AHRD V3.3 *-* A1Y9Q6_9SOLN)		F:GO:0043531	F:ADP binding				3,913	3,460	3,683	5,178	3,918									
Solyc05g054010	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR036388 (G3D	0,639	1,182	0,563	0,510	0,682									
Solyc05g054020	LOW QUALITY:NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q9_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	0,812	0,980	0,430	0,414	0,519									
Solyc05g054030	Zinc finger family protein (AHRD V3.3 *** B9HJL4_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF_C2H2	0,000	0,064	0,000	0,000	0,000									
Solyc05g054040	Transmembrane 9 superfamily member (AHRD V3.3 *** K4C283_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): PTHR10766:SF5	5,166	4,706	4,107	3,978	4,425									
Solyc05g054050	Glutamate decarboxylase (AHRD V3.3 *** K4C284_SOLLC)		F:GO:0004351; P:G(	F:glutamate decarb	EC:4.1.1.15	Glutamate decarboxy	IPR002129 (PFAM): IPR015421 (G3D	0,000	0,039	0,000	0,000	0,000									
Solyc05g054060	UDP-GLUCOSE PYROPHOSPHORYLASE 1 (AHRD V3.3 *** AT3G03250.1)		F:GO:0003983; P:G(	F:UTP:glucose-1-ph	EC:2.7.7.64; EC:2.7.	UTP-monosaccharide	G3DSA:2.160.10.10 (GENE3D): IPR0	0,590	0,509	0,118	0,072	0,046									
Solyc05g054070	60S ribosomal protein L6 (AHRD V3.3 *** RL6_MESCR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000915 (PFAM): IPR005568 (PFA	94,984	98,351	107,907	99,491	99,168									
Solyc05g054080	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			IPR019956 (PRINTS): IPR000626 (SM	55,288	35,145	116,644	118,473	106,844	-0,627	0,016					down		
Solyc05g054090	UDP-3-O-acyl N-acetylglycosamine deacetylase family protein (AHRD V3.3 --* AT1G25210.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	581,552	723,644	50,970	55,018	57,862									
Solyc05g054100	Transmembrane protein 111 (AHRD V3.3 *** A0A0B2RAS8_GLYSO)		C:GO:0016020	C:membrane			IPR002809 (SMART): IPR002809 (PF.	53,387	51,675	76,599	70,335	65,882									
Solyc05g054110	Rho GDP-dissociation inhibitor 1 family protein (AHRD V3.3 *** B9IH83_POPTR)		F:GO:0005094; C:G(	F:Rho GDP-dissociation inhibitor activity; C:cytoplasm			IPR000406 (PRINTS): IPR024792 (G3	0,419	0,825	0,118	0,100	0,141									
Solyc05g054120	Cysteine proteinase inhibitor (AHRD V3.3 *** K4C291_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			IPR000010 (SMART): IPR000010 (PF.	6,704	8,873	1,037	0,845	0,777									
Solyc05g054130	Calcium-binding protein, putative (AHRD V3.3 *** B9T038_RICCO)		F:GO:0004674; P:G(	F:protein serine/thre	EC:2.7.11	Transferring phosphc	IPR013878 (PFAM): IPR011989 (G3D	31,480	29,055	19,666	18,637	20,138									
Solyc05g054140	DNA-directed RNA polymerase I subunit rpa43-like protein (AHRD V3.3 *** T2DMP5_PHAVU)		F:GO:0001054; C:G(	F:RNA polymerase	EC:2.7.7.6	DNA-directed RNA p(	G3DSA:2.40.50.1060 (GENE3D): mob	11,812	11,768	15,283	15,607	13,318									
Solyc05g054150	RAB GTPase homolog A5A (AHRD V3.3 *** AT5G47520.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	12,729	11,741	3,100	2,562	3,971									
Solyc05g054170	GRAS family transcription factor (AHRD V3.3 *** G7JLR5_MEDTR)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM_GRAS	132,454	170,879	37,395	34,401	55,119			0,556	0,020				up	
Solyc05g054180	Potyviral VPg interacting protein 2 (AHRD V3.3 *** G8XRV5_PHAVU)						IPR004082 (PRINTS): IPR001965 (SM	52,041	76,559	33,740	31,698	35,735									
Solyc05g054190	CASP-like protein (AHRD V3.3 *** K4C298_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006702 (PFAM): IPR006459 (TIGF	2,061	1,514	0,267	0,318	0,375									
Solyc05g054200	Transcriptional adapter ADA2 (AHRD V3.3 *** A0A151T6L2_CAJCA)		F:GO:0003677; F:G(	F:DNA binding; F:transcription coactivator activity; F:protein bin			G3DSA:1.10.10.60 (GENE3D): IPR01(	31,952	26,718	19,817	20,010	20,587									
Solyc05g054210	proline-rich protein		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	179,560	135,982	47,700	53,751	48,020									
Solyc05g054220	SNF1-related kinase complex anchoring protein	sip1	F:GO:0005515	F:protein binding			IPR006828 (SMART): IPR006828 (PF.	54,839	44,870	44,533	36,154	39,731									
Solyc05g054230	Nudix hydrolase (AHRD V3.3 *** A0A061GGI6_THECC)		F:GO:0016787	F:hydrolase activity			G3DSA:3.40.630.30 (GENE3D): PF18	8,958	7,772	3,791	3,583	4,531									
Solyc05g054240	Protein arginine n-methyltransferase, putative (AHRD V3.3 *** B9RT51_RICCO)		P:GO:0006479; F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:2.70.160.11 (GENE3D): PF06	50,288	45,925	21,363	18,365	22,234									
Solyc05g054260	Kinesin-like protein (AHRD V3.3 *** K4C2A5_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	57,154	50,873	44,115	44,152	46,943									
Solyc05g054310	eukaryotic translation initiation factor 2 gamma subunit (AHRD V3.3 *** AT1G04170.2)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR015256 (PF	21,671	23,250	19,926	17,938	17,330									
Solyc05g054320	Epoxide hydrolase (AHRD V3.3 *** Q41413_SOLTU)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR029058 (G3	18,472	22,105	8,857	7,044	9,365									
Solyc05g054330	Epoxide hydrolase (AHRD V3.3 *** Q41415_SOLTU)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR000073 (PF	25,083	22,314	4,076	3,481	2,860									
Solyc05g054340	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	31,727	25,615	39,277	39,274	34,053									
Solyc05g054350	alpha/beta hydrolase family protein		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR029058 (G3	205,796	257,271	225,196	296,635	366,936			0,701	0,000	0,400	0,028		up	up
Solyc05g054355	beta-galactosidase 2 (AHRD V3.3 --* AT3G52840.2)						PTHR35488:SF2 (PANTHER): PTHR3	0,000	0,037	0,000	0,000	0,000									
Solyc05g054360	Pectinesterase (AHRD V3.3 *** K4C2B4_SOLLC)		F:GO:0004857; F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR012334 (G3	0,139	0,018	0,094	0,050	0,048									
Solyc05g054365	acyl-CoA dehydrogenase-like protein (AHRD V3.3 *** AT3G06810.1)		F:GO:0016627; F:G(	F:oxidoreductase activity, acting on the CH-CH group of donors			G3DSA:2.40.110.10 (GENE3D): IPR0(	172,895	152,539	70,764	59,887	77,302									
Solyc05g054380	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (PF	0,000	0,096	0,000	0,025	0,000									
Solyc05g054390	Two-component response regulator (AHRD V3.3 *** W9RS74_9ROSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding; F:D			IPR001789 (SMAF_ARR-B	53,139	32,892	32,793	35,190	58,124	-0,665	0,006	0,821	0,000			down	up	
Solyc05g054400	GATA transcription factor, putative (AHRD V3.3 *** B9RZK8_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (SMAF_GATA	14,583	21,040	9,283	9,668	7,862									
Solyc05g054410	telomere binding protein 1	tbp1	F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR001005 (SMART): G3DSA:1.10.24	58,242	53,271	38,355	31,763	40,079									

Solyc05g054420	XH/XS domain-containing family protein (AHRD V3.3 *** B9HTH7_POPTR)		P:GO:0031047	P:gene silencing by RNA			IPR005379 (PFAM): IPR005380 (PFA	25,057	20,372	17,019	18,127	19,739										
Solyc05g054430	DNA replication complex GINS protein PSF2 (AHRD V3.3 *** K4C2C1_SOLLC)		C:GO:0005634; P:G(	C:nucleus; P:DNA replication			IPR021151 (PFAM): G3DSA:1.20.58.1	2,677	2,609	1,581	1,095	1,412										
Solyc05g054435	DNA replication complex GINS protein PSF2 (AHRD V3.3 *-* M1C604_SOLTU)		P:GO:0000727; C:G(	P:double-strand bre	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.58.1020 (GENE3D)	1,240	1,094	0,763	0,289	0,492										
Solyc05g054440	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** G7L028_MEDTR)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR012946 (PF	0,000	0,019	0,000	0,000	0,000										
Solyc05g054450	LOW QUALITY:Microneme/rhoptry antigen (AHRD V3.3 *** A0A1D1Y2V2_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,951	7,773	6,252	5,491	6,457										
Solyc05g054460	Dolichyl-phosphate beta-glucosyltransferase, putative (AHRD V3.3 *** B9SXX8_RICCO)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:protein N-linked glycosyla			IPR001173 (PFAM): IPR029044 (G3D	13,588	14,675	16,295	18,629	16,573										
Solyc05g054480	Actin (AHRD V3.3 *** ACT1_TOBAC)		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): IPR004000 (SM	2,150	3,038	1,848	1,408	1,340										
Solyc05g054490	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** AT3G55360.1)		P:GO:0006629; F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t			IPR001104 (PFAM): G3DSA:3.10.20.9	54,829	55,193	47,545	41,703	42,935										
Solyc05g054493	DNA/RNA-binding protein KIN17 (AHRD V3.3 *** A0A0B2S1P2_GLYSO)		F:GO:0003690; C:G(	F:double-stranded DNA binding; C:nucleus; P:DNA replication; F			IPR019447 (SMART): IPR019447 (PF	82,770	67,860	71,304	74,107	71,155										
Solyc05g054510	Dof zinc finger protein (AHRD V3.3 *** A0A0K9PZW2_ZOSMR)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,077	0,000	0,000	0,000	0,000										
Solyc05g054520	Geranylgeranyl transferase type-1 subunit beta (AHRD V3.3 *** W9SPR0_9ROSA)		F:GO:0003824	F:catalytic activity			IPR001330 (PFAM): G3DSA:1.50.10.2	21,097	20,535	35,732	37,904	34,201										
Solyc05g054530	Transmembrane protein, putative (AHRD V3.3 *** G7KWV5_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,417	0,850	0,621	0,559	0,568										
Solyc05g054540	ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** AT5G59300.1)		P:GO:0000209; F:G(	P:protein polyubiquitination; F:ATP binding; P:ubiquitin-depende			SM00212 (SMART): IPR016135 (G3D	23,797	23,854	23,675	24,420	24,550										
Solyc05g054550	ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** AT5G59300.1)		P:GO:0000209; F:G(	P:protein polyubiquitination; F:ATP binding; P:ubiquitin-depende			SM00212 (SMART): IPR016135 (G3D	12,283	9,431	14,140	13,565	12,188										
Solyc05g054560	CASP-like protein (AHRD V3.3 *** K4C2D4_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006702 (PFAM): mobidb-lite (MOB	48,508	31,817	55,491	65,871	47,297	-0,579	0,032					down		
Solyc05g054570	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein (AHRD V3.3 *** AT3G46450		C:GO:0016021	C:integral component of membrane			IPR001251 (SMART): IPR001251 (PF	25,958	28,285	67,186	88,955	71,694					0,409	0,045			up
Solyc05g054580	60S acidic ribosomal protein P0 (AHRD V3.3 *** K4C2D6_SOLLC)		C:GO:0005622; P:G(	C:intracellular; P:ribosome biogenesis			IPR001790 (PFAM): PF00428 (PFAM)	302,684	366,970	248,890	236,547	235,430									
Solyc05g054590	UDP-glucuronate decarboxylase 1 (AHRD V3.3 *** Q6IVK5_TOBAC)		C:GO:0005737; P:G(	C:cytoplasm; P:D-x	EC:4.1.1.35	UDP-glucuronate dec	G3DSA:3.40.50.720 (GENE3D): IPR0	18,349	21,298	34,116	24,852	31,701									
Solyc05g054600	Methionyl-tRNA synthetase family protein (AHRD V3.3 *** B9HTK5_POPTR)		F:GO:0004825; F:G(	F:methionine-tRNA	EC:6.1.1.1	Methionine--tRNA lig	IPR033911 (PRINTS): G3DSA:1.10.73	11,532	13,279	11,354	9,949	11,220									
Solyc05g054610	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	5,393	6,156	0,465	0,242	0,565									
Solyc05g054620	ACT domain-containing protein (AHRD V3.3 *** AT2G39570.1)						G3DSA:3.30.70.260 (GENE3D): PTHR	118,862	87,392	33,551	30,553	35,831									
Solyc05g054630	Elongator complex protein 1 (AHRD V3.3 *** K4C2E0_SOLLC)		P:GO:0002098; C:G(	P:tRNA wobble uridine modification; C:Elongator holoenzyme co			IPR006849 (PFAM): IPR006849 (PIRS	30,223	30,831	39,003	43,211	39,654									
Solyc05g054640	2-oxoglutarate dehydrogenase E1 component family protein (AHRD V3.3 *** B9HM58_POPTR)		F:GO:0004591; P:G(	F:oxoglutarate dehy	EC:1.2.4.2	Oxoglutarate dehydro	IPR005475 (SMART): IPR005475 (PF	203,207	208,074	224,184	205,655	216,081									
Solyc05g054650	Zinc finger family protein (AHRD V3.3 *** B9HM54_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,037	0,096	0,112	0,123	0,047									
Solyc05g054670	nuclease (AHRD V3.3 *** AT3G63270.1)						IPR027806 (PFAM): mobidb-lite (MOB	6,155	3,427	10,859	10,902	10,047									
Solyc05g054680	protein kinase family protein (AHRD V3.3 *** AT5G54380.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR024788 (PF	4,333	3,108	1,206	1,767	2,842			1,211	0,003				up	
Solyc05g054690	60S ribosomal protein L23a (AHRD V3.3 --* RL23A_TOBAC)						mobidb-lite (MOBIDB_LITE)	0,516	0,493	0,169	0,200	0,094									
Solyc05g054700	MAP kinase phosphatase	mkp1	P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threon	IPR020422 (SMART): IPR029021 (G3	29,012	31,032	32,228	25,877	27,804									
Solyc05g054710	Beta-hexosaminidase (AHRD V3.3 *** E6Y3A5_SOLLC)		F:GO:0004563; P:G(	F:beta-N-acetylhexo	EC:3.2.1.52	Beta-N-acetylhexosa	IPR025705 (PRINTS): IPR029019 (PF	28,259	26,797	20,694	23,053	23,160									
Solyc05g054720	Protein TIC 20, chloroplastic (AHRD V3.3 *** A0A0B2STH9_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR005691 (PFAM): IPR005691 (TIGF	69,572	78,721	149,642	145,615	153,632									
Solyc05g054730	Cation efflux family protein (AHRD V3.3 *** AT2G39450.1)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;			IPR036837 (G3DSA:3.30.70.GENE3D	53,577	43,980	43,388	42,317	39,904									
Solyc05g054740	Sulfate transporter (AHRD V3.3 *** A0A0R5RJV0_HEVBR)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR002645 (PFAM): IPR001902 (TIGF	28,392	22,976	17,355	17,357	20,301									
Solyc05g054750	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)						IPR006476 (PFAM): IPR006476 (TIGF	0,720	0,299	0,449	0,319	0,023									
Solyc05g054760	dehydroascorbate reductase 1	DHAR2	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	202,701	218,406	298,025	197,112	266,077					-0,592	0,001			down
Solyc05g054770	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-like protein (AHRD V3.3 *-* AT2G39435.6)						IPR025486 (PFAM): mobidb-lite (MOB	13,070	23,763	18,043	15,426	17,165	0,886	0,026					up		
Solyc05g054780	Dirigent protein (AHRD V3.3 *** M1C5D5_SOLTU)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAN	0,021	0,101	0,099	0,022	0,023									
Solyc05g054790	LOW QUALITY:plastidic GLC translocator (AHRD V3.3 --* AT5G16150.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,018	0,000	0,000	0,000									
Solyc05g054795	Dirigent protein (AHRD V3.3 *-* M1C5D3_SOLTU)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): mobidb-lite (MOB	0,061	0,075	0,050	0,045	0,024									
Solyc05g054800	LEM3 (Ligand-effect modulator 3) family protein (AHRD V3.3 *** D7L0J9_ARALL)		C:GO:0016020	C:membrane			IPR005045 (PFAM): IPR005045 (PIRS	158,817	186,857	108,044	145,563	120,108					0,433	0,031			up
Solyc05g054810	60S ribosomal protein L35 (AHRD V3.3 *** RL35_EUPES)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001854 (TIGRFAM): G3DSA:1.10.:	177,709	210,760	145,711	127,814	132,444									
Solyc05g054820	LOW QUALITY:Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9HTX5_POPTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): mobidb-lite (MOB	1,098	1,850	0,022	0,000	0,046									
Solyc05g054830	Ankyrin repeat family protein (AHRD V3.3 *** AT3G12360.1)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	179,853	211,599	62,195	82,875	98,075			0,653	0,001				up	
Solyc05g054840	E3 UFM1-protein ligase (AHRD V3.3 *-* A0A199V584_ANACO)		P:GO:0003352	P:regulation of cilium movement			IPR021298 (PFAM): IPR021298 (PAN	4,633	3,835	4,496	5,529	4,257									
Solyc05g054850	membrane-associated kinase regulator (AHRD V3.3 *** AT2G39370.1)		C:GO:0005886; F:G(	C:plasma membrane; F:kinase inhibitor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,380	0,367	0,000	0,000	0,000									
Solyc05g054860	Kinase, putative (AHRD V3.3 *** B9SGH1_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR001245 (PF	28,414	32,862	29,763	43,768	48,605			0,705	0,000	0,559	0,002		up	up
Solyc05g054870	U4/U6 small nuclear Prp3-like ribonucleoprotein (AHRD V3.3 *-* G7IF06_MEDTR)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,821	3,363	3,656	3,647	3,626									
Solyc05g054880	U4/U6 small nuclear ribonucleoprotein Prp3 (AHRD V3.3 *** A0A0B0N7U9_GOSAR)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			IPR010541 (PFAM): IPR013881 (PFA	8,250	9,647	9,548	7,897	9,180									
Solyc05g054890	ABC transporter family protein (AHRD V3.3 *** B9HTY6_POPTR)	ABCG13	F:GO:0005524; F:G(	F:ATP binding; F:ele	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	0,159	0,849	0,629	0,586	0,656									
Solyc05g054910	SAC3/GANP/Nin1/mts3/eIF-3 p25 family (AHRD V3.3 *** AT2G39340.1)						IPR005062 (PFAM): G3DSA:1.25.40.9	54,034	49,990	60,523	62,792	62,654									
Solyc05g054920	Serine/arginine-rich-splicing factor RS2Z32 (AHRD V3.3 *** A0A0M8KRK6_NICAT)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR000504 (SM	364,456	393,647	263,872	280,061	262,743									
Solyc05g054930	CAP-gly domain linker (AHRD V3.3 *** AT3G55060.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,008	2,215	1,486	0,875	1,630									
Solyc05g054940	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (AHRD V3.3 *** AT4G08790		P:GO:0006807	P:nitrogen compound metabolic process			IPR036526 (G3DSA:3.60.110.GENE3	26,491	22,269	54,448	46,003	55,676									
Solyc05g054960	Peroxisome biogenesis protein 12 (AHRD V3.3 *** K4C2H2_SOLLC)		C:GO:0005779; P:G(	C:integral component of peroxisomal membrane; P:protein targe			IPR017375 (PIRSF): IPR006845 (PFA	14,281	14,686	21,506	22,552	21,763									
Solyc05g054970	Ankyrin repeat family protein (AHRD V3.3 *** AT3G04470.1)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	92,975	101,969	81,177	75,613	79,265									
Solyc05g054980	Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha (AHRD V3.3 *** A0A0B0NW47		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.220 (GENE3D): PF1	39,902	38,042	37,240	40,928	37,141									
Solyc05g054990	Ribosomal protein S6 (AHRD V3.3 *** A0A103XMX6_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR000529 (PFAM): IPR014717 (G3D	13,346	15,081	15,247	13,548	16,745									
Solyc05g055000	Cysteine desulfurase family protein (AHRD V3.3 *** B9HNK4_POPTR)		P:GO:0006534; F:G(	P:cysteine metaboli	EC:2.8.1.7	Cysteine desulfurase	IPR015421 (G3DSA:3.40.640.GENE3	33,775	32,808	82,079	82,049	86,494									
Solyc05g055010	RNA-binding protein (AHRD V3.3 *** A0A0K9NRG1_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	31,206	19,188	33,581	30,611	35,241	-0,675	0,022					down		
Solyc05g055020	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT5G28490.1)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM): PTHR31165:SF1	0,155	0,158	0,000	0,000	0,000									
Solyc05g055030	R2R3MYB transcription factor 10	R2R3MYB10	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,159	0,379	0,137	0,123	0,024									
Solyc05g055040	Hexosyltransferase (AHRD V3.3 *** K4C2I1_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR002495 (PFAM): IPR029044 (G3D	13,492	12,534	9,715	10,523	9,344									
Solyc05g055050	Phosphoenolpyruvate carboxylase kinase (AHRD V3.3 *** Q9SDX9_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,058	0,099	0,000	0,000	0,000									
Solyc05g055060	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0I1T1_SOLCH)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	40,088	39,831	59,116	59,457	56,040									
Solyc05g055070	Ethylene receptor homolog (AHRD V3.3 *** Q9XET9_SOLLC)	ETR7	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR001789 (SMART): IPR003018 (SM	29,441	28,428	50,748	55,619	47,473									
Solyc05g055080	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G13030.3)						mobidb-lite (MOBIDB_LITE): PTHR335	0,299	0,144	0,050	0,514	0,023									
Solyc05g055090	Ubiquitin carboxyl-terminal hydrolase 12 (AHRD V3.3 *** UBP12_ARATH)		F:GO:0005515; P:G(	F:protein binding; P	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR002083 (SMART): IPR008974 (G3	86,925	79,360	90,715	89,912	93,463									
Solyc05g055100	Ubiquitin carboxyl-terminal hydrolase 12 (AHRD V3.3 *-* W9RMK9_9ROSA)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR024729 (PF	0,599	0,457	0,025	0,000	0,000									
Solyc05g055110	Nuclear pore complex protein Nup136d (AHRD V3.3 *** W6JJ82_NICBE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	68,883	41,540	29,790	34,962	36,346	-0,703	0,012					down		
Solyc05g055120	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 --* AT1G10900.3)							17,277	12,404	9,951	9,989	9,471									
Solyc05g055130	nuclear pore complex protein (AHRD V3.3 *-* AT3G10650.2)		C:GO:0005635; P:G(	C:nuclear envelope; P:poly(A)+ mRNA export from nucleus; P:nu			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,490	0,242	0,140	0,333	0,281									
Solyc05g055140	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FQW5_THECC)		C:GO:0016020	C:membrane			IPR001841 (SMART): IPR001841 (PF	0,000	0,019	0,000	0,025	0,023									
Solyc05g055160	DnaJ-like protein (AHRD V3.3 *** Q38HT9_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat sho			IPR001623 (PRINTS): IPR001623 (SM	5344,598	4315,846	3787,326	3301,236	3125,987									
Solyc05g055170	Charged multivesicular body protein 5 (AHRD V3.3 *** W9R7A4_9ROSA)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): mobidb-lite (MOB	41,292	40,189	25,841	22,893	24,091									
Solyc05g055180	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT3G44190.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00368 (PRINTS): IPR023753 (PFA	0,019	0,000	0,000	0,000	0,000									
Solyc05g055185	photosystem I reaction center subunit N (AHRD V3.3 *-* AT1G49975.1)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis			PTHR36327 (PANTHER)	0,019	0,175	0,000	0,022	0,000									
Solyc05g055200	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHRI		P:GO:0019538	P:protein metabolic process			IPR036628 (G3DSA:1.10.1780.GENE	0,333	0,575	0,283	0,234	0,379									
Solyc05g055210	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *** ERF1X_ARATH)		F:GO:0003747; C:G(	F:translation release factor activity; C:cytoplasm; P:translationa			IPR005140 (SMART): IPR005140 (PF	106,867	90,855	128,375	106,021	117,134									
Solyc05g055220	ovate family protein 10	OFP10	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (PFAM): IPR006458 (TIGF	0,394	0,041	0,000	0,000	0,000									
Solyc05g055230	40S ribosomal protein S17 (AHRD V3.3 *** RS17_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036401 (G3DSA:1.10.60.GENE3D	80,333	88,698	62,542	52,367	58,562									
Solyc05g055240	I-box binding factor	mybi	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	39,528	34,100	73,361	68,060	65,959									
Solyc05g055260	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT3G11500.2)		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:spliceosomal complex			IPR001163 (SMART): G3DSA:2.30.30	60,615	63,697	72,561	56,534	59,776									
Solyc05g055270	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT5G60570.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,204	0,000	0,000	0,000									
Solyc05g055280	Ferredoxin (AHRD V3.3 *** A0A076FFN2_OCIBA)		F:GO:0009055; P:G(	F:electron transfer activity; P:electron transport chain; F:2 iron,			IPR001041 (PFAM): IPR010241 (TIGF	18,274	24,250	26,911	30,287	29,539									
Solyc05g055290	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)		C:GO:0016020	C:membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,503	0,314	0,047	0,117	0,072									
Solyc05g055300	Protein YIPF (AHRD V3.3 *** K4C2K6_SOLLC)		C:GO:0016020	C:membrane			IPR006977 (PFAM): mobidb-lite (MOB	15,454	17,197	14,330	14,685	13,532									
Solyc05g055310	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G27690.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	98,888	105,618	131,157	125,927	144,586									
Solyc05g055320	Peroxidase (AHRD V3.3 *** K4C2K8_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc05g055330	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *** A0A072VZG4	ABCG41	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	4,478	5,001	2,258	3,118	2,795									
Solyc05g055340	Plant tudor-like RNA-binding protein (AHRD V3.3 *** A0A072UR05_MEDTR)						IPR005491 (SMART): IPR014002 (SM	24,587	14,421	20,488	22,142	21,200	-0,740	0,014					down		
Solyc05g055343	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	5,561	4,091	6,055	4,587	4,060									
Solyc05g055350	Nuclear ribonuclease Z (AHRD V3.3 *** G7K7F6_MEDTR)		P:GO:0034414; F:G(	P:tRNA 3'-trailer cle	EC:3.1.3; EC:3.1.26	Acting on ester bonds	IPR036866 (G3DSA:3.60.15.GENE3D	16,817	20,899	42,349	40,499	46,686									
Solyc05g055360	Mediator of RNA polymerase II transcription subunit 12 (AHRD V3.3 *** A0A0B0MWN8_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	24,703	23,327	29,432	26,178	28,286									
Solyc05g055370	LOW QUALITY:Transmembrane 9 superfamily member (AHRD V3.3 --* A0A199W436_ANACO)						PTHR37725 (PANTHER)	0,021	0,018	0,000	0,025	0,047									
Solyc05g055380	RNase L inhibitor protein-like protein (AHRD V3.3 *** AT5G10070.2)		P:GO:0006364	P:rRNA processing			IPR007177 (PFAM): IPR007209 (PFA	9,903	12,269	14,627	14,638	13,864									
Solyc05g055390	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DVK5_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	4,906	4,553	9,064	7,284	7,685									
Solyc05g055400	Cytochrome P450 (AHRD V3.3 *** D9MWM1_SOLTO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	304,868	181,590	0,478	1,179	0,700									
Solyc05g055420	Exostosin-2 (AHRD V3.3 *** A0A0B0N4C2_GOSAR)		P:GO:0006486; C:G(	P:protein glycosylation; C:integral component of membrane; F:tr			IPR029044 (G3DSA:3.90.550.GENE3	28,030	19,329	18,077	16,531	20,230									
Solyc05g055430	RAP release 2%2C galactose-binding-like domain protein%2C putative (DUF1997) (AHRD V3.3 *** AT5G04		C:GO:0009507	C:chloroplast			IPR018971 (PFAM): PTHR34131 (PAN	1,220	1,676	0,746	1,066	1,407									
Solyc05g055440	Histone H2B (AHRD V3.3 *** K4C2M0_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	123,881	126,109	110,393	118,182	114,132									
Solyc05g055450	RNA-binding Nova-1 (AHRD V3.3 *** A0A0B0MMT7_GOSAR)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR036612 (G3	77,735	91,745	69,263	66,071	71,766									
Solyc05g055470	NAC domain protein, (AHRD V3.3 *** A0A061FNG1_THECC)	NAC048	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	49,107	60,634	96,385	98,505	90,707									
Solyc05g055480	NAC (AHRD V3.3 *** J7H8R1_CESNO)	NAC049	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	18,952	20,210	13,470	11,320	13,814									
Solyc05g055500	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** D7LXI3_ARALL)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,099	0,000	0,022	0,000	0,000									
Solyc05g055510	Pectate lyase (AHRD V3.3 *** K4C2M7_SOLLC)		C:GO:0016021; F:G(	C:integral compone	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	4,521	5,093	2,193	3,595	2,287									
Solyc05g055530	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9IFU5_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR002554 (PIRSF): IPR011989 (G3D	5,767	6,199	2,201	1,960	2,511									
Solyc05g055540	Major facilitator superfamily protein (AHRD V3.3 *** AT2G39210.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR010658 (PFAM): G3DSA:1.20.125	0,179	0,222	0,000	0,092	0,024									
Solyc05g055550	TSA: Wollemia nobilis Ref_Wollemi_Transcript_5463_1093 transcribed RNA sequence (AHRD V3.3 *** A0A		P:GO:0009555	P:pollen development			IPR016621 (PFAM): PTHR35732 (PAN	5,897	7,629	4,352	5,607	7,493			0,776	0,008				up	
Solyc05g055563	APO protein 1 (AHRD V3.3 *-* W9RCK2_9ROSA)		F:GO:0003723	F:RNA binding			IPR023342 (PFAM): PTHR10388:SF5	1,018	0,600	0,071	0,025	0,023									
Solyc05g055567	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *-* A0A0B0PVB3_GOSAR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002937 (PFAM): IPR036188 (G3D	0,279	0,176	0,000	0,025	0,000									
Solyc05g055570	E3 ubiquitin-protein ligase RKP-like protein (AHRD V3.3 *-* G7JA93_MEDTR)		C:GO:0000151; C:G(	C:ubiquitin ligase complex; C:cytoplasm; P:ubiquitin-dependent p			PTHR13363:SF1 (PANTHER): PTHR1:	1,129	1,198	0,096	0,073	0,094									
Solyc05g055590	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *** A0A0B0PVB3_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding; F:oxidoreductase activity; P:o			IPR036388 (G3DSA:1.10.10.GENE3D	1,414	0,988	0,025	0,144	0,023									
Solyc05g055600	Vacuolar protein-sorting protein 33 (AHRD V3.3 *** B9HLH4_POPTR)		P:GO:0006904	P:vesicle docking involved in exocytosis			G3DSA:3.40.50.2060 (GENE3D): G3D	47,550	42,867	51,005	51,026	49,484									
Solyc05g055605	Vacuolar protein sorting-associated protein 33-like protein (AHRD V3.3 *-* W9RWW6_9ROSA)		P:GO:0006904	P:vesicle docking involved in exocytosis			IPR027482 (G3DSA:3.40.50.GENE3D	27,316	26,288	32,966	27,577	29,291									
Solyc05g055610	Met-10+ like family protein / kelch repeat-containing protein (AHRD V3.3 *** AT4G04670.1)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR015915 (G3	12,701	12,611	15,707	14,915	14,308									
Solyc05g055630	S-acyltransferase (AHRD V3.3 *** K4C2N9_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883:SF1	7,158	5,911	11,080	13,015	10,238									
Solyc05g055640	ARM repeat superfamily protein (AHRD V3.3 --* AT1G12930.1)							0,021	0,021	0,000	0,000	0,000									
Solyc05g055650	Quinohemoprotein ethanol dehydrogenase type-1 (AHRD V3.3 *-* A0A0B2Q0Y5_GLYSO)						IPR018391 (SMART): G3DSA:2.140.1	1,186	1,850	1,187	0,949	1,393									
Solyc05g055660	SP6A		F:GO:0008429; P:G(	F:phosphatidylethanolamine binding; P:regulation of flower deve			IPR008914 (PFAM): IPR036610 (G3D	0,000	0,054	0,051	0,022	0,047									
Solyc05g055680	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT5G16250.1)		C:GO:0016020	C:membrane			PTHR34124:SF2 (PANTHER): PTHR3	0,187	0,228	0,000	0,000	0,000									
Solyc05g055690	Protein transport protein Sec24-like family (AHRD V3.3 *** A0A151TQ51_CAJCA)		P:GO:0006886; P:G(	P:intracellular protein transport; P:endoplasmic reticulum to Gol			IPR006895 (PFAM): IPR029006 (G3D	0,336	0,295	0,096	0,072	0,094									
Solyc05g055700	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** I3SE71_MEDTR)		P:GO:0055114	P:oxidation-reduction process			PF16884 (PFAM): G3DSA:3.40.50.72(	14,613	13,061	43,551	41,274	40,866									
Solyc05g055710	L-ascorbate oxidase homolog (AHRD V3.3 *** ASOL_TOBAC)		F:GO:0005507; P:G(	F:copper ion binding; P:oxidation-reduction process			IPR008972 (G3DSA:2.60.40.GENE3D	0,000	0,000	0,000	0,000	0,023									
Solyc05g055730	Methylenetetrahydrofolate reductase (AHRD V3.3 *** K4C2P8_SOLLC)		F:GO:0004489; P:G(	F:methylenetetrahy	EC:1.5.1.2	Methylenetetrahydrol	IPR003171 (PFAM): IPR004621 (TIGF	1,845	2,192	0,072	0,022	0,142									
Solyc05g055740	Tyrosine phosphatase family protein (AHRD V3.3 *** A0A061EYJ9_THECC)		F:GO:0004725; C:G(	F:protein tyrosine p	EC:3.1.3.16; EC:3.1	Protein-serine/threon	IPR004861 (PFAM): IPR029021 (G3D	0,019	0,152	0,000	0,000	0,047									
Solyc05g055745	Seed linoleate 9S-lipoxygenase (AHRD V3.3 --* LOXX_SOYBN)							0,000	0,021	0,000	0,000	0,000									
Solyc05g055750	WRKY transcription factor 34	WRKY34	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,000	0,021	0,000	0,000	0,000									
Solyc05g055760	isopentenyl diphosphate isomerase	IPI2	F:GO:0004452; P:G(	F:isopentenyl-dipho	EC:5.3.3.2	Isopentenyl-diphosph	IPR011876 (PIRSF): IPR011876 (TIGI	29,224	31,484	16,930	11,897	14,467									
Solyc05g055770	Basic leucine zipper and W2 domain-containing 2 (AHRD V3.3 *** A0A0B0NBI1_GOSAR)		F:GO:0005515	F:protein binding			IPR003307 (SMART): IPR016021 (G3	285,968	292,113	392,261	374,594	357,338									
Solyc05g055780	DNA repair protein RecA, putative (AHRD V3.3 *** A0A072V2Z1_MEDTR)		F:GO:0003697; F:G(	F:single-stranded D	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013765 (PRINTS): IPR003593 (SM	5,743	5,905	4,210	4,138	4,240									
Solyc05g055790	Protein phosphatase-2c, putative (AHRD V3.3 *** B9RM68_RICCO)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART): IPR036457 (G3	4,978	6,859	16,474	23,592	19,663					0,522	0,012			up
Solyc05g055800	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G05840.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032861 (PF	6,828	13,204	1,698	2,777	3,149	0,977	0,001					up		
Solyc05g055810	Haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** G7KQL8_MEDTR)		F:GO:0016787	F:hydrolase activity			PTHR43611:SF2 (PANTHER): PTHR4	0,100	0,172	0,025	0,095	0,117									
Solyc05g055820	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** AT1G79790.4)		F:GO:0016787	F:hydrolase activity			PF13419 (PFAM): IPR006439 (TIGRF	0,299	0,541	0,246	0,212	0,280									
Solyc05g055830	R3H domain protein (AHRD V3.3 *** A0A072VLT6_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR001374 (SMART): IPR001374 (PF	7,549	7,289	10,189	11,372	10,524									
Solyc05g055840	Glycosyltransferase (AHRD V3.3 *** B6EWY8_LYCBA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	4,149	9,383	0,980	1,702	4,219	1,200	0,000	2,086	0,000			up	up	
Solyc05g055845	Glycosyltransferase (AHRD V3.3 *-* B6EWY8_LYCBA)		C:GO:0043231; F:G(	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl			G3DSA:3.40.50.2000 (GENE3D): PTH	2,210	3,767	0,494	0,942	1,707									
Solyc05g055850	resistance to phytophthora 1 (AHRD V3.3 *** AT2G48070.2)		C:GO:0009507; P:G(	C:chloroplast; P:positive regulation of hydrogen peroxide biosyn			mobidb-lite (MOBIDB_LITE): PTHR363	8,262	14,355	7,321	8,930	16,173	0,826	0,010	1,136	0,000			up	up	
Solyc05g055860	Kinase family protein (AHRD V3.3 *** D7L628_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,138	0,202	0,050	0,025	0,070									
Solyc05g055870	F-box protein family (AHRD V3.3 *** A0A151U5P0_CAJCA)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): PTHR32278 (PAN	61,902	78,851	23,344	26,131	25,459									
Solyc05g055880	NOP56-like pre RNA processing ribonucleoprotein (AHRD V3.3 *** AT5G27120.1)		F:GO:0030515; C:G(	F:snoRNA binding; C:box C/D snoRNP complex; C:small-subunit			IPR012976 (SMART): IPR002687 (PF	1,707	3,009	1,913	1,817	1,873									
Solyc05g055890	DNA-directed RNA polymerase subunit (AHRD V3.3 *** K4C2R4_SOLLC)		F:GO:0003676; P:G(	F:nucleic acid binding; P:transcription, DNA-templated; F:zinc io			IPR001222 (SMART): G3DSA:2.20.25	11,649	12,218	10,230	9,707	10,046									

Solyc05g055910	vacuolar sorting-associated protein (DUF946) (AHRD V3.3 *** AT3G04350.1)						IPR009291 (PFAM): IPR000008 (PFA	11,428	14,647	8,455	8,195	11,055									
Solyc05g055930	Cysteine-rich repeat secretory protein (AHRD V3.3 *** A0A0K9P487_ZOSMR)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane			IPR002902 (PFAM): IPR038408 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc05g055940	Myb-like transcription factor family protein (AHRD V3.3 *** G7KXD8_MEDTR)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	23,743	26,490	19,087	20,869	24,036									
Solyc05g055950	LOW QUALITY:Ankyrin repeat-containing-like protein (AHRD V3.3 *-* A0A061FUD1_THECC)		C:GO:0016020; P:G(	C:membrane; P:regulation of response to stimulus			IPR026961 (PFAM): PTHR24177 (PAN	0,000	0,018	0,050	0,047	0,000									
Solyc05g055960	Ankyrin repeat-containing-like protein (AHRD V3.3 *-* A0A061FUD1_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:regulation of defense res			IPR026961 (PFAM): PTHR24177 (PAN	0,080	0,018	0,050	0,000	0,024									
Solyc05g055970	Ankyrin repeat-containing-like protein (AHRD V3.3 *-* A0A061FUD1_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:regulation of defense res			IPR026961 (PFAM): PTHR24177 (PAN	0,057	0,142	0,071	0,094	0,070									
Solyc05g055980	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G12620.2)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	5,839	4,892	3,271	2,326	3,080									
Solyc05g055990	plasma membrane intrinsic protein 2.12	PIP2.12	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (TI(	0,171	0,474	0,000	0,000	0,000									
Solyc05g056000	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G19290.1)		C:GO:0016020	C:membrane			IPR029058 (G3DSA:3.40.50.GENE3D	107,871	98,364	155,633	168,697	163,200									
Solyc05g056010	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151RYX6_CAJCA)						IPR019557 (PFAM): PTHR45083 (PAN	29,419	27,274	42,741	38,849	39,981									
Solyc05g056020	V-type proton ATPase subunit G (AHRD V3.3 *** A0A199UG74_ANACO)		C:GO:0016471; F:G(	C:vacuolar proton-t	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:1.20.5.620 (GENE3D): IPR00!	13,093	16,744	51,253	53,772	52,478									
Solyc05g056030	Patatin (AHRD V3.3 *** K4C2S8_SOLLC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.1090.10 (GENE3D): IPR(	96,538	82,406	138,798	151,789	138,673									
Solyc05g056040	Auxin Response Factor 24	ARF24	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR003340 (SMAF ARF	53,420	86,733	24,379	21,922	32,045									
Solyc05g056050	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4C2T0_SOLLC)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460 GENE	28,986	116,577	17,095	29,338	61,080	2,036	0,000	1,832	0,000	0,783	0,013	up	up	up
Solyc05g056055	Ubiquitin-like protein (AHRD V3.3 *** A0A0B0NRY4_GOSAR)		F:GO:0005515	F:protein binding			IPR000626 (SMART): G3DSA:3.10.20	26,777	26,088	19,348	19,419	20,528									
Solyc05g056060	Cation transporter/ E1-E2 ATPase family protein (AHRD V3.3 --* AT4G11730.1)							0,000	0,043	0,025	0,025	0,023									
Solyc05g056070	photosystem 1 protein	TOMPS1	P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460 GENE	175,863	462,248	92,449	102,604	263,927	1,423	0,000	1,510	0,000			up	up	
Solyc05g056080	zinc finger B-box protein (AHRD V3.3 *** AT5G45410.5)		C:GO:0009507; P:G(	C:chloroplast; P:defense response to bacterium, incompatible ir			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,513	0,711	0,259	0,535	0,444									
Solyc05g056090	Transmembrane 70, mitochondrial (AHRD V3.3 *** A0A0B0MH90_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR009724 (PFAM): mobidb-lite (MOB	10,407	12,130	15,156	14,948	13,886									
Solyc05g056100	Double-stranded RNA-binding (AHRD V3.3 *** A0A118K5W9_CYNCS)		F:GO:0003723	F:RNA binding			IPR014720 (SMART): G3DSA:3.30.16	34,257	36,474	50,531	45,610	43,244									
Solyc05g056110	decapping 2 (AHRD V3.3 *** AT5G13570.1)		F:GO:0003723; F:G(	F:RNA binding; F:hydrolase activity; F:manganese ion binding			IPR007722 (SMART): G3DSA:3.90.79	28,333	18,201	26,448	25,792	24,324	-0,611	0,025					down		
Solyc05g056120	GATA transcription factor (AHRD V3.3 *** K4C2T6_SOLLC)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ior			IPR000679 (SMAF GATA	206,899	73,319	27,413	48,748	64,218	-1,472	0,000	1,224	0,000	0,831	0,001	down	up	up
Solyc05g056130	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (AHRD V3.3 *** A0A0V0IGM4_SO		F:GO:0004579; C:G(	F:dolichyl-diphosph	EC:2.4.1.119	Glycosyltransferases	IPR007676 (PFAM): IPR007676 (PAN	54,031	61,418	65,478	58,438	61,479									
Solyc05g056140	Zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 *** A0A061FV73_THECC)						IPR002035 (SMART): IPR001841 (SM	7,055	7,871	7,833	9,864	8,877									
Solyc05g056150	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (AH		P:GO:0000105; F:G(	P:histidine biosynth	EC:5.3.1.16	1-(5-phosphoribosyl)-	IPR006062 (PFAM): IPR013785 (G3D	5,155	5,446	6,165	6,531	6,789									
Solyc05g056160	Proteasome subunit beta type (AHRD V3.3 *** K4C2U0_SOLLC)		F:GO:0004298; C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000243 (PRINTS): IPR001353 (PF	82,696	90,906	132,853	133,164	127,934									
Solyc05g056170	phenylalanine ammonia-lyase 2	PAL	C:GO:0005737; P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l			G3DSA:1.20.200.10 (GENE3D): IPR0(	22,277	19,224	2,238	2,694	2,691									
Solyc05g056180	LOW QUALITY:Protein TIC 214 (AHRD V3.3 --* TI214_CITSI)							0,000	0,000	0,000	0,025	0,000									
Solyc05g056190	LOW QUALITY:ARM repeat superfamily protein (AHRD V3.3 --* AT1G24330.2)							0,057	0,124	0,168	0,117	0,093									
Solyc05g056200	Kinase family protein (AHRD V3.3 *** A9P9S2_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	2,938	3,644	6,150	6,442	5,310									
Solyc05g056210	Methyltransferase MT-A70 family protein isoform 1 (AHRD V3.3 *** A0A061FJR2_THECC)		F:GO:0003676; F:G(	F:nucleic acid binding; F:methyltransferase activity; P:methylati			IPR007757 (PFAM): mobidb-lite (MOB	87,531	82,243	108,978	112,612	110,373									
Solyc05g056220	Methyltransferase MT-A70 family protein isoform 1 (AHRD V3.3 *** A0A061FJR2_THECC)		F:GO:0003676; F:G(	F:nucleic acid binding; F:methyltransferase activity; P:methylati			IPR007757 (PFAM): mobidb-lite (MOB	178,799	125,653	119,854	121,293	122,900									
Solyc05g056230	Calreticulin (AHRD V3.3 *** G7KRL3_MEDTR)		F:GO:0005509; C:G(	F:calcium ion binding; C:endoplasmic reticulum; P:protein folding			IPR001580 (PRINTS): IPR001580 (PF	339,418	317,087	249,829	209,519	245,693									
Solyc05g056240	Acyl carrier protein (AHRD V3.3 *** K4C2U8_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR003231 (TIGRFAM): IPR036736 ((	127,228	141,547	125,256	143,741	130,120									
Solyc05g056250	Aspartate--tRNA ligase (AHRD V3.3 *** A0A0K9PY91_ZOSMR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:6.1.1.12	Aspartate--tRNA ligas	IPR002312 (PRINTS): G3DSA:3.30.93	44,851	42,831	56,960	53,695	52,974									
Solyc05g056255	Phenylalanyl-tRNA synthetase, putative (AHRD V3.3 *** B9SSI2_RICCO)		F:GO:0000049; F:G(	F:tRNA binding; F:p	EC:6.1.1.2	Phenylalanine--tRNA	IPR005121 (SMART): G3DSA:3.30.93	33,604	43,790	78,608	74,730	82,297									
Solyc05g056270	Isocitrate lyase (AHRD V3.3 *** A0A0K9PVT1_ZOSMR)		F:GO:0003824	F:catalytic activity			IPR040442 (G3DSA:3.20.20.GENE3D	69,783	72,349	154,074	147,219	168,448									
Solyc05g056290	biotin carboxylase carrier	bccp1	F:GO:0003729; C:G(	F:mRNA binding; C:U1 snRNP; P:mRNA splice site selection			IPR004882 (PFAM): mobidb-lite (MOB	34,673	40,919	40,989	38,481	38,759									
Solyc05g056295	Biotin carboxyl carrier acetyl-CoA carboxylase (AHRD V3.3 *** G7KRK6_MEDTR)		F:GO:0003989; P:G(	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR001249 (PRINTS): IPR000089 (PF	34,269	45,068	68,288	74,373	78,790									
Solyc05g056300	Thioredoxin (AHRD V3.3 *** A0A103YEZ4_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): G3DSA:3.40.30.1	45,648	53,682	29,359	31,220	41,777			0,507	0,001				up	
Solyc05g056310	T-complex protein 1 subunit gamma (AHRD V3.3 *** K4C2V5_SOLLC)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR027413 (G3	180,140	196,544	252,855	218,972	239,582									
Solyc05g056320	smr (Small MutS Related) domain-containing protein (AHRD V3.3 *** AT5G23520.2)		C:GO:0005737	C:cytoplasm			IPR013899 (SMART): IPR002625 (SM	63,654	76,321	70,336	71,901	78,927									
Solyc05g056325	Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial (AHRD V3.3 --* AT3G02660.2)							6,005	6,402	6,589	6,543	6,802									
Solyc05g056330	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q2QRE9_ORYSJ)						IPR027806 (PFAM): PTHR22930 (PAN	2,676	3,869	3,255	3,645	3,228									
Solyc05g056340	Peptidyl-prolyl cis-trans isomerase G isoform 1 (AHRD V3.3 *** A0A061FAS4_THECC)		P:GO:0016575	P:histone deacetylation			IPR013951 (PFAM): mobidb-lite (MOB	98,544	86,666	114,884	109,161	109,731									
Solyc05g056350	Cleft lip and palate transmembrane protein, putative (AHRD V3.3 *** B9RW92_RICCO)		C:GO:0016021	C:integral component of membrane			IPR008429 (PFAM): mobidb-lite (MOB	90,386	94,614	106,814	105,332	96,245									
Solyc05g056360	Protein Mei2 (AHRD V3.3 *-* A0A0U9HRM8_KLEFL)		F:GO:0003676	F:nucleic acid binding			IPR007201 (PFAM): IPR034865 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc05g056370	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9P3X9_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR001611 (PF	22,245	20,745	13,974	17,128	18,143									
Solyc05g056380	patatin-like phospholipase domain protein (AHRD V3.3 *** AT1G76980.1)						mobidb-lite (MOBIDB_LITE): PTHR341	0,249	1,277	0,022	0,101	0,024									
Solyc05g056390	10 kDa chaperonin (AHRD V3.3 *** CH10_BRANA)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding			IPR020818 (PRINTS): IPR020818 (SM	7,438	6,598	12,804	9,072	10,861									
Solyc05g056400	Protein disulfide-isomerase (AHRD V3.3 *** K4C2W4_SOLLC)		F:GO:0003756; P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	PR00421 (PRINTS): G3DSA:3.40.30.1	0,063	0,158	0,000	0,000	0,024									
Solyc05g056430	Small auxin up-regulated RNA56	SAUR56	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF1	0,123	0,135	0,097	0,070	0,046									
Solyc05g056440	Small auxin up-regulated RNA57	SAUR57	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	0,042	0,175	0,222	0,202	0,024									
Solyc05g056450	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT2G03200.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	0,138	0,217	0,094	0,097	0,024									
Solyc05g056460	arginine/glutamate-rich 1 protein (AHRD V3.3 *** AT5G13340.1)						IPR033371 (PFAM): mobidb-lite (MOB	38,476	29,902	41,791	32,419	34,569					-0,364	0,039			down
Solyc05g056470	ABC transporter family protein (AHRD V3.3 *** B9H498_POPTR)	ABCG14	F:GO:0005524; C:G(	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF	0,667	1,213	0,412	0,048	0,073									
Solyc05g056480	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** A0A068TWC7_COFCA)		F:GO:0016624	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR001017 (PFAM): G3DSA:3.40.50.9	38,693	21,359	27,862	24,898	35,764	-0,827	0,001					down		
Solyc05g056490	3(2),5-bisphosphate nucleotidase HAL2 (AHRD V3.3 *** A0A103XK20_CYNCS)		P:GO:0006790; F:G(	P:sulfur compound r	EC:3.1.3.7; EC:3.1.3	3'(2'),5'-bisphosphate	IPR000760 (PRINTS): G3DSA:3.30.54	0,398	0,373	0,482	0,630	0,474									
Solyc05g056500	U-box domain-containing protein 25 (AHRD V3.3 *** W9QUC2_9ROSA)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR003613 (SMART): IPR003613 (PF	0,021	0,205	0,186	0,096	0,165									
Solyc05g056510	Mucin-like protein (AHRD V3.3 *** Q8S2G4_ORYSJ)						IPR021036 (PFAM): PTHR35476:SF3	33,828	38,004	47,914	43,053	43,369									
Solyc05g056520	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G32170.1)		F:GO:0008757; P:G(	F:S-adenosylmethionine-dependent methyltransferase activity; I			IPR012901 (SMART): IPR012901 (PF	7,859	7,281	6,165	6,000	7,122									
Solyc05g056530	DDT domain-containing protein (AHRD V3.3 *** A0A103XFB7_CYNCS)		C:GO:0005634	C:nucleus			IPR018501 (SMART): IPR018501 (PF	5,161	6,314	2,834	2,446	3,691									
Solyc05g056540	Alcohol dehydrogenase (AHRD V3.3 *** M8AF04_TRIUA)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): IPR0	20,481	15,508	17,797	22,173	23,148									
Solyc05g056545	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9RHN6_RICCO)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): IPR0	23,701	17,814	20,924	27,603	29,168			0,477	0,004				up	
Solyc05g056560	hikeshi-like protein (AHRD V3.3 *** AT1G66080.1)						IPR008493 (PFAM): IPR031318 (PAN	8,213	7,078	10,704	10,281	10,062									
Solyc05g056570	Calcium dependent protein kinase (AHRD V3.3 *** Q93XI9_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (SMART): IPR000719 (SM	7,232	9,436	8,807	9,952	9,200									
Solyc05g056580	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G64030.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	127,930	126,953	122,849	117,459	112,866									
Solyc05g056595	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G08710.1)						IPR000408 (PRINTS): IPR009091 (G3	15,353	17,228	16,596	14,387	19,538									
Solyc05g056620	Ontology_term=GO:0046982	mc	F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	24,469	20,665	30,576	30,132	28,533									
Solyc06g005000	RING/U-box superfamily protein (AHRD V3.3 *** AT5G37560.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR001841 (SMART): IPR002867 (SM	14,501	11,839	8,142	5,763	7,398									
Solyc06g005040	LOW QUALITY:ABC transporter G family member (AHRD V3.3 *-* A0A0K9PPQ0_ZOSMR)		F:GO:0000166; C:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR19241:SF290 (PANTHER): PTHI	0,000	0,021	0,000	0,000	0,000									
Solyc06g005050	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR032675 (G3D	1,023	0,430	0,287	0,376	0,446									
Solyc06g005060	elongation factor 1-alpha		F:GO:0003746; F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004160 (PF	1987,018	2205,246	1566,937	1403,703	1473,287									
Solyc06g005070	Major facilitator superfamily protein (AHRD V3.3 *** AT1G68570.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,358	0,633	0,325	0,047	0,024									
Solyc06g005080	Vacuolar protein sorting-associated protein 18-like protein (AHRD V3.3 *** W9RNF4_9ROSA)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport			IPR000547 (PFAM): IPR007810 (PFA	90,834	90,520	109,639	117,558	111,403									
Solyc06g005090	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)						IPR004883 (PFAM LBD	0,000	0,021	0,000	0,000	0,000									
Solyc06g005100	Phosphatidylinositol transfer protein (AHRD V3.3 *** A0A103YF13_CYNCS)		F:GO:0005548; C:G(	F:phospholipid transporter activity; C:intracellular; P:phospholipi			IPR001666 (PRINTS): IPR001666 (PF	27,258	45,548	19,769	24,087	27,884									
Solyc06g005110	40S ribosomal protein S23 (AHRD V3.3 *** RS23_FRAAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR006032 (PFAM): G3DSA:2.40.50.1	22,988	17,941	12,115	10,777	10,490									
Solyc06g005130	Dof zinc finger protein (AHRD V3.3 *** W9RMR9_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,532	0,954	0,000	0,025	0,163									
Solyc06g005140	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H877_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	12,550	12,688	12,363	11,596	11,775									
Solyc06g005150	Ascorbate peroxidase (AHRD V3.3 *** Q52QQ4_SOLLC)	APX2	F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR002207 (PF	172,827	167,070	158,951	135,073	146,682									
Solyc06g005160	Ascorbate peroxidase (AHRD V3.3 *** Q9SMD3_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS): IPR002016 (PF	533,815	512,585	651,126	573,980	653,552									
Solyc06g005170	mitogen-activated protein kinase 3	mpk3	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	296,474	172,625	31,406	94,626	73,088			1,215	0,001	1,590	0,000		up	up
Solyc06g005180	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9GPB9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,000	0,000	0,000	0,050	0,000									
Solyc06g005190	CCR4-NOT transcription complex subunit 4 (AHRD V3.3 *** W9SKU7_9ROSA)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ubiquitin-protein transferase activity; C			IPR003954 (SMART): IPR013083 (G3	112,456	131,667	109,971	107,621	110,637									
Solyc06g005200	Ribonuclease P subunit p30 (AHRD V3.3 *-* A0A0B0MN27_GOSAR)		F:GO:0004540; P:G(	F:ribonuclease activity; P:tRNA processing			G3DSA:3.20.20.140 (GENE3D): IPR0(	8,887	9,252	11,871	12,781	11,769									
Solyc06g005210	LOW QUALITY:Cytochrome P450 like_TBP (AHRD V3.3 *-* O04892_TOBAC)							0,038	0,106	0,000	0,076	0,071									
Solyc06g005220	LOW QUALITY:Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	1,882	1,491	1,686	2,089	1,748									
Solyc06g005230	Kinase (AHRD V3.3 *** A0A061GXM4_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	46,768	33,619	29,194	27,687	32,487									
Solyc06g005240	Ankyrin repeat family protein (AHRD V3.3 *** AT1G07710.2)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR020683 (PF	0,000	0,019	0,000	0,000	0,000									
Solyc06g005250	Transmembrane protein, putative (AHRD V3.3 *** G7J5E4_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR12242 (PANTHER): PTHR12242	11,303	17,677	7,176	9,327	10,331	0,671	0,023					up		
Solyc06g005260	Glutaredoxin (AHRD V3.3 *** GLRX_SOLLC)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR014025 (PRINTS): IPR002109 (PF	89,713	113,772	141,800	132,500	120,549									
Solyc06g005270	histone H2A deubiquitinase (DUF3755) (AHRD V3.3 *** AT3G07565.3)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): IPR02	0,021	0,021	0,000	0,000	0,000									
Solyc06g005280	LOW QUALITY:Exocyst subunit exo70 family protein (AHRD V3.3 *** G7IUA9_MEDTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): G3DSA:1.20.128	0,276	0,041	0,022	0,949	0,070									
Solyc06g005290	UDP-galactose transporter 5 (AHRD V3.3 *** AT3G46180.1)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM): PTHR10778 (PAN	12,880	14,441	12,450	12,413	13,050									
Solyc06g005300	TOX high mobility group box family member 4-A, putative isoform 1 (AHRD V3.3 *** A0A061H046_THECC)						IPR012862 (PFAM): PTHR33431:SF2	0,814	0,196	0,558	2,444	1,836			1,661	0,004	2,079	0,001		up	up
Solyc06g005310	MYB transcription factor		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,019	0,021	0,000	0,000	0,000									
Solyc06g005320	MYB-related transcription factor (AHRD V3.3 *-* A0A059PRS8_SALMI)		F:GO:0003677	F:DNA binding			mobidb-lite (MOBIDB_LITE): PTHR106	0,019	0,018	0,000	0,000	0,000									
Solyc06g005330	R2R3MYB transcription factor 59	R2R3MYB59	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,118	0,136	0,000	0,000	0,024									
Solyc06g005350	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G59840.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	0,316	0,274	0,025	0,171	0,000									
Solyc06g005360	Actin-depolymerizing factor family protein (AHRD V3.3 *** B9HPK1_POPTR)		F:GO:0003779; C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymei			IPR002108 (SMART): IPR029006 (G3	216,860	236,742	302,060	311,036	271,729									
Solyc06g005370	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (AHRD V3.3 *** A0A0B0PFE1_GOSAR)		F:GO:0046537; F:G(	F:2,3-bisphosphogl	EC:5.4.2.1	Intramolecular transf	IPR017849 (G3DSA:3.40.720.GENE3I	48,399	37,115	61,334	60,390	56,478									
Solyc06g005380	F-box family protein (AHRD V3.3 *** B9H9Z2_POPTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001611 (PF	7,253	7,435	7,540	7,288	6,850									
Solyc06g005390	Histone H2B (AHRD V3.3 *** K4C323_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	3,271	2,987	8,589	7,995	6,625									
Solyc06g005410	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* G7KIF8_MEDTR)		P:GO:0007165; F:G(	P:signal transduction; F:ADP binding			G3DSA:3.40.50.300 (GENE3D): IPR02	8,605	12,298	10,412	10,115	9,914									
Solyc06g005420	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	34,981	41,741	36,466	27,900	31,100					-0,382	0,028			down
Solyc06g005430	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677; F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	9,433	12,148	5,475	3,402	4,321					-0,681	0,026			down
Solyc06g005435	heat shock protein 70 (AHRD V3.3 *** AT3G12580.1)		F:GO:0005524	F:ATP binding			IPR013126 (PRINTS): G3DSA:3.30.42	2,510	2,129	1,108	1,339	1,175									
Solyc06g005460	LOW QUALITY:Pectinesterase inhibitor (AHRD V3.3 *** PMEI_ACTDE)		P:GO:0043086; F:G(	P:negative regulation of catalytic activity; F:pectinesterase inhil			IPR006501 (SMART): IPR006501 (TI(	0,021	0,000	0,000	0,000	0,000									
Solyc06g005470	Metallothionein-like protein type 2 (AHRD V3.3 *** MT2Z_SOLLC)		F:GO:0046872	F:metal ion binding			IPR000347 (PFAM): PTHR33543:SF1	0,021	0,000	0,050	0,000	0,024									
Solyc06g005475	Outer envelope pore protein 16, chloroplastic (AHRD V3.3 *-* A0A0K9PH60_ZOSMR)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:vacuole; P:response			PTHR15371:SF2 (PANTHER): PTHR1!	4,310	3,471	5,098	6,079	5,122									
Solyc06g005480	Plant-specific domain TIGR01615 family protein (AHRD V3.3 *** G7KW44_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (I	12,924	16,971	9,552	14,234	11,392					0,577	0,018			up
Solyc06g005490	triosephosphate isomerase (AHRD V3.3 *** AT3G55440.1)		F:GO:0004807; P:G(	F:triose-phosphate	EC:5.3.1.1	Triose-phosphate iso	IPR000652 (TIGRFAM): IPR000652 (I	105,842	90,852	401,362	357,476	401,205									
Solyc06g005500	tomato protein kinase 1b	tpk1b	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	83,652	107,803	20,916	24,452	29,130									
Solyc06g005520	Protein kinase (AHRD V3.3 *** C6ZRV6_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	4,902	9,322	6,151	5,378	6,229	0,955	0,007					up		
Solyc06g005550	XH/XS domain-containing family protein (AHRD V3.3 *** B9HTH7_POPTR)		P:GO:0031047	P:gene silencing by RNA			IPR005380 (PFAM): IPR005379 (PFA	0,000	0,000	0,000	0,048	0,000									
Solyc06g005560	expansin9	EXPA9	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	3,259	3,317	0,599	0,798	0,629									
Solyc06g005570	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT2G32910.1)						IPR013989 (SMART): IPR013989 (PF	45,438	37,410	63,981	53,014	54,618									
Solyc06g005590	Telomere-binding family protein (AHRD V3.3 *** B9HPG4_POPTR)		F:GO:0003677	F:DNA binding			PTHR21717 (PAN MYB_related	28,700	23,677	21,885	20,390	19,469									
Solyc06g005600	Scarecrow-like transcription factor 11, putative isoform 1 (AHRD V3.3 *** A0A061GX35_THECC)		C:GO:0000176; P:G(	C:nuclear exosome (RNase complex); P:maturation of 5.8S rRN			mobidb-lite (MOBIDB_LITE): mobidb-lit	21,240	17,613	17,721	18,510	16,239									
Solyc06g005610	LOW QUALITY:RTL5-like protein (AHRD V3.3 *** F5C0G8_SOLCH)						IPR012552 (PFAM): mobidb-lite (MOB	0,177	0,713	0,075	0,000	0,000									
Solyc06g005620	zinc transporter		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR003689 (PFAM): PTHR11040 (PAN	0,019	0,018	0,000	0,072	0,024									
Solyc06g005630	RING/U-box superfamily protein (AHRD V3.3 *** AT3G55530.1)		C:GO:0012505; C:G(	C:endomembrane system; C:integral component of membrane; I			IPR001841 (SMART): IPR001841 (PF	8,245	8,337	5,729	5,782	5,612									
Solyc06g005640	Unknown protein (AHRD V3.3)							6,583	6,152	5,719	4,872	5,449									
Solyc06g005650	LOW QUALITY:E3 ubiquitin-protein ligase RING1-like protein (AHRD V3.3 *** A0A072V012_MEDTR)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR039525 (PFAM): mobidb-lite (MOB	199,964	118,262	84,869	174,303	100,108					1,041	0,000			up
Solyc06g005660	TRIO/F-actin-binding protein (AHRD V3.3 *** AT2G37070.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,060	0,025	0,000	0,000									
Solyc06g005670	Pumilio-like protein (AHRD V3.3 *** A0A0B0PMB1_GOSAR)		F:GO:0003723	F:RNA binding			IPR001313 (SMART): IPR001313 (PF	94,922	73,865	230,486	227,754	211,780									
Solyc06g005680	Two-component response regulator (AHRD V3.3 *** W9RUI2_9ROSA)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(G2-like	0,889	2,405	3,883	2,391	4,084	1,448	0,023					up		
Solyc06g005690	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A124SCR9_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,715	0,717	0,485	0,428	0,497									
Solyc06g005700	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061H009_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (I	1,135	1,056	1,473	1,406	1,342									
Solyc06g005710	Protein plastid transcriptionally active 16, chloroplastic (AHRD V3.3 *** PTA16_ARATH)						IPR016040 (PFAM): G3DSA:3.40.50.7	9,295	27,766	3,866	6,586	13,526	1,606	0,002	1,796	0,000	0,768	0,040	up	up	up
Solyc06g005720	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G29260.1),Pfam:PF13561						IPR002347 (PRINTS): IPR002347 (PF	2,804	2,149	2,362	2,623	2,673									
Solyc06g005730	LOW QUALITY:Pumilio, putative (AHRD V3.3 *-* B9SDY2_RICCO)		F:GO:0003723	F:RNA binding			IPR011989 (G3DSA:1.25.10.GENE3D	0,283	0,154	0,115	0,244	0,235									
Solyc06g005740	LOW QUALITY:Sulfhydryl oxidase 1 (AHRD V3.3 --* QSOX1_ARATH)							0,080	0,093	0,118	0,195	0,072									
Solyc06g005750	sterol 4-alpha-methyl-oxidase 2-1 (AHRD V3.3 *** AT1G07420.1)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR11863:SF9	1,867	1,959	4,177	3,778	3,249									
Solyc06g005755	O-methyltransferase family protein (AHRD V3.3 --* AT1G21130.2)							0,376	0,179	0,291	0,319	0,190									
Solyc06g005770	Non-specific lipid-transfer protein (AHRD V3.3 *** K4C359_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	18,710	36,969	2,309	1,766	2,974									
Solyc06g005780	Non-specific lipid-transfer protein (AHRD V3.3 *** A0A0V0GS93_SOLCH)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): G3DSA:1.10.11	0,000	0,021	0,000	0,000	0,000									
Solyc06g005790	DNA-directed RNA polymerase II subunit (AHRD V3.3 *** W9RUB8_9ROSA)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:2.7.7.6	DNA-directed RNA po	IPR005576 (PFAM): G3DSA:2.40.50.1	22,284	21,606	22,817	25,162	24,417									
Solyc06g005800	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0I8D9_SOLCH)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	19,869	21,307	21,085	19,951	19,666									
Solyc06g005810	Ras-related protein Rab11C (AHRD V3.3 *** RB11C_LOTJA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	6,669	9,246	5,289	5,389	4,326									

Solyc06g005820	Copper transporter, putative (AHRD V3.3 *** A0A061GWU0_THECC)		F:GO:0005375; C:G(	F:copper ion transmembrane transporter activity; C:integral com			IPR007274 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,022	0,000									
Solyc06g005840	Mitochondrial import inner membrane translocase subunit Tim10-like protein (AHRD V3.3 *** A0A0B0MQW2		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion complex			IPR004217 (PFAM): IPR035427 (G3D	1,398	1,533	1,746	1,335	1,016									
Solyc06g005850	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT5G59000.1)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	3,495	2,097	11,530	10,022	7,814			-0,564	0,031				down	
Solyc06g005860	Exosome complex component (AHRD V3.3 *** W9QJQ0_9ROSA)		C:GO:0000176; C:G(	C:nuclear exosome (RNase complex); C:cytoplasmic exosome (			IPR015847 (PFAM): IPR027408 (G3D	8,933	9,762	10,829	8,304	8,616									
Solyc06g005865	DNA-directed RNA polymerase (AHRD V3.3 *** G7KSV3_MEDTR)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:protein dimerization activity			IPR009025 (PFAM): IPR036603 (G3D	4,650	5,732	4,656	5,371	5,222									
Solyc06g005880	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			SM00365 (SMART): IPR000719 (SMA	1,626	4,187	0,583	0,718	0,874	1,384	0,012					up		
Solyc06g005890	DUF674 family protein (AHRD V3.3 *** G7L1B1_MEDTR)						IPR007750 (PFAM): IPR007750 (PAN	73,760	64,154	34,055	36,570	34,364									
Solyc06g005910	Tubulin beta chain (AHRD V3.3 *** M1BVE7_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	0,566	0,851	0,118	0,145	0,094									
Solyc06g005930	Protein SENSITIVITY TO RED LIGHT REDUCED 1 (AHRD V3.3 *-* SRR1_ARATH)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM): IPR036397 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc06g005940	Protein disulfide-isomerase (AHRD V3.3 *** K4C376_SOLLC)		F:GO:0003756; P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	PR00421 (PRINTS): G3DSA:3.40.30.1	129,647	129,977	630,315	886,562	599,134					0,495	0,011			up
Solyc06g005950	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** G7K6A4_MEDTR)		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003593 (SMART): IPR000642 (PF	55,090	49,023	85,935	84,989	86,077									
Solyc06g005960	dentin sialophosphoprotein (AHRD V3.3 *-* AT1G07330.2)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,049	0,197	0,141									
Solyc06g005970	Glycosyl hydrolase family protein (AHRD V3.3 *** AT3G47000.1)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR036881 (G3	39,324	35,156	55,099	47,402	55,296									
Solyc06g005980	Anthranilate synthase (AHRD V3.3 *** A0A0K9NQE9_ZOSMR)		P:GO:0009058	P:biosynthetic process			IPR019999 (PRINTS): IPR006805 (PF	0,551	0,802	0,433	1,204	0,842									
Solyc06g005990	Helicase, putative (AHRD V3.3 *** B9S370_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:RI	EC:3.6.1.15	Nucleoside-triphosph	IPR012961 (SMART): IPR014001 (SM	58,643	46,073	70,165	73,188	69,723									
Solyc06g006000	Maternal effect embryo arrest 59 (AHRD V3.3 *** A0A061GXA8_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,692	2,193	0,312	0,505	1,169	1,672	0,001					up		
Solyc06g006010	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT5G46330.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): IPR000719 (SM	0,716	1,716	0,328	0,487	0,402	1,278	0,039					up		
Solyc06g006020	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	0,063	0,386	0,000	0,150	0,142									
Solyc06g006030	Receptor-like kinase (AHRD V3.3 *-* A0A072TRW0_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,000	0,041	0,000	0,000	0,000									
Solyc06g006040	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR000719 (SMA	0,000	0,158	0,000	0,000	0,000									
Solyc06g006050	Receptor-kinase, putative (AHRD V3.3 *** B9SZK5_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	0,000	0,039	0,000	0,000	0,048									
Solyc06g006057	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *-* AT5G46330.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	0,021	0,171	0,025	0,100	0,047									
Solyc06g006080	thiamine biosynthesis protein ThiC		P:GO:0009228; F:G(	P:thiamine biosynthetic process; F:carbon-carbon lyase activity			IPR025747 (PFAM): IPR038521 (G3D	728,490	546,813	204,584	94,097	166,937					-1,118	0,000			down
Solyc06g006090	LOW QUALITY:JOSEPHIN-like protein, putative (AHRD V3.3 *-* A0A061GWC4_THECC)						mobidb-lite (MOBIDB_LITE): PTHR343	10,321	11,832	1,151	0,329	0,725									
Solyc06g006100	Anthranilate synthase (AHRD V3.3 *** A0A0K9NQE9_ZOSMR)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.1.3.27	Anthranilate synthase	IPR019999 (PRINTS): IPR015890 (PF	168,243	155,156	1431,918	1506,743	1338,621									
Solyc06g006110	vacuolar cation/proton exchanger (AHRD V3.3 *** AT1G55720.2)		P:GO:0006816; F:G(	P:calcium ion transport; F:calcium:proton antiporter activity; C:ir			IPR004837 (PFAM): G3DSA:1.20.142	0,386	1,006	0,118	0,203	0,117									
Solyc06g007110	Smr domain-containing protein, putative (AHRD V3.3 *** A0A061GWE6_THECC)						IPR002625 (SMART): IPR013899 (SM	36,100	33,335	28,001	28,250	28,813									
Solyc06g007120	PI-phospholipase C4		F:GO:0004435; P:G(	F:phosphatidylinosit	EC:3.1.4.11; EC:3.1.	Phosphoinositide phc	IPR001192 (PRINTS): IPR000008 (SM	3,569	4,671	1,111	1,570	1,480									
Solyc06g007130	omega-3 fatty acid desaturase-3	LeFAD3	P:GO:0006629; F:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR021863 (PFAM): IPR005804 (PFA	4,446	3,467	0,908	0,435	0,709									
Solyc06g007140	Omega-3 fatty acid desaturase		P:GO:0006629; F:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR021863 (PFAM): IPR005804 (PFA	1,113	0,962	8,986	7,055	7,825									
Solyc06g007150	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G58370.3)		F:GO:0005525	F:GTP binding			IPR006073 (PFAM): IPR019987 (TIGF	6,586	6,370	9,206	10,750	9,386									
Solyc06g007160	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial (AHRD V3.3 *-* INDA1_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			G3DSA:3.50.50.100 (GENE3D): PTHR	0,080	0,799	0,022	0,000	0,142									
Solyc06g007165	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial (AHRD V3.3 *** INDA1_SOLTU)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00368 (PRINTS): IPR023753 (PFA	0,059	0,991	0,047	0,000	0,188									
Solyc06g007170	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFA	3,372	2,285	0,344	0,242	0,235									
Solyc06g007180	asparagine synthetase 1	as1	F:GO:0004066; P:G(	F:asparagine synth	EC:6.3.5.4	Asparagine synthase	IPR006426 (TIGRFAM): IPR014729 ((	2,734	6,557	2,612	5,951	5,863			1,155	0,014	1,183	0,005		up	up
Solyc06g007190	Protein phosphatase 2C (AHRD V3.3 *** Q3V656_SOLTU)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	3,670	1,629	0,756	1,723	0,634									
Solyc06g007200	Protein phosphatase 2C (AHRD V3.3 *** Q3V656_SOLTU)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001714 (PRINTS): IPR001932 (SM	82,007	83,439	78,329	71,305	71,243									
Solyc06g007210	60S ribosomal protein L41 (AHRD V3.3 -** RL41_ARATH)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR007836 (PFAM): mobidb-lite (MOB	68,894	83,630	59,577	55,200	55,710									
Solyc06g007220	60S ribosomal protein L41 (AHRD V3.3 -** RL41_ARATH)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR007836 (PFAM): mobidb-lite (MOB	23,765	29,557	18,597	15,125	14,927									
Solyc06g007240	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** A0A0B2PCD3_GLYSO)		F:GO:0051087	F:chaperone binding			IPR000626 (PFAM): IPR036533 (G3D	1,865	1,712	0,215	0,201	0,211									
Solyc06g007250	Leucine-rich repeat containing protein, putative (AHRD V3.3 *** B9SKU7_RICCO)		F:GO:0005515	F:protein binding			SM00364 (SMART): IPR000626 (SMA	24,213	21,234	33,105	29,952	31,979									
Solyc06g007260	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,312	1,214	1,265	1,291	1,485									
Solyc06g007270	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	1,188	1,420	1,087	1,413	1,036									
Solyc06g007280	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	2,304	1,860	1,764	2,286	1,530									
Solyc06g007300	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	4,794	3,694	2,857	2,982	3,104									
Solyc06g007310	TatD family (AHRD V3.3 *** A0A103XH13_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			G3DSA:3.20.20.140 (GENE3D): IPR0(	14,434	13,889	22,564	22,066	22,115									
Solyc06g007320	Ubiquitin activating enzyme E1 (AHRD V3.3 *** G1FER0_CAMSI)		P:GO:0006464; F:G(	P:cellular protein modification process; F:ubiquitin-like modifier a			IPR000011 (PRINTS): IPR018965 (SM	143,767	132,998	203,890	205,552	190,913									
Solyc06g007330	Gamma interferon inducible lysosomal thiol reductase (AHRD V3.3 *** G7J0S1_MEDTR)						IPR004911 (PFAM): IPR004911 (PAN	3,538	3,214	5,151	3,377	4,975									
Solyc06g007340	Gamma interferon inducible lysosomal thiol reductase (AHRD V3.3 *** G7J0S1_MEDTR)						G3DSA:3.40.30.10 (GENE3D): IPR00	39,791	41,642	66,373	64,302	66,175									
Solyc06g007350	Protein phosphatase 2C family protein (AHRD V3.3 *** AT2G30170.1)		F:GO:0003824	F:catalytic activity			IPR001932 (SMART): IPR036457 (G3	9,454	13,410	17,075	16,395	23,401			0,453	0,027				up	
Solyc06g007355	LOW QUALITY:Protein kinase (AHRD V3.3 *-* A0A0K9NJ18_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,337	0,375	0,679	0,518	0,545									
Solyc06g007360	40S ribosomal protein S4 (AHRD V3.3 *** RS4_SOLTU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR005824 (SMART): IPR005824 (PF	72,042	75,270	54,107	46,102	48,827									
Solyc06g007370	LOW QUALITY:6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** AT2G30230.1)						IPR025322 (PFAM): mobidb-lite (MOB	0,377	0,483	0,071	0,000	0,093									
Solyc06g007380	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamilyprotein (AHRD V3.3 *** ,		F:GO:0008168; C:G(	F:methyltransferase activity; C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D): PTHR	0,060	0,039	0,000	0,022	0,000									
Solyc06g007390	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4B8_RICCO)						IPR004883 (PFAM_LBD	0,019	0,021	0,000	0,000	0,024									
Solyc06g007430	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IRP8_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	82,697	63,890	63,226	65,088	66,024									
Solyc06g007440	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C3C6_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR004041 (PF	2,740	18,230	0,610	0,608	1,432	2,759	0,000					up		
Solyc06g007460	Epidermal patterning factor-like protein (AHRD V3.3 *** G7K0R6_MEDTR)		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): IPR039455 (PANTH	0,871	0,824	0,571	0,291	0,423									
Solyc06g007465	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (AHRD V3.3 --* HMDH1_ARATH)							0,000	0,000	0,022	0,025	0,000									
Solyc06g007470	40S ribosomal protein S26-like protein (AHRD V3.3 *** I3S2G2_MEDTR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR038551 (G3DSA:3.30.1740.GENE	499,340	493,225	282,885	261,037	262,685									
Solyc06g007480	INO80 complex subunit C (AHRD V3.3 *** A0A151QTB1_CAJCA)		P:GO:0006338; C:G(	P:chromatin remodeling; C:Ino80 complex			IPR013272 (SMART): IPR013272 (PF	10,441	8,180	12,444	12,020	12,249									
Solyc06g007490	Lipase, GDSL (AHRD V3.3 *** A0A124S9Z4_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,058	0,037	0,050	0,070	0,000									
Solyc06g007510	Ubiquitin-conjugating enzyme E2-like protein (AHRD V3.3 *** Q2PYY4_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART): IPR000608 (PFA	888,703	794,491	900,353	926,463	823,608									
Solyc06g007515	Disease resistance protein (TIR-NBS class) (AHRD V3.3 --* AT1G17615.1)							59,103	48,539	56,090	65,114	53,368									
Solyc06g007520	60S ribosomal protein L10 (AHRD V3.3 *** RL10_SOLME)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036920 (G3DSA:3.90.1170.GENE	153,678	163,806	204,230	185,476	181,046									
Solyc06g007530	LOW QUALITY:B3 domain-containing protein (AHRD V3.3 *** M8AKJ2_AEGTA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF_B3	6,891	6,793	4,305	3,380	4,162									
Solyc06g007540	Cytochrome b-c1 complex subunit 8 (AHRD V3.3 *** QCR8_SOLTU)		C:GO:0005743; F:G(	C:mitochondrial inne	EC:1.1.2; EC:1.1.2.2	Acting on diphenols a	IPR020101 (PFAM): IPR020101 (PAN	42,877	41,663	87,128	83,418	79,960									
Solyc06g007550	LOW QUALITY:UV-B-induced protein, chloroplastic (AHRD V3.3 *** A0A199VW76_ANACO)						IPR008479 (PFAM): PTHR31808:SF2	0,000	0,000	0,049	0,125	0,096									
Solyc06g007560	UV-B-induced protein, chloroplastic (AHRD V3.3 *** A0A199VW76_ANACO)						IPR008479 (PFAM): IPR038925 (PAN	0,042	0,019	0,000	0,000	0,000									
Solyc06g007570	40S ribosomal protein S8 (AHRD V3.3 *** K4C3D8_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.10.450 (GENE3D): G3DS	58,854	63,847	81,861	72,061	72,067									
Solyc06g007580	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (F	9,822	13,178	8,929	10,302	17,856			0,994	0,000				up	
Solyc06g007590	Histidine triad family protein (AHRD V3.3 *** Q672P8_SOLLC)		F:GO:0003824	F:catalytic activity			IPR001310 (PRINTS): IPR036265 (G3	11,682	13,050	16,062	14,923	15,893									
Solyc06g007600	serine-rich protein-like protein (AHRD V3.3 --* AT3G56500.1)						PTHR33132:SF29 (PANTHER): PTHR:	2,584	2,002	0,807	0,774	0,610									
Solyc06g007610	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DM50_THECC)						IPR029068 (G3DSA:3.10.180.GENE3I	1,743	1,534	0,100	0,194	0,304									
Solyc06g007620	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT3G07470.3)						IPR007493 (PFAM): IPR036758 (G3D	61,857	23,527	28,250	49,336	44,101	-1,368	0,000	0,639	0,000	0,806	0,000	down	up	up
Solyc06g007630	2Fe-2S ferredoxin-like protein (AHRD V3.3 *** Q9SRR8_ARATH)		F:GO:0009055; F:G(	F:electron transfer activity; F:iron-sulfur cluster binding			IPR012675 (G3DSA:3.10.20.GENE3D	33,451	33,004	53,482	44,768	45,624									
Solyc06g007640	Protein FRIGIDA-like protein (AHRD V3.3 *** A0A0B0PA17_GOSAR)		P:GO:0009908; P:G(	P:flower development; P:cell differentiation			IPR012474 (PFAM): mobidb-lite (MOB	96,099	102,162	86,894	83,126	87,179									
Solyc06g007660	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *-* AT5G19480.4)		F:GO:0008134; C:G(	F:transcription factor binding; C:mediator complex; P:positive re			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,490	10,260	16,022	18,572	13,869									
Solyc06g007670	60S ribosomal protein L5 (AHRD V3.3 *** RL5_CUCSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR005485 (PRINTS): G3DSA:3.30.42	280,850	315,684	299,594	288,037	267,721									
Solyc06g007680	F-box/LRR protein (AHRD V3.3 *** A0A072TPF2_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001810 (PF	8,335	7,683	9,825	7,705	9,962									
Solyc06g007690	WD-40 repeat family protein / beige-like protein (AHRD V3.3 --* AT2G45540.6)							0,962	1,072	1,302	1,108	1,057									
Solyc06g007700	Peroxisomal membrane protein 13 (AHRD V3.3 *** A0A0B2RMJ5_GLYSO)		C:GO:0005777; C:G(	C:peroxisome; C:integral component of membrane; P:protein im			mobidb-lite (MOBIDB_LITE): mobidb-lit	125,324	193,673	146,929	143,923	144,228									
Solyc06g007710	Mitochondrial import receptor subunit tom40, putative (AHRD V3.3 *** B9RGH8_RICCO)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:protein transmembrane tran			IPR027246 (PFAM): IPR023614 (G3D	30,830	36,673	61,837	60,363	55,527									
Solyc06g007720	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT2G41720.3)							0,101	0,161	0,068	0,095	0,094									
Solyc06g007730	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	0,573	0,333	0,269	0,311	0,233									
Solyc06g007740	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,691	2,109	2,273	2,189	2,783									
Solyc06g007760	YCF54 (AHRD V3.3 *** AT5G58250.1)						IPR038409 (G3DSA:3.30.70.GENE3D	27,079	55,932	27,448	32,246	50,818	1,074	0,000	0,885	0,000			up	up	
Solyc06g007770	ER lumen protein retaining receptor family protein (AHRD V3.3 *** AT3G25160.1)		P:GO:0006621; C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS): IPR000133 (PF	1,986	2,023	0,655	0,530	0,635									
Solyc06g007780	Nuclear transport factor 2 family protein with RNA binding domain, putative isoform 2 (AHRD V3.3 *** A0A06		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	16,507	13,532	13,125	11,664	11,309									
Solyc06g007790	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *-* G7L045_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR36760 (PANTHER)	0,161	0,138	0,115	0,073	0,144									
Solyc06g007800	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion complex			IPR039175 (PANTHER): PTHR14110:	32,151	26,532	49,808	46,504	48,340									
Solyc06g007810	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	0,778	0,324	0,115	0,120	0,024									
Solyc06g007820	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	0,333	0,169	0,112	0,050	0,235									
Solyc06g007850	Pentatricopeptide repeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	7,561	6,538	3,542	3,348	3,626									
Solyc06g007860	LOW QUALITY:S-norcoclaurine synthase (AHRD V3.3 *** A0A0B2SNQ7_GLYSO)		P:GO:0006952	P:defense response			IPR023393 (G3DSA:3.30.530.GENE3I	0,430	0,333	0,118	0,000	0,071									
Solyc06g007870	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DV39_THECC)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): IPR013083 (G3	18,235	18,830	23,343	22,595	20,389									
Solyc06g007880	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G13100.9)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): PF13920 (PFAM	0,555	0,589	0,415	0,169	0,446									
Solyc06g007890	Gibberellin-regulated family protein (AHRD V3.3 *** AT1G74670.1)						IPR003854 (PFAM): PTHR23201 (PAI	0,059	0,136	0,000	0,000	0,000									
Solyc06g007910	Gibberellin-regulated family protein (AHRD V3.3 *** AT1G74670.1)						IPR003854 (PFAM): PTHR23201:SF4	1,697	1,887	0,629	0,553	0,328									
Solyc06g007920	Gibberellin-regulated family protein (AHRD V3.3 *** AT1G74670.1)						IPR003854 (PFAM): PTHR23201 (PAI	0,300	0,708	0,000	0,000	0,000									
Solyc06g007930	Cytochrome b5 (AHRD V3.3 *** CYB5_TOBAC)		C:GO:0005789; F:G(	C:endoplasmic retic	EC:1.7.1.1; EC:1.7.9	Nitrate reductase (N/	IPR001199 (PRINTS): IPR001199 (SM	28,483	34,300	82,931	84,543	76,015									
Solyc06g007940	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G48800.1)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0:	0,536	0,700	0,606	0,694	0,447									
Solyc06g007960	Caffeic O-methyltransferase (AHRD V3.3 *** A0A068FLE8_PUNGR)		F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity			G3DSA:3.40.50.150 (GENE3D): IPR0:	0,102	0,059	0,000	0,000	0,000									
Solyc06g007970	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G48850.1)		F:GO:0005515	F:protein binding			IPR019734 (PFAM): IPR011990 (G3D	0,077	0,118	0,631	0,758	0,353									
Solyc06g007980	UDP-glucose:sterol 3-O-glucosyltransferase (AHRD V3.3 *** Q8H9B4_PANGI)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:transferase activity, trans			IPR004276 (PFAM): G3DSA:3.40.50.2	207,812	186,777	80,302	76,950	87,234									
Solyc06g007990	transmembrane protein (AHRD V3.3 *** AT4G13220.1)		C:GO:0016021	C:integral component of membrane			PTHR36777 (PANTHER)	3,702	5,669	6,655	5,350	6,446									
Solyc06g008010	Mediator of RNA polymerase II transcription subunit 18 (AHRD V3.3 *** A0A0S2LKM0_REHGL)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR019095 (PANTHER)	11,718	15,360	17,599	14,766	16,692									
Solyc06g008020	HIT zinc finger protein (AHRD V3.3 *** A0A072VLZ0_MEDTR)		F:GO:0046872	F:metal ion binding			IPR007529 (PFAM): G3DSA:3.30.60.1	2,608	3,008	3,835	3,935	3,861									
Solyc06g008030	bHLH transcription factor 041	PIF1b	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF_bHLH	9,605	7,210	12,690	12,276	10,353									
Solyc06g008040	CLIP-associating 1 (AHRD V3.3 *** A0A0B0MGS3_GOSAR)		F:GO:0005515	F:protein binding			IPR034085 (SMART): IPR024395 (PF	97,072	67,851	93,242	98,652	90,192									
Solyc06g008050	Flavin-containing monooxygenase (AHRD V3.3 *** D2IGV3_SOLLC)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.:	Flavin-containing mo	IPR000103 (PRINTS): PR00368 (PRIN	0,940	1,877	27,267	21,881	21,922									
Solyc06g008065	cullin 1 (AHRD V3.3 *-* AT4G02570.4)		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			IPR001373 (PFAM): G3DSA:1.20.131	0,021	0,000	0,025	0,000	0,000									
Solyc06g008090	Myosin (AHRD V3.3 *** W5ZTD6_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:t	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR001609 (SM	51,333	41,228	50,444	48,708	46,045									
Solyc06g008100	Unknown protein (AHRD V3.3)							0,101	0,101	0,046	0,022	0,047									
Solyc06g008110	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G20330.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	62,858	54,866	71,448	65,977	69,969									
Solyc06g008120	Mitochondrial import receptor subunit TOM22 (AHRD V3.3 *** A0A0K9PK98_ZOSMR)		C:GO:0005741; P:G(	C:mitochondrial outer membrane; P:intracellular protein transpor			IPR005683 (PFAM): IPR017411 (PIRS	45,449	57,812	29,745	27,008	29,788									
Solyc06g008130	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9QWZ0_9ROSA)		F:GO:0018024	F:histone-lysine N-r	EC:2.1.1.43	Histone-lysine N-met	IPR018848 (PFAM): G3DSA:1.10.8.85	28,236	28,182	39,864	47,127	40,897									
Solyc06g008150	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						IPR015410 (PFAM): mobidb-lite (MOB	18,393	19,373	24,321	22,133	20,275									
Solyc06g008160	Protein FLUORESCENT IN BLUE LIGHT, chloroplastic (AHRD V3.3 *** FLU_ARATH)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13424 (PFAM	6,436	8,096	10,109	10,454	11,396									
Solyc06g008170	50S ribosomal protein L14 (AHRD V3.3 *** A0A0K9PMD0_ZOSMR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000218 (SMART): IPR000218 (PF	135,997	153,395	169,982	150,910	150,507									
Solyc06g008180	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 *** AT1G09900.1)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	8,576	9,917	21,729	19,477	19,620									
Solyc06g008190	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SVN3_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	1,806	2,090	1,210	1,635	1,577									
Solyc06g008195	3-ketoacyl-CoA synthase 7 (AHRD V3.3 --* AT1G71160.1)							0,697	0,712	0,358	0,562	0,306									
Solyc06g008200	Myb-like transcription factor family protein (AHRD V3.3 *** G7KXD8_MEDTR)		F:GO:0003677	F:DNA binding			IPR025756 (PFAM_G2-like	26,398	25,993	38,108	38,191	34,744									
Solyc06g008210	breast cancer associated RING 1 (AHRD V3.3 *** AT1G04020.1)		P:GO:0006281; F:G(	P:DNA repair; F:metal ion binding			IPR001841 (SMART): IPR001357 (SM	5,319	4,903	1,270	1,391	1,390									
Solyc06g008220	DAG protein (AHRD V3.3 *** A0A0K9Q0F0_ZOSMR)		P:GO:0016554	P:cytidine to uridine editing			mobidb-lite (MOBIDB_LITE): PTHR313	29,010	33,841	34,548	28,923	38,587									
Solyc06g008230	Tetratricopeptide repeat 7A (AHRD V3.3 *** A0A0B0PQU8_GOSAR)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	27,049	18,877	59,535	63,841	55,953									
Solyc06g008235	NDH-dependent cyclic electron flow 5 (AHRD V3.3 --* AT1G55370.2)							0,019	0,018	0,047	0,045	0,024									
Solyc06g008240	ROP-interactive CRIB motif protein (AHRD V3.3 *** A0A072U2K9_MEDTR)						IPR000095 (SMART): IPR000095 (PF	0,000	0,059	0,000	0,000	0,000									
Solyc06g008250	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G28550.1)		F:GO:0005096; C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (SMART): G3DSA:1.10.8.2	11,840	9,789	27,062	28,430	25,923									
Solyc06g008260	60S ribosomal protein L14, putative (AHRD V3.3 *** B9SS61_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR002784 (PFAM): IPR014722 (G3D	150,427	166,418	134,950	116,824	126,347									
Solyc06g008265	Leucine-rich repeat receptor-like protein kinase family protein, putative (AHRD V3.3 *** A0A061GI31_THEC(		F:GO:0005515	F:protein binding			IPR003591 (SMART): SM00365 (SMA	0,082	1,727	0,674	1,281	0,841									
Solyc06g008290	Vacuolar protein sorting-associated protein 2 homolog 2 (AHRD V3.3 *** VPS2B_ARATH)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): mobidb-lite (MOB	10,808	19,963	18,075	17,008	15,981	0,911	0,008					up		
Solyc06g008295	Calcium-dependent phosphotriesterase superfamily protein (AHRD V3.3 --* AT3G57020.2)							0,059	0,059	0,296	0,605	0,473									
Solyc06g008300	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding			SM00365 (SMART): IPR003591 (SMA	1,965	12,162	47,651	96,061	70,812	2,649	0,000	0,569	0,001	1,013	0,000	up	up	up
Solyc06g008310	WD40 repeat-containing protein (AHRD V3.3 *** A0A103YA92_CYNCS)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	29,798	30,803	47,961	44,253	45,688									
Solyc06g008315	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072UAN6_MEDTR)						IPR025558 (PFAM): mobidb-lite (MOB	0,042	0,000	0,025	0,045	0,047									
Solyc06g008320	Casein kinase, putative (AHRD V3.3 *-* B9SV24_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	71,619	54,391	51,550	46,573	47,368									
Solyc06g008330	Protein kinase (AHRD V3.3 *** Q40547_TOBAC)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phosphc	IPR000961 (SMART): IPR000719 (SM	12,560	10,353	20,700	23,239	18,285									
Solyc06g008340	Adaptin ear-binding coat-associated protein 1 (AHRD V3.3 *** A0A072VLL1_MEDTR)		P:GO:0006897; C:G(	P:endocytosis; C:membrane			IPR012466 (PFAM): IPR011993 (G3D	17,267	17,541	44,535	44,273	40,693									
Solyc06g008350	Serine/threonine-protein kinase 19 (AHRD V3.3 *** A0A199URZ6_ANACO)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR018865 (PFAM): mobidb-lite (MOB	11,075	10,735	26,873	30,516	25,072									

Solyc06g008360	NAC domain protein, (AHRD V3.3 *** A0A061DNM9_THECC)	NAC050	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	1,086	1,061	2,624	2,693	2,420									
Solyc06g008380	Mi1.4		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	0,094	0,083	0,025	0,000	0,047									
Solyc06g008390	NBS-LRR resistance protein-like protein (AHRD V3.3 *-* A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding				0,316	0,569	0,072	0,288	0,094									
Solyc06g008400	Mi1.5		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,040	0,117	0,000	0,000	0,023									
Solyc06g008420	LOW QUALITY:L-aspartate oxidase (AHRD V3.3 *-* AT5G14760.1)		F:GO:0008734: P:G(	F:L-aspartate oxida	EC:1.4.3.16: EC:1.4.	L-aspartate oxidase; L-amino-acid oxidase		0,080	0,043	0,050	0,000	0,046									
Solyc06g008450	Mi1.6		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	9,347	12,670	2,406	2,212	3,318									
Solyc06g008470	Protein TRANSPORT INHIBITOR RESPONSE 1 (AHRD V3.3 *-* TIR1_ARATH)						IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,022	0,000									
Solyc06g008490	Transcription factor jumonji family protein (AHRD V3.3 *** A0A072VM93_MEDTR)		P:GO:0006338: F:G(	P:chromatin remodeling: F:methyltransferase activity: P:methyla			IPR003347 (SMART): IPR003349 (SM	20,160	13,970	24,032	23,758	22,806									
Solyc06g008500	Ankyrin repeat domain protein, putative (AHRD V3.3 *** B9T1B3_RICCO)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	4,030	4,076	1,088	1,496	2,301			1,074	0,034				up	
Solyc06g008510	CDT1-like protein a, chloroplastic (AHRD V3.3 *** A0A0B0P9Z8_GOSAR)		P:GO:0000076: P:G(	P:DNA replication checkpoint: P:mitotic cytokinesis: C:kinetoch			IPR014939 (SMART): IPR032054 (PF	3,379	3,449	6,819	4,561	5,874									
Solyc06g008520	Bet1-like SNARE 1-1 family protein (AHRD V3.3 *** B9H8J7_POPTR)		P:GO:0015031: C:G(	P:protein transport; C:integral component of Golgi membrane			IPR039897 (PANTHER): PTHR12791:	43,342	37,105	40,080	41,443	37,660									
Solyc06g008530	Myosin XI, putative (AHRD V3.3 *** B9S7I4_RICCO)		F:GO:0003774: F:G(	F:motor activity: F:ı	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR000048 (SM	2,311	2,274	1,719	1,528	1,714									
Solyc06g008560	ternary complex factor MIP1 leucine-zipper protein (Protein of unknown function, DUF547) (AHRD V3.3 *** AT2G39690.1)						IPR025757 (PFAM): IPR006869 (PFA	0,038	0,113	0,000	0,000	0,000									
Solyc06g008580	auxin-regulated IAA22	IAA22	F:GO:0005515: C:G(	F:protein binding: C:nucleus: P:regulation of transcription, DNA-t			IPR033389 (PFAM): G3DSA:3.10.20.9	2,364	1,870	0,025	0,000	0,000									
Solyc06g008590	auxin-regulated IAA17	IAA17	F:GO:0005515: C:G(	F:protein binding: C:nucleus: P:regulation of transcription, DNA-t			IPR033389 (PFAM): G3DSA:3.10.20.9	32,868	38,041	0,580	0,412	0,681									
Solyc06g008600	E3 ubiquitin protein ligase DRIP2 (AHRD V3.3 *** W9RBR4_9ROSA)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): PF13923 (PFAM	15,435	15,526	15,367	16,492	16,107									
Solyc06g008610	WRKY transcription factor 21	WRKY21	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of transc			IPR003657 (SMAF WRKY	31,257	47,082	28,624	23,550	27,855	0,618	0,021					up		
Solyc06g008620	LOW QUALITY:tolB protein-like protein (AHRD V3.3 *** AT4G01870.2)						IPR011659 (PFAM): IPR011042 (G3D	4,867	10,581	2,146	4,544	4,680	1,142	0,002	1,118	0,005	1,083	0,014	up	up	up
Solyc06g008663	low-molecular-weight cysteine-rich 48 (AHRD V3.3 -** AT3G48231.1)						IPR015333 (PANTHER): PS51257 (PF	0,000	0,019	0,000	0,000	0,000									
Solyc06g008690	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9GSL6_POPTR)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR015915 (G3	8,660	7,573	3,620	3,185	4,398									
Solyc06g008700	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit (AHRD V3.3 *** K4C3Q0_SOLLC)		F:GO:0005515: P:G(	F:protein binding; P:RNA (guanine-N7)-methylation			IPR001680 (SMART): IPR001680 (PF	20,559	22,072	26,341	24,639	21,953									
Solyc06g008710	Cullin 1 (AHRD V3.3 *** A0A0D4D5H0_SOLLC)		P:GO:0006511: F:G(	P:ubiquitin-dependent protein catabolic process: F:ubiquitin prot			IPR019559 (SMART): IPR016158 (SM	3,430	4,580	0,648	1,055	1,085									
Solyc06g008720	CW-type zinc finger protein (AHRD V3.3 *-* E9NZV0_PHAVU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	86,699	71,611	86,515	97,041	89,435									
Solyc06g008730	Cell division cycle protein 48 homolog (AHRD V3.3 *** CDC48_CAPAN)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:3.40.50	59,940	66,066	64,796	70,764	66,913									
Solyc06g008740	Zinc finger transcription factor 40	C3H40	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	23,973	16,425	21,708	18,627	21,374									
Solyc06g008750	Glutaredoxin (AHRD V3.3 *** E9NZT9_PHAVU)		F:GO:0009055: F:G(	F:electron transfer activity: F:protein disulfide oxidoreductase a			IPR014025 (PRINTS): G3DSA:3.40.30	0,063	0,142	0,022	0,000	0,000									
Solyc06g008760	Glutaredoxin (AHRD V3.3 *** B3F8F2_SOLTU)		F:GO:0009055: F:G(	F:electron transfer activity: F:protein disulfide oxidoreductase a			IPR014025 (PRINTS): IPR011905 (TI(	8,702	6,172	7,045	8,251	8,685									
Solyc06g008770	CNL4		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,621	1,484	0,050	0,049	0,140	1,281	0,046					up		
Solyc06g008780	Transport inhibitor response 1 (AHRD V3.3 *** C7E4R3_TOBAC)		F:GO:0005488: P:G(	F:binding: P:cell communication: P:response to auxin: P:post-en			IPR006553 (SMART): IPR032675 (G3	0,000	0,000	0,000	0,025	0,000									
Solyc06g008790	Mi-1.1	Mi1-1	F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,917	1,035	0,149	0,022	0,210									
Solyc06g008800	CNL6		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,042	0,021	0,000	0,000	0,000									
Solyc06g008803	Transport inhibitor response 1-like protein (AHRD V3.3 *-* A0A097F6G5_9ROSA)		F:GO:0000822: P:G(	F:inositol hexakisphosphate binding: P:auxin-activated signaling			IPR032675 (G3DSA:3.80.10.GENE3D	1,270	0,878	1,774	2,193	1,530									
Solyc06g008805	Transport inhibitor response 1 (AHRD V3.3 *-* C7E4R3_TOBAC)		F:GO:0000822: P:G(	F:inositol hexakisphosphate binding: P:auxin-activated signaling			IPR032675 (G3DSA:3.80.10.GENE3D	0,101	0,122	0,096	0,173	0,047									
Solyc06g008807	Transport inhibitor response 1 (AHRD V3.3 *-* I7FHQ5_CAMSI)		F:GO:0005488: P:G(	F:binding: P:cell communication: P:multicellular organism develo			G3DSA:1.20.1280.50 (GENE3D): IPR(	0,280	0,194	0,420	0,725	0,446									
Solyc06g008810	Transport inhibitor response 1 (AHRD V3.3 *-* C7E4R3_TOBAC)		F:GO:0000822: P:G(	F:inositol hexakisphosphate binding: P:auxin-activated signaling			IPR032675 (G3DSA:3.80.10.GENE3D	0,333	0,481	0,760	0,706	0,708									
Solyc06g008820	Na+/H+ antiporter 1	nhx1	C:GO:0005774: C:G(	C:vacuolar membrane: C:plasma membrane: P:sodium ion trans			IPR004709 (PRINTS): IPR038770 (G3	16,823	14,320	3,998	3,395	3,566									
Solyc06g008830	Protein kinase superfamily protein (AHRD V3.3 *-* AT3G56760.1)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,019	0,099	0,000	0,000	0,023									
Solyc06g008840	BRCT domain-containing DNA repair protein, putative isoform 1 (AHRD V3.3 *-* A0A061ENE5_THECC)						IPR001357 (SMART): IPR036420 (G3	1,213	0,587	0,496	0,398	0,424									
Solyc06g008850	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT2G32910.1)						IPR013989 (SMART): IPR013989 (PF	27,180	23,913	32,455	30,619	30,592									
Solyc06g008860	u1 small nuclear ribonucleoprotein C		P:GO:0000387: F:G(	P:spliceosomal snRNP assembly: F:nucleic acid binding: C:U1 s			IPR003604 (SMART): IPR017340 (PIF	18,430	23,062	28,734	28,808	26,911									
Solyc06g008870	Gid1-like gibberellin receptor (AHRD V3.3 *** M9N8R2_NICAT)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	8,196	9,750	44,849	67,968	47,240					0,604	0,001			up
Solyc06g008880	WD40 repeat-containing protein (AHRD V3.3 *** A0A118JWM1_CYNCS)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	48,333	37,831	87,310	85,400	89,637									
Solyc06g008890	Kinase family protein (AHRD V3.3 *** D7LZE6_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,302	0,629	0,169	0,744	0,447									
Solyc06g008900	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03000.2)		F:GO:0016874	F:ligase activity			PF13920 (PFAM): IPR013083 (G3DSA	10,393	9,081	12,679	12,180	11,895									
Solyc06g008910	Hexosyltransferase (AHRD V3.3 *** K4C3S1_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR002495 (PFAM): IPR029044 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc06g008920	AMP dependent ligase, putative (AHRD V3.3 *** B9R8M5_RICCO)		F:GO:0003824	F:catalytic activity			IPR025110 (PFAM): G3DSA:3.30.300	9,409	6,719	82,661	78,485	57,631			-0,523	0,010				down	
Solyc06g008930	MLP-like protein 31 (AHRD V3.3 -** A0A151QPB6_CAJCA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,188	0,137	0,025	0,116	0,118									
Solyc06g008940	Elongation factor Tu (AHRD V3.3 *** K4C3S4_SOLLC)		F:GO:0003746: F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004161 (PF	22,894	24,225	27,965	23,141	21,840									
Solyc06g008950	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G19090.5)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	0,000	0,000	0,022	0,000	0,000									
Solyc06g008960	Mediator of RNA polymerase II transcription subunit 33A (AHRD V3.3 *** G7IKE7_MEDTR)		C:GO:0016592: P:G(	C:mediator complex: P:regulation of phenylpropanoid metabolic			IPR039638 (PANTHER): PTHR33739:	53,667	38,830	79,057	84,014	76,966									
Solyc06g008970	RNA helicase DEAH-box18	DEAH18	F:GO:0003677: F:G(	F:DNA binding: F:A	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR001945 (PRINTS): IPR006554 (SM	14,260	12,083	15,589	14,705	13,793									
Solyc06g008980	F-box/WD repeat-containing 10 (AHRD V3.3 *** A0A0B0NKC4_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,274	0,368	0,025	0,000	0,000									
Solyc06g009000	Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 *-* A0A061GBF7_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc06g009010	Nuclear transcription factor Y protein (AHRD V3.3 *** I3TAW4_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	0,057	0,021	0,000	0,000	0,000									
Solyc06g009020	Glutathione S-transferase (AHRD V3.3 *** A5YWI8_SOLCO)	GSTF2	F:GO:0005515	F:protein binding			IPR004046 (PFAM): IPR004045 (PFA	19,282	21,513	36,573	33,807	32,308									
Solyc06g009040	Glutathione S-transferase (AHRD V3.3 *** A5YWI8_SOLCO)	GSTF3	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	0,019	0,186	0,000	0,050	0,024									
Solyc06g009050	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT2G47710.1)						IPR006015 (PRINTS): IPR006016 (PF	47,145	52,464	821,631	905,960	733,549									
Solyc06g009055	U2 snRNP auxilliary factor, large subunit, splicing factor (AHRD V3.3 --* AT4G36690.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	39,665	47,396	47,917	43,870	42,922									
Solyc06g009060	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G02840.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	54,032	59,899	61,473	61,634	60,624									
Solyc06g009070	Zinc finger transcription factor 41	C3H41	F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding; F:metal ion binding			IPR014001 (SMART): IPR000571 (SM	22,454	18,977	28,560	27,200	28,159									
Solyc06g009080	Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT4G33490.2)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,000	0,019	0,000	0,022	0,000									
Solyc06g009090	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *-* AT4G33490.2)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc06g009110	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT4G33490.2)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	62,440	115,698	12,110	14,009	18,548									
Solyc06g009120	LYR motif-containing protein 7 isoform 1 (AHRD V3.3 *** A0A061DSK3_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	24,721	23,498	16,533	13,968	14,874									
Solyc06g009125	with no lysine (K) kinase 1 (AHRD V3.3 --* AT3G04910.3)							0,200	0,234	0,097	0,072	0,095									
Solyc06g009130	Magnesium/proton exchanger family member (AHRD V3.3 *** K4C3U3_SOLLC)		C:GO:0016021: P:G(	C:integral component of membrane: P:transmembrane transport			IPR004837 (PFAM): G3DSA:1.20.142	26,682	17,391	12,034	13,274	12,328	-0,588	0,034					down		
Solyc06g009140	Late embryogenesis abundant protein (AHRD V3.3 *** E3W6T3_SESPO)		C:GO:0005739	C:mitochondrion			IPR004926 (PFAM): mobidb-lite (MOB	248,298	291,458	152,675	263,156	183,979					0,789	0,000			up
Solyc06g009150	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G02360.1)						IPR007493 (PFAM): IPR036758 (G3D	0,000	0,018	0,025	0,000	0,000									
Solyc06g009160	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857: P:G(	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	G3DSA:3.90.226.10 (GENE3D): G3DS	41,992	31,458	56,169	47,601	51,876									
Solyc06g009170	Epoxide hydrolase (AHRD V3.3 *** A0A072UF47_MEDTR)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR000073 (PF	12,913	19,397	10,969	12,282	14,624	0,615	0,028					up		
Solyc06g009180	Pectinesterase (AHRD V3.3 *** K4C3U8_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR000070 (PF	0,000	0,000	0,025	0,000	0,000									
Solyc06g009190	Pectinesterase (AHRD V3.3 *** K4C3U9_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a	EC:3.1.1.11: EC:3.1.	Pectinesterase: Cart	IPR006501 (SMART): IPR012334 (G3	59,642	39,649	0,539	0,144	0,374									
Solyc06g009200	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G07830.1)	PG45	F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc06g009210	Ribosomal protein L19 (AHRD V3.3 *** K4C3V1_SOLLC)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: P:translatio			IPR000196 (SMART): G3DSA:1.10.12	620,524	641,429	457,787	400,312	424,576									
Solyc06g009220	Isoamylase, putative (AHRD V3.3 *** B9RJQ8_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			IPR006047 (SMART): IPR004193 (PF	49,329	49,218	59,024	64,525	61,891									
Solyc06g009225	Translation factor GUF1 homolog, mitochondrial (AHRD V3.3 --* GUF1_ORYSI)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carbohydrate metabolic process: F:cation bi				1,894	2,378	2,786	3,171	2,616									
Solyc06g009240	Cation/H(+) antiporter 15 (AHRD V3.3 *** W9SYW9_9ROSA)		P:GO:0006812: F:G(	P:cation transport: F:solute:proton antiporter activity: C:integral			IPR006153 (PFAM): IPR038770 (G3D	0,840	0,816	0,642	0,267	0,426									
Solyc06g009250	LOW QUALITY:F-box family protein (AHRD V3.3 *-* D7LS19_ARALL)		F:GO:0005515	F:protein binding			PTHR44918 (PANTHER): IPR036047 (	0,021	0,000	0,000	0,025	0,000									
Solyc06g009260	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 --* AT3G14980.6)		P:GO:0006415: C:G(	P:translational termination: C:chloroplast: F:translation release factor activity, codon specific: F:riboson				3,197	2,590	4,720	5,160	5,133									
Solyc06g009270	Diacylglycerol kinase (AHRD V3.3 *** K4C3V7_SOLLC)		F:GO:0003951: F:G(	F:NAD+ kinase acti	EC:2.7.1.23: EC:2.7.	NAD(+) kinase: Diac	IPR000756 (SMART): IPR001206 (SM	33,421	96,673	20,188	17,609	22,658	1,555	0,001					up		
Solyc06g009280	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	ABCB8	F:GO:0005524: C:G(	F:ATP binding: C:int	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	0,000	0,306	0,022	0,000	0,071									
Solyc06g009290	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	ABCB9	F:GO:0005524: C:G(	F:ATP binding: C:int	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	5,208	14,188	2,410	2,118	2,792	1,472	0,002					up		
Solyc06g009330	Outward rectifying potassium channel protein (AHRD V3.3 *** G7KUL6_MEDTR)		F:GO:0005267: C:G(	F:potassium channel activity: C:membrane: P:potassium ion tra			IPR003280 (PRINTS): G3DSA:1.10.23	7,073	8,256	3,762	4,061	3,607									
Solyc06g009340	Chaperone protein DnaJ (AHRD V3.3 *-* A0A1D1YHH5_9ARAE)		C:GO:0016021	C:integral component of membrane			IPR036869 (SUPERFAMILY)	16,699	13,819	10,863	11,222	10,167									
Solyc06g009380	Transmembrane protein, putative (AHRD V3.3 *** G7IBT3_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR12242 (PANTHER): PTHR12242	26,059	28,435	79,843	92,086	77,889									
Solyc06g009390	Protein phosphatase 2C-like protein (AHRD V3.3 *** G7IBT6_MEDTR)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	4,987	7,496	9,064	8,691	6,890									
Solyc06g009400	PII-like protein	piiglb1	P:GO:0006808: F:G(	P:regulation of nitrogen utilization; F:enzyme regulator activity			IPR002187 (PRINTS): IPR002187 (SM	88,165	86,594	138,417	167,712	179,414									
Solyc06g009425	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT1G75920.4)							2,845	3,121	2,059	1,958	1,861									
Solyc06g009440	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *-* A0A151TXI4_CAJCA)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc06g009455	Nitrogen regulatory protein P-II (AHRD V3.3 --* A0A199V912_ANACO)		C:GO:0009536: P:G(	C:plastid; P:regulation of biological process			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,024									
Solyc06g009480	R2R3MYB transcription factor 24	R2R3MYB24	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,042	0,018	0,000	0,025	0,024									
Solyc06g009490	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A0B2SEE4_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	6,014	4,884	2,928	2,801	3,381									
Solyc06g009500	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2SEE4_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,466	1,810	1,065	1,343	1,739									
Solyc06g009510	Transcription factor, putative (AHRD V3.3 *** B9RNB4_RICCO)		F:GO:0046983	F:protein dimerization activity			PTHR33124 (PANTHER): PTHR33124	0,000	0,019	0,000	0,047	0,023									
Solyc06g009520	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RNC1_RIC	GUN1	F:GO:0005515	F:protein binding			IPR002625 (SMART): IPR033443 (PF	53,811	70,777	80,703	78,656	91,238									
Solyc06g009530	Carbohydrate-binding-like fold protein (AHRD V3.3 *** A0A097PPL4_SOLLC)		C:GO:0005774: C:G(	C:vacuolar membrane: C:endoplasmic reticulum membrane: C:G			PF13620 (PFAM): IPR013783 (G3DSA	88,455	84,534	103,437	105,180	101,611									
Solyc06g009560	LOW QUALITY:DNA helicase homolog, putative (AHRD V3.3 *-* Q1EPC6_MUSAC)						IPR013955 (PFAM): G3DSA:2.40.50.1	0,000	0,021	0,000	0,000	0,000									
Solyc06g009600	LOW QUALITY:HIT zinc finger,PAPA-1-like conserved region, putative (AHRD V3.3 *-* A0A061F305_THEC(		P:GO:0006338: C:G(	P:chromatin remodeling; C:Ino80 complex			IPR006880 (SMART): IPR007529 (PF	2,517	2,699	0,049	0,000	0,047									
Solyc06g009610	LOW QUALITY:GRAS family transcription factor, putative (AHRD V3.3 *** A0A061E	GRAS					IPR005202 (PFAM GRAS	0,021	0,021	0,124	0,076	0,093									
Solyc06g009620	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061F8B1_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	4,398	5,318	2,967	3,460	3,450									
Solyc06g009630	CP12 (AHRD V3.3 *** O24136_TOBAC)		C:GO:0009507: P:G(	C:chloroplast: P:negative regulation of reductive pentose-phosp			IPR003823 (SMART): IPR003823 (PF	167,393	232,510	208,829	209,575	292,311			0,482	0,004				up	
Solyc06g009640	BZIP transcription factor (AHRD V3.3 *** Q1HW69_CAPAN)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of transc			IPR004827 (SMAF bZIP	43,835	34,807	22,544	38,257	35,874			0,667	0,000	0,764	0,000		up	up
Solyc06g009650	Vps51/Vps67 family (components of vesicular transport) protein (AHRD V3.3 *** AT4G02030.1)		C:GO:0000938: C:G(	C:GARP complex: C:trans-Golgi network: C:cytosol: P:Golgi org			PF08700 (PFAM): mobidb-lite (MOBID	51,312	44,896	48,076	54,299	50,071									
Solyc06g009660	GTP-binding protein (AHRD V3.3 *** W9QX75_9ROSA)		F:GO:0005525: C:G(	F:GTP binding; C:intracellular; P:intracellular protein transport			IPR006689 (PRINTS): SM00178 (SMA	0,946	0,800	0,861	0,807	0,637									
Solyc06g009670	DNAJ heat shock N-terminal domain-containing family protein (AHRD V3.3 *** B9GSH4_POPTR)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	1,520	0,570	0,680	0,471	0,589	-1,370	0,045					down		
Solyc06g009680	BRCT domain-containing protein (AHRD V3.3 *** A0A124SIE7_CYNCS)		F:GO:0046872	F:metal ion binding			IPR001357 (SMART): IPR036420 (G3	5,517	5,653	2,113	1,463	1,868									
Solyc06g009690	ARM repeat superfamily protein, putative (AHRD V3.3 *** A0A061FLE8_THECC)						PTHR14873 (PANTHER): IPR016024 (	8,263	6,261	7,149	6,200	6,714									
Solyc06g009695	DUF4050 family protein (AHRD V3.3 --* AT1G15350.2)							0,000	0,018	0,000	0,000	0,000									
Solyc06g009710	R2R3MYB transcription factor 111	R2R3MYB111	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,019	0,083	0,076	0,025	0,000									
Solyc06g009750	importin alpha	kap	F:GO:0005515: C:G(	F:protein binding: C:nucleus: C:cytoplasm: P:protein import into			IPR000225 (SMART): IPR036975 (G3	104,991	95,628	138,150	126,147	124,267									
Solyc06g009760	LOW QUALITY:CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,155	0,347	0,000	0,000	0,000									
Solyc06g009770	Flagellar biosynthesis protein flhA (AHRD V3.3 *-* A0A1D1YQS8_9ARAE)						PTHR33702 (PANTHER): PTHR33702	34,856	27,557	0,025	0,050	0,024									
Solyc06g009780	Kinesin-like protein (AHRD V3.3 *** F8UN41_TOBAC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001715 (SMART): IPR001752 (SM	1,600	1,562	0,172	0,342	0,588									
Solyc06g009783	Kinesin-like protein (AHRD V3.3 *-* F8UN41_TOBAC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	1,807	1,386	0,358	0,286	0,304									
Solyc06g009790	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A061ENJ0_THECC)	PG48-1	F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	14,821	10,469	11,101	11,525	11,876									
Solyc06g009795	Pectin lyase-like superfamily protein (AHRD V3.3 *-* AT3G16850.1)		F:GO:0004650: C:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR024535 (PFAM): IPR012334 (G3D	5,918	4,209	5,358	4,329	4,740									
Solyc06g009800	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *-* A0A151SLA5_CAJCA)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	1,418	1,715	1,633	1,287	1,343									
Solyc06g009810	Ethylene-responsive transcription factor, putative (AHRD V3.3 --* A0A061G219_THECC)							5,660	4,306	2,990	1,988	3,320									
Solyc06g009820	Fumarate hydratase 1 family protein (AHRD V3.3 *-* B9GSD7_POPTR)		F:GO:0004333: P:G(	F:fumarate hydratas	EC:4.2.1.2	Fumarate hydratase	G3DSA:1.20.200.10 (GENE3D): IPR0;	9,109	7,094	9,215	8,710	8,042									
Solyc06g009830	Fumarate hydratase 2 (AHRD V3.3 *-* B3H477_ARATH)		F:GO:0004333: P:G(	F:fumarate hydratas	EC:4.2.1.2	Fumarate hydratase	IPR000362 (PRINTS): IPR022761 (PF	2,108	2,189	2,334	2,928	1,998									
Solyc06g009840	Fumarate hydratase 2 (AHRD V3.3 *-* B3H477_ARATH)		F:GO:0004333: P:G(	F:fumarate hydratas	EC:4.2.1.2	Fumarate hydratase	G3DSA:1.20.200.10 (GENE3D): G3DS	1,739	1,347	2,075	2,159	1,971									
Solyc06g009850	Sulfurtransferase (AHRD V3.3 *-* W9R534_9ROSA)		F:GO:0016740	F:transferase activity			IPR036873 (G3DSA:3.40.250.GENE3I	0,021	0,021	0,000	0,000	0,000									
Solyc06g009860	Sulfurtransferase (AHRD V3.3 *-* A0A0D2SL37_GOSRA)		F:GO:0004792: F:G(	F:thiosulfate sulfurtransferase activity; F:transferase activity			IPR036873 (G3DSA:3.40.250.GENE3I	0,000	0,021	0,000	0,000	0,000									
Solyc06g009890	PHD finger family protein (AHRD V3.3 --* AT3G17460.1)							0,094	0,021	0,000	0,000	0,000									
Solyc06g009900	Emsy N terminus domain-containing family protein (AHRD V3.3 *** B9HPS6_POPTR)		P:GO:0050832	P:defense response to fungus			IPR005491 (SMART): IPR005491 (PF	1,508	1,012	0,825	0,804	1,104									
Solyc06g009940	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_ENCLE)		C:GO:0009522: P:G(	C:photosystem I: P:photosynthesis: C:integral component of me			IPR001280 (PFAM): IPR036408 (G3D	0,038	0,206	0,275	0,391	0,235									
Solyc06g009950	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522: P:G(	C:photosystem I: P:photosynthesis: C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,000	0,025	0,075	0,047									
Solyc06g009960	Elongation factor 1-alpha (AHRD V3.3 *-* EF1A_SOLLC)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR000795 (PF	83,572	88,119	70,302	59,415	66,137									
Solyc06g009970	Elongation factor 1-alpha (AHRD V3.3 *** EF1A_SOLLC)		F:GO:0003746: F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004160 (PF	1288,899	1408,817	1052,626	885,249	958,020									
Solyc06g009985	LOW QUALITY:50S ribosomal protein L2, chloroplastic (AHRD V3.3 *-* A0A0N7BD77_CORYI)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014726 (G3DSA:4.10.950.GENE3I	0,161	0,510	0,000	0,148	0,234									
Solyc06g010000	SUMO E3 ligase SIZ1 (AHRD V3.3 *** A0A0X9AQ43_SOLLC)		C:GO:0005634: F:G(	C:nucleus: F:zinc ion binding: P:cell growth: P:protein sumoylati			IPR003034 (SMART): IPR001965 (SM	31,424	28,073	48,675	49,309	47,048									
Solyc06g010030	MLO-like protein (AHRD V3.3 *-* K4C430_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): PTHR31942 (PAN	1,155	6,155	0,390	0,443	0,980	2,433	0,000					up		
Solyc06g010033	MLO-like protein (AHRD V3.3 *** K4C430_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	6,329	28,017	1,985	3,614	5,726	2,168	0,000	1,524	0,000			up	up	
Solyc06g010050	LOW QUALITY:O-acyltransferase (WSD1-like) family protein (AHRD V3.3 --* AT5G53380.1)							0,000	0,041	0,000	0,000	0,000									
Solyc06g010060	Protein transport protein Sec61 subunit beta, putative (AHRD V3.3 *** B9SK56_RICCO)		C:GO:0005784: P:G(	C:Sec61 translocon complex; P:intracellular protein transport			IPR016482 (PFAM): IPR030671 (PIRS	12,028	10,454	13,872	11,726	13,716									
Solyc06g010100	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *-* A0A061E		C:GO:0005634: F:G(	C:nucleus: F:zinc ion binding: P:cell growth: P:protein sumoylati			IPR001965 (SMART): PF13086 (PFAM	0,157	0,895	0,047	0,000	0,023									
Solyc06g010120	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V		F:GO:0008270: C:G(	F:zinc ion binding; C:integral component of membrane			PTHR10887 (PANTHER): PTHR10887	0,040	0,079	0,191	0,094	0,094									
Solyc06g010170	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		P:GO:0001522: F:G(	P:pseudouridine synthesis: F:RNA binding: F:pseudouridine syn			IPR007877 (PFAM): PTHR31210:SF3	4,443	4,025	3,545	2,227	4,409									
Solyc06g010200	Chromatin remodeling complex subunit, putative isoform 2 (AHRD V3.3 *-* A0A061GY85_THECC)		F:GO:0005524: P:G(	F:ATP binding; P:chromatin silencing			IPR001650 (PFAM): G3DSA:3.40.50.3	84,461	68,342	74,750	80,261	78,334									
Solyc06g010240	Helicase protein MOM1 (AHRD V3.3 *-* A0A0B2QJF7_GLYSO)		P:GO:0006342	P:chromatin silencing			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,220	4,031	4,445	5,730	6,189									
Solyc06g010250	High-affinity nitrate transporter (AHRD V3.3 *** Q76IH8_PRUPE)		C:GO:0016021: P:G(	C:integral component of membrane: P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,061	0,319	0,025	0,000	0,000									

Solyc06g010260	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** A0A151TNE8_CAJCA)		F:GO:0005515; P:G(	F:protein binding; P:response to sucrose; P:cellular response to			IPR006828 (SMART): IPR006828 (PF.	6,303	5,470	6,868	6,555	7,095									
Solyc06g010270	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061GX52_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	0,131	0,060	0,000	0,000	0,000									
Solyc06g011270	LOW QUALITY:Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 --* AT4G13410.3)							0,019	0,000	0,306	0,485	0,210									
Solyc06g011280	Elongation factor 1-gamma 1 (AHRD V3.3 *** EF1G1_ORYSJ)	EF1By1	F:GO:0003746; F:G(	F:translation elongation factor activity; F:protein binding; P:trans			IPR001662 (SMART): IPR004046 (PF.	542,155	601,743	384,497	334,443	344,183									
Solyc06g011350	plasma membrane intrinsic protein 2.4	PIP2.4	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	4,527	5,899	6,165	8,150	6,463									
Solyc06g011370	Chaperone protein (AHRD V3.3 *** W9QX74_9ROSA)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:response to heat; P:protein meta			IPR001270 (PRINTS): IPR019489 (SM	235,305	170,559	701,612	615,608	713,914									
Solyc06g011374	Coiled-coil domain-containing protein 93 (AHRD V3.3 --* A0A1D1Y1J3_9ARAE)							2,138	2,494	2,060	2,066	2,640									
Solyc06g011375	Coiled-coil domain-containing 93 (AHRD V3.3 *-* A0A0B0N531_GOSAR)						PTHR16441:SF0 (PANTHER): IPR039	3,263	2,620	2,671	1,533	3,157									
Solyc06g011440	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7J8B2_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc06g011450	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT4G32285.2)		F:GO:0005545; C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART): IPR008942 (G3	18,039	15,604	2,783	2,775	4,506									
Solyc06g011460	LOW QUALITY:DNA/RNA polymerases superfamily protein (AHRD V3.3 *-* A0A061FNI4_THECC)		F:GO:0005488	F:binding			IPR005162 (PFAM): mobidb-lite (MOB	0,040	0,000	0,022	0,025	0,023									
Solyc06g011470	LOW QUALITY:beta-amylase 5 (AHRD V3.3 --* AT4G15210.4)							7,455	10,605	1,694	1,694	2,601									
Solyc06g011490	Unknown protein (AHRD V3.3)							0,486	0,906	1,136	0,975	0,540									
Solyc06g011495	30S ribosomal protein S18, chloroplastic (AHRD V3.3 --* RR18_ORYSJ)		F:GO:0003677; F:G(	F:DNA binding; F:transposase activity; P:transposition, DNA-me			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc06g011510	40S ribosomal protein S23 (AHRD V3.3 *-* RS23_EUPES)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.50.140 (GENE3D): IPR0(	0,000	0,078	0,025	0,047	0,047									
Solyc06g011540	Myosin (AHRD V3.3 *-* W5ZT55_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.120.720 (GENE3D): IPR(	0,240	0,160	0,093	0,050	0,235									
Solyc06g011550	Myosin-11 (AHRD V3.3 *-* MYO11_ARATH)		F:GO:0000146; F:G(	F:microfilament mot	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): PTHR131	22,178	18,607	13,382	14,178	14,276									
Solyc06g011560	transmembrane protein (AHRD V3.3 *** AT1G70505.4)		C:GO:0016021	C:integral component of membrane			PTHR12242:SF10 (PANTHER): PTHR	0,143	0,178	0,503	0,912	0,569									
Solyc06g011570	haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *-* AT2G25870.1)		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR023091 (G3DSA:3.40.390.GENE3I	5,411	5,520	3,763	3,185	3,929									
Solyc06g011580	LOW QUALITY:precursor of peptide 1 (AHRD V3.3 --* AT5G64900.1)							0,499	0,236	0,717	1,191	0,615									
Solyc06g011590	Major facilitator superfamily protein (AHRD V3.3 *** AT2G28120.1)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,492	0,215	0,093	0,385	0,119									
Solyc06g011620	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *-* G7IF78_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR24223:SF189 (PANTHER): PTHI	0,138	0,176	0,116	0,192	0,165									
Solyc06g011630	LOW QUALITY:nucleotide-sensitive chloride conductance regulator (ICln) family protein (AHRD V3.3 *-* AT5		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:cytosol; C:plasma membrane; P:chloride transport; P:cell volume h(				0,019	0,000	0,050	0,000	0,000									
Solyc06g011660	zinc induced facilitator-like 1 (AHRD V3.3 *-* AT5G13750.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,019	0,000	0,000	0,025	0,000									
Solyc06g016670	LOW QUALITY:histone acetyltransferase subunit NuA4-domain protein (AHRD V3.3 --* AT4G14385.8)							0,000	0,000	0,025	0,000	0,000									
Solyc06g016695	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AHRD V3.3 --* AT2G02765.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,197	0,000	0,022	0,094									
Solyc06g016750	nuclear factor Y, subunit C10 (AHRD V3.3 *-* AT1G07980.1)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM NF-YC	25,916	25,034	21,221	20,482	18,242									
Solyc06g016760	gamma-secretase subunit (AHRD V3.3 *-* AT5G09310.1)		C:GO:0005798; C:G(	C:Golgi-associated vesicle; C:integral component of membrane			IPR019379 (PFAM): mobidb-lite (MOB	11,623	12,299	23,176	21,798	21,241									
Solyc06g016770	RING/U-box superfamily protein (AHRD V3.3 *** AT5G60580.3)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	4,280	3,325	2,803	3,371	2,737									
Solyc06g016790	Hydroxyproline-rich glycoprotein (AHRD V3.3 *-* B9HQ96_POPTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	8,279	10,728	1,428	2,059	1,100									
Solyc06g016800	LOW QUALITY:CTP synthase (AHRD V3.3 *** K4AVQ0_SOLLC)		F:GO:0003883; P:G(	F:CTP synthase ac	EC:6.3.4.2	CTP synthase (glutar	IPR029062 (G3DSA:3.40.50.GENE3D	2,701	4,886	0,448	0,391	0,677									
Solyc06g016820	LOW QUALITY:7-deoxyloganetin glucosyltransferase (AHRD V3.3 --* UGT6_CATRO)							0,040	0,000	0,051	0,025	0,024									
Solyc06g017850	FAR1-related sequence 7 (AHRD V3.3 --* AT3G06250.3)							0,703	0,591	0,443	0,681	0,400									
Solyc06g017860	Carboxypeptidase (AHRD V3.3 *** K4C4B4_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	3,478	3,990	0,358	1,076	0,376									
Solyc06g017970	Ubiquitin carboxyl-terminal hydrolase 13 (AHRD V3.3 *** W9RB05_9ROSA)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR008974 (G3	98,706	89,252	116,079	120,089	118,010									
Solyc06g018000	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PANTHER): IPR027417 (:	0,000	0,021	0,050	0,124	0,023									
Solyc06g018004	tetraspanin10 (AHRD V3.3 --* AT1G63260.6)							0,954	0,644	0,535	0,741	0,637									
Solyc06g018050	mitochondrial calcium uniporter complex protein-like		F:GO:0005509; P:G(	F:calcium ion binding; P:mitochondrial calcium ion transmembrai			IPR002048 (SMART): IPR002048 (PF.	26,032	23,076	30,499	29,619	25,957									
Solyc06g018100	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT4G33490.2)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM): IPR021109 (G3D	8,308	11,119	5,048	3,355	5,102									
Solyc06g018110	RNA binding protein		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (SMART): IPR000504 (SM	7,113	8,043	8,257	8,526	7,120									
Solyc06g018115	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2QRD1_ORYSJ)		F:GO:0003677	F:DNA binding			IPR025525 (PFAM): PTHR23272 (PAI	0,042	0,041	0,000	0,000	0,000									
Solyc06g019170	Delta-1-pyrroline-5-carboxylate synthetase (AHRD V3.3 *** G3M3X3_SOLTO)		F:GO:0004350; C:G(	F:glutamate-5-semi	EC:1.2.1.41	Glutamate-5-semiald	IPR001057 (PRINTS): IPR005766 (PII	189,361	171,874	491,642	455,468	465,191									
Solyc06g019190	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151R878_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,062	0,000	0,047	0,000									
Solyc06g019200	Ethylene-dependent gravitropism-deficient and yellow-green-like 2 isoform 2 (AHRD V3.3 *** A0A061FLR5_T		F:GO:0008233; C:G(	F:peptidase activity; C:chloroplast thylakoid membrane; C:integi			mobidb-lite (MOBIDB_LITE): mobidb-lit	14,057	29,278	8,642	12,574	24,875	1,086	0,000	1,518	0,000			up	up	
Solyc06g024200	BSD domain-containing protein (AHRD V3.3 --* AT1G26300.3)						PTHR33047:SF20 (PANTHER): PTHR:	0,134	0,308	0,118	0,448	0,379									
Solyc06g024207	alpha-1,2-Mannosidase (AHRD V3.3 --* D8RTN8_SELML)							0,203	0,176	0,491	0,366	0,259									
Solyc06g024210	LOW QUALITY:Senescence-associated protein (AHRD V3.3 *-* A0A072THV8_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR330	10,997	13,798	12,091	25,959	15,377					1,109	0,002			up
Solyc06g024230	LOW QUALITY:Senescence-associated protein, putative (AHRD V3.3 *-* A0A072THY4_MEDTR)						PTHR45345 (PANTHER): PTHR45345	0,097	0,126	0,100	0,151	0,118									
Solyc06g024240	LOW QUALITY:ribosomal protein 1 (AHRD V3.3 --* AT1G43170.4)							0,000	0,021	0,000	0,000	0,000									
Solyc06g024245	Class II aaRS and biotin synthetases superfamily protein (AHRD V3.3 --* AT3G44740.5)						mobidb-lite (MOBIDB_LITE)	8,581	11,738	8,967	15,748	10,448									
Solyc06g024310	LOW QUALITY:Elongation defective 1 family protein (AHRD V3.3 *-* B9GM49_POPTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:transferase			PTHR10774:SF158 (PANTHER): PTHI	2,687	1,940	0,025	0,000	0,000									
Solyc06g024340	LOW QUALITY:S-adenosylmethionine synthase (AHRD V3.3 --* METK_BRARP)							0,097	0,146	0,148	0,251	0,143									
Solyc06g024370	LOW QUALITY:calcium-dependent protein kinase 30 (AHRD V3.3 --* AT1G74740.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,038	0,021	0,000	0,099	0,000									
Solyc06g024375	Cytochrome c oxidase subunit 1 (AHRD V3.3 --* COX1_AEGCO)							0,000	0,043	0,000	0,000	0,000									
Solyc06g024380	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT1G08260.2)						mobidb-lite (MOBIDB_LITE): PTHR330	13,066	16,828	12,876	25,724	15,313									
Solyc06g024386	Alpha-mannosidase (AHRD V3.3 --* A0A059AHM8_EUCGR)		C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated; F:sequ(			PTHR33047 (PANTHER)	0,098	0,375	0,197	0,343	0,167									
Solyc06g024415	DNA-BINDING TRANSCRIPTION FACTOR 2 (AHRD V3.3 --* AT3G18380.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,282	0,256	0,293	0,371	0,283									
Solyc06g025415	Mediator of RNA polymerase II transcription subunit 14 (AHRD V3.3 --* MED14_ARATH)							0,000	0,000	0,000	0,000	0,024									
Solyc06g025425	Spc97 / Spc98 family of spindle pole body (SBP) component (AHRD V3.3 --* AT3G43610.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc06g030470	Domain of Uncharacterized protein function, putative (AHRD V3.3 *** A0A061GWB6_THECC)						IPR021182 (PIRSF): IPR010369 (PFA	24,395	26,352	31,980	85,019	75,684			1,241	0,000	1,414	0,000		up	up
Solyc06g030490	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0HV59_SOLCH)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	22,625	21,493	38,508	36,615	38,006									
Solyc06g030510	hAT transposon superfamily (AHRD V3.3 *** AT4G15020.2)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM): IPR007021 (PFA	13,110	10,150	17,005	13,694	15,133									
Solyc06g030540	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9P5V6_ZOSMR)		F:GO:0018024	F:histone-lysine N-r	EC:2.1.1.43	Histone-lysine N-met	G3DSA:1.10.8.850 (GENE3D): IPR01	47,872	45,612	45,625	45,485	46,847									
Solyc06g030570	Ribosomal RNA large subunit methyltransferase N (AHRD V3.3 *** A0A0B0P4H5_GOSAR)		F:GO:0008173; P:G(	F:RNA methyltransferase activity; P:tRNA methylation; F:iron-su			IPR006638 (SMART): IPR013785 (G3	23,079	29,495	53,591	61,443	56,394									
Solyc06g030590	Serine palmitoyltransferase (AHRD V3.3 *** B3Y000_NICBE)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR004839 (PFAM): IPR015421 (G3D	0,038	0,000	0,025	0,025	0,023									
Solyc06g031670	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G30630.1)		F:GO:0005524; F:G(	F:ATP binding; F:kinase activity			IPR010488 (PFAM): PTHR31153:SF9	0,019	0,000	0,000	0,000	0,000									
Solyc06g031675	FYVE zinc finger protein (AHRD V3.3 *-* G7JR48_MEDTR)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation; F:metal ion binding			PTHR13856 (PANTHER): PTHR13856	0,098	0,019	0,022	0,069	0,048									
Solyc06g031690	Ankyrin repeat family protein (AHRD V3.3 *** B9IKF9_POPTR)		F:GO:0005515	F:protein binding			PF13857 (PFAM): IPR036770 (G3DS/	30,232	27,985	35,852	34,047	33,911									
Solyc06g031710	Sl Nodulin-like protein		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF1	0,021	0,019	0,000	0,000	0,000									
Solyc06g031740	ABC transporter G family member 22 (AHRD V3.3 --* A0A1D1YL65_9ARAE)							0,019	0,092	0,000	0,000	0,070									
Solyc06g032740	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,025	0,025	0,000									
Solyc06g033790	LOW QUALITY:RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	0,078	0,098	0,000	0,000	0,000									
Solyc06g033800	LOW QUALITY:RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,000	0,018	0,000	0,000	0,000									
Solyc06g033810	LOW QUALITY:RNA-binding family protein (AHRD V3.3 *** B9GTK9_POPTR)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:snRNA stem-loop binding			PTHR10501:SF20 (PANTHER): PTHR	0,325	0,194	0,000	0,000	0,000									
Solyc06g033850	Dehydration responsive element-binding factor protein (AHRD V3.3 --* A0A0K0K9Y3_ELECO)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; F:GT			PTHR31241:SF18 (PANTHER): PTHR:	2,599	1,120	1,421	1,057	1,526									
Solyc06g033860	Glutamate dehydrogenase (AHRD V3.3 *** K4C4L0_SOLLC)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:oxidoreductase activ			IPR006095 (PRINTS): IPR006096 (SM	0,098	0,083	0,022	0,150	0,166									
Solyc06g033870	LOW QUALITY:R2R3MYB transcription factor 105	R2R3MYB105	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,040	0,000	0,000	0,022	0,000									
Solyc06g033890	DNA-directed RNA polymerase II subunit RPB7 (AHRD V3.3 *** A0A0B0PUV3_GOSAR)		C:GO:0000419; F:G(	C:RNA polymerase	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:2.40.50.140 (GENE3D): PTHR	0,019	0,000	0,000	0,000	0,000									
Solyc06g033920	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT3G24240.1)		F:GO:0005515	F:protein binding			IPR003591 (SMART): IPR013210 (PF.	0,000	0,019	0,000	0,000	0,000									
Solyc06g033980	LOW QUALITY:Ribonuclease H (AHRD V3.3 *** Q2HUA4_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	IPR036397 (G3DSA:3.30.420.GENE3I	1,940	2,369	1,907	2,008	2,020									
Solyc06g034020	methionine sulfoxide reductase A3		F:GO:0008113; P:G(	F:peptide-methionin	EC:1.8.4.11	Peptide-methionine (:	IPR036509 (G3DSA:3.30.1060.GENE:	33,665	30,675	56,334	55,219	53,265									
Solyc06g034030	myb-like transcription factor family protein (AHRD V3.3 *-* AT5G47390.1)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR001005 (SMAF MYB_related	0,021	0,000	0,000	0,000	0,023									
Solyc06g034040	Oleosin (AHRD V3.3 *** K4C4M8_SOLLC)		C:GO:0012511; C:G(	C:monolayer-surrounded lipid storage body; C:integral compone			IPR000136 (PFAM): PTHR33203:SF7	61,189	68,327	6,148	14,327	1,390									
Solyc06g034063	PIF1 helicase, putative (AHRD V3.3 *-* A0A061ECN6_THECC)		P:GO:0000723; F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR010285 (PFAM): G3DSA:2.40.50.1	0,021	0,000	0,022	0,025	0,000									
Solyc06g034070	AT hook motif-containing protein, putative, expressed (AHRD V3.3 *-* Q2QZU2_ORYSJ)		P:GO:0000723; F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR003840 (PFAM): G3DSA:3.40.50.3	0,000	0,000	0,050	0,047	0,094									
Solyc06g034080	50S ribosomal protein L20, chloroplastic (AHRD V3.3 --* RK20_ACUOB)							5,420	4,828	4,600	3,817	3,826									
Solyc06g034090	LOW QUALITY:NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 --* AT3G53880.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,021	0,000	0,000	0,000									
Solyc06g034100	ubiquinol-cytochrome C chaperone family protein (AHRD V3.3 *** AT5G51220.1)		C:GO:0005739	C:mitochondrion			IPR021150 (PFAM): PTHR12184:SF1	16,332	19,202	26,016	25,939	26,210									
Solyc06g034110	Tomato acid phosphatase	aps1	F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR005519 (PFAM): IPR014403 (PIRS	8,904	9,519	38,913	47,719	42,427									
Solyc06g034120	Oxidoreductase, zinc-binding dehydrogenase family protein, expressed (AHRD V3.3 *** Q10T48_ORYSJ)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): G3DSA:3.40.50	50,908	49,971	47,883	41,317	48,598									
Solyc06g034140	B3 domain-containing protein (AHRD V3.3 *-* W9RYD5_9ROSA)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,214	0,214	0,025	0,171	0,024									
Solyc06g034150	8-amino-7-oxononanoate synthase (AHRD V3.3 *** A0A0B2R2H1_GLYSO)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR004839 (PFAM): IPR015422 (G3D	6,722	6,146	3,891	5,127	4,621									
Solyc06g034160	Autophagy-related protein 3 (AHRD V3.3 *** K4C4P0_SOLLC)		C:GO:0005737; P:G(	C:cytoplasm; P:autophagy; P:protein transport			IPR007134 (PFAM): IPR019461 (PFA	45,163	35,842	87,775	88,897	82,296									
Solyc06g034180	2-phosphoglycerate kinase (AHRD V3.3 *** A0A0B2RDC0_GLYSO)						PF13238 (PFAM): G3DSA:3.40.50.30(	0,217	0,167	0,047	0,000	0,000									
Solyc06g034200	Phosphate transporter (AHRD V3.3 *** K4C4P4_SOLLC)		F:GO:0005315; P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph			IPR005828 (PFAM): IPR004738 (TIGF	0,021	0,000	0,172	0,069	0,070									
Solyc06g034220	Vesicle-associated 1-1-like protein (AHRD V3.3 *** A0A0B0MV36_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR016763 (PIRSF): IPR013783 (G3I	19,778	20,311	37,607	36,682	33,873									
Solyc06g034230	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *-* AT1G71850.1)						IPR021099 (PFAM): PTHR31476 (PAI	3,570	3,582	3,589	3,751	3,167									
Solyc06g034234	Cytochrome P450 (AHRD V3.3 *-* Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3I	0,000	0,021	0,000	0,000	0,000									
Solyc06g034236	Cytochrome P450 (AHRD V3.3 *-* Q9M7M3_CAPAN)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PFAM): IPR036396 (G3D	0,037	0,021	0,000	0,000	0,000									
Solyc06g034290	Glycerol-3-phosphate transporter, putative (AHRD V3.3 *** B9R9S6_RICCO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	5,353	7,176	8,351	19,277	23,709			1,498	0,000	1,208	0,000		up	up
Solyc06g034300	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT1G53190.2)							0,077	0,043	0,165	0,047	0,047									
Solyc06g034310	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** G7LIE6_MEDTR)						IPR024752 (PFAM): mobidb-lite (MOB	0,095	0,122	0,022	0,259	0,118									
Solyc06g034320	transmembrane protein (AHRD V3.3 *** AT4G25225.2)						IPR027854 (PFAM): PTHR33528:SF1	3,408	2,624	4,943	6,080	4,808									
Solyc06g034330	E3 ubiquitin protein ligase RIN2 (AHRD V3.3 *** W8QCW8_9ROSI)		F:GO:0005515	F:protein binding			IPR001841 (SMART): G3DSA:1.10.8.1	82,098	61,575	90,144	96,902	88,599									
Solyc06g034340	NAC domain protein, (AHRD V3.3 *** A0A061G781_THECC)	NAC051	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,199	0,230	0,097	0,143	0,071									
Solyc06g034350	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_PHAAO)		F:GO:0003676	F:nucleic acid binding				0,058	0,132	0,000	0,000	0,000									
Solyc06g034360	Pectinesterase (AHRD V3.3 *** K4C4Q7_SOLLC)		F:GO:0004857; F:G(	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (TIC	0,019	0,179	0,384	0,496	0,328									
Solyc06g034370	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62350.1)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (SMART): IPR035513 (G3	3,375	14,520	3,378	1,815	3,244	2,127	0,000					up		
Solyc06g034380	60S ribosomal protein L9 (AHRD V3.3 *** A0A0B0NWI7_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR036789 (G3DSA:3.90.930.GENE3I	0,315	0,226	0,119	0,100	0,235									
Solyc06g034390	Phosphate-responsive 1 family protein (AHRD V3.3 *** G7JP91_MEDTR)		C:GO:0009505; C:G(	C:plant-type cell wall; C:plasmodesma; C:integral component of			IPR006766 (PFAM): IPR006766 (PAN	5,989	2,991	0,553	0,193	0,165									
Solyc06g034410	DUF1442 family protein (AHRD V3.3 *** B7FH79_MEDTR)						IPR009902 (PFAM): G3DSA:3.40.50.1	0,098	0,043	0,000	0,050	0,046									
Solyc06g035410	Purine permease (AHRD V3.3 *-* G7KBC7_MEDTR),Pfam:PF16913		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	0,061	0,079	0,174	0,241	0,141									
Solyc06g035430	AT hook motif DNA-binding family protein (AHRD V3.3 *** AT4G25320.1)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	0,315	0,583	1,817	2,357	1,252									
Solyc06g035440	Cell cycle regulated microtubule associated protein, putative (AHRD V3.3 *** A0A061G0R3_THECC)		C:GO:0005819; C:G(	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027330 (PFAM): mobidb-lite (MOB	0,756	1,341	0,832	1,677	2,252			1,414	0,019				up	
Solyc06g035450	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9R9L5_RICCO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR011545 (PF.	1011,291	893,833	642,019	586,212	529,652									
Solyc06g035480	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,272	0,098	0,391	0,490	0,118									
Solyc06g035490	bHLH transcription factor 042		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase			IPR011598 (SMAF bHLH	0,974	6,016	0,190	0,192	0,186	2,644	0,000					up		
Solyc06g035520	Gibberellin receptor GID1 (AHRD V3.3 *** A0A151RHF2_CAJCA)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	1,205	1,122	0,797	0,608	1,129									
Solyc06g035530	gibberellin 20-oxidase-2		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	0,219	0,183	0,166	0,149	0,000									
Solyc06g035555	MADS-box transcription factor (AHRD V3.3 *** A0A023JBH3_9ROSI)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM): IPR002487 (PRC	0,326	0,641	0,600	0,389	0,615									
Solyc06g035560	MADS-box transcription factor (AHRD V3.3 *-* G7L1F7_MEDTR)		F:GO:0000977; P:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINTS): IPR002100 (SM	0,155	0,081	0,025	0,099	0,309									
Solyc06g035580	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT5G51950.3)		F:GO:0016614; F:G(	F:oxidoreductase activity, acting on CH-OH group of donors; F:f			IPR007867 (PFAM): IPR000172 (PFA	292,963	248,028	4,208	10,983	3,676					1,384	0,001			up
Solyc06g035610	RNA-binding family protein (AHRD V3.3 *** A0A061F5T2_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	7,134	3,083	0,954	0,626	1,056	-1,179	0,001					down		
Solyc06g035620	GRAS family transcription factor (AHRD V3.3 *** D4QD66_DIACA)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	0,795	0,454	0,399	0,484	0,378									
Solyc06g035690	Post-GPI attachment-like factor-protein (AHRD V3.3 *** A0A072UAB4_MEDTR)		C:GO:0000139; P:G(	C:Golgi membrane; P:GPI anchor biosynthetic process; C:integi			IPR007217 (PFAM): PTHR13148:SF5	34,047	14,764	38,473	41,429	41,271	-1,175	0,000					down		
Solyc06g035700	Dehydration responsive element binding transcription factor (AHRD V3.3 *** W6FIY4_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	3,522	4,025	1,579	1,909	2,915									
Solyc06g035710	Protein DETOXIFICATION (AHRD V3.3 *** K4C4U3_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	0,021	0,018	0,000	0,000	0,000									
Solyc06g035720	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** BAG2_ARATH)		F:GO:0051087	F:chaperone binding			IPR003103 (SMART): IPR000626 (PF.	206,357	137,381	16,899	8,804	12,356					-0,939	0,001			down
Solyc06g035760	Cytochrome P450 (AHRD V3.3 *** R4R2I7_9SOLA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	3,907	5,867	0,025	0,000	0,000									
Solyc06g035770	LOW QUALITY:paired amphipathic helix Sin3-like protein (AHRD V3.3 --* AT1G10450.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,022	0,046									
Solyc06g035790	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G00750.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	9,769	8,571	6,409	4,765	5,754									
Solyc06g035810	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT4G00750.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): IPR004159 (PAN	0,038	0,163	0,100	0,101	0,047									
Solyc06g035820	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MRN6_ARALL)						IPR016140 (SMART): IPR016140 (PF.	0,019	0,000	0,000	0,000	0,000									
Solyc06g035830	LOW QUALITY:Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G43500.9)							0,119	0,041	0,076	0,000	0,071									
Solyc06g035840	LOW QUALITY:SIN3-like 3 (AHRD V3.3 --* AT1G24190.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,059	0,036	0,050	0,025	0,023									
Solyc06g035850	LOW QUALITY:BnaC04g27970D protein (AHRD V3.3 -** A0A078E1W4_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,019	0,046	0,000	0,023									
Solyc06g035860	multidrug resistance-associated protein 3 (AHRD V3.3 --* AT3G13080.4)							1,277	0,995	0,861	0,881	0,756									
Solyc06g035870	Membrane steroid-binding protein (AHRD V3.3 *** G5DXK7_SILLA)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			IPR001199 (SMART): IPR001199 (PF.	149,009	140,780	262,453	233,708	230,961									
Solyc06g035920	Remorin (AHRD V3.3 *** REMO_SOLTU)		C:GO:0005886; P:G(	C:plasma membrane; P:cell-cell signaling; F:galacturonate bindi			IPR005518 (PFAM): IPR005516 (PFA	80,269	75,360	48,510	47,982	48,801									
Solyc06g035930	LOW QUALITY:CYCLIN B2-4 (AHRD V3.3 --* AT1G76310.4)							1,182	0,548	0,440	0,313	0,352									
Solyc06g035940	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			IPR002913 (SMAF HD-ZIP	0,344	0,336	0,237	0,210	0,284									

Solyc06g035960	4-coumarate:CoA ligase-like protein (AHRD V3.3 *** A0A0A1ETC4_ALBBR)	4CL-Like	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): IPR025110 (PFA	43,197	84,293	36,508	70,302	52,658					0,947	0,000			up
Solyc06g035970	Tubulin beta chain (AHRD V3.3 *** TBB_HORVU)		F:GO:0003924: F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	0,061	0,043	0,025	0,224	0,069									
Solyc06g035980	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G11620.9)							0,037	0,021	0,025	0,000	0,000									
Solyc06g036000	DNA-directed RNA polymerase III subunit RPC3 (AHRD V3.3 *** A0A0B0MV99_GOSAR)		F:GO:0003697: F:GC	F:single-stranded D	EC:2.7.7.6	DNA-directed RNA pc	IPR036388 (G3DSA:1.10.10.GENE3D	4,998	5,321	5,354	4,611	5,209									
Solyc06g036040	LOW QUALITY:Oxidoreductase/transition metal ion-binding protein, putative (AHRD V3.3 *-* A0A072UAG3		C:GO:0016020	C:membrane			PTHR33740 (PANTHER): PTHR33740	0,000	0,021	0,000	0,000	0,000									
Solyc06g036050	60S ribosomal protein L36 (AHRD V3.3 *** K4C4X4_SOLLC)		F:GO:0003735: C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000509 (PFAM): IPR038097 (G3D	162,098	189,853	124,895	116,460	120,897									
Solyc06g036060	Zinc finger, C2H2 (AHRD V3.3 *-* A0A103YJ68_CYNCS)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	19,204	17,269	9,074	8,080	10,334									
Solyc06g036070	SKP1 family protein (AHRD V3.3 *** B9I474_POPTR)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR001232 (SMART): G3DSA:3.30.71	12,648	12,641	16,048	19,010	17,201									
Solyc06g036080	MAP kinase kinase kinase 37		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	26,801	24,334	24,164	20,562	24,753									
Solyc06g036100	Divalent ion symporter (AHRD V3.3 *** AT1G02260.2)		C:GO:0016021: P:GC	C:integral component of membrane; P:transmembrane transport			IPR004680 (PFAM): mobidb-lite (MOB	3,865	2,472	0,849	1,323	1,267									
Solyc06g036110	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G23950.2)						IPR000008 (SMART): IPR000008 (PF	23,340	73,784	34,241	40,712	38,272	1,682	0,000					up		
Solyc06g036120	alpha-1,2-Mannosidase (AHRD V3.3 --* A0A0A0KLY9_CUCSA)							3,336	3,713	3,280	3,005	2,519									
Solyc06g036130	Protein DETOXIFICATION (AHRD V3.3 *** K4C4Y2_SOLLC)		P:GO:0006855: F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	22,243	41,231	160,574	200,435	183,310									
Solyc06g036170	gras9	GRAS9	F:GO:0003700: C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM_GRAS	135,640	87,449	303,550	461,910	306,433					0,609	0,001			up
Solyc06g036180	Protein arginine N-methyltransferase 5 (AHRD V3.3 --* ANM5_ORYSI)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,104	1,740	1,129	1,783	1,104									
Solyc06g036200	Transcription initiation factor TFIID subunit 13 (AHRD V3.3 *** A0A0B0MGR7_GOSAR)		P:GO:0006366: F:GC	P:transcription by RNA polymerase II; F:protein heterodimerizati			IPR003195 (PFAM): IPR009072 (G3D	0,000	0,082	0,000	0,025	0,000									
Solyc06g036210	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 *-* NDHK_SOLLC)		F:GO:0005506: F:GC	F:iron ion binding; F	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	G3DSA:3.40.50.12280 (GENE3D): PT	0,000	0,200	0,121	0,145	0,212									
Solyc06g036230	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *-* D7LUP2_ARALL)		F:GO:0005504: P:GC	F:fatty acid binding; P:systemic acquired resistance			PTHR33122:SF14 (PANTHER): IPR03	0,262	0,101	0,044	0,000	0,047									
Solyc06g036231	Pleiotropic drug resistance transporter 1 (AHRD V3.3 *-* A0A096VPM7_PANGI)		F:GO:0000166: F:GC	F:nucleotide binding; F:ATP binding; C:membrane; C:integral coi			PTHR19241 (PANTHER): PTHR19241	0,063	0,000	0,075	0,000	0,000									
Solyc06g036234	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TUG3_ACAMN)		F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): IPR013581 (PFA	0,159	0,260	0,477	0,580	0,423									
Solyc06g036236	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TUG3_ACAMN)		F:GO:0000166: F:GC	F:nucleotide binding; F:ATP binding; C:membrane; C:integral coi			PTHR19241:SF437 (PANTHER): PTHI	0,021	0,000	0,000	0,025	0,000									
Solyc06g036238	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *-* A0A072UG71_MEDTR)		C:GO:0016020	C:membrane			IPR013525 (PFAM): PTHR19241 (PAN	0,253	0,175	0,366	0,759	0,752									
Solyc06g036240	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TUG3_ACAMN)	ABCG59	F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	0,155	0,203	0,285	0,265	0,188									
Solyc06g036250	stress response NST1-like protein (AHRD V3.3 *** AT4G25670.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,576	1,676	6,024	4,153	2,053			-1,549	0,000				down	
Solyc06g036260	beta-carotene hydroxylase-1	BCH1	F:GO:0005506: P:GC	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): PTHR31899:SF7	85,240	67,280	61,367	58,619	68,648									
Solyc06g036290	heat shock protein 90	hsp90	F:GO:0005524: P:GC	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS): IPR003594 (SM	178,581	88,836	181,559	197,869	170,685	-0,980	0,004					down		
Solyc06g036300	translation initiation factor (AHRD V3.3 --* AT1G44780.2)						mobidb-lite (MOBII_MYB_related	0,000	0,000	0,000	0,025	0,000									
Solyc06g036305	MYB transcription factor (AHRD V3.3 *** A1DR87_CATRO)		F:GO:0003677	F:DNA binding			IPR001005 (SMART): IPR006447 (TIC	15,015	10,552	24,687	23,140	22,624									
Solyc06g036310	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A072TW71_MEDTR)		P:GO:0030001: F:GC	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	86,471	126,777	8,814	9,018	13,682									
Solyc06g036320	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SGZ7_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAI	0,000	0,000	0,025	0,000	0,000									
Solyc06g036330	LOW QUALITY:Ornithine cyclodeaminase/mu-crystallin (AHRD V3.3 *** B7FJU0_MEDTR)		C:GO:0005737: P:GC	C:cytoplasm; P:arginine catabolic process; C:integral componer			IPR023401 (G3DSA:3.30.1780.GENE	80,601	79,712	51,575	52,789	58,423									
Solyc06g036340	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT3G49140.1)						IPR037119 (G3DSA:3.20.180.GENE3I	11,315	10,751	34,979	39,477	34,566									
Solyc06g036350	NADH-ubiquinone oxidoreductase-like protein (AHRD V3.3 *** AT5G52840.1)		C:GO:0005747: P:GC	C:mitochondrial respiratory chain complex I; P:respiratory electi			IPR006806 (PFAM): mobidb-lite (MOB	68,346	61,574	99,088	85,046	85,173									
Solyc06g036420	SGT1 (AHRD V3.3 *** A0A023GU62_CAPAN)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR008978 (G3	0,181	0,890	0,118	0,346	0,444									
Solyc06g036430	Reticulon-like protein (AHRD V3.3 *** K4C509_SOLLC)		C:GO:0005789: C:GC	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994 (PAI	52,961	49,397	37,227	34,946	35,196									
Solyc06g036440	S-type anion channel (AHRD V3.3 *** A0A098GMQ9_9ROSI)		P:GO:0006873: F:GC	P:cellular ion homeostasis; F:voltage-gated anion channel activ			IPR004695 (PFAM): IPR038665 (G3D	1,375	1,883	0,125	0,292	0,282									
Solyc06g036460	Membrane-associated kinase regulator-like protein, putative (AHRD V3.3 *** A0A072U8P3_MEDTR)		F:GO:0016301: P:GC	F:kinase activity; P:phosphorylation			PTHR34576 (PANTHER): PTHR34576	0,040	0,060	0,044	0,000	0,000									
Solyc06g036463	vacuole protein (AHRD V3.3 *-* AT4G33625.2)		C:GO:0005774: C:GC	C:vacuolar membrane; C:integral component of membrane			PTHR34965 (PANTHER)	3,261	3,096	3,423	4,064	3,227									
Solyc06g036467	Protein kinase, putative (AHRD V3.3 *-* Q1EP57_MUSBA)		F:GO:0004674: F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,445	0,418	0,335	0,450	0,260									
Solyc06g036470	Serine/threonine-protein kinase (AHRD V3.3 *** K4BEK1_SOLLC)		P:GO:0048544	P:recognition of pollen			IPR001480 (SMART): IPR036426 (G3	0,021	0,000	0,000	0,000	0,000									
Solyc06g036500	LOW QUALITY:Proline-rich cell wall-like protein (AHRD V3.3 *-* A0A072V261_MEDTR)		C:GO:0000813: F:GC	C:ESCRT I complex; F:ubiquitin binding; P:ubiquitin-dependent protein catabolic process via the multive				0,000	0,000	0,051	0,000	0,000									
Solyc06g036520	Transmembrane protein, putative (AHRD V3.3 *-* G7JB45_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35288:SF1 (PANTHER): PTHR3	71,606	62,329	115,561	98,390	107,062									
Solyc06g036540	Transmembrane protein, putative (AHRD V3.3 *-* G7JB45_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR352	54,451	48,122	83,286	72,605	78,156									
Solyc06g036550	LOW QUALITY:3-ketoacyl-CoA synthase 6 (AHRD V3.3 --* AT1G68530.1)							0,061	0,000	0,025	0,000	0,000									
Solyc06g036580	U4/U6 small nuclear ribonucleoprotein Prp3 (AHRD V3.3 *** A0A0B2RPV3_GLYSO)		P:GO:0000398: C:GC	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			IPR013881 (PFAM): IPR010541 (PFA	30,708	30,467	35,111	34,155	35,409									
Solyc06g036590	U4/U6 small nuclear Prp3-like ribonucleoprotein (AHRD V3.3 *-* G7IF06_MEDTR)		P:GO:0000398: C:GC	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc06g036600	RNA binding protein (AHRD V3.3 *-* AT2G43410.6)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	0,208	0,076	0,000	0,000	0,000									
Solyc06g036630	Ankyrin repeat domain-containing protein 13B (AHRD V3.3 *-* A0A0B0NR41_GOSAR)						IPR021832 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc06g036640	alpha-(1,6)-fucosyltransferase (AHRD V3.3 *** AT5G28910.2)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.11350 (GENE3D): PT	39,191	26,778	70,152	67,579	80,758									
Solyc06g036660	LOW QUALITY:homeodomain GLABROUS 2 (AHRD V3.3 --* AT1G05230.9)							0,000	0,018	0,000	0,000	0,000									
Solyc06g036670	SET domain-containing protein (AHRD V3.3 *-* AT3G55080.1)		F:GO:0008168: P:GC	F:methyltransferase activity; P:methylation			IPR015353 (PFAM): IPR036464 (G3D	0,100	0,174	0,022	0,000	0,000									
Solyc06g036680	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2 (AHRD V3.3 --* BAME2_ARATH)							0,021	0,037	0,000	0,000	0,023									
Solyc06g036690	RING/U-box protein (AHRD V3.3 --* AT3G05670.3)							0,000	0,019	0,000	0,000	0,000									
Solyc06g036700	SET domain-containing protein (AHRD V3.3 *-* AT3G55080.1)		F:GO:0008168: P:GC	F:methyltransferase activity; P:methylation			G3DSA:3.90.1410.10 (GENE3D): PTH	0,137	0,222	0,000	0,070	0,047									
Solyc06g036720	Ubiquitin family protein (AHRD V3.3 *** B9N6Y0_POPTR)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): IPR000626 (SM	68,803	65,655	81,234	72,798	73,614									
Solyc06g036770	LOW QUALITY:CASP-like protein (AHRD V3.3 --* A0A0L9UWM4_PHAAN)							0,257	0,155	0,099	0,122	0,190									
Solyc06g036780	magnesium transporter, putative (DUF803) (AHRD V3.3 *** AT5G11960.1)		F:GO:0015095: P:GC	F:magnesium ion transmembrane transporter activity; P:magnes			PTHR12570:SF9 (PANTHER): IPR008	8,160	7,421	8,145	8,026	8,000									
Solyc06g042950	SANT domain-containing protein 2 (AHRD V3.3 *** A0A1D1YHB5_9ARAE)						PTHR34958 (PANTHER)	18,005	16,688	20,771	19,919	20,417									
Solyc06g042960	SANT domain-containing protein 2 (AHRD V3.3 *** A0A1D1YHB5_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,220	5,236	7,401	8,282	7,823									
Solyc06g042990	ATPase subunit 4 (AHRD V3.3 *-* A0A0K1ZEU7_SOLCA)		C:GO:0000276: F:GC	C:mitochondrial proton-transporting ATP synthase complex, cou			IPR008688 (PFAM): PTHR37774 (PAI	0,000	0,021	0,000	0,025	0,000									
Solyc06g043020	Atp synthase subunit alpha (AHRD V3.3 *** A0A061S892_9CHLO)		F:GO:0003676: C:GC	F:nucleic acid binding; C:chloroplast			PTHR38146 (PANTHER)	0,237	0,490	0,465	0,395	0,469									
Solyc06g043030	Affected trafxn,cking 2 isoform 1 (AHRD V3.3 *** A0A061FTS2_THECC)		P:GO:0006886: P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR029390 (SMART): IPR029390 (PF	47,373	37,720	44,325	46,914	43,467									
Solyc06g043032	Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 --* AT2G25770.2)							0,239	0,197	0,326	0,245	0,166									
Solyc06g043036	Ycf68 (AHRD V3.3 *-* A0A1B0ZD71_EUCUL)		C:GO:0009507	C:chloroplast			IPR022546 (PFAM): PTHR34890 (PAI	0,063	0,082	0,125	0,146	0,189									
Solyc06g043038	Ycf68 (AHRD V3.3 *-* K4PN21_LOLMU)		C:GO:0005739: C:GC	C:mitochondrion; C:chloroplast				0,021	0,018	0,025	0,025	0,096									
Solyc06g043070	FMN-binding split barrel (AHRD V3.3 *** A0A103YIL6_CYNCS)		F:GO:0048037	F:cofactor binding			IPR012349 (G3DSA:2.30.110.GENE3I	13,986	15,081	15,217	14,538	13,700									
Solyc06g043113	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151R878_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc06g043140	Autophagy protein 5 (AHRD V3.3 *** K4C567_SOLLC)		C:GO:0005737: P:GC	C:cytoplasm; P:autophagy			G3DSA:3.10.20.90 (GENE3D): IPR00	4,060	4,766	5,558	5,568	4,674									
Solyc06g043150	cell cycle switch 52B		F:GO:0005515: F:GC	F:protein binding; F:anaphase-promoting complex binding; F:ubi			IPR001680 (SMART): IPR001680 (PF	0,331	0,617	0,000	0,075	0,000									
Solyc06g043160	LOW QUALITY:Pre-mRNA-processing-splicing factor 8 (AHRD V3.3 *-* W9R414_9ROSA)		P:GO:0000244: F:GC	P:spliceosomal tri-snRNP complex assembly; F:second spliceos			IPR012984 (PFAM): G3DSA:3.40.140	0,000	0,039	0,025	0,000	0,024									
Solyc06g043170	Unknown protein (AHRD V3.3)							0,222	0,039	0,457	0,292	0,234									
Solyc06g043175	Actin/actin-like family protein (AHRD V3.3 *** U5G2L8_POPTR)						IPR004000 (SMART): G3DSA:3.30.42	0,000	0,059	0,000	0,025	0,024									
Solyc06g043280	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT3G59210.5)							0,000	0,000	0,022	0,000	0,000									
Solyc06g043352	SKP1-like protein (AHRD V3.3 *** A0A0P0CFU9_CATRO)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR001232 (SMART): G3DSA:3.30.71	0,000	0,039	0,328	0,612	0,353									
Solyc06g048390	NADP-malic enzyme 3 (AHRD V3.3 --* AT5G25880.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc06g048410	iron superoxide dismutase	fesod	F:GO:0004784: P:GC	F:superoxide dismu	EC:1.15.1.1	Superoxide dismutas	IPR001189 (PRINTS): IPR036324 (G3	270,183	395,975	307,451	279,165	390,558	0,579	0,031					up		
Solyc06g048420	Superoxide dismutase (AHRD V3.3 *** K4C589_SOLLC)		F:GO:0004784: P:GC	F:superoxide dismu	EC:1.15.1.1	Superoxide dismutas	IPR036314 (G3DSA:2.40.500.GENE3I	0,082	0,116	0,097	0,142	0,047									
Solyc06g048430	ATP synthase epsilon chain (AHRD V3.3 *** A0A0K9P5X2_ZOSMR)		P:GO:0015986: C:GC	P:ATP synthesis co	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036771 (G3DSA:2.60.15.GENE3D	3,136	2,481	1,597	1,059	1,458									
Solyc06g048440	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* A0A0U1WME9_9ORYZ)		F:GO:0003899: P:GC	F:DNA-directed 5'-3' RNA polymerase activity; P:RNA biosynthe			IPR010800 (PFAM): mobidb-lite (MOB	34,649	35,210	2,918	3,135	7,140									
Solyc06g048450	Anaphase-promoting complex subunit 1 (AHRD V3.3 *** A0A118K619_CYNCS)		C:GO:0005680	C:anaphase-promoting complex			IPR024990 (PFAM): IPR024990 (PAN	16,416	13,085	12,223	14,160	14,164									
Solyc06g048460	Anaphase-promoting complex subunit 1 (AHRD V3.3 *** W9RQW6_9ROSA)		C:GO:0005680	C:anaphase-promoting complex			PF18122 (PFAM): IPR024990 (PANTH	18,535	16,397	17,011	15,451	16,865									
Solyc06g048470	COP1-interacting-like protein, putative (AHRD V3.3 *** A0A072V1D3_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	88,834	62,877	8,683	7,059	7,686									
Solyc06g048480	Transducin/WD40 repeat protein (AHRD V3.3 *** G7J9R1_MEDTR)						PTHR31789 (PANTHER): SSF69322 (	21,927	21,152	24,023	23,570	22,053									
Solyc06g048510	WD repeat domain phosphoinositide-interacting protein 3 (AHRD V3.3 *** W9S9Q2_9ROSA)		F:GO:0005515	F:protein binding			IPR001680 (SMART): mobidb-lite (MO	49,236	42,951	57,633	55,641	53,388									
Solyc06g048520	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01960.1)		C:GO:0016021: F:GC	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	16,589	16,262	32,272	33,915	28,903									
Solyc06g048530	Hydroxyacylglutathione hydrolase (AHRD V3.3 *** K7VP97_SOLTU)		F:GO:0004416: P:GC	F:hydroxyacylglutat	EC:3.1.2.6	Hydroxyacylglutathioi	IPR001279 (SMART): IPR013103 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc06g048540	ABC transporter family protein (AHRD V3.3 *** A0A097P9T8_HEVBR)	ABCI6	F:GO:0005524: F:GC	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	39,209	51,235	110,443	112,319	117,343									
Solyc06g048570	Methyl esterase 17 (AHRD V3.3 *** A0A061FZJ0_THECC)		P:GO:0033473: P:GC	P:indoleacetic acid	EC:3.1.1.1	Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	2,543	2,603	0,568	1,151	1,058									
Solyc06g048590	Transmembrane receptor, eukaryota (AHRD V3.3 *** A0A124SFZ6_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR009637 (PFAM): PTHR21229:SF1	18,080	17,576	10,804	10,433	10,756									
Solyc06g048600	Response regulator 7	RRA7	P:GO:0000160	P:phosphorelay signal transduction system			IPR001789 (SMART): G3DSA:3.40.50	0,000	0,060	0,000	0,025	0,000									
Solyc06g048610	Nucleic acid-binding, OB-fold-like protein (AHRD V3.3 *** Q93VB0_ARATH)		F:GO:0000049	F:tRNA binding			IPR002547 (PFAM): G3DSA:1.20.105	37,961	39,180	53,198	53,620	49,751									
Solyc06g048620	Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** A0A072V1G8_MEDTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS): IPR003591 (SMA	12,322	5,748	1,104	2,007	1,756	-1,068	0,020					down		
Solyc06g048630	methionine sulfoxide reductase A1	MSRA1	F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (SMAF_bZIP	37,983	36,630	17,720	18,862	19,604									
Solyc06g048633	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-containing protein (AHRD V3.3 --* AT3G10310.2)							4,662	1,707	2,077	2,049	2,100	-1,423	0,001					down		
Solyc06g048637	Exosome complex exonuclease RRP44 (AHRD V3.3 *-* A0A068EX93_COCNU)		F:GO:0004518: P:GC	F:nuclease activity; P:nucleic acid metabolic process				12,798	7,837	7,809	5,756	7,099									
Solyc06g048640	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT1G11270.3)							0,594	0,120	0,399	0,267	0,450									
Solyc06g048700	LOW QUALITY:B-cell lymphoma 6 protein, putative (AHRD V3.3 -** A0A061GDG5_THECC)		P:GO:0010227	P:floral organ abscission			PTHR33599:SF10 (PANTHER): IPR03	0,857	0,250	0,225	0,224	0,282									
Solyc06g048710	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611: P:GC	P:response to wounding; P:jasmonic acid metabolic process; P:			IPR004993 (PFAM): IPR004993 (PAN	0,056	0,057	0,000	0,000	0,000									
Solyc06g048717	initiation factor 4F subunit (DUF1350) (AHRD V3.3 --* AT3G43540.2)							0,021	0,021	0,000	0,047	0,000									
Solyc06g048720	LOW QUALITY:NHL repeat-containing family protein (AHRD V3.3 *-* B9HJT0_POPTR)		C:GO:0016021	C:integral component of membrane			PTHR13833:SF42 (PANTHER): PTHR	0,198	0,134	0,022	0,000	0,047									
Solyc06g048730	Uroporphyrinogen decarboxylase (AHRD V3.3 *** K4C5B9_SOLLC)	HEME/UROD	F:GO:0004853: P:GC	F:uroporphyrinogen	EC:4.1.1.37	Uroporphyrinogen de	IPR000257 (PFAM): IPR006361 (TIGF	26,342	41,141	45,350	48,666	58,006	0,670	0,005					up		
Solyc06g048740	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR003591 (SM	0,021	0,186	0,047	0,145	0,284									
Solyc06g048750	Unknown protein (AHRD V3.3)							2,173	2,125	0,000	0,025	0,000									
Solyc06g048770	syntaxin of plants 51 (AHRD V3.3 --* AT1G16240.3)							3,030	3,130	0,025	0,000	0,070									
Solyc06g048780	LOW QUALITY:PLAC8 family protein (AHRD V3.3 *-* AT3G10980.1)		F:GO:0009975: C:GC	F:cyclase activity; C:integral component of membrane; P:sesqu			IPR021369 (PFAM): mobidb-lite (MOB	0,040	0,156	0,000	0,000	0,023									
Solyc06g048790	Plant cadmium resistance 10-like protein (AHRD V3.3 *** A0A0B0N332_GOSAR)		C:GO:0016020	C:membrane			IPR006461 (PFAM): IPR006461 (TIGF	0,000	0,037	0,025	0,000	0,000									
Solyc06g048800	LOW QUALITY:Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 --* AT4G19890.1)							0,042	0,018	0,050	0,000	0,000									
Solyc06g048810	Protein PLANT CADMIUM RESISTANCE 8 (AHRD V3.3 *** A0A1D1Y0F1_9ARAE)		C:GO:0016021	C:integral component of membrane			IPR006461 (TIGRFAM): IPR006461 (F	38,285	44,895	29,058	33,200	32,693									
Solyc06g048820	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR016533 (PIRSF): IPR009798 (PFA	27,233	36,264	7,535	7,751	10,553									
Solyc06g048840	Late embryogenesis abundant protein (AHRD V3.3 *** H2E688_HORVU),Pfam:PF00477		C:GO:0005829: P:GC	C:cytosol; P:response to abscisic acid			IPR038956 (PFAM): mobidb-lite (MOB	3,871	12,137	12,513	26,160	2,339									
Solyc06g048850	methionine-S-oxide reductase (AHRD V3.3 *-* AT2G17705.1)						PTHR33674 (PANTHER): PTHR33674	0,000	0,039	0,000	0,025	0,000									
Solyc06g048860	Laccase (AHRD V3.3 *** A0A022PYV8_ERYGU)		F:GO:0005507: P:GC	F:copper ion binding	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR017761 (TIGRFAM): IPR008972 (C	0,059	0,081	0,206	0,287	0,400									
Solyc06g048865	basic pentacysteine 6 (AHRD V3.3 --* AT5G42520.3)							1,661	1,360	1,065	1,340	1,034									
Solyc06g048870	WRKY transcription factor 19	WRKY19	F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF_WRKY	0,019	0,041	0,000	0,000	0,024									
Solyc06g048890	Protein kinase (AHRD V3.3 *-* A0A0K9NZM3_ZOSMR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PTHF	5,274	3,692	4,539	3,661	4,812									
Solyc06g048893	Protein kinase (AHRD V3.3 *** A0A0K9NZM3_ZOSMR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR011989 (G3DSA:1.25.10.GENE3D	21,203	16,593	19,518	18,949	18,799									
Solyc06g048897	LOW QUALITY:Polyprotein, putative (AHRD V3.3 *-* Q0KIN7_SOLDE)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): PTHR23272 (PAI	0,021	0,000	0,000	0,073	0,023									
Solyc06g048900	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061FSK4_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,909	2,541	3,226	3,186	3,101									
Solyc06g048910	LOW QUALITY:Disease resistance protein (AHRD V3.3 *** W9RZV6_9ROSA)		F:GO:0005515: F:GC	F:protein binding; F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,019	0,000	0,000	0,000	0,000									
Solyc06g048920	Glycerol-3-phosphate dehydrogenase [NAD(+)] (AHRD V3.3 *** K4C5D8_SOLLC)		F:GO:0004367: C:GC	F:glycerol-3-phosph	EC:1.1.1.8; EC:1.1.1	Glycerol-3-phosphate	IPR006168 (PRINTS): G3DSA:3.40.50	13,668	13,923	15,538	18,715	17,916									
Solyc06g048930	Tomato Response regulator 16,17	TRR 16/17	P:GO:0000160	P:phosphorelay signal transduction system			IPR001789 (SMART): G3DSA:3.40.50	2,973	2,421	4,802	7,000	5,063									
Solyc06g048935	Ferritin (AHRD V3.3 --* F6GXT8_VITVI)							0,696	0,873	1,060	1,323	1,314									
Solyc06g048940	Transmembrane 9 superfamily member (AHRD V3.3 *** K4C5E0_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): IPR004240 (PAN	21,577	26,795	25,031	31,837	29,900									
Solyc06g048950	Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** A0A072V1G8_MEDTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS): IPR003591 (SMA	9,129	7,601	0,688	0,663	0,893									
Solyc06g048960	Dicer-like 2a	DCL2a	F:GO:0003676: F:GC	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR001650 (SMART): IPR000999 (SM	12,828	11,317	8,390	8,123	8,171									
Solyc06g048970	Cation-transporting ATPase 4 (AHRD V3.3 *** A0A0B0MJG4_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	14,772	11,871	7,855	6,964	8,107									
Solyc06g049010	EIN3-binding F-box-like protein (AHRD V3.3 *** G7I706_MEDTR)	EBF4	F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001611 (PF	0,040	0,054	0,000	0,000	0,000									
Solyc06g049020	Sorghum bicolor protein targeted either to mitochondria or chloroplast proteins T50848 (AHRD V3.3 *** C7IVU8_9POAL)						PTHR35127 (PANTHER)	79,026	18,846	24,725	72,259	27,324	-2,042	0,000			1,552	0,000	down		up
Solyc06g049030	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FT40_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	8,204	7,088	1,990	1,127	1,553									
Solyc06g049040	BZIP transcription factor (AHRD V3.3 *** A0A072V8H4_MEDTR)		F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (SMAF_bZIP	3,463	3,564	0,626	0,479	0,845									
Solyc06g049050	expansin 2	EXPA2	C:GO:0005576: P:GC	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	0,423	0,921	0,243	0,286	0,234									
Solyc06g049060	Reticulon-like protein (AHRD V3.3 *** A0A0V0HSV9_SOLCH)		C:GO:0005789: C:GC	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): mobidb-lite (MOB	13,716	15,909	11,451	11,924	11,717									
Solyc06g049070	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT2G30460.2)		F:GO:0005464: C:GC	F:UDP-xylose transmembrane transporter activity; C:Golgi appa			IPR004853 (PFAM): PTHR44159:SF1	38,311	45,505	27,187	33,732	26,811									
Solyc06g049080	thioredoxin peroxidase 1	tpx1	F:GO:0004784: P:GC	F:superoxide dismu	EC:1.15.1.1	Superoxide dismutas	IPR001189 (PRINTS): IPR019831 (PF	13,952	14,391	28,300	22,391	28,305									
Solyc06g049090	N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative (AHRD V3.3 *** B9SAN0_RICCO)		F:GO:0003723: F:GC	F:RNA binding; F:tRNA (guanine-N2-)-methyltransferase activity			G3DSA:3.30.56.70 (GENE3D): IPR00	2,149	2,419	3,391	2,657	4,034									
Solyc06g049100	N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative (AHRD V3.3 *-* B9SAN0_RICCO)		F:GO:0003723: F:GC	F:RNA binding; F:tRNA (guanine-N2-)-methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	1,782	2,721	2,694	2,401	3,535									
Solyc06g050110	Gibberellin 20-oxidase (AHRD V3.3 *** Q9M4A0_SOLDU)		F:GO:0016491: P:GC	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR026992 (PFA	0,061	0,039	0,000	0,000	0,000									
Solyc06g050120	60S ribosomal protein L7A-like (AHRD V3.3 *** Q2VCI3_SOLTU)		P:GO:0000470: F:GC	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large ribc			IPR001921 (PRINTS): IPR018492 (PF	361,472	331,129	403,968	314,602	339,918					-0,357	0,049			down
Solyc06g050130	Alpha-galactosidase (AHRD V3.3 *** K4C5G0_SOLLC)		F:GO:0004553: P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbc			IPR002241 (PRINTS): PF17801 (PFA	41,694	34,336	31,208	26,911	38,587									
Solyc06g050140	LOW QUALITY:Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G17150.6)		P:GO:0010227	P:floral organ abscission			mobidb-lite (MOBIDB_LITE): IPR0396	0,337	0,356	0,050	0,266	0,117									
Solyc06g050160	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)		F:GO:0003677: F:GC	F:DNA binding; F:lipid binding			IPR002913 (SMAF_HD-ZIP	0,077	0,021	0,590	0,561	0,591									

Solyc06g050170	Potassium transporter (AHRD V3.3 *** W8NQ93_OLEEU)		F:GO:0015079: C:G(	F:potassium ion transmembrane transporter activity; C:membrai		IPR003855 (PFAM): IPR003855 (TIGF	82,514	66,505	43,883	43,815	44,864									
Solyc06g050210	TLC ATP/ADP transporter (AHRD V3.3 *** A0A061FRW5_THECC)		F:GO:0005471: P:G(	F:ATP:ADP antiporter activity; P:nucleotide transport; C:integral		IPR004667 (PFAM): mobidb-lite (MOB	12,480	10,568	14,084	14,645	13,279									
Solyc06g050220	Alpha-soluble NSF attachment protein (AHRD V3.3 *-* SNAA_SOLTU)		F:GO:0005515	F:protein binding		PF14938 (PFAM): IPR011990 (G3DSA	4,796	6,637	4,608	4,028	4,563									
Solyc06g050230	Dual specificity protein phosphatase, putative (AHRD V3.3 *** B9S4C7_RICCO)		P:GO:0006470: F:G(	P:protein dephosph EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR029021 (G3	78,319	70,517	84,944	95,352	88,552									
Solyc06g050250	Adenine/guanine permease AZG1 (AHRD V3.3 *** AZG1_ARATH)		F:GO:0005345: P:G(	F:purine nucleobase transmembrane transporter activity; P:purii		IPR006043 (PFAM): IPR029950 (PTH	4,179	2,638	3,404	3,183	3,073									
Solyc06g050270	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C5H2_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR004041 (PF.	0,075	0,138	0,025	0,051	0,023									
Solyc06g050280	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C5H3_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR004041 (PF.	0,000	0,060	0,025	0,000	0,000									
Solyc06g050290	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C5H4_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): IPR004041 (PF.	0,019	0,037	0,050	0,122	0,047									
Solyc06g050300	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C5H5_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): G3DSA:3.30.31	35,938	35,331	40,994	54,272	39,040					0,406	0,024			up
Solyc06g050310	Haloacid dehalogenase-like hydrolase superfamily protein (AHRD V3.3 *** A0A097PQD8_SOLLC)					IPR023214 (G3DSA:3.40.50.GENE3D	31,446	31,301	47,259	47,129	54,069									
Solyc06g050320	High mobility group (HMG) box domain-containing protein (AHRD V3.3 *** A0A103YDE8_CYNCS)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus		PTHR13711:SF147 (PANTHER): PTHI	5,718	8,666	3,176	6,199	5,399			0,756	0,049	0,964	0,004		up	up
Solyc06g050330	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_MUTAC)						0,181	0,122	0,022	0,097	0,143									
Solyc06g050340	villin 4 (AHRD V3.3 --* AT4G30160.4)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,879	0,550	0,071	0,525	0,541									
Solyc06g050350	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT2G38370.2)		C:GO:0005829: P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac		IPR008545 (PFAM): mobidb-lite (MOB	21,482	17,276	4,533	4,289	5,910									
Solyc06g050360	Polycomb group protein FERTILIZATION-INDEPENDENT SEED 2 (AHRD V3.3 --* FIS2C_ARATH)						1,543	1,229	1,040	0,850	0,843									
Solyc06g050370	LOW QUALITY:OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 --* AT4G25850.2)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation		PTHR33257:SF17 (PANTHER): PTHR:	6,671	8,436	0,802	0,597	0,653									
Solyc06g050390	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G48120.1)					IPR019557 (PFAM): mobidb-lite (MOB	0,116	0,120	0,000	0,000	0,000									
Solyc06g050400	Lysine--tRNA ligase (AHRD V3.3 *-* A0A0V0IK21_SOLCH)		F:GO:0000049: F:G(	F:tRNA binding; F:ly EC:6.1.1.6	Lysine--tRNA ligase	G3DSA:3.30.930.10 (GENE3D): PTHF	0,019	0,059	0,022	0,025	0,024									
Solyc06g050430	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4B8_RICCO)					IPR004883 (PFAM LBD	0,277	0,238	0,277	0,225	0,187									
Solyc06g050440	Peroxidase (AHRD V3.3 *** K4C5I8_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activil EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	1,455	1,455	1,643	1,846	1,337									
Solyc06g050460	Unknown protein (AHRD V3.3)						0,040	0,000	0,000	0,025	0,000									
Solyc06g050500	Abscisic acid receptor (AHRD V3.3 *** G7KT83_MEDTR)		F:GO:0004864: C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm		IPR019587 (PFAM): IPR023393 (G3D	20,384	19,048	5,254	5,033	5,219									
Solyc06g050510	DNA repair rhp54 (AHRD V3.3 *** A0A0B0NS67_GOSAR)		F:GO:0005524	F:ATP binding		IPR014001 (SMART): IPR001650 (SM	145,290	133,358	72,080	63,500	77,066									
Solyc06g050520	dehydration responsive element binding protein 1	dreb1	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec		IPR001471 (PRINT ERF	1,004	0,797	3,723	2,379	2,382									
Solyc06g050530	Laccase (AHRD V3.3 *** I1M7Q3_SOYBN)		F:GO:0005507: P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a		IPR008972 (G3DSA:2.60.40.GENE3D	3,798	1,648	0,543	0,656	1,102	-1,159	0,034					down		
Solyc06g050540	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT1G48490.4)						0,019	0,019	0,000	0,000	0,047									
Solyc06g050550	sorting nexin 2B (AHRD V3.3 *** AT5G07120.2)		F:GO:0035091	F:phosphatidylinositol binding		IPR001683 (SMART): IPR001683 (PF.	106,593	91,937	143,485	136,365	134,629									
Solyc06g050560	Receptor-like kinase (AHRD V3.3 *** C4TP22_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro		PR00019 (PRINTS): SM00365 (SMAR	0,368	0,459	0,115	0,000	0,000									
Solyc06g050570	PRA1 family protein (AHRD V3.3 *** K4C5K1_SOLLC)		C:GO:0016021	C:integral component of membrane		IPR004895 (PFAM): mobidb-lite (MOB	43,239	44,735	27,304	26,353	24,670									
Solyc06g050590	Biotin carboxyl carrier protein (AHRD V3.3 *** A0A0H5BV69_PEA)		C:GO:0009507: P:G(	C:chloroplast; P:negative regulation of fatty acid biosynthetic pr		G3DSA:2.40.50.100 (GENE3D): IPR0(	71,352	78,339	91,061	98,655	104,557									
Solyc06g050600	Kelch repeat-containing family protein (AHRD V3.3 *-* B9IGK0_POPTR)		F:GO:0005515	F:protein binding		PR00501 (PRINTS): IPR006652 (SMA	0,611	1,123	0,172	0,167	0,213									
Solyc06g050610	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT3G11000.1)					IPR013989 (SMART): IPR013989 (PF.	1,264	1,409	0,193	0,215	0,373									
Solyc06g050620	DUF399 family protein, putative (DUF399 and DUF3411) (AHRD V3.3 *** AT2G40400.2)					G3DSA:3.40.50.11550 (GENE3D): IPI	24,817	23,079	19,971	20,084	22,016									
Solyc06g050630	arogenate dehydrogenase (AHRD V3.3 *-* AT5G34930.3)		F:GO:0004665: P:G(	F:prephenate dehyc EC:1.3.1.12; EC:1.3.	Prephenate dehydroc	G3DSA:3.40.50.720 (GENE3D): IPR0(	11,601	17,210	7,568	17,853	17,259			1,187	0,000	1,240	0,000		up	up
Solyc06g050640	Nascent polypeptide-associated complex subunit beta (AHRD V3.3 *-* BTF3L_ARATH)		P:GO:0009651	P:response to salt stress		IPR038187 (G3DSA:2.20.70.GENE3D	0,000	0,018	0,000	0,000	0,023									
Solyc06g050720	Ca(2+)-dependent nuclease family protein (AHRD V3.3 *** AT2G40410.2)		F:GO:0003676: F:G(	F:nucleic acid binding; F:nuclease activity; F:aminoacyl-tRNA lic		IPR016071 (SMART): G3DSA:1.20.12	0,063	0,021	0,047	0,000	0,046									
Solyc06g050730	Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic (AHRD V3.3 --* STAD_SIMCH)					mobidb-lite (MOBIDB_LITE): mobidb-lit	6,753	7,350	9,274	11,115	9,486									
Solyc06g050760	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane		IPR016533 (PIRSF): IPR009798 (PFA	94,925	109,129	93,323	68,454	77,756					-0,444	0,005			down
Solyc06g050770	Alpha-soluble NSF attachment protein (AHRD V3.3 *** SNAA_SOLTU)		F:GO:0005515: P:G(	F:protein binding; P:intracellular protein transport		IPR000744 (PRINTS): IPR019734 (SM	89,451	88,883	124,647	122,924	115,614									
Solyc06g050790	Amino acid transporter, putative (AHRD V3.3 *** B9S4A2_RICCO)		P:GO:0003333: F:G(	P:amino acid transmembrane transport; F:amino acid transmem		IPR013057 (PFAM): PTHR22950 (PAI	7,220	6,829	7,701	8,871	8,500									
Solyc06g050800	Amino acid transporter family protein (AHRD V3.3 *** B9HYI5_POPTR)		P:GO:0003333: F:G(	P:amino acid transmembrane transport; F:amino acid transmem		IPR013057 (PFAM): PTHR22950:SF3:	9,162	6,436	4,186	4,007	6,001									
Solyc06g050810	LURP-one-like protein (AHRD V3.3 *** G7KW19_MEDTR)					IPR007612 (PFAM): IPR038595 (G3D	5,032	15,728	1,257	1,359	3,039	1,663	0,030					up		
Solyc06g050820	Nop53 protein (AHRD V3.3 *-* AT2G40430.3)		P:GO:0000027: C:G(	P:ribosomal large subunit assembly; C:nucleolus; P:rRNA proce		IPR011687 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,049	0,000									
Solyc06g050830	Pectinesterase (AHRD V3.3 --* A0A103YG83_CYNCS)						2,799	3,402	0,666	1,173	1,198									
Solyc06g050833	alpha-1,2-Mannosidase (AHRD V3.3 --* M7ZA92_TRIUA)					mobidb-lite (MOBIDB_LITE)	7,696	8,345	2,599	3,061	3,870									
Solyc06g050840	bHLH transcription factor135		F:GO:0046983	F:protein dimerization activity		IPR036638 (G3DS bHLH	3,553	3,174	0,072	0,236	0,281									
Solyc06g050860	BTB/POZ domain-containing protein (AHRD V3.3 *** AT3G56230.1)		F:GO:0005515	F:protein binding		IPR000210 (SMART): G3DSA:1.25.40	0,021	0,000	0,000	0,000	0,000									
Solyc06g050870	Hypoxia-responsive family protein (AHRD V3.3 *** A0A061FYY0_THECC)		C:GO:0016021	C:integral component of membrane		IPR007667 (PFAM): IPR040153 (PAN	2,452	0,817	1,515	1,965	3,845			1,322	0,005				up	
Solyc06g050880	Protein kinase superfamily protein (AHRD V3.3 --* AT5G02290.2)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation		mobidb-lite (MOBIDB_LITE): mobidb-lit	9,021	10,921	10,102	9,527	8,988									
Solyc06g050890	LOW QUALITY:Ethylene receptor 3 (AHRD V3.3 --* ETR3_ORYSJ)						1,051	1,043	0,121	0,050	0,211									
Solyc06g050900	Major facilitator superfamily protein (AHRD V3.3 *** AT2G40460.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmem		IPR000109 (PFAM): IPR000109 (PAN	0,735	0,845	0,071	0,047	0,094									
Solyc06g050910	Protein transport protein Sec61 subunit gamma (AHRD V3.3 --* A0A0B2SM00_GLYSO)						0,042	0,039	0,000	0,000	0,000									
Solyc06g050920	Trichome birefringence-like protein (AHRD V3.3 *** G7K771_MEDTR)		C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace		IPR025846 (PFAM): IPR026057 (PFA	0,297	0,344	0,169	0,295	0,255									
Solyc06g050930	Cytosolic endo-beta-N-acetylglucosaminidase (AHRD V3.3 *** A0A0B0NZD9_GOSAR)		C:GO:0005737: F:G(	C:cytoplasm; F:mar EC:3.2.1.96	Mannosyl-glycoprote	IPR005201 (PFAM): IPR008979 (G3D	34,960	48,438	25,720	26,616	31,121									
Solyc06g050950	LOB domain-containing protein, putative (AHRD V3.3 *** B9S461_RICCO)					IPR004883 (PFAM LBD	0,431	0,243	1,052	0,524	0,333									
Solyc06g050980	Ferritin (AHRD V3.3 *** K4C5P1_SOLLC)		P:GO:0006826: P:G(	P:iron ion transport; P:cellular iron ion homeostasis; F:ferric iror		IPR012347 (G3DSA:1.20.1260.GENE	206,198	206,962	206,901	183,435	243,367									
Solyc06g050990	Multiple inositol polyphosphate phosphatase 1 (AHRD V3.3 *** W9QKJ4_9ROSA)		F:GO:0016791	F:phosphatase activity		IPR016274 (PIRSF): IPR000560 (PFA	23,449	22,839	31,870	34,994	32,056									
Solyc06g051000	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT3G56080.1)		F:GO:0008168	F:methyltransferase activity		G3DSA:3.40.50.150 (GENE3D): IPR0(	0,000	0,057	0,000	0,025	0,000									
Solyc06g051010	LOW QUALITY:Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein (AHRD V3.3 *** AT5(		C:GO:0005773	C:vacuole		IPR021102 (PFAM): PTHR31104:SF2	12,493	17,879	15,191	23,568	16,212					0,633	0,003			up
Solyc06g051020	LOW QUALITY:Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein (AHRD V3.3 *** AT5(		C:GO:0005773	C:vacuole		IPR021102 (PFAM): IPR021102 (PAN	67,777	45,802	156,252	145,270	140,979									
Solyc06g051030	Protein kinase family protein, putative, expressed (AHRD V3.3 *** A0A0K9Q4P0_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:1.10.510.10 (GENE3D): IPR0	79,760	67,877	24,885	39,263	42,206			0,759	0,001	0,658	0,011		up	up
Solyc06g051040	Mad3/BUB1 region 1, putative isoform 1 (AHRD V3.3 *** A0A061FM29_THECC)		P:GO:0007094	P:mitotic spindle assembly checkpoint		IPR013212 (SMART): IPR013212 (PF	0,440	0,571	0,047	0,025	0,048									
Solyc06g051045	LOW QUALITY:Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** A0A061FKX6_THECC),Pfam:PF01190					PF01190 (PFAM): PTHR31614:SF10 (	0,000	0,000	0,000	0,000	0,024									
Solyc06g051080	UDP-glucose pyrophosphorylase (AHRD V3.3 *** G7JBW8_MEDTR)		F:GO:0070569	F:uridylyltransferase activity		IPR029044 (G3DSA:3.90.550.GENE3	27,089	26,693	62,053	56,659	58,162									
Solyc06g051090	U-box domain-containing protein 13 (AHRD V3.3 *** W9RRI9_9ROSA)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot		IPR000225 (SMART): IPR003613 (SM	0,081	0,060	0,146	0,025	0,024									
Solyc06g051120	Transcription factor, putative (AHRD V3.3 *** B9SQQ1_RICCO)		C:GO:0005634: F:G(	C:nucleus; F:sequence-specific DNA binding; F:transcription rec		PF13837 (PFAM): Trihelix	16,784	17,920	19,753	21,054	20,060									
Solyc06g051130	LOW QUALITY:Transferase family protein (AHRD V3.3 *** B9HSL5_POPTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3	8,654	6,317	1,193	0,826	1,339									
Solyc06g051140	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *-* A0A072VRU4_MEDTR)					PTHR44422:SF1 (PANTHER): PTHR4	0,000	0,540	0,025	0,025	0,241									
Solyc06g051160	DnaJ/Hsp40 cysteine-rich domain superfamily protein, putative (AHRD V3.3 *** A0A061FJK4_THECC)					PTHR15852 (PANTHER): PTHR15852	7,339	7,647	11,730	10,027	11,695									
Solyc06g051190	RNA-dependent RNA polymerase (AHRD V3.3 *** K4C5R0_SOLLC)		F:GO:0003968	F:RNA-directed 5'-3 EC:2.7.7.48	RNA-directed RNA pc	IPR007855 (PFAM): PTHR23079:SF1	7,749	6,888	2,509	1,771	2,975									
Solyc06g051200	Ribosomal protein L3 family protein (AHRD V3.3 *** AT2G43030.1)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		IPR000597 (PFAM): G3DSA:2.40.30.1	31,579	47,461	61,686	62,693	71,478	0,616	0,030					up		
Solyc06g051210	Bromodomain-containing protein (AHRD V3.3 *** B9R8P3_RICCO)		F:GO:0005515	F:protein binding		IPR001487 (PRINTS): IPR001487 (SM	10,651	13,129	8,435	8,338	7,981									
Solyc06g051230	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G44410.1)		F:GO:0016874: F:G(	F:ligase activity; F:metal ion binding		IPR001841 (SMART): PF13920 (PFAM	0,178	0,096	0,090	0,122	0,071									
Solyc06g051235	RING/U-box superfamily protein (AHRD V3.3 *** AT2G44410.1)		F:GO:0016874: F:G(	F:ligase activity; F:metal ion binding		IPR001841 (SMART): IPR013083 (G3	0,021	0,000	0,000	0,000	0,000									
Solyc06g051240	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G34420.1)						0,042	0,082	0,025	0,075	0,000									
Solyc06g051250	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FKY9_THECC)		C:GO:0016021: P:G(	C:integral component of membrane; P:protein ubiquitination		IPR001841 (SMART): IPR013083 (G3	4,678	3,489	2,280	2,227	1,850									
Solyc06g051260	bHLH transcription factor 043		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat		IPR011598 (SMAF bHLH	16,245	14,625	1,902	1,499	2,353									
Solyc06g051270	Mannose-1-phosphate guanylyltransferase, putative (AHRD V3.3 *** B9SE08_RICCO)		P:GO:0009058: F:G(	P:biosynthetic process; F:nucleotidyltransferase activity		IPR001451 (PFAM): IPR029044 (G3D	73,120	69,340	73,180	65,194	69,267									
Solyc06g051300	Chromosome transmission fidelity protein 8 (AHRD V3.3 *** A0A1D1XTK7_9ARAE)		P:GO:0007064: C:G(	P:mitotic sister chromatid cohesion; C:Ctf18 RFC-like complex		IPR018607 (PFAM): PTHR28605:SF1	1,264	0,904	0,115	0,000	0,093									
Solyc06g051310	Clathrin heavy chain (AHRD V3.3 *** K4C5S4_SOLLC)		F:GO:0005198: P:G(	F:structural molecule activity; P:intracellular protein transport; P		IPR000547 (SMART): IPR016341 (PIF	260,714	239,425	220,186	221,940	218,698									
Solyc06g051320	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061EWX8_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3	0,383	0,194	0,049	0,000	0,047									
Solyc06g051330	IQ-domain 30 (AHRD V3.3 --* AT1G18840.3)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,751	0,341	1,053	1,166	1,506									
Solyc06g051350	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G55990.1)		P:GO:0050826	P:response to freezing		IPR026057 (PFAM): IPR025846 (PFA	3,662	2,290	0,122	0,164	0,071									
Solyc06g051360	Gibberellin 2-beta-dioxygenase 1-like protein (AHRD V3.3 *** A0A0B0PL18_GOSAR)		F:GO:0051213: P:G(	F:dioxygenase activity; P:oxidation-reduction process		IPR027443 (G3DSA:2.60.120.GENE3	33,648	27,734	29,233	24,873	24,977									
Solyc06g051370	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524: C:G(	F:ATP binding; C:chloroplast		IPR008543 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,123	0,000									
Solyc06g051380	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *-* AT5G05570.2)		F:GO:0005515	F:protein binding		IPR001680 (SMART): IPR015943 (G3	9,938	6,556	12,575	14,589	12,307									
Solyc06g051390	Transducin family protein / WD-40 repeat family protein, putative isoform 5 (AHRD V3.3 *** A0A061EQ99_TI		F:GO:0005515: C:G(	F:protein binding; C:integral component of membrane; P:vesicle		G3DSA:1.20.5.110 (GENE3D): IPR01	29,471	24,302	43,729	43,314	42,373									
Solyc06g051400	Omega-3 fatty acid desaturase (AHRD V3.3 *** Q7X7I9_SOLLC)	fad	P:GO:0006629: F:G(	P:lipid metabolic prc EC:1.14.19	Acting on paired donc	IPR021863 (PFAM): IPR005804 (PFA	62,975	187,130	100,901	96,660	117,798	1,598	0,000					up		
Solyc06g051410	Phosphoribosylanthranilate isomerase (AHRD V3.3 *** F1BPW4_SOLPN)	PRAI	F:GO:0004640: P:G(	F:phosphoribosylan EC:5.3.1.24	Phosphoribosylanthra	IPR013785 (G3DSA:3.20.20.GENE3D	11,098	17,841	21,512	27,015	29,704	0,713	0,012					up		
Solyc06g051420	nucleic acid-binding protein		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:histone binding		IPR001965 (SMART): IPR013083 (G3	27,910	29,366	45,427	41,978	41,771									
Solyc06g051440	Protein POLLEN DEFECTIVE IN GUIDANCE 1 (AHRD V3.3 *** POD1_ARATH)		C:GO:0016021	C:integral component of membrane		IPR008010 (PFAM): mobidb-lite (MOB	39,651	31,438	22,020	18,947	21,554									
Solyc06g051450	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT3G56510.5)						8,285	9,046	5,627	5,031	5,628									
Solyc06g051460	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHRI		F:GO:0005524: P:G(	F:ATP binding; P:protein metabolic process		G3DSA:3.40.50.300 (GENE3D): IPR0(	22,013	19,827	2,474	2,066	2,045									
Solyc06g051500	Kinase family protein (AHRD V3.3 *** B9HHQ2_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): G3DSA:3.30.20	20,539	13,608	12,000	10,209	10,756									
Solyc06g051520	CTD small phosphatase-like protein (AHRD V3.3 *** W9S4E3_9ROSA)		F:GO:0016791	F:phosphatase activity		IPR004274 (SMART): IPR011948 (TIC	15,069	15,351	34,180	42,186	35,734									
Solyc06g051540	Serine/threonine-protein kinase (AHRD V3.3 *** W0TR71_ACAMN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (SMART): G3DSA:1.10.51	13,970	8,058	12,009	14,733	12,951	-0,768	0,021					down		
Solyc06g051550	fe inefficient	fer	F:GO:0046983	F:protein dimerization activity		IPR011598 (SMAF bHLH	0,000	0,019	0,000	0,000	0,023									
Solyc06g051560	Flavoprotein wrbA (AHRD V3.3 *-* A0A1D1ZBK1_9ARAE)		F:GO:0003955: F:G(	F:NAD(P)H dehydrc EC:1.6.5.2	NAD(P)H dehydroger	IPR029039 (G3DSA:3.40.50.GENE3D	0,412	0,701	2,995	4,353	2,981									
Solyc06g051570	NF-X1-type zinc finger protein NFXL2 (AHRD V3.3 *-* AT5G05660.1)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR000967 (SMAF NF-X1	10,626	8,988	11,307	9,720	10,008									
Solyc06g051573	Monoterpene synthase (AHRD V3.3 --* S4S654_THYCA)						0,737	0,702	0,711	0,551	0,634									
Solyc06g051577	NF-X1-type zinc finger protein NFXL2 (AHRD V3.3 *** AT5G05660.1)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR000967 (SMART): IPR000967 (PF.	12,463	10,578	13,035	12,709	12,628									
Solyc06g051600	Ubiquitin carboxyl-terminal hydrolase-related protein (AHRD V3.3 --* AT1G65130.4)		F:GO:0003676	F:nucleic acid binding		IPR013087 (SMART): G3DSA:3.30.16	0,019	0,019	0,000	0,000	0,000									
Solyc06g051620	PI-phospholipase C PLC2		F:GO:0004435: P:G(	F:phosphatidylinosit EC:3.1.4.11; EC:3.1.	Phosphoinositide phc	IPR001192 (PRINTS): IPR000008 (SM	24,104	39,522	37,160	40,474	40,710	0,739	0,017					up		
Solyc06g051630	PI-phospholipase C PLC5		F:GO:0004435: P:G(	F:phosphatidylinosit EC:3.1.4.11; EC:3.1.	Phosphoinositide phc	IPR001192 (PRINTS): IPR000008 (SM	7,154	7,055	3,915	3,311	2,924									
Solyc06g051650	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** Q5GA61_SOLLC)		P:GO:0000413: F:G(	P:protein peptidyl-pi EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR029000 (G3	31,870	29,178	39,238	37,587	36,270									
Solyc06g051680	Protein EARLY FLOWERING 4 (AHRD V3.3 *-* A0A0B2RPG0_GLYSO)		P:GO:0042753	P:positive regulation of circadian rhythm		IPR009741 (PFAM): PTHR33469:SF5	0,042	0,000	0,000	0,022	0,000									
Solyc06g051720	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RQI9_CAJCA)		C:GO:0048046	C:apoplast		IPR036514 (G3DSA:3.40.50.GENE3D	20,588	16,698	24,907	25,612	24,012									
Solyc06g051730	ABC1 family protein (AHRD V3.3 *** B9HHP1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR004147 (PFAM): PTHR43173 (PAI	16,241	12,930	20,607	24,777	19,876									
Solyc06g051740	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT2G29780.2)						0,822	0,786	1,346	0,929	0,825									
Solyc06g051745	LYR family of Fe/S cluster biogenesis protein (AHRD V3.3 *** AT1G76065.1)					IPR008011 (PFAM): IPR026868 (PAN	2,211	1,811	2,536	1,937	2,264									
Solyc06g051750	Cytochrome P450 (AHRD V3.3 *** Q70Z22_TOBAC)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc		IPR002401 (PRINTS): IPR001128 (PF	59,238	42,257	98,614	109,376	89,654									
Solyc06g051760	Arginyl-tRNA--protein transferase (AHRD V3.3 *** K4C5W5_SOLLC)		F:GO:0004057: P:G(	F:arginyltransferase EC:2.3.2.8	Arginyltransferase	IPR017137 (PIRSF): IPR007471 (PFA	32,069	30,532	31,655	32,394	32,516									
Solyc06g051770	LOW QUALITY:B3 domain protein (AHRD V3.3 *** AT5G26805.1)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus		PTHR36264 (PANTHER)	0,057	0,116	0,000	0,000	0,000									
Solyc06g051790	protein HESO1-like		F:GO:0016779	F:nucleotidyltransferase activity		G3DSA:1.10.1410.10 (GENE3D): G3D	22,038	37,677	27,018	24,979	24,192	0,800	0,006					up		
Solyc06g051795	LOW QUALITY:D-lactate dehydrogenase [cytochrome], mitochondrial (AHRD V3.3 *-* A0A1D1Z183_9ARAE		F:GO:0003824: F:G(	F:catalytic activity; F:flavin adenine dinucleotide binding		IPR004113 (PFAM): IPR016164 (SUP	0,000	0,039	0,645	1,486	0,921									
Solyc06g051800	expansin 1	EXPA1	C:GO:0005576: P:G(	C:extracellular region; P:plant-type cell wall organization		IPR002963 (PRINTS): IPR007118 (PF	7,235	14,680	765,129	830,390	629,307									
Solyc06g051810	XH/XS domain-containing family protein (AHRD V3.3 *** B9HTH7_POPTR)		P:GO:0031047	P:gene silencing by RNA		IPR005379 (PFAM): IPR005380 (PFA	238,360	205,724	234,218	236,606	230,673									
Solyc06g051815	Oxygen-evolving enhancer protein 2-3, chloroplastic (AHRD V3.3 --* PSBP3_TOBAC)						3,722	6,081	4,640	5,479	4,923									
Solyc06g051820	myosin heavy chain-like protein (AHRD V3.3 *** AT5G53310.1)		F:GO:0003774: C:G(	F:motor activity; C:r EC:3.6.1.15	Nucleoside-triphosph	IPR010926 (PFAM): mobidb-lite (MOB	14,327	22,108	14,301	17,697	16,908									
Solyc06g051830	Potassium transporter (AHRD V3.3 *** K4C5X2_SOLLC)		F:GO:0015079: C:G(	F:potassium ion transmembrane transporter activity; C:membrai		IPR003855 (PFAM): PTHR30540:SF1	0,197	0,474	0,047	0,000	0,142									
Solyc06g051835	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061FVD3_THECC)		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM): mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc06g051840	Solanum lycopersicum Cytokinin Response Factor 6	CRF8	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec		IPR001471 (PRINT ERF	1,703	2,844	0,872	0,294	0,607									
Solyc06g051850	phosphate transporter 4	pt5	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport		IPR005828 (PFAM): mobidb-lite (MOB	0,181	0,272	0,022	0,048	0,046									
Solyc06g051860	mycorrhiza-inducible inorganic phosphate transporter 4		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport		IPR005828 (PFAM): mobidb-lite (MOB	30,277	21,464	60,204	59,398	67,569									
Solyc06g051900	Folylpolyglutamate synthase (AHRD V3.3 *** F1BPW5_SOLPN)	FPGS	F:GO:0004326: F:G(	F:tetrahydrofolylpol EC:6.3.2.17	Tetrahydrofolate syn	IPR013221 (PFAM): IPR036565 (G3D	10,020	8,430	9,602	8,597	8,802									
Solyc06g051905	actin-binding FH2 (formin-like) protein (AHRD V3.3 --* AT3G32420.1)						0,775	0,805	0,841	0,781	0,609									
Solyc06g051910	Polypyrimidine tract-binding protein (AHRD V3.3 *-* A0A0H5DID0_RHOSS)		F:GO:0003676	F:nucleic acid binding		mobidb-lite (MOBIDB_LITE): PTHR443	0,038	0,019	0,022	0,025	0,047									
Solyc06g051920	Cyclic nucleotide gated channel CNGC5 (AHRD V3.3 *** A0A0B4U1Q6_SOLLC)		F:GO:0005216: P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer		IPR000595 (SMART): IPR000595 (PF.	33,260	39,459	29,968	35,643	30,645									
Solyc06g051930	pyruvate kinase superfamily protein		F:GO:0000287: F:G(	F:magnesium ion bi EC:2.7.1.4	Pyruvate kinase	IPR040442 (G3DSA:3.20.20.GENE3D	6,851	4,615	7,319	8,086	8,437									
Solyc06g051940	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)		F:GO:0004722: P:G(	F:protein serine/thr EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	47,079	26,108	60,767	41,383	48,723	-0,821	0,014			-0,553	0,004	down		down
Solyc06g051950	Nuclear migration protein nudC (AHRD V3.3 *** A0A1D1YN56_9ARAE)		C:GO:0005737: P:G(	C:cytoplasm; P:protein folding; P:developmental process; F:unfc		IPR007052 (PFAM): IPR008978 (G3D	0,314	0,214	1,074	1,394	0,802									
Solyc06g051960	Pectinesterase (AHRD V3.3 *** K4C5Y2_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR035513 (G3	0,139	0,232	0,000	0,000	0,000									
Solyc06g051970	Calcineurin B-like protein (AHRD V3.3 *** V5R531_9ROSA)		F:GO:0005509	F:calcium ion binding		PR00450 (PRINTS): IPR002048 (SMA	0,059	0,331	0,100	0,025	0,047									
Solyc06g051980	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4C5Y4_SOLLC)		F:GO:0005509: F:G(	F:calcium ion binding; F:protein binding; C:nucleus; P:ubiquitin-d		PR00450 (PRINTS): IPR002048 (SMA	14,629	11,792	16,737	15,521	14,297									
Solyc06g051990	Defective in meristem silencing 3 (AHRD V3.3 *** A0A061G2F1_THECC)					PTHR33566:SF1 (PANTHER): PTHR3:	1,688	2,153	0,205	0,392	0,258									
Solyc06g052000	LOW QUALITY:Eukaryotic translation initiation factor 3 subunit I (AHRD V3.3 *** A0A0K9NVH2_ZOSMR)		F:GO:0005515	F:protein binding		IPR015943 (G3DSA:2.130.10.GENE3	0,159	0,124	0,122	0,125	0,046									
Solyc06g052010	SUN-like protein 16	SUN16	F:GO:0005515	F:protein binding		IPR000048 (SMART): G3DSA:1.20.5.1	4,961	2,729	1,387	1,043	1,129									
Solyc06g052020	Transmembrane protein, putative (AHRD V3.3 -** A0A072V1A4_MEDTR)					mobidb-lite (MOBIDB_LITE): PTHR344	0,114	0,037	0,047	0,025	0,000									
Solyc06g052030	Importin subunit beta-1 (AHRD V3.3 *** A0A0B0MVG3_GOSAR)		P:GO:0006606: F:G(	P:protein import into nucleus; F:protein transporter activity		IPR011989 (G3DSA:1.25.10.GENE3D	88,680	75,296	105,675	110,245	102,165									
Solyc06g052040	Calcium-binding EF hand family protein (AHRD V3.3 *** AT4G27790.1)		F:GO:0005509	F:calcium ion binding		IPR002048 (SMART): IPR002048 (PF.	0,019	0,000	0,000	0,022	0,000									
Solyc06g052050	Heat shock protein 70 (AHRD V3.3 *** Q9M4E8_CUCSA)		F:GO:0005524: C:G(	F:ATP binding; C:er EC:1.3.1.74	2-alkenal reductase (	IPR013126 (PRINTS): IPR013126 (PF	6,348	7,728	20,632	15,299	17,021									

Solyc06g052055	Heat shock protein 70 (AHRD V3.3 *-* Q9M4E8_CUCSA)		F:GO:0005524: C:G(	F:ATP binding: C:nu	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR029048 (G3DSA:1.20.1270.GENE	1,076	1,566	3,317	2,027	2,827									
Solyc06g052060	Pentatricopeptide repeat-containing protein At5g12100, mitochondrial (AHRD V3.3 *-* A0A1D1Y140_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,400	9,688	3,611	3,204	3,732									
Solyc06g052070	WD-repeat protein, putative (AHRD V3.3 *** B9T7W7_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	27,512	21,651	14,444	33,432	23,919			0,723	0,001	1,210	0,000		up	up
Solyc06g052080	RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003723	F:RNA binding			mobidb-lite (MOBIDB_LITE): PTHR105	19,769	22,146	34,150	31,819	30,948									
Solyc06g052090	LOW QUALITY:RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	0,245	0,401	0,050	0,050	0,047									
Solyc06g052100	RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			PTHR10501:SF20 (PANTHER): PTHR	0,236	0,276	0,000	0,025	0,000									
Solyc06g052110	LOW QUALITY:RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	0,253	0,154	0,022	0,000	0,000									
Solyc06g052130	RNA-binding family protein (AHRD V3.3 *-* B9GTK9_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,171	0,055	0,022	0,000	0,000									
Solyc06g052140	RNA-binding family protein (AHRD V3.3 --* B9GTK9_POPTR)		P:GO:0000398: F:G(	P:mRNA splicing, via spliceosome; F:snRNA stem-loop binding			PTHR10501 (PANTHER): PTHR10501	0,264	0,265	0,000	0,000	0,000									
Solyc06g053140	Rhodanese-like domain-containing protein (AHRD V3.3 *** T1E126_SILLA)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:chloroplast envelope; F:tra			IPR001763 (SMART): IPR001763 (PF.	14,089	21,822	7,394	7,981	13,279			0,839	0,000				up	
Solyc06g053145	Photosystem II CP47 reaction center protein (AHRD V3.3 --* PSBB_CHLRE)							0,141	0,314	0,046	0,050	0,072									
Solyc06g053150	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G46620.1)		F:GO:0005524	F:ATP binding			IPR003593 (SMART): G3DSA:3.40.50	2,734	4,519	2,068	2,515	2,110									
Solyc06g053160	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G27680.1)		F:GO:0005524	F:ATP binding			PR00830 (PRINTS): IPR003593 (SMA	36,354	44,101	39,310	35,167	39,763									
Solyc06g053170	Leucine-rich repeat family protein, putative, expressed (AHRD V3.3 --* Q10QT0_ORYSJ)							0,580	0,533	0,599	0,506	0,497									
Solyc06g053180	Cytochrome b5 (AHRD V3.3 *-* A5Z1Y7_MALDO)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:heme bindi			IPR001199 (PFAM): IPR036400 (G3D	37,364	40,935	57,743	57,372	52,665									
Solyc06g053190	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT3G49350.1)		F:GO:0005096: C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (SMART): G3DSA:1.10.8.2	41,247	30,041	33,147	29,836	34,030									
Solyc06g053200	6-phosphogluconolactonase (AHRD V3.3 *** B6UAK0_MAIZE)		P:GO:0005975: P:G(	P:carbohydrate met	EC:3.1.1.31; EC:3.1.	6-phosphogluconolac	G3DSA:3.40.50.1360 (GENE3D): IPR(	83,436	74,028	113,433	103,934	104,189									
Solyc06g053210	Ubiquitin (AHRD V3.3 *** J7G5B5_ROSRU)		F:GO:0003735: F:G(	F:structural constituent of ribosome; F:protein binding; C:riboso			IPR019956 (PRINTS): IPR000626 (SM	4,955	3,284	3,497	3,030	3,285									
Solyc06g053220	Homeobox leucine zipper protein (AHRD V3.3 *** B8YIB0_MIRJA)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRINT HD-ZIP	0,038	0,064	0,169	0,118	0,093									
Solyc06g053230	Transmembrane protein, putative (AHRD V3.3 *** G7J878_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR341	55,568	33,883	49,364	49,483	48,611	-0,685	0,002					down		
Solyc06g053245	transmembrane protein (AHRD V3.3 --* AT1G15640.2)							0,063	0,018	0,000	0,000	0,000									
Solyc06g053250	SET domain protein 35 (AHRD V3.3 --* AT1G26760.1)							0,082	0,019	0,000	0,000	0,023									
Solyc06g053260	SAUR-like auxin-responsive family protein (AHRD V3.3 *** G7J880_MEDTR)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF1	0,000	0,018	0,000	0,166	0,186									
Solyc06g053290	SAUR-like auxin-responsive family protein (AHRD V3.3 *** G7J880_MEDTR)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	1,906	1,513	6,305	9,817	6,462					0,641	0,015			up
Solyc06g053300	RNA-binding protein, putative (AHRD V3.3 *** B9T1D4_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR009818 (PF.	44,093	43,146	60,659	56,209	54,734									
Solyc06g053310	Hydroxyacylglutathione hydrolase (AHRD V3.3 *** G7IS04_MEDTR)		F:GO:0004416: P:G(	F:hydroxyacylglutat	EC:3.1.2.6	Hydroxyacylglutathio	IPR001279 (SMART): IPR001279 (PF.	63,597	87,956	114,491	121,400	125,250									
Solyc06g053320	RNA-binding protein (AHRD V3.3 *** E5GC87_CUCME)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	38,636	40,285	32,661	33,359	32,563									
Solyc06g053330	DNA-directed RNA polymerase I subunit rpa49, putative (AHRD V3.3 *** A0A061G333_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	IPR009668 (PFAM): mobidb-lite (MOB	42,165	51,794	43,427	42,666	40,054									
Solyc06g053340	F-box protein SKIP16 (AHRD V3.3 *** A0A0B2PAG4_GLYSO)		F:GO:0005515	F:protein binding			IPR037883 (G3DSA:3.40.1580.GENE	13,123	10,736	37,189	39,347	32,278									
Solyc06g053350	BZIP transcription factor (AHRD V3.3 *** G7IHV8_MEDTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	17,034	19,066	18,544	19,532	18,141									
Solyc06g053360	ENHANCED DISEASE RESISTANCE-like protein (DUF1336) (AHRD V3.3 *** AT1G06050.1)						IPR009769 (PFAM): mobidb-lite (MOB	3,345	2,780	7,423	8,421	5,825									
Solyc06g053370	Rhomboid protein (AHRD V3.3 *** E5GC88_CUCME)		F:GO:0004252: C:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bo	IPR022764 (PFAM): IPR035952 (G3D	5,726	3,942	7,488	7,901	6,509									
Solyc06g053380	Chitinase (AHRD V3.3 *** A0A1B1HY32_9APIA)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR001002 (SMART): IPR000726 (PF.	2,772	1,398	0,143	0,115	0,190									
Solyc06g053385	Signal recognition particle 14 kDa protein (AHRD V3.3 *** A0A061EJC2_THECC)		C:GO:0005786: P:G(	C:signal recognition particle, endoplasmic reticulum targeting; P			IPR009018 (G3DSA:3.30.720.GENE3	9,267	11,133	12,965	13,047	12,922									
Solyc06g053400	Isopropylmalate synthase (AHRD V3.3 *** K4C627_SOLLC)		F:GO:0003852: P:G(	F:2-isopropylmalate	EC:2.3.3.13	2-isopropylmalate sy	IPR013709 (SMART): G3DSA:3.30.16	45,327	41,637	54,028	52,634	51,469									
Solyc06g053410	External alternative NAD(P)H-ubiquinone oxidoreductase B1, mitochondrial (AHRD V3.3 --* ENDB1_SOLTU)							0,000	0,000	0,044	0,000	0,071									
Solyc06g053420	C2 domain-containing protein / GRAM domain-containing protein (AHRD V3.3 *** AT3G59660.1)						IPR000008 (PRINTS): IPR000008 (SM	1,116	0,999	0,165	0,195	0,047									
Solyc06g053430	selenoprotein family protein		C:GO:0016021	C:integral component of membrane			IPR014912 (PFAM): IPR038219 (G3D	26,598	26,296	40,003	39,601	36,642									
Solyc06g053440	Serine/Threonine-kinase (AHRD V3.3 *** AT3G59680.2)						mobidb-lite (MOBIDB_LITE): PTHR367	0,470	0,210	0,072	0,000	0,024									
Solyc06g053450	SUN-like protein 17	SUN17	F:GO:0005515	F:protein binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	85,154	80,617	109,112	112,125	116,772									
Solyc06g053455	Protein IQ-DOMAIN 14-like protein (AHRD V3.3 *** A0A0B0PMG6_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	113,233	111,188	156,437	149,093	161,725									
Solyc06g053470	Proteasome assembly chaperone 4 (AHRD V3.3 *** A0A0B0PA50_GOSAR)		P:GO:0043248	P:proteasome assembly			IPR032157 (PFAM): IPR032157 (PAN	7,333	6,805	10,358	9,801	9,113									
Solyc06g053480	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A0V0I9I2_SOLCH)		P:GO:0006631: F:G(	P:fatty acid metabo	EC:1.14.19.2; EC:1.	Stearoyl-[acyl-carrier	IPR012348 (G3DSA:1.10.620.GENE3	99,326	108,598	75,098	68,256	71,026									
Solyc06g053490	FAM136A-like protein (DUF842) (AHRD V3.3 *** AT2G31725.1)						IPR008560 (PFAM): IPR008560 (PAN	2,389	2,745	1,972	1,822	1,859									
Solyc06g053500	cytochrome oxidase assembly protein (AHRD V3.3 *** AT2G43780.4)		C:GO:0016021	C:integral component of membrane			PTHR36744 (PANTHER)	4,930	4,631	9,514	8,152	7,937									
Solyc06g053520	spermidine synthase (AHRD V3.3 *** AT1G23820.1)		F:GO:0003824	F:catalytic activity			PF01564 (PFAM): G3DSA:3.40.50.15(	0,000	0,019	0,000	0,050	0,000									
Solyc06g053530	Tetratricopeptide repeat protein 7A (AHRD V3.3 *** A0A0B2P0K1_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR019734 (PF.	31,231	28,118	27,255	27,820	27,860									
Solyc06g053550	Peroxisomal membrane protein PMP22 (AHRD V3.3 *** A0A199UZZ3_ANACO)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM): PTHR11266:SF4	0,353	0,523	0,458	0,391	0,401									
Solyc06g053560	Casein kinase, putative (AHRD V3.3 *** B9SS69_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	30,057	31,826	47,565	50,204	44,830									
Solyc06g053585	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** G7I4M8_MEDTR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR023210 (PF	5,979	8,697	5,135	5,615	7,337									
Solyc06g053590	Nuclear-pore anchor protein (AHRD V3.3 *** A0A142CD35_9LAMI)		P:GO:0006606	P:protein import into nucleus			IPR012929 (PFAM): mobidb-lite (MOB	164,706	124,558	137,973	131,810	138,989									
Solyc06g053600	Oxidoreductase, aldo/keto reductase family protein, expressed (AHRD V3.3 *-* Q10GW3_ORYSJ)		F:GO:0004032: P:G(	F:alditol:NADP+ 1-o	EC:1.1.1.21; EC:1.1.	Aldehyde reductase;	IPR023210 (PFAM): IPR036812 (G3D	2,540	3,255	2,769	2,347	3,671									
Solyc06g053610	R2R3MYB transcription factor 14	R2R3MYB14	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,747	0,901	0,234	0,169	0,189									
Solyc06g053620	phosphoenolpyruvate carboxylase kinase 2	ppck2	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,719	2,488	219,585	176,823	140,234									
Solyc06g053625	Phosphoenolpyruvate carboxylase kinase 2 (AHRD V3.3 *-* Q84JP7_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	1,527	1,304	136,200	121,452	92,822									
Solyc06g053630	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0I5T8_SOLCH)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	105,449	94,726	77,004	97,231	96,942									
Solyc06g053640	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EMD3_THECC)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	4,391	5,030	1,515	0,771	1,146									
Solyc06g053653	HR-like lesion-inducing protein-like protein (AHRD V3.3 *** AT1G04340.1)		C:GO:0016021	C:integral component of membrane			IPR008637 (PFAM): PTHR31474 (PAN	7,485	9,297	4,791	4,646	4,601									
Solyc06g053660	HR-like lesion-inducing protein-like protein (AHRD V3.3 *** AT1G04340.1)		C:GO:0016021	C:integral component of membrane			IPR008637 (PFAM): PTHR31474:SF4	1,246	1,330	1,207	1,078	1,219									
Solyc06g053670	Enoyl-CoA hydratase/isomerase family protein (AHRD V3.3 *** D7MH17_ARALL)		F:GO:0003824	F:catalytic activity			G3DSA:3.90.226.10 (GENE3D): IPR0(	64,806	76,852	106,817	94,651	94,958									
Solyc06g053675	tRNA (Adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A (AHRD V3.3 *-* A0A0B0N2D0_GOS/		F:GO:0016429: P:G(	F:tRNA (adenine-N1-)-methyltransferase activity; P:tRNA methy			G3DSA:3.40.50.150 (GENE3D): G3DS	0,000	0,000	0,000	0,048	0,023									
Solyc06g053700	ATBET12, putative (AHRD V3.3 *** B9STJ3_RICCO)						mobidb-lite (MOBIDB_LITE): PTHR339	2,379	3,883	3,199	2,220	2,004									
Solyc06g053710	ethylene receptor homolog (ETR4)	ETR4	F:GO:0000155: P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR003018 (SMART): IPR003661 (SM	92,593	129,946	553,414	622,420	476,908									
Solyc06g053715	S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61390.2)							10,328	12,567	52,780	60,842	46,222									
Solyc06g053720	Zinc finger, C2H2 (AHRD V3.3 *** A0A124SAQ3_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,021	0,168	0,000	0,000	0,000									
Solyc06g053730	Protein kinase (AHRD V3.3 *** A2Q436_MEDTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	2,263	2,190	0,022	0,073	0,046									
Solyc06g053740	MATH domain-containing protein (AHRD V3.3 *-* W9QVS1_9ROSA)						mobidb-lite (MOBIDB_LITE): PTHR263	39,454	37,251	93,712	98,727	87,031									
Solyc06g053750	MATH domain-containing protein (AHRD V3.3 *** W9QVS1_9ROSA)		F:GO:0005515	F:protein binding			IPR002083 (SMART): IPR002083 (PF.	83,157	58,392	64,909	57,053	63,320									
Solyc06g053760	Syntaxin, putative (AHRD V3.3 *** B9SHK3_RICCO)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART): IPR006011 (SM	0,408	0,543	0,366	0,883	0,422									
Solyc06g053770	DNA-repair protein XRCC4, putative (AHRD V3.3 *** B9RTD9_RICCO)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:double-strand break repair; P:DNA			IPR010585 (PFAM): G3DSA:1.20.5.37	5,313	4,760	5,137	4,469	5,036									
Solyc06g053780	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT3G23090.4)						IPR027329 (PFAM): mobidb-lite (MOB	9,214	9,620	1,999	1,862	2,573									
Solyc06g053790	StAR-related lipid transfer protein 7, mitochondrial (AHRD V3.3 *** A0A0B0PQH2_GOSAR)		F:GO:0008289	F:lipid binding			IPR023393 (G3DSA:3.30.530.GENE3	208,011	214,516	333,720	357,214	316,180									
Solyc06g053800	Nonsense-mediated mRNA decay NMD3 family protein (AHRD V3.3 *** B9H0C6_POPTR)		F:GO:0043023	F:ribosomal large subunit binding			IPR007064 (PFAM): mobidb-lite (MOB	31,739	35,673	47,951	45,943	41,400									
Solyc06g053805	cytochrome P450, family 71, subfamily B, polypeptide 30 pseudogene (AHRD V3.3 --* AT3G53290.1)							0,076	0,178	0,097	0,047	0,163									
Solyc06g053810	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G04280.2)		F:GO:0005524: F:G(	F:ATP binding; F:kinase activity			IPR010488 (PFAM): PTHR31153 (PAN	10,747	11,819	10,500	12,773	14,613									
Solyc06g053820	Chloroplast omega-3 fatty acid desaturase (AHRD V3.3 --* Q0GQS4_JATCU)							35,903	33,889	28,878	22,975	25,877									
Solyc06g053830	auxin-regulated IAA7	IAA7	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			G3DSA:3.10.20.90 (GENE3D): IPR03	6,415	2,302	1,047	0,462	0,843	-1,445	0,001					down		
Solyc06g053840	auxin-regulated IAA4	IAA4	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			G3DSA:3.10.20.90 (GENE3D): IPR03	49,241	40,104	15,625	19,165	20,146									
Solyc06g053850	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RTF6_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,715	2,185	1,835	2,043	1,820									
Solyc06g053860	alpha-1,2-Mannosidase (AHRD V3.3 *** K4C673_SOLLC)		F:GO:0004571: F:G(	F:mannosyl-oligosa	EC:3.2.1.113; EC:3.	Mannosyl-oligosacch	IPR001382 (PRINTS): IPR001382 (PF	19,981	17,233	41,726	45,370	36,817									
Solyc06g053870	3-ketoacyl-CoA synthase (AHRD V3.3 *** A0A023PL08_TOBAC)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR012392 (PIRSF): IPR013747 (PFA	0,021	0,000	0,000	0,045	0,000									
Solyc06g053900	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4C677_SOLLC)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR012392 (PIRSF): IPR016039 (G3D	0,019	0,000	4,642	1,357	1,726			-1,423	0,020	-1,769	0,000		down	down
Solyc06g053910	DUF506 family protein (AHRD V3.3 *** A0A072VMZ8_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (F	56,432	46,959	51,724	42,223	52,971									
Solyc06g053920	inactive purple acid phosphatase-like protein (AHRD V3.3 *-* AT1G42430.1)		P:GO:0005982: C:G(	P:starch metabolic process; C:chloroplast stroma; C:starch grai			mobidb-lite (MOBIDB_LITE): mobidb-lit	20,870	20,135	19,100	16,619	20,658									
Solyc06g053930	Calmodulin, putative (AHRD V3.3 *** B9RTI5_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): G3DSA:1.10.23	0,019	0,343	0,556	0,461	0,518									
Solyc06g053950	Heat shock transcription factor (AHRD V3.3 *-* A0A076L230_GOSHI)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			PTHR10015:SF260 (PANTHER): IPR0	4,028	6,792	67,554	59,174	52,425									
Solyc06g053960	SolycHsfA6b	HSF-14	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRINT HSF	10,826	13,569	149,932	168,378	141,053									
Solyc06g053970	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *** AT4G14723.1),Pfam:PF17181		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): PTHR33109:SF34 (	0,913	1,106	0,389	0,498	0,443									
Solyc06g053980	Chlorophyllase (AHRD V3.3 *** F1BPW6_SOLPN)	CLH1	P:GO:0015996: F:G(	P:chlorophyll catabo	EC:3.1.1.14; EC:3.1.	Chlorophyllase; Carb	IPR029058 (G3DSA:3.40.50.GENE3D	29,712	49,387	8,724	5,561	11,996	0,758	0,027					up		
Solyc06g054010	inositol-1,4,5-triphosphate-5-phosphatase 3	5pt3	P:GO:0046856	P:phosphatidylinositol dephosphorylation			IPR000300 (SMART): IPR036691 (G3	9,292	11,661	4,329	4,443	5,410									
Solyc06g054020	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G05460.2)		F:GO:0003723: F:G(	F:RNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): PF13	95,985	82,554	116,981	109,103	117,139									
Solyc06g054030	LOW QUALITY:Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9NBN8_POPTF		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR016140 (SMART): IPR016140 (PF.	0,000	0,021	0,025	0,050	0,071									
Solyc06g054050	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G05460.1)		F:GO:0003723: F:G(	F:RNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	PF13086 (PFAM): G3DSA:3.40.50.30(	0,042	0,041	0,025	0,025	0,046									
Solyc06g054060	LOW QUALITY:Lipid transfer protein (AHRD V3.3 *** Q5MJA5_CAPAN)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding; C:integral component of membra			IPR016140 (SMART): IPR016140 (PF.	0,060	0,021	0,000	0,000	0,024									
Solyc06g054070	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR016140 (SMART): G3DSA:1.10.11	6,996	7,721	1,455	1,193	1,319									
Solyc06g054080	PHP (AHRD V3.3 *** A0A097PLE9_SOLLC)		P:GO:0006368: P:G(	P:transcription elongation from RNA polymerase II promoter; P:I			IPR031336 (PFAM): IPR038103 (G3D	0,000	0,039	0,000	0,000	0,023									
Solyc06g054090	LOW QUALITY:Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** A0A072VQW9_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR000182 (PFAM): G3DSA:3.40.630.	0,080	0,244	0,100	0,022	0,165									
Solyc06g054100	Major facilitator superfamily protein (AHRD V3.3 *-* AT2G32040.1)		C:GO:0016021	C:integral component of membrane			IPR039309 (PFAM): IPR039309 (PAN	0,136	0,043	0,025	0,022	0,023									
Solyc06g054120	Major facilitator superfamily protein (AHRD V3.3 *** AT2G32040.1)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1250.20 (GENE3D): IPR(	1,411	1,097	0,175	0,264	0,375									
Solyc06g054130	LOW QUALITY:DUF1677 family protein (AHRD V3.3 *** G7K3P0_MEDTR)						IPR012876 (PFAM): mobidb-lite (MOB	0,098	0,132	0,075	0,025	0,024									
Solyc06g054140	FBD, F-box and Leucine Rich Repeat domains containing protein (AHRD V3.3 --* AT3G49030.2)						PTHR35986 (PANTHER)	0,837	0,816	0,402	0,339	0,562									
Solyc06g054145	Exocyst complex component SEC5 (AHRD V3.3 --* AT1G21170.2)						mobidb-lite (MOBIDB_LITE): PTHR359	2,368	1,801	1,201	1,018	0,985									
Solyc06g054150	LOW QUALITY:17.6 kDa class II heat shock protein (AHRD V3.3 *** A0A061EM62_THECC)		C:GO:0016021	C:integral component of membrane			PTHR33879:SF3 (PANTHER): PTHR3	0,803	2,124	1,084	1,605	1,540	1,412	0,010					up		
Solyc06g054160	LOW QUALITY:Protein OBERON 1-like protein (AHRD V3.3 *-* A0A0B0NZZ1_GOSAR)						IPR032881 (PFAM): PTHR33345:SF2	0,019	0,000	0,000	0,000	0,000									
Solyc06g054200	Protein OBERON 1-like protein (AHRD V3.3 *-* A0A0B0NZZ1_GOSAR)						IPR032881 (PFAM): PTHR33345:SF2	0,000	0,043	0,000	0,000	0,000									
Solyc06g054210	LOW QUALITY:Protein OBERON 1 (AHRD V3.3 *-* A0A0B2RKS8_GLYSO)						PTHR33345 (PANTHER)	0,000	0,043	0,000	0,000	0,000									
Solyc06g054220	Photosystem II reaction center PsbP family protein (AHRD V3.3 --* AT4G15510.1)						mobidb-lite (MOBIDB_LITE)	1,713	2,159	2,794	2,538	2,571									
Solyc06g054230	Protein OBERON 1 (AHRD V3.3 *-* A0A0B2RKS8_GLYSO)						PTHR33345 (PANTHER)	0,019	0,018	0,049	0,000	0,047									
Solyc06g054240	5'-nucleotidase surE (AHRD V3.3 *** W9QLZ8_9ROSA)		F:GO:0008252	F:nucleotidase acti	EC:3.1.3.31	Nucleotidase	IPR002828 (PFAM): IPR002828 (TIGF	2,724	2,221	2,185	1,434	2,659									
Solyc06g054250	5'-nucleotidase surE (AHRD V3.3 *** W9QLZ8_9ROSA)		F:GO:0008252	F:nucleotidase acti	EC:3.1.3.31	Nucleotidase	IPR036523 (G3DSA:3.40.1210.GENE	64,428	60,914	72,846	60,822	69,602									
Solyc06g054260	photosystem 1 reaction center protein subunit 2	psad	C:GO:0009538: P:G(	C:photosystem I reaction center; P:photosynthesis			IPR003685 (PFAM): G3DSA:3.30.147(	194,037	485,294	140,632	206,563	401,056	1,351	0,000	1,508	0,000	0,560	0,042	up	up	up
Solyc06g054270	Sugar transporter protein 11	STP11	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	3,333	8,298	0,582	3,072	6,126	1,342	0,002	3,334	0,000	2,345	0,000	up	up	up
Solyc06g054280	LOW QUALITY:E3 UFM1-protein ligase 1 homolog (AHRD V3.3 --* UFL1_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,024									
Solyc06g054290	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	1,351	1,691	1,158	0,929	1,387									
Solyc06g054310	LOW QUALITY:Fantastic four-like protein (AHRD V3.3 *** G7IE53_MEDTR)						IPR021410 (PFAM): PTHR33155 (PAN	0,081	0,161	0,025	0,000	0,024									
Solyc06g054313	WUSCHEL related homeobox 2 (AHRD V3.3 --* AT5G59340.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,600	3,060	5,373	5,925	4,757									
Solyc06g054317	NPK1-related protein kinase 3 (AHRD V3.3 --* AT3G06030.1)							0,918	0,360	1,002	0,950	1,111									
Solyc06g054323	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_GOSBA)							0,019	0,000	0,025	0,025	0,000									
Solyc06g054327	maturase K (AHRD V3.3 --* ATCG00040.1)							1,174	0,812	1,443	1,440	1,721									
Solyc06g054330	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G06060.2)		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS): IPR002347 (PF	13,292	14,497	20,911	20,778	18,449									
Solyc06g054360	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9SZS6_RICCO)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	0,021	0,000	0,000	0,000	0,000									
Solyc06g054370	Stem-specific TSJT1 (AHRD V3.3 *** A0A0B0MRD0_GOSAR)						IPR024286 (SMART): IPR029055 (G3	0,321	0,260	0,000	0,025	0,000									
Solyc06g054380	RNA binding protein (AHRD V3.3 *-* B6TNV4_MAIZE)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	3,091	3,794	7,195	8,580	9,227									
Solyc06g054390	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2P6Y2_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM): mobidb-lite (MOB	0,685	0,674	0,022	0,125	0,164									
Solyc06g054400	Translation initiation factor (AHRD V3.3 *** G7ID01_MEDTR)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR000795 (PF	0,080	0,062	0,047	0,025	0,048									
Solyc06g054410	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9SWZ5_RICCO)		F:GO:0016787	F:hydrolase activity			IPR002933 (PFAM): IPR017439 (TIGF	6,032	5,680	3,496	3,197	3,256									
Solyc06g054420	Serinc-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 *** AT3G06170.1)		C:GO:0016020	C:membrane			IPR005016 (PFAM): PTHR10383:SF2	95,671	61,067	86,285	84,678	83,220	-0,620	0,014					down		
Solyc06g054430	F-box family protein (AHRD V3.3 *-* D7MAH5_ARALL)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	1,263	0,898	1,263	1,087	0,960									
Solyc06g054440	F-box/LRR protein (AHRD V3.3 *** G7IFP9_MEDTR)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR032675 (G3	10,950	11,465	12,039	11,873	11,351									
Solyc06g054450	UPF0454 protein C12orf49 like (AHRD V3.3 *** A0A0B2PF05_GLYSO)		P:GO:0006487: F:G(	P:protein N-linked g	EC:2.4.1.155	Alpha-1,6-mannosyl-	IPR019352 (PFAM): IPR026116 (PFA	12,057	9,153	11,732	11,215	12,015									
Solyc06g054455	F-box/LRR-repeat 4-like protein (AHRD V3.3 *-* A0A0B0Q196_GOSAR)		P:GO:0006289: P:G(	P:nucleotide-excision repair; P:response to UV-C			PTHR45517 (PANTHER)	0,040	0,076	0,071	0,121	0,187									
Solyc06g054460	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 *** K4C6D2_SOLLC)		F:GO:0004014: P:G(	F:adenosylmethioni	EC:4.1.1.5	Adenosylmethionine	IPR001985 (PIRSF): G3DSA:3.30.360	0,821	0,931	0,358	0,314	0,399									
Solyc06g054470	LOW QUALITY:Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain-containing protein (AHRD V3.3 --* AT2G32415.3)						PF15365 (PFAM): mobidb-lite (MOBID	4,162	5,044	2,740	2,059	2,446									
Solyc06g054480	Kinase family protein (AHRD V3.3 *** D7LYI7_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	2,933	3,502	1,791	2,321	2,157									
Solyc06g054490	Prolyl 4-hydroxylase alpha subunit, putative (AHRD V3.3 *** B9RSW4_RICCO)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR006620 (SMART): IPR003582 (SM	45,979	45,850	57,583	55,773	48,883									
Solyc06g054510	Acyl carrier protein (AHRD V3.3 *** K4C6D7_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR036736 (G3DSA:1.10.1200.GENE	224,686	245,926	315,578	349,604	334,947									
Solyc06g054530	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G39080.1)						G3DSA:3.40.50.720 (GENE3D): PTHR	21,918	21,376	34,347	34,470	32,058									
Solyc06g054540	CHY-type/CTCHY-type/RING-type Zinc finger protein (AHRD V3.3 *** AT5G18650.1)		F:GO:0008270: P:G(	F:zinc ion binding; P:protein ubiquitination			IPR001841 (SMART): IPR008913 (PF.	1,195	1,538	0,414	1,107	1,033									
Solyc06g054550	Lipase (AHRD V3.3 *** B6V3M3_JATCU)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	15,860	15,317	22,685	23,196	22,428									
Solyc06g054560	RNA helicase DEAH-box19	DEAH19	F:GO:0003677: F:G(	F:DNA binding; F:A	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR014001 (SMART): IPR001005 (SM	56,743	52,498	52,537	46,806	51,245									
Solyc06g054570	Glutaredoxin family protein (AHRD V3.3 *** D7LYE9_ARALL)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR014025 (PRINTS): IPR011905 (TI(	0,000	0,000	0,000	0,025	0,024									

Solyc06g054580	RING/U-box superfamily protein (AHRD V3.3 *** AT2G39100.1)		P:GO:0006397	P:mRNA processing			IPR001841 (SMART): IPR002483 (PF	6,182	12,201	8,133	8,341	7,752	1,004	0,010					up		
Solyc06g054590	transmembrane protein (AHRD V3.3 *** AT5G09270.2)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	10,355	9,845	12,693	11,643	10,804									
Solyc06g054610	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_HELAN)							4,326	4,241	3,906	3,649	5,110									
Solyc06g054620	Zinc finger transcription factor 43	C3H43	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	3,550	2,744	1,655	1,828	2,496									
Solyc06g054625	Zinc finger CCCH domain-containing protein 32 (AHRD V3.3 *-* A0A151STD4_CAJCA)		F:GO:0046872	F:metal ion binding			IPR000571 (SMART): G3DSA:4.10.10	4,662	3,713	3,298	2,467	4,265									
Solyc06g054630	Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9NXK4_ZOSMR)		F:GO:0003677: F:G(	F:DNA binding: F:DNA-binding transcription factor activity: P:rec			IPR001471 (PRIN ERF	0,021	0,730	0,391	0,051	0,071									
Solyc06g054640	DUF506 family protein (AHRD V3.3 *** G7LD84_MEDTR)						IPR006502 (PFAM): IPR006502 (TIGF	0,042	0,078	0,046	0,147	0,094									
Solyc06g054650	uncharacterized protein		P:GO:0071786	P:endoplasmic reticulum tubular network organization			IPR019273 (PFAM): mobidb-lite (MOB	25,145	22,654	31,439	31,005	28,939									
Solyc06g054660	LOW QUALITY:tracheary element differentiation-related 7 (AHRD V3.3 --* AT5G48920.1)		C:GO:0016020	C:membrane			PTHR35697 (PANTHER): PTHR35697	0,080	0,152	0,000	0,000	0,000									
Solyc06g054670	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A118HPD5_CYNCS)		P:GO:0006631: F:G(	P:fatty acid metabo	EC:1.14.19.2: EC:1.'	Stearoyl-[acyl-carrier	IPR005067 (PFAM): IPR012348 (G3D	0,159	0,096	0,425	0,151	0,167									
Solyc06g054690	DNA binding protein, putative (AHRD V3.3 *** B9SRR8_RICCO)		F:GO:0003743: P:G(	F:translation initiation factor activity: P:translational initiation: P			mobidb-lite (MOBIDB_LITE): mobidb-lit	66,776	80,754	40,480	48,881	47,460									
Solyc06g059710	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A118HPD5_CYNCS)		P:GO:0006631: F:G(	P:fatty acid metabo	EC:1.14.19.2: EC:1.'	Stearoyl-[acyl-carrier	IPR012348 (G3DSA:1.10.620.GENE3I	0,000	0,019	1,610	1,687	1,671									
Solyc06g059720	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A118HPD5_CYNCS)		P:GO:0006631: F:G(	P:fatty acid metabo	EC:1.14.19.2: EC:1.'	Stearoyl-[acyl-carrier	IPR005067 (PFAM): IPR005067 (PIRS	9,306	3,939	899,577	807,138	681,020									
Solyc06g059730	SIPIN6	PIN6	C:GO:0016021: P:G(	C:integral component of membrane: P:transmembrane transport			IPR014024 (TIGRFAM): IPR004776 (F	0,857	9,671	0,147	0,075	0,236	3,509	0,000					up		
Solyc06g059740	Alcohol dehydrogenase (AHRD V3.3 *** ADH_MALDO)		P:GO:0055114	P:oxidation-reduction process			IPR013154 (PFAM): G3DSA:3.90.180	1142,184	1077,841	3859,037	4094,449	3593,702									
Solyc06g059750	Transcriptional corepressor SEUSS, putative (AHRD V3.3 *** B9S2M5_RICCO)		P:GO:0000122: F:G(	P:negative regulation of transcription by RNA polymerase II: F:F			IPR029005 (PFAM): mobidb-lite (MOB	64,589	63,545	66,774	68,167	68,000									
Solyc06g059755	Transcriptional corepressor SEUSS (AHRD V3.3 *-* A0A151TS77_CAJCA)		P:GO:0000122: F:G(	P:negative regulation of transcription by RNA polymerase II: F:F			IPR029005 (PANTHER): PTHR10378:	4,974	5,509	6,478	4,593	4,851									
Solyc06g059760	Transcriptional corepressor SEUSS, putative (AHRD V3.3 *** B9S2M5_RICCO)		P:GO:0000122: F:G(	P:negative regulation of transcription by RNA polymerase II: F:F			IPR029005 (PFAM): mobidb-lite (MOB	60,061	59,071	70,245	65,754	66,279									
Solyc06g059790	Non-specific lipid-transfer protein (AHRD V3.3 *** M1D161_SOLTU)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (SM	0,000	0,019	0,000	0,000	0,000									
Solyc06g059800	ACT domain-containing protein						IPR002912 (PFAM): G3DSA:3.30.70.2	127,831	128,704	17,279	15,440	20,479									
Solyc06g059805	F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)						IPR017451 (TIGRFAM): IPR006527 (F	5,501	6,140	0,590	0,981	1,173									
Solyc06g059840	branched chain alpha-keto acid dehydrogenase E1-alpha subunit		F:GO:0016624	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR001017 (PFAM): G3DSA:3.40.50.9	3,903	2,244	0,071	0,192	0,048									
Solyc06g059850	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** D7KXE8_ARALL)		F:GO:0016624	F:oxidoreductase activity, acting on the aldehyde or oxo group (			G3DSA:3.40.50.970 (GENE3D): IPR0(	1,129	1,037	0,022	0,000	0,023									
Solyc06g059860	patatin-like phospholipase domain protein (AHRD V3.3 *** AT1G76980.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,029	0,647	1,356	2,153	1,556									
Solyc06g059870	subunit of exocyst complex 8 (AHRD V3.3 --* AT3G10380.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	26,225	34,835	3,485	4,824	4,123									
Solyc06g059880	Acetolactate synthase		F:GO:0000287: F:G(	F:magnesium ion bi	EC:2.2.1.6	Acetolactate synthas	IPR011766 (PFAM): G3DSA:3.40.50.1	0,481	0,373	0,022	0,025	0,140									
Solyc06g059885	Germacrene synthase (AHRD V3.3 *** G1JUH6_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM): IPR036965 (G3D	0,000	0,095	0,000	0,000	0,000									
Solyc06g059900	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 --* NU1C_CHLAT)						mobidb-lite (MOBIDB_LITE)	7,276	7,316	5,229	7,352	6,097									
Solyc06g059930	sesquiterpene synthase 1	sstle1	F:GO:0000287: F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR008949 (G3DSA:1.10.600.GENE3I	0,040	0,499	0,000	0,000	0,000									
Solyc06g059960	Histone-lysine N-methyltransferase ASHH2 (AHRD V3.3 *-* W9QJR6_9ROSA)		C:GO:0000785: C:G(	C:chromatin: C:nucl	EC:2.1.1.43	Histone-lysine N-met	mobidb-lite (MOBIDB_LITE): mobidb-lit	8,276	7,913	8,516	9,474	9,070									
Solyc06g059965	histone-lysine N-methyltransferase (AHRD V3.3 *-* AT1G77300.2)		F:GO:0005515: C:G(	F:protein binding: C	EC:2.1.1.43	Histone-lysine N-met	IPR006560 (SMART): IPR001214 (SM	25,821	19,585	24,550	27,052	25,700									
Solyc06g059970	TPI	TPI	F:GO:0000977: P:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	0,429	0,211	0,000	0,025	0,000									
Solyc06g059980	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G03810.2)		C:GO:0005794: P:G(	C:Golgi apparatus: P:fucose metabolic process: C:chloroplast: I			IPR019378 (PFAM): mobidb-lite (MOB	18,875	13,308	22,773	25,387	21,801									
Solyc06g059990	Alkyl transferase (AHRD V3.3 *** K7W9N9_SOLLC)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR001441 (PFAM): IPR036424 (G3D	0,249	0,207	0,196	0,000	0,116									
Solyc06g060010	Terpene synthase (AHRD V3.3 *** G5CV42_SOLLC)		F:GO:0010333	F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,315	0,218	0,165	0,267	0,165									
Solyc06g060013	Terpene synthase (AHRD V3.3 *** G5CV42_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM): IPR008949 (G3D	0,114	0,222	0,068	0,171	0,094									
Solyc06g060017	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR001128 (PFAM): IPR036396 (G3D	0,098	0,280	0,521	0,381	0,259									
Solyc06g060050	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IK16_POPTR)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	2,581	2,563	1,797	1,881	2,144									
Solyc06g060060	NAD kinase 2 (AHRD V3.3 *** AT1G21640.1)		F:GO:0003951: P:G(	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR002504 (PFAM): IPR017438 (G3D	36,185	26,511	35,807	36,192	39,322									
Solyc06g060070	1-aminocyclopropane-1-carboxylate oxidase (AHRD V3.3 *** A0A0G3FFL2_FICCA)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,019	0,021	0,000	0,000	0,000									
Solyc06g060080	Mitochondrial ATP synthase 6 kDa subunit (AHRD V3.3 *** A0A0K9PE24_ZOSMR)		C:GO:0016021	C:integral component of membrane			PTHR34565 (PANTHER)	33,146	37,545	37,355	35,276	40,850									
Solyc06g060090	DnaJ domain protein (AHRD V3.3 *** A0A072V0L9_MEDTR)		C:GO:0005737: P:G(	C:cytoplasm: P:receptor-mediated endocytosis: F:clathrin bindir			IPR036869 (G3DSA:1.10.287.GENE3I	140,987	191,375	90,252	91,646	114,349									
Solyc06g060100	Mannose-6-phosphate isomerase (AHRD V3.3 *** K4C6J1_SOLLC)		F:GO:0004476: P:G(	F:mannose-6-phosp	EC:5.3.1.8	Mannose-6-phosphat	IPR016305 (PRINTS): IPR016305 (PII	14,910	17,137	10,018	12,609	11,406									
Solyc06g060110	amino acid transporter 2	aap2	P:GO:0003333: C:G(	P:amino acid transmembrane transport: C:plasma membrane: F:			IPR013057 (PFAM): PTHR22950:SF4	157,246	168,966	61,349	69,314	86,687									
Solyc06g060120	SWI/SNF complex subunit SWI3C (AHRD V3.3 *** A0A0B2RTB1_GLYSO)		F:GO:0003677: F:G(	F:DNA binding; F:protein binding			IPR001005 (SMART): IPR007526 (PF	116,586	87,568	79,234	71,817	77,410									
Solyc06g060130	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT4G33490.2)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR032799 (PFA	75,909	62,708	21,327	19,584	26,351									
Solyc06g060140	Kinesin-like protein (AHRD V3.3 *** A0A061FI31_THECC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	9,091	9,500	2,255	2,351	3,318									
Solyc06g060150	replication factor C subunit 3 (AHRD V3.3 *** AT1G77470.1)		F:GO:0003677: F:G(	F:DNA binding; F:ATP binding; P:DNA replication			IPR003593 (SMART): IPR003959 (PF	20,421	20,332	17,161	17,344	17,165									
Solyc06g060160	U-box domain-containing protein 13 (AHRD V3.3 *** W9R751_9ROSA)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR000008 (SM	0,546	0,683	0,308	0,173	0,117									
Solyc06g060170	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G33440.1)	PG52	F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	4,109	5,042	5,757	8,764	6,939					0,611	0,020			up
Solyc06g060180	Terpene synthase (AHRD V3.3 *** G5CV42_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR036965 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc06g060190	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,000	0,000	0,000	0,548	0,023									
Solyc06g060210	Ras-related GTP-binding family protein (AHRD V3.3 *** B9N6W1_POPTR)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	0,042	0,081	0,047	0,097	0,070									
Solyc06g060230	NAC domain-containing protein, putative (AHRD V3.3 *** B9S2X2_RICCO)	NAC052	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	35,928	43,758	52,490	91,425	39,216					0,804	0,000			up
Solyc06g060240	LOW QUALITY:DnaJ protein (AHRD V3.3 *-* A0A199VN04_ANACO)		P:GO:0006457: F:G(	P:protein folding; F:unfolded protein binding			G3DSA:2.60.260.20 (GENE3D): IPR0(	0,000	0,000	0,000	0,000	0,024									
Solyc06g060250	Aldehyde dehydrogenase (AHRD V3.3 *** K4C6K6_SOLLC)		P:GO:0006081: F:G(	P:cellular aldehyde metabolic process: F:oxidoreductase activit			IPR012394 (PIRSF): IPR015590 (PFA	47,484	38,679	37,937	31,429	35,633									
Solyc06g060260	stromal ascorbate peroxidase 7	APX7	F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS): IPR002016 (PF	43,930	58,218	131,759	120,842	125,656									
Solyc06g060270	DUF630 family protein, putative (DUF630 and DUF632) (AHRD V3.3 *** AT1G21740.1)		P:GO:0071249	P:cellular response to nitrate			IPR006868 (PFAM): IPR006867 (PFA	6,210	3,383	3,636	4,439	3,843									
Solyc06g060290	Protein disulfide-isomerase (AHRD V3.3 *** A0A0V0IRM2_SOLCH)		F:GO:0003756: P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	PR00421 (PRINTS): IPR005792 (TIGF	165,170	157,037	209,668	190,909	189,842									
Solyc06g060300	zinc-ribbon domain protein (AHRD V3.3 *** AT1G44414.1)						IPR031493 (PFAM): PTHR36718 (PAI	0,038	0,021	0,098	0,120	0,047									
Solyc06g060310	Chlorophyllide a oxygenase (AHRD V3.3 *** W9SD87_9ROSA)	CAO	F:GO:0010277: F:G(	F:chlorophyllide a o	EC:1.13.12: EC:1.14	Acting on single donc	IPR017941 (PFAM): IPR036922 (G3D	12,611	16,729	12,936	17,856	20,168			0,638	0,001	0,468	0,031		up	up
Solyc06g060320	Filament-like plant protein (AHRD V3.3 *** FPP_SOLLC)						IPR008587 (PFAM): mobidb-lite (MOB	0,000	0,039	0,000	0,000	0,023									
Solyc06g060340	photosystem II subunit S		C:GO:0009523: C:G(	C:photosystem II: C:chloroplast thylakoid membrane: P:photosy			IPR023329 (G3DSA:1.10.3460.GENE	43,744	151,681	25,046	31,010	81,808	1,820	0,000	1,703	0,000			up	up	
Solyc06g060350	ATPase family AAA domain-containing protein 5 (AHRD V3.3 *** A0A0B0MDF2_GOSAR)		C:GO:0005634: P:G(	C:nucleus; P:DNA repair			IPR003593 (SMART): G3DSA:1.10.8.6	21,977	18,366	20,027	21,435	20,379									
Solyc06g060360	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G44760.2)		F:GO:0016787	F:hydrolase activity			IPR014729 (G3DSA:3.40.50.GENE3D	0,999	1,521	0,363	0,173	0,375									
Solyc06g060370	EamA-like transporter family protein (AHRD V3.3 *** AT1G77610.1)		F:GO:0005459: F:G(	F:UDP-galactose transmembrane transporter activity: F:UDP-gl			IPR004853 (PFAM): PTHR44674 (PAI	51,167	57,515	55,653	58,744	58,339									
Solyc06g060380	Sister chromatid cohesion PDS5-like protein (AHRD V3.3 *-* A0A072VH41_MEDTR)		P:GO:0007064	P:mitotic sister chromatid cohesion			IPR011989 (G3DSA:1.25.10.GENE3D	17,348	23,956	18,723	23,568	21,241									
Solyc06g060390	Histone-lysine N-methyltransferase ASHR1-like protein (AHRD V3.3 *** A0A0B0MR97_GOSAR)		F:GO:0005515	F:protein binding			IPR001214 (SMART): IPR002893 (PF	8,980	7,684	11,679	10,908	11,656									
Solyc06g060400	Ribosomal protein L15 (AHRD V3.3 *** K4C6M0_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000439 (SMART): IPR000439 (PF	76,888	67,130	48,463	36,970	43,367									
Solyc06g060410	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 *** B9H7C8_POPTR)		C:GO:0016021: F:G(	C:integral component of membrane: F:kinase activity: P:phosph			IPR003409 (SMART): G3DSA:2.20.11	0,973	0,591	2,508	1,132	0,729									
Solyc06g060420	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein (AHRD V3.3 *** AT1G44835.2)		F:GO:0002161	F:aminoacyl-tRNA (	EC:3.1.1.1	Carboxylesterase	IPR007214 (PFAM): IPR036754 (G3D	32,606	31,264	41,324	41,290	41,251									
Solyc06g060440	Transmembrane emp24 domain-containing protein 10, putative (AHRD V3.3 *** B9RJ70_RICCO)		C:GO:0005789: C:G(	C:endoplasmic reticulum membrane: C:endoplasmic reticulum-G			IPR009038 (SMART): IPR009038 (PF	0,038	0,140	0,025	0,050	0,024									
Solyc06g060450	Transmembrane emp24 domain-containing protein 10, putative (AHRD V3.3 *** B9RJ70_RICCO)		C:GO:0005789: C:G(	C:endoplasmic reticulum membrane: C:endoplasmic reticulum-G			IPR009038 (SMART): IPR009038 (PF	0,075	0,202	5,343	8,331	5,185					0,646	0,017			up
Solyc06g060460	transmembrane protein (AHRD V3.3 *** AT1G21370.2)		C:GO:0016021	C:integral component of membrane			PTHR28110 (PANTHER)	14,473	13,793	13,904	15,289	11,540									
Solyc06g060470	LOW QUALITY:VQ motif-containing protein, putative (AHRD V3.3 *** A0A061FH83_THECC)		C:GO:0005634: P:G(	C:nucleus: P:defense response signaling pathway, resistance g			IPR008889 (PFAM): mobidb-lite (MOB	0,000	0,036	0,025	0,025	0,023									
Solyc06g060480	Zinc finger family protein (AHRD V3.3 *** B9HPY6_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMART): PF13912 (PFAI	0,624	0,184	0,022	0,051	0,047									
Solyc06g060490	BZIP transcription factor (AHRD V3.3 *** A0A0K9NU16_ZOSMR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR004827 (SMAF bZIP	35,146	36,122	28,407	24,044	28,097									
Solyc06g060500	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TPA5_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR014476 (PIRSF): IPR005175 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc06g060510	LOW QUALITY:Plant/F17O14-7 protein (AHRD V3.3 *** G7KY86_MEDTR)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): IPR010605 (PFA	2,033	2,592	0,146	1,491	0,983									
Solyc06g060520	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT3G08600.1)		C:GO:0016021	C:integral component of membrane			IPR010605 (PFAM): mobidb-lite (MOB	1,884	1,942	0,271	0,169	0,117									
Solyc06g060530	Protein DETOXIFICATION (AHRD V3.3 *** K4C6N3_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport: F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	0,272	0,160	0,000	0,000	0,000									
Solyc06g060535	AT hook, DNA-binding motif-containing protein (AHRD V3.3 --* A0A103XG23_CYNCS)						mobidb-lite (MOBIDB_LITE)	0,778	1,147	0,755	0,695	0,753									
Solyc06g060540	AT hook motif DNA-binding family protein (AHRD V3.3 *-* AT5G51590.1)		F:GO:0003680	F:AT DNA binding			PTHR31500:SF0 (PANTHER): IPR039	0,099	0,062	0,050	0,022	0,071									
Solyc06g060550	Cornichon family protein (AHRD V3.3 *** AT1G12390.1)		P:GO:0016192	P:vesicle-mediated transport			IPR003377 (SMART): IPR003377 (PF	5,590	4,683	6,378	7,661	6,025									
Solyc06g060560	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)						PTHR33270:SF7 (PANTHER): IPR040	6,424	5,356	0,228	0,413	0,868									
Solyc06g060570	Dihydrofolate reductase (AHRD V3.3 *** A0A0B0NHA3_GOSAR)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm			IPR005645 (PFAM): IPR029058 (G3D	7,198	7,681	75,955	88,461	73,747									
Solyc06g060580	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4C6N8_SOLLC)		C:GO:0016021: F:G(	C:integral component of membrane: F:sugar transmembrane tra			G3DSA:1.20.1280.290 (GENE3D): IPF	0,042	0,018	0,000	0,000	0,047									
Solyc06g060590	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4C6N9_SOLLC)		C:GO:0016021: F:G(	C:integral component of membrane: F:sugar transmembrane tra			IPR004316 (PFAM): G3DSA:1.20.128	0,097	0,079	0,396	0,479	0,308									
Solyc06g060600	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** A0A0V0IC82_SOLCH)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process			G3DSA:3.30.70.1020 (GENE3D): IPR(	0,081	0,076	0,585	0,673	0,583									
Solyc06g060610	Flavin-containing monooxygenase (AHRD V3.3 *** K4C6P1_SOLLC)		F:GO:0004499: F:G(	F:N,N-dimethylanilir	EC:1.14.13.8: EC:1.'	Flavin-containing mo	IPR000960 (PRINTS): IPR036188 (G3	10,196	11,252	10,047	9,450	12,070									
Solyc06g060620	Nitrate transporter (AHRD V3.3 *** Q852P7_TOBAC)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			IPR000109 (PFAM): G3DSA:1.20.125	32,690	49,458	4,193	5,528	6,889	0,622	0,049					up		
Solyc06g060640	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** A0A061DW53_THECC)						IPR016140 (SMART): G3DSA:1.10.11	0,000	0,000	0,118	0,000	0,046									
Solyc06g060670	Arginine N-methyltransferase family protein (AHRD V3.3 *** B9GYA9_POPTR)		P:GO:0006479: F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:2.70.160.11 (GENE3D): G3DS	19,118	19,109	13,553	12,728	12,701									
Solyc06g060680	Kinase family protein (AHRD V3.3 *** B9GPM5_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (PFAM): PIRSF000654 (P	24,147	11,382	17,876	45,225	23,965	-1,060	0,002			1,344	0,000	down		up
Solyc06g060690	Kinase family protein (AHRD V3.3 *** B9GPM5_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	45,716	31,634	7,588	19,718	12,619			0,728	0,031	1,374	0,000		up	up
Solyc06g060700	Protein kinase superfamily protein (AHRD V3.3 --* AT3G57720.1)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	PTHR27005:SF38 (PANTHER): PTHR:	2,741	3,545	0,830	1,466	1,058									
Solyc06g060710	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 *** AT4G16600.1)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity: P:protein glycosylation: (			IPR029044 (G3DSA:3.90.550.GENE3I	13,848	46,403	5,425	6,951	6,558	1,766	0,001					up		
Solyc06g060720	Peroxisome biogenesis protein 19-2 (AHRD V3.3 *** A0A0B2PL27_GLYSO)		C:GO:0005777	C:peroxisome			IPR038322 (G3DSA:1.20.120.GENE3I	37,716	38,648	39,719	35,557	39,896									
Solyc06g060730	FER-like regulator of iron uptake (AHRD V3.3 --* AT2G28160.1)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR003604 (SMART): IPR022755 (PF	17,764	17,370	22,089	21,823	20,103									
Solyc06g060740	Zinc finger family protein (AHRD V3.3 *** B9IBW4_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	3,818	3,621	2,197	1,322	1,619									
Solyc06g060750	O-fucosyltransferase family protein (AHRD V3.3 *** AT4G16650.2)		P:GO:0006004: C:G(	P:fucose metabolic process: C:integral component of membrane			IPR024709 (PIRSF): IPR019378 (PFA	15,839	14,961	17,507	17,545	16,193									
Solyc06g060760	tonoplast intrinsic protein 2.3	TIP2.3	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,249	0,663	0,647	2,172	0,705					1,709	0,032			up
Solyc06g060770	Methionyl-tRNA formyltransferase (AHRD V1 *-*- FMT_STAEQ)		P:GO:0006189: F:G(	P:'de novo' IMP bio	EC:3.5.1.1	Formyltetrahydrofolat	IPR004810 (PRINTS): IPR002376 (PF	0,061	0,244	0,093	0,198	0,047									
Solyc06g060780	phosphatidylserine decarboxylase	psd	F:GO:0004609: C:G(	F:phosphatidylserin	EC:4.1.1.65	Phosphatidylserine d	IPR033177 (TIGRFAM): IPR003817 (F	13,683	13,770	13,715	12,911	12,776									
Solyc06g060790	3-isopropylmalate dehydratase, putative (AHRD V3.3 *** B9SXE3_RICCO)		F:GO:0016836	F:hydro-lyase activity			IPR015928 (G3DSA:3.20.19.GENE3D	67,733	81,869	170,400	151,127	159,740									
Solyc06g060800	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G16765.6)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR026992 (PFA	3,743	2,869	16,585	20,809	15,308									
Solyc06g060810	Nogo-B receptor (AHRD V3.3 *** A0A0B0NTE7_GOSAR)		P:GO:0001525: F:G(	P:angiogenesis: F:transferase activity, transferring alkyl or aryl			IPR036424 (G3DSA:3.40.1180.GENE:	15,585	16,284	20,596	23,193	22,470									
Solyc06g060820	30S ribosomal protein S7, chloroplastic (AHRD V3.3 --* RR7_SAGLA)		C:GO:0016021	C:integral component of membrane			IPR008480 (PFAM): mobidb-lite (MOB	0,993	1,656	0,586	0,915	0,590									
Solyc06g060830	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GYL8_POPTR)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR000047 (PRIN HD-ZIP	8,199	2,520	2,261	2,754	1,735	-1,672	0,000					down		
Solyc06g060840	Oleosin (AHRD V3.3 *** K4C6R4_SOLLC)		C:GO:0012511: C:G(	C:monolayer-surrounded lipid storage body: C:integral compone			IPR000136 (PFAM): IPR000136 (PAN	0,000	0,019	0,100	0,173	0,046									
Solyc06g060850	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** K4C6R5_SOLLC)		F:GO:0004843: C:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001578 (PRINTS): IPR001578 (PF	26,346	25,416	28,550	23,760	26,532									
Solyc06g060860	ATP-dependent caseinolytic protease/crotonase family protein (AHRD V3.3 *** A0A061G4B1_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,760	1,704	0,351	0,099	0,095									
Solyc06g060870	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GB30_THECC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.50.12520 (GENE3D): IPF	0,060	0,019	0,000	0,000	0,000									
Solyc06g060880	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT2G35660.1)	ZEP1	F:GO:0071949	F:FAD binding			PR00420 (PRINTS): IPR002938 (PFA	3,550	4,401	0,826	0,804	1,106									
Solyc06g060890	Dynamin-like 120 kDa protein, putative isoform 1 (AHRD V3.3 *** A0A061GB21_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,399	9,757	10,585	10,283	10,815									
Solyc06g060900	LOW QUALITY:PRLI-interacting factor (AHRD V3.3 --* AT5G19900.5)		C:GO:0016020: C:G(	C:membrane: C:integral component of membrane: F:kinase acti			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,064	0,000	0,000	0,000									
Solyc06g060910	Glycerol-3-phosphate transporter, putative (AHRD V3.3 *** B9T0L8_RICCO)		C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport			IPR000849 (PIRSF): G3DSA:1.20.125	3,279	2,906	8,614	9,429	10,132									
Solyc06g060920	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 (AHRD V3.3 --* METE2_ARATH)						PTHR35749 (PANTHER)	3,666	4,053	5,997	5,386	5,461									
Solyc06g060925	Arogenate dehydrogenase (AHRD V3.3 *-* A0A061GQ11_THECC)		F:GO:0004665: P:G(	F:prephenate dehydrogenase (NADP+) activity: P:tyrosine bios			PTHR43207 (PANTHER)	0,000	0,000	0,025	0,000	0,073									
Solyc06g060940	GATA transcription factor, putative (AHRD V3.3 *** B9SYZ6_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR000679 (SMAF GATA	8,852	10,306	27,671	27,326	23,540									
Solyc06g060950	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G19970.5)							0,343	0,499	0,392	0,220	0,379									
Solyc06g060960	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *-* W9S0E6_9ROSA)		F:GO:0005515: C:G(	F:protein binding: C	EC:2.1.1.43	Histone-lysine N-met	IPR003105 (SMART): IPR001214 (SM	0,481	0,291	0,377	0,530	0,117									
Solyc06g060970	Expansin-like protein (AHRD V3.3 *** Q0WRS3_ARATH)	EXLB3	C:GO:0005576	C:extracellular region			IPR007118 (PRINTS): IPR007117 (PF	0,271	0,301	0,398	0,050	0,281									
Solyc06g060990	Coiled-coil domain-containing 97 (AHRD V3.3 *** A0A0B0M5J9_GOSAR)						IPR040233 (PFAM): mobidb-lite (MOB	14,353	14,072	20,304	18,440	18,168									
Solyc06g061000	Casein kinase II subunit beta (AHRD V3.3 *** K4C6T0_SOLLC)		C:GO:0005956: F:G(	C:protein kinase CK2 complex: F:protein kinase regulator activi			IPR000704 (PRINTS): IPR000704 (SM	262,532	251,507	202,323	181,645	195,735									
Solyc06g061010	senescence-associated family protein (DUF581) (AHRD V3.3 *-* AT4G17670.1)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR007650 (PFAM): mobidb-lite (MOB	1,323	1,416	0,389	0,594	0,588									
Solyc06g061020	SBP (S-ribonuclease-binding protein) family protein (AHRD V3.3 *** G7JYN7_MEDTR)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity: P:protein ubiquitination:			PF13920 (PFAM): IPR013083 (G3DSA	130,032	54,718	197,173	200,548	204,502	-1,222	0,000					down		
Solyc06g061030	Two-component response regulator-like protein (AHRD V3.3 *** W9RZ29_9ROSA)		P:GO:0000160: F:G(	P:phosphorelay signal transduction system; F:DNA binding			IPR001789 (SMAF ARR-B	17,138	15,695	4,669	4,682	6,351									
Solyc06g061040	Ribose-phosphate pyrophosphokinase (AHRD V3.3 *** G7JHM7_MEDTR)		F:GO:0000287: F:G(	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	SM01400 (SMART): IPR029099 (PFAI	1,118	1,252	0,673	0,686	1,104									
Solyc06g061050	Tobamovirus multiplication protein 2B (AHRD V3.3 *** U5GN76_POPTR)						mobidb-lite (MOBIDB_LITE)	0,760	0,688	1,758	2,202	1,579									
Solyc06g061055	Chloroplast 40 kDa outer membrane envelope protein (AHRD V3.3 *** A0A144L7G4_PEA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	44,268	42,942	57,029	49,010	52,228									
Solyc06g061070	Glycine cleavage system protein H (AHRD V3.3 *** A9PG07_POPTR)		C:GO:0005960: P:G(	C:glycine cleavage complex: P:glycine decarboxylation via glyci			G3DSA:2.40.50.100 (GENE3D): IPR0	52,351	97,107	38,467	45,635	75,810	0,919	0,007	0,976	0,000			up	up	
Solyc06g061080	NAC domain protein, (AHRD V3.3 *** A0A061GAH7_THECC)	NAC053	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,944	1,708	1,102	1,390	1,111									
Solyc06g061090	Interferon-induced protein 44 (AHRD V3.3 *** A0A1D1XKP6_9ARAE)		C:GO:0009507	C:chloroplast			IPR006571 (PFAM): PTHR14241:SF1	0,077	0,094	0,025	0,022	0,000									
Solyc06g061100	aluminum activated malate transporter family protein (AHRD V3.3 *** AT5G46610.1)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): IPR006571 (PFA	0,040	0,019	0,025	0,000	0,000									
Solyc06g061110	Seed maturation protein (AHRD V3.3 *** Q2XSJ3_GLYTO)		P:GO:0009793	P:embryo development ending in seed dormancy			IPR005513 (PFAM): mobidb-lite (MOB	0,973	1,505	0,272	0,703	0,162									
Solyc06g061120	SAC3/GANP/Nin1/mts3/eIF-3 p25 (AHRD V3.3 *** A0A103XWK1_CYNCS)		C:GO:0005737: P:G(	C:cytoplasm: P:poly(A)+ mRNA export from nucleus: C:transcrip			IPR005062 (PFAM): G3DSA:1.25.40.9	33,141	26,592	35,055	36,792	32,602									
Solyc06g061130	Gag-Pol polyprotein/retrotransposon (AHRD V3.3 *** AT2G38695.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR343	2,003	3,295	2,557	2,483	3,161									
Solyc06g061140	phospholipid hydroperoxide glutathione peroxidase (AHRD V3.3 *** AT4G17960.1)						mobidb-lite (MOBIDB_LITE): PTHR357	7,844	8,630	8,526	6,680	6,665									
Solyc06g061150	AP-2 complex subunit mu (AHRD V3.3 *** AP2M_ARATH)		P:GO:0006886: P:G(	P:intracellular protein transport: P:vesicle-mediated transport: C			IPR001392 (PRINTS): G3DSA:3.30.45	37,554	38,877	44,974	46,868	40,283									
Solyc06g061170	Mitochondrial carrier protein (AHRD V3.3 *** B1N662_SOLLC)		F:GO:0022857: P:G(	F:transmembrane transporter activity: P:transmembrane transpo			IPR002067 (PRINTS): IPR023395 (G3	11,792	13,079	256,875	332,098	205,430									

Solyc06g061180	Abscisic acid receptor PYR1 (AHRD V3.3 *** PYR1_ARATH)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR019587 (PFAM); IPR023393 (G3D	22,562	21,985	5,863	4,735	7,109									
Solyc06g061190	VQ motif-containing protein (AHRD V3.3 *** AT2G35230.3)		P:GO:0009960; P:G(	P:endosperm development; P:regulation of seed growth	IPR008889 (PFAM); mobidb-lite (MOB	19,763	15,075	10,088	22,296	15,665			0,632	0,039	1,145	0,000		up	up
Solyc06g061200	glycine-rich protein 1				PR01228 (PRINTS)	185,961	177,597	39,908	34,721	32,929									
Solyc06g061230	Metallocarboxypeptidase inhibitor (AHRD V3.3 -** M1D4V9_SOLTU)		F:GO:0004180; P:G(	F:carboxypeptidase activity; P:proteolysis; C:membrane; C:inte	IPR009632 (PRODOM)	0,966	0,869	0,700	0,172	0,569									
Solyc06g061240	PLATZ transcription factor family protein (AHRD V3.3 *** G7KDS6_MEDTR)		F:GO:0008270	F:zinc ion binding	IPR006734 (PFAM); mobidb-lite (MOB	19,563	19,316	17,899	16,223	13,639									
Solyc06g061250	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GAA2_THECC)		F:GO:0008270	F:zinc ion binding	IPR001841 (SMART); IPR013083 (G3	1,738	1,599	1,110	1,481	1,225									
Solyc06g061280	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *** B9S247_RICCO)	CCR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding	G3DSA:3.40.50.720 (GENE3D); IPR0(	0,325	0,920	0,681	0,925	0,304									
Solyc06g062280	Thioredoxin superfamily protein (AHRD V3.3 *-* A0A061FEH2_THECC)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.30.10 (GENE3D); IPR01:	44,483	37,581	40,635	42,905	40,488									
Solyc06g062290	Glycosyltransferase (AHRD V3.3 *** K4C6W0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM); G3DSA:3.40.50.2	2,163	2,303	2,290	1,955	2,110									
Solyc06g062300	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *-* B9GL08_POPTR)		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic	IPR027443 (G3DSA:2.60.120.GENE3	1,504	1,975	1,276	1,777	1,576									
Solyc06g062305	Flavin-containing monooxygenase (AHRD V3.3 *-* M1BEB5_SOLTU)		F:GO:0004499; F:G(	F:N,N-dimethylanilir EC:1.14.13.8; EC:1.· Flavin-containing mo	PR00419 (PRINTS); PF13450 (PFAM)	0,042	0,019	0,025	0,000	0,000									
Solyc06g062310	Flavin-containing monooxygenase (AHRD V3.3 *** K4C6W2_SOLLC)		F:GO:0004499; F:G(	F:N,N-dimethylanilir EC:1.14.13.8; EC:1.· Flavin-containing mo	PR00419 (PRINTS); IPR036188 (G3D	1,180	0,862	0,797	0,621	0,947									
Solyc06g062320	Flavin-containing monooxygenase (AHRD V3.3 *-* M1BEB5_SOLTU)		F:GO:0004499; F:G(	F:N,N-dimethylanilir EC:1.14.13.8; EC:1.· Flavin-containing mo	IPR036188 (G3DSA:3.50.50.GENE3D	1,805	1,440	1,314	1,240	1,390									
Solyc06g062330	Glycosyltransferase (AHRD V3.3 *** M1BEA1_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR(	1,527	2,814	1,867	1,060	1,699									
Solyc06g062340	Unknown protein (AHRD V3.3)					0,021	0,000	0,000	0,025	0,000									
Solyc06g062350	RuvB-like helicase (AHRD V3.3 *** K4C6W6_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:In EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); G3DS	16,249	17,259	17,336	14,678	15,851									
Solyc06g062360	Syntaxin-like protein (AHRD V3.3 *** Q3HRZ4_SOLTU)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport	IPR000727 (SMART); IPR006011 (SM	33,113	30,653	40,554	36,245	35,357									
Solyc06g062370	Acid phosphatase-like protein 1 (AHRD V3.3 *** V9MHL3_9ROSA)		F:GO:0003993	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR014403 (PIRSF); IPR010028 (TIGI	0,000	0,041	0,000	0,000	0,024									
Solyc06g062375	LOW QUALITY:Acid phosphatase 1 (AHRD V3.3 *** N1R2I4_AEGTA)		F:GO:0003993; P:G(	F:acid phosphatase activity; P:dephosphorylation	IPR005519 (PFAM); IPR023214 (G3D	0,000	0,039	0,000	0,000	0,000									
Solyc06g062380	Acid phosphatase-like protein 1 (AHRD V3.3 *** V9MHL3_9ROSA)		F:GO:0003993	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR023214 (G3DSA:3.40.50.GENE3D	0,987	4,551	0,197	0,050	0,166	2,220	0,002					up		
Solyc06g062390	Acid phosphatase-like protein 1 (AHRD V3.3 *** V9MHL3_9ROSA)		F:GO:0003993	F:acid phosphatase EC:3.1.3.2 Acid phosphatase	IPR014403 (PIRSF); IPR005519 (PFA	0,118	0,060	0,000	0,025	0,000									
Solyc06g062400	Protein CHUP1, chloroplastic (AHRD V3.3 *** A0A0B2RCB9_GLYSO)		C:GO:0009707; C:G(	C:chloroplast outer membrane; C:integral component of membra	mobidb-lite (MOBIDB_LITE); mobidb-lit	9,374	6,926	4,342	3,855	4,913									
Solyc06g062420	transmembrane protein (AHRD V3.3 -** AT3G21351.1)				PTHR36328 (PANTHER)	0,178	0,927	0,147	0,690	0,735									
Solyc06g062430	Myo-inositol oxygenase (AHRD V3.3 *** K7VPE5_SOLTU)		F:GO:0005506; C:G(	F:iron ion binding; C EC:1.13.99.1 Inositol oxygenase	IPR007828 (PFAM); PTHR12588:SF2	25,094	17,501	17,017	19,619	18,138									
Solyc06g062440	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	14,625	18,769	10,367	13,432	14,993			0,527	0,038				up	
Solyc06g062450	Leucine-rich repeat protein kinase family protein, putative (AHRD V3.3 *** A0A061GIV3_THECC)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation	IPR024788 (PFAM); PTHR27003 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc06g062460	bHLH transcription factor136		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,291	0,380	0,046	0,045	0,070									
Solyc06g062480	Protein EARLY FLOWERING 3-like protein (AHRD V3.3 *** A0A0B0MJA5_GOSAR)		P:GO:2000028	P:regulation of photoperiodism, flowering	mobidb-lite (MOBIDB_LITE); mobidb-lit	16,870	18,384	19,848	23,995	20,250									
Solyc06g062500	60S ribosomal protein L28, putative (AHRD V3.3 *** B9RKC5_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:3.30.390.110 (GENE3D); IPR(	87,584	88,977	43,524	42,421	44,313									
Solyc06g062510	Charged multivesicular body 1 (AHRD V3.3 *** A0A0B0N7X7_GOSAR)		P:GO:0007034	P:vacuolar transport	IPR005024 (PFAM); mobidb-lite (MOB	126,834	133,044	182,030	166,614	162,684									
Solyc06g062520	Dof zinc finger protein (AHRD V3.3 *** W9QMS6_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM Dof	3,101	5,686	1,817	2,876	2,860	0,899	0,032					up		
Solyc06g062530	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B (AHRD V3.3 *** K4C6Y4_SOLLC)		C:GO:0000159; F:G(	C:protein phosphatase type 2A complex; F:protein binding; F:pr	IPR000009 (PRINTS); IPR001680 (SM	39,881	38,303	34,129	34,506	33,242									
Solyc06g062540	putative acid phosphatase	psi14c	F:GO:0016791	F:phosphatase activity	IPR023214 (G3DSA:3.40.50.GENE3D	1,804	1,746	0,415	0,459	0,541									
Solyc06g062550	LES459817 putative phosphatase 14A	psi14a	F:GO:0016791	F:phosphatase activity	IPR016965 (PIRSF); IPR023214 (G3I	0,141	0,103	0,118	0,195	0,023									
Solyc06g062570	LOW QUALITY:Agenet-like domain-containing protein (AHRD V3.3 *** A0A103YGJ9_CYNCS)				IPR014002 (SMART); PTHR31917:SF	0,019	0,000	0,000	0,000	0,000									
Solyc06g062580	Beta-galactosidase (AHRD V3.3 *** BGAL_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS); IPR008979 (G3	5,825	7,546	0,742	0,406	0,609									
Solyc06g062590	Transmembrane 9 superfamily member (AHRD V3.3 *** A0A0V0IMM7_SOLCH)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM); IPR004240 (PAN	101,924	105,810	510,073	485,516	424,559									
Solyc06g062600	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G72970.1)		F:GO:0016614; F:G(	F:oxidoreductase activity, acting on CH-OH group of donors; F:	IPR007867 (PFAM); IPR012132 (PIRS	21,880	18,222	93,391	121,945	77,240									
Solyc06g062610	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YL18_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,922	2,174	1,631	1,987	2,142									
Solyc06g062627	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT4G26460.2)					0,040	0,000	0,000	0,000	0,000									
Solyc06g062630	LOB domain-containing protein, putative (AHRD V3.3 *-* B9SN30_RICCO)				IPR004883 (PFAM LBD	0,000	0,000	0,025	0,000	0,000									
Solyc06g062660	Beta-galactosidase (AHRD V3.3 *** K4C6Z7_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS); IPR008979 (G3	34,876	33,895	39,699	48,662	43,341									
Solyc06g062670	zinc finger family protein		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	35,568	38,446	19,988	21,799	25,252									
Solyc06g062680	Polyadenylate-binding protein (AHRD V3.3 *-* K4DGU3_SOLLC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	1,663	2,987	0,423	0,391	0,703									
Solyc06g062690	Nucleosome assembly protein 1-1 (AHRD V3.3 *-* NAP1A_ORYSJ)		C:GO:0005634; P:G(	C:nucleus; P:nucleosome assembly	IPR002164 (PFAM); G3DSA:3.30.112(	21,574	22,720	47,932	37,158	46,983					-0,364	0,020			down
Solyc06g062700	SMAD/FHA domain-containing protein (AHRD V3.3 *-* AT3G13780.1)		F:GO:0005515	F:protein binding	G3DSA:2.60.200.20 (GENE3D); mobic	11,808	12,318	10,826	8,940	9,644									
Solyc06g062720	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT3G13224.2)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	0,019	0,155	0,022	0,098	0,023									
Solyc06g062730	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT1G17640.3)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	0,021	0,000	0,000	0,051	0,048									
Solyc06g062740	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT3G13224.2)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR000504 (PF.	0,021	0,000	0,000	0,000	0,000									
Solyc06g062750	5'-nucleotidase surE (AHRD V3.3 *** A0A0B2RK49_GLYSO)		F:GO:0008252	F:nucleotidase acti EC:3.1.3.31 Nucleotidase	IPR002828 (PFAM); IPR036523 (G3D	0,339	0,138	0,000	0,000	0,000									
Solyc06g062760	50S ribosomal protein L34 (AHRD V3.3 *** W9QNR0_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000271 (TIGRFAM); IPR000271 (F	9,550	8,520	8,168	8,666	7,800									
Solyc06g062770	DEAD-box ATP-dependent RNA helicase (AHRD V3.3 *** AT5G57000.2)				mobidb-lite (MOBIDB_LITE); mobidb-lit	12,061	10,676	18,290	18,393	18,849									
Solyc06g062780	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IZF4_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	PR00119 (PRINTS); IPR032631 (PFA	87,482	81,808	23,939	27,795	29,372									
Solyc06g062790	Casein kinase, putative (AHRD V3.3 *** B9S5V9_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	72,009	68,073	155,631	164,498	143,973									
Solyc06g062795	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 --* G7LI91_MEDTR)				IPR021899 (PFAM); PTHR33193 (PAN	0,000	0,043	0,100	0,166	0,024									
Solyc06g062800	RNA helicase DEAD19	DEAD19	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR001650 (SMART); IPR014001 (SM	1,004	1,968	4,354	7,546	3,917					0,797	0,046			up
Solyc06g062805	Outer arm dynein light chain 1 protein (AHRD V3.3 --* AT4G03260.4)					0,405	0,415	0,265	0,288	0,165									
Solyc06g062810	Glycylpeptide N-tetradecanoyltransferase (AHRD V3.3 *** K4C712_SOLLC)		F:GO:0004379; P:G(	F:glycylpeptide N-te EC:2.3.1.97 Glycylpeptide N-tetra	IPR022677 (PFAM); G3DSA:3.40.630	39,147	46,882	37,312	35,433	34,717									
Solyc06g062820	protein kinase family protein (AHRD V3.3 *-* AT5G26150.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); IPR000719 (PF.	0,040	0,115	0,000	0,000	0,000									
Solyc06g062830	60S ribosomal L18a-like protein (AHRD V3.3 *** AT5G57060.9)		C:GO:0005840; C:G(	C:ribosome; C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,685	2,325	2,781	2,719	2,758									
Solyc06g062840	DNA polymerase epsilon catalytic subunit A (AHRD V3.3 --* DPOE1_ARATH)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc06g062845	Threonine synthase, putative (AHRD V3.3 *** B9RK44_RICCO)		F:GO:0004795; P:G(	F:threonine synthas EC:4.2.3.1 Threonine synthase	G3DSA:3.40.50.1100 (GENE3D); IPR(	3,673	3,474	2,668	2,192	2,922									
Solyc06g062850	PHD finger alfin-like protein (AHRD V3.3 *** A0A072V846_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding	IPR001965 (SMART); IPR013083 (G3	10,972	9,492	17,419	17,843	17,110									
Solyc06g062860	Ataxin-2 related protein (AHRD V3.3 *** A2PZE4_IPONI)		C:GO:0010494; P:G(	C:cytoplasmic stress granule; P:regulation of cytoplasmic mRN/	IPR009604 (SMART); IPR009604 (PF.	53,803	63,350	56,576	54,506	55,165									
Solyc06g062880	Brevis radix-like protein (AHRD V3.3 *** A0A072TLT2_MEDTR)				IPR027988 (PFAM); IPR013591 (PFA	0,751	0,688	0,097	0,025	0,024									
Solyc06g062883	Ethylene-responsive transcription factor 1B (AHRD V3.3 --* W9SHC2_9ROSA)					3,476	3,090	1,252	1,817	2,277									
Solyc06g062887	Transcription initiation factor TFIID subunit 12 (AHRD V3.3 *-* W9RRR4_9ROSA)		C:GO:0000124; C:G(	C:SAGA complex; C:transcription factor TFIID complex; P:DNA-	IPR003228 (PFAM); IPR009072 (G3D	5,651	6,717	1,879	2,013	3,202									
Solyc06g062890	Unknown protein (AHRD V3.3)					1,091	1,017	0,530	0,436	0,898									
Solyc06g062900	Transcription initiation factor TFIID subunit 12 (AHRD V3.3 *-* W9RRR4_9ROSA)		C:GO:0000124; C:G(	C:SAGA complex; C:transcription factor TFIID complex; C:SLIK	mobidb-lite (MOBIDB_LITE); mobidb-lit	4,404	5,652	1,743	1,901	2,683									
Solyc06g062905	global transcription factor group E8 (AHRD V3.3 --* AT3G27260.4)					3,021	4,087	2,178	1,322	1,884									
Solyc06g062910	LOW QUALITY:AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT4G33280.1)					3,873	4,466	3,109	1,944	2,736									
Solyc06g062920	auxin-regulated dual specificity cytosolic kinase		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM); G3DSA:1.10.510	47,963	17,819	1,567	1,645	2,083	-1,404	0,000					down		
Solyc06g062930	LOW QUALITY:Plant regulator RWP-RK family protein (AHRD V3.3 --* AT1G76350.4)				mobidb-lite (MOBIDB_LITE); PTHR347	0,040	0,021	0,000	0,000	0,000									
Solyc06g062940	RING-box protein (AHRD V3.3 *** Q2PYP4_ARAHY)		F:GO:0008270	F:zinc ion binding	IPR024766 (PFAM); IPR013083 (G3D	40,749	44,958	55,412	51,842	51,495									
Solyc06g062960	DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)				IPR012876 (PFAM); IPR012876 (PAN	2,619	2,973	0,694	1,058	1,618									
Solyc06g062970	LOW QUALITY:Early auxin response protein (AHRD V3.3 *-* Q69P88_ORYSJ)				PTHR34045 (PANTHER); PTHR34045	0,019	0,055	0,022	0,000	0,047									
Solyc06g062980	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT3G14080.2)		P:GO:0000956	P:nuclear-transcribed mRNA catabolic process	IPR001163 (SMART); IPR001163 (PF.	4,282	5,398	4,140	4,203	3,153									
Solyc06g062990	Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9N7F2_POPTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis	IPR004140 (PFAM); mobidb-lite (MOB	19,163	28,095	16,411	17,806	14,261									
Solyc06g063000	RNA-binding family protein (AHRD V3.3 *** A0A061GD25_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART); IPR012677 (G3	295,963	249,440	261,927	238,783	258,368									
Solyc06g063010	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 --* RPOA_ARATH)				mobidb-lite (MOBIDB_LITE); mobidb-lit	3,936	2,779	5,409	6,459	6,106									
Solyc06g063015	DNA binding protein, putative (AHRD V3.3 *** B9ST76_RICCO)		F:GO:0008168; F:G(	F:methyltransferase activity; F:transferase activity; P:methylatic	mobidb-lite (MOBIDB_LITE); mobidb-lit	55,200	40,395	78,878	85,541	75,409									
Solyc06g063020	Zinc finger transcription factor 44	C3H44	F:GO:0046872	F:metal ion binding	IPR003034 (SMAF C3H	21,738	19,275	18,995	15,584	15,664									
Solyc06g063030	25. vesicle transport protein (AHRD V3.3 *** A0A1D1XNZ8_9ARAE)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo	IPR010908 (SMART); G3DSA:1.20.5.1	23,400	20,263	32,441	30,011	27,563									
Solyc06g063040	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR020843 (SMART); G3DSA:3.90.18	5,619	5,173	5,486	6,087	3,487			-0,653	0,047				down	
Solyc06g063050	Erect panicle 2 protein (AHRD V3.3 *-* I2AW35_9POAL)				mobidb-lite (MOBIDB_LITE); mobidb-lit	2,831	2,601	5,284	4,862	6,920									
Solyc06g063060	Auxin-repressed protein-like protein (AHRD V3.3 *** Q84KS0_TOBAC)				IPR008406 (PFAM); mobidb-lite (MOB	2,360	4,743	2,583	1,923	2,782									
Solyc06g063070	Ethylene Response Factor A.3	ERF.E2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	759,204	841,763	1994,426	2097,426	1956,996									
Solyc06g063080	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G14250.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART); IPR002867 (PF.	0,021	0,019	0,000	0,025	0,000									
Solyc06g063090	alanine aminotransferase 2 (AHRD V3.3 *** AT1G72330.1)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	IPR004839 (PFAM); IPR015422 (G3D	41,746	44,571	90,880	73,699	84,964									
Solyc06g063100	Ubiquitin-conjugating enzyme (AHRD V3.3 *** B7FML7_MEDTR)		P:GO:0000209; C:G(	P:protein polyubiquitination; C:endoplasmic reticulum; C:integral	SM00212 (SMART); IPR016135 (G3D	11,701	13,407	15,417	15,132	12,783									
Solyc06g063110	RING/U-box superfamily protein (AHRD V3.3 *** AT1G72310.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination	IPR001841 (SMART); IPR001841 (PF.	0,161	0,153	0,297	0,213	0,332									
Solyc06g063120	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G50420.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane	IPR019378 (PFAM); G3DSA:3.40.50.1	0,625	1,085	0,144	0,123	0,210									
Solyc06g063130	K+-H+ exchange-like protein (AHRD V3.3 *** AT1G53760.1)		C:GO:0005774; P:G(	C:vacuolar membrane; P:potassium ion transport; C:plastid; C:ir	IPR018786 (PFAM); mobidb-lite (MOB	0,244	0,241	0,093	0,195	0,233									
Solyc06g063140	26S protease regulatory subunit, putative (AHRD V3.3 *** B9RR13_RICCO)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata	IPR003593 (SMART); IPR018786 (PF.	123,262	131,717	184,983	181,129	170,135									
Solyc06g063150	Kinase (AHRD V3.3 *** A0A0K9NP62_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	G3DSA:1.10.510.10 (GENE3D); IPR0(	6,751	5,108	8,586	5,665	9,937									
Solyc06g063160	Beta-glucosidase, GBA2 type family protein (AHRD V3.3 --* AT4G10060.2)				mobidb-lite (MOBIDB_LITE)	1,093	1,110	0,457	0,859	0,821									
Solyc06g063170	Glutamate receptor (AHRD V3.3 *** K4C748_SOLLC)		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART); IPR017103 (PIF	11,839	11,732	6,373	6,511	7,465									
Solyc06g063180	glutamate receptor-like 2.2		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART); IPR001828 (PF.	5,829	16,718	0,875	1,769	3,358	1,540	0,018	1,927	0,001			up	up	
Solyc06g063190	glutamate receptor-like 2.3		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART); IPR001638 (PF.	0,222	2,454	0,072	0,145	0,475	3,455	0,000					up		
Solyc06g063200	glutamate receptor-like 2.4		F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART); IPR017103 (PIF	0,021	0,566	0,121	0,162	0,237									
Solyc06g063210	glutamate receptor-like 2.5	GLR2_5	F:GO:0004970; C:G(	F:ionotropic glutamate receptor activity; C:membrane	IPR001320 (SMART); G3DSA:3.40.50	1,533	4,774	3,533	5,995	7,269	1,663	0,000	1,034	0,001	0,762	0,046	up	up	up
Solyc06g063220	ATP synthase subunit epsilon, mitochondrial (AHRD V3.3 *** ATP5E_IPOBA)		C:GO:0000275; P:G(	C:mitochondrial pro EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR036742 (G3DSA:1.10.1620.GENE	38,481	34,663	36,725	31,276	33,064									
Solyc06g063230	WD repeat-containing protein 49 isoform 1 (AHRD V3.3 *** A0A061G8I2_THECC)				PTHR37201 (PANTHER)	48,312	39,839	23,914	17,796	24,966									
Solyc06g063240	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G51630.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane	IPR024709 (PIRSF); IPR019378 (PFA	343,191	248,905	63,898	49,752	54,207									
Solyc06g063250	Metal tolerance protein C4 (AHRD V3.3 *** X5D917_TOBAC)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;	IPR002524 (TIGRFAM); IPR027469 ((	6,328	6,694	4,222	5,372	5,347									
Solyc06g063260	alpha-1,2-Mannosidase (AHRD V3.3 *** K4C757_SOLLC)		F:GO:0004571; F:G(	F:mannosyl-oligosa EC:3.2.1.113; EC:3.; Mannosyl-oligosacch	IPR001382 (PRINTS); IPR012341 (G3	1,796	2,609	1,835	1,012	1,462									
Solyc06g063270	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT4G33495.1)				IPR021099 (PFAM); mobidb-lite (MOB	6,331	5,169	4,686	4,515	4,054									
Solyc06g063280	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HV28_POPTR)	BBX30	F:GO:0008270	F:zinc ion binding	IPR000315 (SMART); PTHR31717:SF	4,528	6,575	4,830	3,874	4,755									
Solyc06g063290	Pyridoxamine 5'-phosphate oxidase-related, FMN-binding (AHRD V3.3 *** A0A0K9NPW0_ZOSMR)		F:GO:0048037	F:cofactor binding	PF13883 (PFAM); IPR012349 (G3DS/	23,765	26,517	33,496	31,224	30,841									
Solyc06g063295	F-box/kelch-repeat protein (AHRD V3.3 *** A0A0B2P9A5_GLYSO)		F:GO:0005515	F:protein binding	PF13418 (PFAM); IPR015915 (G3DS/	14,520	11,117	11,793	9,776	10,814									
Solyc06g063300	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 -** AT2G42130.5)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	3,607	2,651	1,678	2,914	2,364									
Solyc06g063305	Maturase K (AHRD V3.3 --* W8T6W3_9ROSI)					0,277	0,544	0,338	0,312	0,332									
Solyc06g063310	Fiber protein Fb15 (AHRD V3.3 *** K7WJQ5_SOLTU)		C:GO:0005753; C:G(	C:mitochondrial proton-transporting ATP synthase complex; C:p	PTHR36059 (PANTHER)	88,649	91,787	143,250	121,440	125,039									
Solyc06g063320	Serine/arginine repetitive matrix protein 2, putative isoform 1 (AHRD V3.3 *-* A0A061G9S9_THECC)				PTHR33972:SF2 (PANTHER); PTHR3:	80,628	61,903	69,421	70,375	60,618									
Solyc06g063330	vacuolar ATP synthase subunit A (AHRD V3.3 *** AT1G78900.2)		F:GO:0005524; P:G(	F:ATP binding; P:A1 EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR031686 (PFAM); G3DSA:3.40.50.3	1,094	1,301	1,085	1,236	1,412									
Solyc06g063340	DUF1666 family protein (DUF1666) (AHRD V3.3 *** AT3G20260.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR012870 (PFAM); mobidb-lite (MOB	4,978	6,505	0,459	0,412	0,633									
Solyc06g063345	Reticulon family protein (AHRD V3.3 *** AT1G78895.1)		C:GO:0016021	C:integral component of membrane	IPR003388 (PFAM); PTHR10994:SF9	0,542	0,841	0,197	0,314	0,308									
Solyc06g063350	Magnesium-chelatase subunit ChlD, chloroplastic (AHRD V3.3 --* CHLD_ORYSJ)	CHLD				0,000	0,041	0,000	0,000	0,000									
Solyc06g063360	chlorophyll a-b binding protein Cab9		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	G3DSA:1.10.510.10 (GENE3D); IPR0(	3,650	2,678	2,014	2,258	2,301									
Solyc06g063365	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT4G19120.3)					0,059	0,000	0,000	0,000	0,000									
Solyc06g063370	Type I (26 kD) CP29 polypeptide		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane	IPR022796 (PFAM); IPR023329 (G3D	406,528	983,198	306,779	385,419	706,647	1,302	0,001	1,200	0,000			up	up	
Solyc06g063390	Wound-induced basic protein (AHRD V3.3 *** PR4_PHAVU)		C:GO:0005829; P:G(	C:cytosol; P:response to cytokinin	IPR012643 (PFAM); mobidb-lite (MOB	0,021	0,060	0,075	0,000	0,116									
Solyc06g063400	Wound-induced basic protein (AHRD V3.3 *** PR4_PHAVU)		C:GO:0005829; P:G(	C:cytosol; P:response to cytokinin	IPR012643 (PFAM); mobidb-lite (MOB	0,115	0,078	0,047	0,022	0,047									
Solyc06g063410	ATP-dependent clp protease ATP-binding subunit clpx, putative (AHRD V3.3 *** B9S1U1_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding	IPR003593 (SMART); IPR019489 (SM	22,527	21,340	36,360	37,576	35,491									
Solyc06g063420	General transcription factor 3C polypeptide 3 (AHRD V3.3 *** A0A0B2PD46_GLYSO)		F:GO:0001004; P:G(	F:RNA polymerase III transcription regulator recruiting activity; I	IPR019734 (SMART); IPR011990 (G3	22,923	16,966	21,583	24,008	21,256									
Solyc06g063430	NAC domain-containing protein, putative (AHRD V3.3 *** B9T5U4_RICCO)	NAC055	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,000	0,018	0,000	0,000	0,000									
Solyc06g064430	Vesicle-associated membrane family protein (AHRD V3.3 *** B9IDQ1_POPTR)		C:GO:0016021	C:integral component of membrane	G3DSA:3.30.450.50 (GENE3D); PTHF	4,356	3,838	3,224	2,043	1,952									
Solyc06g064440	RING/U-box superfamily protein, putative (AHRD V3.3 *-* A0A061FJ88_THECC)		P:GO:0006511; C:G(	P:ubiquitin-dependent protein catabolic process; C:integral com	IPR001841 (SMART); IPR013083 (G3	12,882	15,103	4,743	5,111	4,887									
Solyc06g064445	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_PINKO)					0,828	1,111	0,362	0,219	0,282									
Solyc06g064450	Cytoplasmic membrane protein (AHRD V3.3 *** G7J0A0_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR018639 (PFAM); PTHR35102 (PAI	13,286	12,623	14,840	16,134	15,944									
Solyc06g064460	60S ribosomal protein L7A-like protein (AHRD V3.3 *** Q2XPW4_SOLTU)		P:GO:0000470; F:G(	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large rib(	IPR001921 (PRINTS); IPR018492 (PF	92,079	88,639	53,874	50,771	50,034									
Solyc06g064470	60S ribosomal protein L7A-like protein (AHRD V3.3 *** Q2XPW4_SOLTU)		P:GO:0000470; F:G(	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large rib(	IPR018492 (PRINTS); IPR001921 (PF	211,615	226,705	143,188	128,805	129,292									
Solyc06g064480	Exostosin family protein (AHRD V3.3 *** A0A061GMU3_THECC)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyc(	IPR004263 (PFAM); IPR004263 (PAN	14,019	9,996	10,537	11,583	9,586									
Solyc06g064500	O-methyltransferase (AHRD V3.3 *** F6M2M1_VITPS)	ASMT07	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR016461 (PIRSF); IPR012967 (PFA	19,321	15,675	64,899	73,473	50,366									
Solyc06g064510	O-methyltransferase (AHRD V3.3 *** A0A1B4Z3W3_9ROSA)	ASMT08	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR036388 (G3DSA:1.10.10.GENE3D	3,173	2,741	3,543	3,425	3,094									
Solyc06g064520	(1-4)-beta-mannan endohydrolase precursor	man2	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001547 (PFAM); G3DSA:3.20.20.8	0,096	0,328	0,000	0,139	0,236									
Solyc06g064525	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 (AHRD V3.3 *-* W9S6E2_9ROSA)		C:GO:0005739	C:mitochondrion		0,220	0,323	0,115	0,264	0,165									
Solyc06g064530	Major facilitator superfamily protein (AHRD V3.3 --* AT1G22570.2)					0,019	0,085	0,044	0,094	0,024									
Solyc06g064550	Aspartokinase-homoserine dehydrogenase (AHRD V3.3 *** O63067_SOYBN)		F:GO:0004072; P:G(	F:aspartate kinase EC:2.7.2.4 Aspartate kinase	G3DSA:3.30.2130.10 (GENE3D); IPR(	84,693	67,622	3,214	1,612	3,032					-0,987	0,021			down
Solyc06g064560	UvrABC system protein C (AHRD V3.3 *** A0A1D1YTR9_9ARAE)		P:GO:0000712	P:resolution of meiotic recombination intermediates	PF12826 (PFAM); G3DSA:1.10.150.2(	1,933	1,924	2,357	1,875	2,540									
Solyc06g064570	SNARE associated Golgi protein family (AHRD V3.3 *** AT1G22850.1)		C:GO:0016021	C:integral component of membrane	IPR032816 (PFAM); mobidb-lite (MOB	15,145	14,447	35,486	37,693	39,276									

Solyc06g064590	bHLH transcription factor 045		F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	0,000	0,000	0,025	0,000	0,000									
Solyc06g064600	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9I6N6_POPTR)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,979	1,507	2,181	1,994	1,579									
Solyc06g064610	LOW QUALITY:Glucan endo-1,3-beta-glucosidase (AHRD V3.3 -** A0A0B0PK92_GOSAR)				mobidb-lite (MOBIDB_LITE): PTHR351	0,289	0,601	0,072	0,050	0,072									
Solyc06g064630	Ribosomal protein L15 (AHRD V3.3 *** K4C793_SOLLC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000439 (SMART); IPR024794 (G3	117,292	146,418	93,798	80,725	89,850									
Solyc06g064640	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G10030.1)		F:GO:0004620; P:GC	F:phospholipase activity; P:lipid biosynthetic process; P:respon	IPR029058 (G3DSA:3.40.50.GENE3D	9,355	11,022	10,505	10,736	10,710									
Solyc06g064650	hydroxysteroid dehydrogenase 5 (AHRD V3.3 *** AT4G10020.1)		C:GO:0016021; F:GC	C:integral component of membrane; F:oxidoreductase activity; F	IPR002347 (PRINTS); G3DSA:3.40.50	11,582	9,163	0,688	1,946	0,162									
Solyc06g064660	Protein kinase family protein (AHRD V3.3 *** Q9LQ29_ARATH)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:1.10.51	0,434	0,536	0,071	0,190	0,635									
Solyc06g064680	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q8_SOLLC)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	3,079	2,189	0,096	0,073	0,140									
Solyc06g064720	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G40060.1)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	0,255	0,751	0,097	0,076	0,118									
Solyc06g064740	LOW QUALITY:Nuclear nucleic acid-binding protein C1D (AHRD V3.3 *-* A0A0B0NSY9_GOSAR)				mobidb-lite (MOBIDB_LITE); IPR0110	0,061	0,000	0,121	0,050	0,142									
Solyc06g064750	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q8_SOLLC)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); G3DSA:3.40.50.3	0,685	0,781	0,427	0,894	0,591									
Solyc06g064760	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR002182 (PFA	0,019	0,036	0,025	0,146	0,047									
Solyc06g064770	LOW QUALITY:UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT2G28080.1)					0,021	0,061	0,000	0,000	0,000									
Solyc06g064800	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G33800.1)		P:GO:0045492	P:xylan biosynthetic process	IPR021148 (PFAM); IPR006514 (TIGF	0,000	0,000	0,396	0,738	0,071									
Solyc06g064810	Zinc finger and BTB domain-containing protein 11 isoform 1 (AHRD V3.3 *** A0A061FI49_THECC)		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:chloroplast envelope	mobidb-lite (MOBIDB_LITE); mobidb-lit	8,034	9,986	12,125	12,345	10,995									
Solyc06g064820	GDSL esterase/lipase (AHRD V3.3 *** W9S0Q7_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	1,644	1,677	0,049	0,152	0,023									
Solyc06g064830	WD-40 repeat protein AY032884		F:GO:0005515	F:protein binding	IPR020472 (PRINTS); IPR001680 (SM	34,953	33,266	43,937	42,600	40,303									
Solyc06g064840	AGAMOUS MADS box factor transcription factor (AHRD V3.3 *** A0A0K9Q4Y3_ZOSMR)		F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRINTS); IPR002100 (SM	35,421	56,055	15,303	26,932	27,574	0,688	0,046	0,845	0,002	0,816	0,000	up	up	up
Solyc06g064850	NTGP4 (AHRD V3.3 *** Q9ZRD1_TOBAC)		F:GO:0005525	F:GTP binding	IPR006703 (PFAM); G3DSA:3.40.50.3	0,305	0,738	0,222	0,145	0,165									
Solyc06g064860	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A061FL24_THE		F:GO:0005525	F:GTP binding	IPR006703 (PFAM); G3DSA:3.40.50.3	0,077	0,043	0,025	0,000	0,047									
Solyc06g064870	methyl esterase 12 (AHRD V3.3 *** AT4G09900.1)		P:GO:0009694; P:GC	P:jasmonic acid me EC:3.1.1.1 Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	14,116	17,480	5,165	5,909	5,302									
Solyc06g064880	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (AHRD V3.3 *** AT5G12040		P:GO:0006807	P:nitrogen compound metabolic process	IPR003010 (PFAM); IPR036526 (G3D	0,101	0,078	0,022	0,073	0,071									
Solyc06g064890	Transcription initiation factor IIE subunit beta (AHRD V3.3 *** A0A166FP58_DAUCA)		C:GO:0005673; P:GC	C:transcription factor TFIIE complex; P:transcription initiation fr	IPR003166 (PFAM); PF18121 (PFAM)	44,095	43,370	76,040	70,722	65,817									
Solyc06g064895	Aldehyde dehydrogenase, putative (AHRD V3.3 *-* B9SH74_RICCO)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process	IPR016162 (G3DSA:3.40.605.GENE3I	2,175	1,505	5,207	6,221	5,342									
Solyc06g064900	Aldehyde dehydrogenase (AHRD V3.3 --* Q7FWR0_MAIZE)					0,433	0,281	2,280	2,655	2,126									
Solyc06g064910	T-complex protein 11 (AHRD V3.3 *** U5FVQ2_POPTR)				IPR008862 (PFAM); IPR008862 (PAN	81,467	65,551	108,729	103,599	103,619									
Solyc06g064930	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT1G33970.3)		F:GO:0005525	F:GTP binding	G3DSA:3.40.50.300 (GENE3D); IPR0	0,019	0,000	0,000	0,000	0,000									
Solyc06g064940	Patellin-like protein (AHRD V3.3 *** A0A072UTX7_MEDTR)				IPR001251 (SMART); IPR011074 (SM	51,168	48,810	120,668	136,509	123,844									
Solyc06g064970	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	0,038	0,043	0,000	0,000	0,000									
Solyc06g064980	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	0,019	0,096	0,075	0,000	0,000									
Solyc06g064990	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,019	0,043	0,000	0,000	0,000									
Solyc06g065000	LOW QUALITY:Hero resistance protein (AHRD V3.3 *** Q8GSM1_SOLLC)		F:GO:0043531	F:ADP binding	IPR002182 (PFAM); G3DSA:3.40.50.3	0,019	0,000	0,047	0,069	0,047									
Solyc06g065010	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	2,765	3,427	0,318	0,222	0,211									
Solyc06g065020	Major facilitator superfamily protein (AHRD V3.3 *** AT1G22540.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen	G3DSA:1.20.1250.20 (GENE3D); IPR	146,770	110,084	107,822	118,372	123,610									
Solyc06g065030	Transmembrane 9 superfamily member (AHRD V3.3 *** K4C7D2_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM); IPR004240 (PAN	4,066	11,252	4,894	9,852	9,415	1,493	0,000	0,937	0,001	1,008	0,000	up	up	up
Solyc06g065040	bHLH transcription factor 086		F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	6,405	4,604	20,684	22,903	20,170									
Solyc06g065050	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 *** A0A072UTU9_MEDTR)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.120.20 (GENE3D); IPR02	3,913	4,621	1,170	2,000	0,541									
Solyc06g065055	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 --* AT1G22600.1)		C:GO:0016021	C:integral component of membrane	PTHR23241:SF92 (PANTHER); PTHR2	0,021	0,000	0,000	0,000	0,000									
Solyc06g065060	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061GF79_THECC)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI	IPR006094 (PFAM); G3DSA:3.40.462	0,000	0,000	0,025	0,000	0,000									
Solyc06g065080	LOW QUALITY:Di-glucose binding protein with Kinesin motor domain-containing protein (AHRD V3.3 --* AT2G22610.3)				mobidb-lite (MOBIDB_LITE); PTHR330	0,042	0,057	0,049	0,045	0,000									
Solyc06g065100	R2R3MYB transcription factor 3	R2R3MYB3	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	9,665	12,431	13,535	12,784	11,722									
Solyc06g065130	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* A0A072U140_MEDTR)		P:GO:0007165; F:GC	P:signal transduction; F:ADP binding		0,000	0,019	0,000	0,000	0,000									
Solyc06g065140	Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 *-* A0A072TZ76_MEDTR)		P:GO:0007165; F:GC	P:signal transduction; F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,022	0,000	0,000									
Solyc06g065150	Disease resistance protein N-like protein (AHRD V3.3 *** A0A0H4BH71_9SOLA)		F:GO:0005515	F:protein binding	IPR001611 (PFAM); IPR032675 (G3D	0,000	0,041	0,000	0,000	0,000									
Solyc06g065160	LOW QUALITY:clathrin adaptor complexes medium subunit family protein (AHRD V3.3 --* AT2G20790.4)					0,000	0,018	0,000	0,000	0,000									
Solyc06g065170	vacuolar protein sorting 11 (AHRD V3.3 *** AT2G05170.1)		F:GO:0005515; P:GC	F:protein binding; P:intracellular protein transport; P:vesicle-mec	IPR016528 (PIRSF); IPR011990 (G3D	48,399	45,461	62,762	60,474	60,585									
Solyc06g065180	SLL1 protein (AHRD V3.3 *** I3S1M4_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR36003 (PANTHER)	73,727	81,045	95,320	83,125	83,737									
Solyc06g065190	TCP transcription factor 13	TCP13	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR017887 (PFAM TCP	5,327	4,653	1,968	1,169	2,137									
Solyc06g065200	Uncharacterized protein				PTHR35715 (PANTHER)	4,760	4,614	5,055	5,844	5,060									
Solyc06g065210	alkaline/neutral invertase		F:GO:0033926	F:glycopeptide alph EC:3.2.1.97 Endo-alpha-N-acetylg	IPR024746 (PFAM); IPR012341 (G3D	27,116	23,828	17,930	18,584	19,432									
Solyc06g065215	DNA replication licensing factor MCM4 (AHRD V3.3 --* MCM4_ORYSJ)					0,082	0,060	0,025	0,000	0,046									
Solyc06g065230	N-acetyltransferase (AHRD V3.3 *** K7WTW4_SOLTU)		F:GO:0004596; P:GC	F:peptide alpha-N-a EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	IPR000182 (PFAM); G3DSA:3.40.630	32,116	33,375	60,779	58,461	52,294									
Solyc06g065240	alpha-1,4-fucosyltransferase	fut13	P:GO:0006486; F:GC	P:protein glycosylation; F:fucosyltransferase activity; C:membra	IPR001503 (PFAM); IPR017177 (PIRS	22,434	16,630	22,881	22,420	21,486									
Solyc06g065260	Receptor-like protein kinase HSL1 (AHRD V3.3 *** W9T2E3_9ROSA)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR003591 (SMART); IPR000719 (SM	32,141	27,409	33,220	31,164	42,090									
Solyc06g065270	Adenylate kinase (AHRD V3.3 *** G7JRB1_MEDTR)		F:GO:0004017; F:GC	F:adenylate kinase EC:2.7.4.4; EC:2.7.4 Nucleoside-phosphat	IPR000850 (PRINTS); G3DSA:3.40.50	62,587	72,853	128,327	119,349	116,817									
Solyc06g065290	Protein phosphatase 1 regulatory subunit inhibitor protein (AHRD V3.3 *** G7IAP0_MEDTR)		F:GO:0004865; P:GC	F:protein serine/threonine phosphatase inhibitor activity; P:nega	IPR011107 (PFAM); mobidb-lite (MOB	9,654	9,465	14,222	14,256	12,046									
Solyc06g065300	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *-* AT1G20960.2)		F:GO:0003676; F:GC	F:nucleic acid bindi EC:3.6.1.15 Nucleoside-triphosph	IPR004179 (SMART); IPR035892 (G3	0,140	0,080	0,215	0,240	0,164									
Solyc06g065305	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *-* AT1G20960.2)		F:GO:0003676; F:GC	F:nucleic acid bindi EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D); PTHF	0,095	0,018	0,099	0,075	0,095									
Solyc06g065310	Biotin/lipoate A/B protein ligase family (AHRD V3.3 *** AT3G29010.3)		P:GO:0006464	P:cellular protein modification process	G3DSA:3.30.930.10 (GENE3D); PTHF	1,984	2,105	2,632	2,569	2,595									
Solyc06g065320	Disulfide isomerase-like protein (AHRD V3.3 *** A0A061FKQ2_THECC)		P:GO:0045454	P:cell redox homeostasis	PR00421 (PRINTS); G3DSA:3.40.30.1	35,085	37,682	42,585	42,830	37,961									
Solyc06g065330	RING/U-box superfamily protein (AHRD V3.3 *** AT1G35625.1)		C:GO:0000306; P:GC	C:extrinsic component of vacuolar membrane; P:ubiquitin-deper	IPR001841 (SMART); IPR003137 (PF	3,453	1,822	9,026	9,105	7,341									
Solyc06g065340	LOW QUALITY:Ca(2+)-dependent nuclease family protein (AHRD V3.3 --* AT2G40410.2)				IPR007789 (PFAM); mobidb-lite (MOB	1,003	1,463	0,097	0,022	0,163									
Solyc06g065345	Erythroid differentiation-related factor 1 (AHRD V3.3 *-* A0A061FK10_THECC)					0,019	0,019	0,000	0,025	0,117									
Solyc06g065360	Erythroid differentiation-related factor 1 (AHRD V3.3 *** A0A061FK10_THECC)				mobidb-lite (MOBIDB_LITE); mobidb-lit	29,979	24,472	28,895	30,319	31,364									
Solyc06g065370	Subtilisin-like protease (AHRD V3.3 *** A0A1D1XUI7_9ARAE)		F:GO:0004866; C:GC	F:endopeptidase inhibitor activity; C:cytosol; C:plasma membra	IPR010259 (PFAM); IPR037045 (G3D	80,957	73,249	80,016	70,836	69,511									
Solyc06g065380	Calcium-dependent protein kinase (AHRD V3.3 *** H6UM40_TOBAC)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR002048 (SMART); IPR000719 (SM	0,170	0,628	0,000	0,022	0,000									
Solyc06g065390	50S ribosomal protein L21, chloroplastic (AHRD V3.3 *** A0A199W1N6_ANACO)		F:GO:0003723; F:GC	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR001787 (TIGRFAM); IPR028909 (F	22,992	34,691	31,193	34,511	40,504	0,621	0,017	0,374	0,042			up	up	
Solyc06g065400	SNARE associated Golgi protein family (AHRD V3.3 *** AT1G71940.1)		C:GO:0016021	C:integral component of membrane	IPR032816 (PFAM); PTHR43220:SF3	16,728	21,447	15,645	19,602	17,774									
Solyc06g065410	NAC domain-containing protein, putative (AHRD V3.3 *** B9SLE9_RICCO)	NAC056	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,019	0,059	0,000	0,025	0,000									
Solyc06g065420	Cytochrome P450 (AHRD V3.3 *** A0A103XLH6_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR002401 (PRINTS); IPR001128 (PF	0,000	0,000	0,000	0,000	0,023									
Solyc06g065430	Cytochrome P450 (AHRD V3.3 *** A0A061G8S3_THECC)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS); IPR002401 (PF	0,042	0,000	0,000	0,000	0,000									
Solyc06g065440	Protein SENSITIVE TO PROTON RHIZOTOXICITY 1 (AHRD V3.3 *** STOP1_ARATH)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	18,804	15,745	5,186	4,268	6,317									
Solyc06g065450	PSL1a (AHRD V3.3 *** F5A7N5_9SOLN)		F:GO:0005515	F:protein binding	IPR000253 (SMART); IPR002716 (PF	0,080	0,142	0,000	0,000	0,000									
Solyc06g065470	DUF668 family protein (AHRD V3.3 *** A0A072VPK0_MEDTR)				IPR007700 (PFAM); IPR021864 (PFA	59,325	83,194	53,108	52,171	55,217									
Solyc06g065475	RNA-binding family protein (AHRD V3.3 *** A0A061GTK7_THECC)		F:GO:0003729; C:GC	F:mRNA binding; C:nucleus; C:cytoplasm; P:RNA processing	IPR008111 (PRINTS); IPR000504 (SM	43,584	44,444	53,761	53,113	48,507									
Solyc06g065480	Protein tyrosine phosphatase (AHRD V3.3 *** Q6J2K7_PHAVU)		F:GO:0004725; P:GC	F:protein tyrosine p EC:3.1.3.16; EC:3.1. Protein-serine/threor	IPR000242 (PRINTS); IPR000242 (SM	61,993	58,321	75,665	80,441	75,034									
Solyc06g065490	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** A0A0F7CYM1_9ROSI)		F:GO:0005509; C:GC	F:calcium ion binding; C:photosystem II oxygen evolving comple	IPR002683 (PFAM); IPR016123 (G3D	1,023	3,288	1,156	1,433	3,362	1,700	0,003	1,528	0,000			up	up	
Solyc06g065500	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H3L0_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	49,855	54,731	67,954	75,223	73,822									
Solyc06g065510	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RS99_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR002885 (PFA	7,546	6,786	7,440	6,681	6,531									
Solyc06g065520	T-complex protein 1 subunit eta (AHRD V3.3 *** TCPH_ARATH)		F:GO:0005524; P:GC	F:ATP binding; P:protein folding; F:unfolded protein binding	IPR017998 (PRINTS); IPR027413 (G3	80,329	84,029	86,535	76,141	74,119									
Solyc06g065530	GDSL-like lipase/acylhydrolase superfamily protein		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	2,151	1,291	0,050	0,073	0,000									
Solyc06g065540	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** A0A151S8H9_CAJCA)		F:GO:0005524; F:GC	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;	IPR002498 (SMART); IPR027484 (G3	44,072	34,217	57,513	61,409	52,452									
Solyc06g065550	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT5G40590.1)				mobidb-lite (MOBIDB_LITE)	0,099	0,096	0,144	0,234	0,256									
Solyc06g065560	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1CGV7_SOLTU)		P:GO:0006633; C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a	IPR013747 (PFAM); IPR012392 (PIRS	32,437	35,413	16,065	17,677	21,458									
Solyc06g065570	acyl-CoA N-acyltransferases (NAT) superfamily protein		P:GO:0007064; F:GC	P:mitotic sister chrc EC:2.3.1.5 Arylamine N-acetyltra	IPR000182 (PFAM); G3DSA:3.40.630	30,731	34,832	82,379	83,282	84,247									
Solyc06g065580	Uridine kinase (AHRD V3.3 *** K4C7I7_SOLLC)		F:GO:0004849; F:GC	F:uridine kinase act EC:2.7.1.48 Uridine kinase	PR00988 (PRINTS); IPR006083 (PFA	30,125	28,480	51,042	54,121	47,849									
Solyc06g065590	60S ribosomal protein L18a (AHRD V3.3 *** K4C7I8_SOLLC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:3.10.20.10 (GENE3D); IPR02	106,713	119,682	111,424	95,438	97,189									
Solyc06g065610	Protein phosphatase 2C (AHRD V3.3 *** A0A103PU55_CYNCS)		F:GO:0004722; P:GC	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART); IPR036457 (G3	15,456	17,981	23,340	23,343	21,337									
Solyc06g065620	probable protein phosphatase 2C		P:GO:0042138	P:meiotic DNA double-strand break formation	IPR034566 (PANTHER)	0,637	0,455	0,259	0,192	0,213									
Solyc06g065630	flavin monooxygenase	tofzy	F:GO:0004499; F:GC	F:N,N-dimethylanilir EC:1.14.13.8; EC:1. Flavin-containing mo	IPR000103 (PRINTS); PR00368 (PRIN	0,118	0,423	0,000	0,000	0,000									
Solyc06g065640	Transcriptional corepressor LEUNIG (AHRD V3.3 *** W9SY16_9ROSA)		F:GO:0005515	F:protein binding	IPR001680 (SMART); IPR006594 (SM	115,830	106,089	137,974	135,694	134,472									
Solyc06g065650	Protein TIFY 8 (AHRD V3.3 *** A0A151RAB6_CAJCA)		C:GO:0005634; P:GC	C:nucleus; P:response to wounding; P:regulation of defense res	IPR010399 (SMART); IPR010399 (PF	37,747	30,027	92,432	83,822	76,945									
Solyc06g065655	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *-* G7JU55_MEDTR)		C:GO:0016020	C:membrane	IPR013525 (PFAM); PTHR19241 (PAN	2,103	1,451	0,118	0,075	0,023									
Solyc06g065670	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG42	F:GO:0005524; C:GC	F:ATP binding; C:me EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART); IPR013525 (PF	59,988	37,124	1,192	1,125	1,778									
Solyc06g065680	cyclin A2	cyca2	C:GO:0005634	C:nucleus	IPR004367 (SMART); IPR013763 (SM	3,265	3,051	0,069	0,167	0,259									
Solyc06g065690	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9GTV0_POPTR)		C:GO:0000159; P:GC	C:protein phosphatase type 2A complex; P:signal transduction;	IPR002554 (PFAM); IPR002554 (PIRS	25,878	24,167	11,000	8,860	10,226									
Solyc06g065700	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT1G11160.4)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS); IPR001680 (SM	43,717	39,417	49,954	54,898	49,857									
Solyc06g065710	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *** A0A0B2R5L9_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion	G3DSA:2.30.30.140 (GENE3D); mobic	176,402	168,115	226,846	213,913	211,619									
Solyc06g065720	DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein (/		P:GO:0017004; F:GC	P:cytochrome complex assembly; F:heme binding	IPR006593 (SMART); IPR005018 (SM	41,710	47,242	51,909	59,315	52,959									
Solyc06g065730	chromatin remodeling factor CHD3 (PICKLE) (AHRD V3.3 *** AT2G25170.4)		F:GO:0005524	F:ATP binding	IPR000953 (SMART); IPR001650 (SM	78,837	76,762	93,828	101,493	94,255									
Solyc06g065740	Golgi SNAP receptor complex member 1 (AHRD V3.3 *** K4C7K3_SOLLC)		C:GO:0000139; C:GC	C:Golgi membrane; C:cis-Golgi network; P:endoplasmic reticulu	IPR018876 (PFAM); PF12352 (PFAM)	14,488	14,655	16,335	18,082	15,800									
Solyc06g065800	Mitochondrial glycoprotein family protein (AHRD V3.3 *** AT4G31930.1)		C:GO:0005759	C:mitochondrial matrix	IPR003428 (PFAM); IPR036561 (G3D	4,209	5,110	3,465	4,139	3,655									
Solyc06g065820	Ethylene Response Factor H.1	ERF_H_1	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,727	0,984	1,320	2,345	3,675			1,463	0,001				up	
Solyc06g065825	dipeptide transport ATP-binding protein (AHRD V3.3 *** AT3G05570.1)				mobidb-lite (MOBIDB_LITE); PTHR336	8,748	13,279	27,132	25,660	26,490									
Solyc06g065840	Trafficking particle complex subunit 9 (AHRD V3.3 *** A0A0B0PZ32_GOSAR)		P:GO:0000919; C:GC	P:cell plate assembly; C:early endosome; C:trans-Golgi network	IPR013935 (PFAM); IPR013935 (PAN	67,317	58,320	72,861	68,965	70,238									
Solyc06g065850	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT5G25260.1)				IPR001107 (PFAM); G3DSA:3.30.479	0,000	0,000	0,050	0,000	0,000									
Solyc06g065870	transmembrane protein (AHRD V3.3 *** AT2G25270.1)		C:GO:0005886; C:GC	C:plasma membrane; C:plasmodesma; C:integral component of	PTHR31414:SF13 (PANTHER); IPR04	0,098	0,254	0,000	0,000	0,047									
Solyc06g065890	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G41740.1)					0,078	0,101	0,022	0,050	0,000									
Solyc06g065900	Serine-rich protein-related (AHRD V3.3 *** A0A061GN42_THECC)				PTHR33132:SF12 (PANTHER); PTHR3	57,629	29,083	85,292	71,052	68,988	-0,958	0,001					down		
Solyc06g065910	Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repeat-containing protein (AHRD		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR000270 (SM	0,678	0,781	2,546	3,195	1,967									
Solyc06g065920	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G17090.1)		F:GO:0004722; P:GC	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART); IPR036457 (G3	6,461	4,840	3,010	2,703	2,400									
Solyc06g065930	ER membrane protein complex subunit-like protein (AHRD V3.3 *** G7JAF8_MEDTR)		F:GO:0030246; C:GC	F:carbohydrate binding; C:ER membrane protein complex	IPR019008 (PFAM); IPR039163 (PAN	0,121	0,119	0,093	0,147	0,142									
Solyc06g065945	Protein FAR1-RELATED SEQUENCE 6 (AHRD V3.3 *** A0A0B2QKT7_GLYSO)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR018289 (PFAM); IPR031052 (PAN	0,061	0,238	0,000	0,025	0,047									
Solyc06g065950	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9RP23_RICCO)		C:GO:0016021; P:GC	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS); IPR010908 (SM	13,666	11,594	5,422	4,414	5,571									
Solyc06g065960	LOW QUALITY:cysteine-rich repeat secretory protein, putative (DUF26) (AHRD V3.3 --* AT3G21980.1)		C:GO:0005634; P:GC	C:nucleus; P:multicellular organism development; F:transcription	factor binding; F:sequence-specific DN	0,786	0,478	0,097	0,246	0,234									
Solyc06g065970	14 kDa proline-rich protein DC2.15, putative (AHRD V3.3 *** B9RP24_RICCO)				IPR016140 (SMART); IPR027923 (PF	2,252	3,486	0,025	0,073	0,000									
Solyc06g065980	Alba DNA/RNA-binding protein (AHRD V3.3 *** AT2G34160.1)		F:GO:0003676	F:nucleic acid binding	IPR014560 (PIRSF); IPR002775 (PFA	45,863	41,887	39,649	37,073	38,391									
Solyc06g065990	ATP synthase subunit b (AHRD V3.3 *** A0A0K9PIX0_ZOSMR)		F:GO:0015078; P:GC	F:proton transmembrane transporter activity; P:ATP synthesis c	IPR002146 (PFAM); PTHR33445 (PAN	4,708	12,613	0,332	0,459	0,840	1,449	0,019					up		
Solyc06g066000	ATP synthase subunit b (AHRD V3.3 *** A0A0K9PIX0_ZOSMR)		F:GO:0015078; P:GC	F:proton transmembrane transporter activity; P:ATP synthesis c	IPR002146 (PFAM); PTHR33445 (PAN	81,661	151,081	56,691	62,488	101,021	0,915	0,001	0,831	0,000			up	up	
Solyc06g066010	U11/U12 small nuclear ribonucleoprotein 25 kDa (AHRD V3.3 *** A0A0B0PAC5_GOSAR)		P:GO:0000398; F:GC	P:mRNA splicing, via spliceosome; F:protein binding; C:U12-typ	IPR000626 (SMART); PF18036 (PFAM	4,475	8,369	3,444	4,050	3,688	0,928	0,014					up		
Solyc06g066020	auxin-regulated IAA36	IAA36	F:GO:0005515; C:GC	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t	IPR033389 (PFAM); G3DSA:3.10.20.9	2,412	4,542	0,213	0,099	0,164									
Solyc06g066030	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT4G32330.4)				IPR027329 (PFAM); mobidb-lite (MOB	173,917	165,993	55,638	52,510	59,396									
Solyc06g066040	pfkB-like carbohydrate kinase family protein (AHRD V3.3 --* AT5G37850.4)		F:GO:0046872	F:metal ion binding	PTHR33304:SF2 (PANTHER); PTHR3	0,059	0,043	0,025	0,047	0,046									
Solyc06g066050	DUF4050 family protein (AHRD V3.3 *** G7JE31_MEDTR)				IPR025124 (PFAM); mobidb-lite (MOB	7,610	8,811	12,065	12,952	12,249									
Solyc06g066060	CGI-144	cgi1	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding	IPR014001 (SMART); IPR001650 (SM	99,922	110,021	117,969	107,976	105,879									
Solyc06g066070	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT4G32390.1)		C:GO:0005768; C:GC	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte	IPR004853 (PFAM); mobidb-lite (MOB	0,276	0,174	0,000	0,025	0,000									
Solyc06g066080	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XZP2_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding	IPR032867 (PFAM); IPR002885 (PFA	3,140	3,157	2,829	2,651	2,898									
Solyc06g066090	Lactation elevated protein 1 (AHRD V3.3 *** A0A0B0NJ47_GOSAR)		F:GO:0005524	F:ATP binding	IPR005654 (PFAM); IPR005654 (PAN	2,885	3,639	11,625	14,014	16,004			0,458	0,044				up	
Solyc06g066100	Alba DNA/RNA-binding protein (AHRD V3.3 *** AT2G34160.1)		F:GO:0003676	F:nucleic acid binding	IPR014560 (PIRSF); IPR002775 (PFA	23,608	24,117	30,506	29,539	28,969									
Solyc06g066110	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)				IPR012876 (PFAM); PTHR33108:SF1	0,102	0,183	0,146	0,076	0,094									
Solyc06g066120	Endoglucanase (AHRD V3.3 *** B9RQY0_RICCO)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001701 (PFAM); IPR012341 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc06g066140	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)		F:GO:0046872	F:metal ion binding	PTHR33304 (PANTHER); PTHR33304	0,000	0,141	0,000	0,000	0,023									
Solyc06g066160	Isoflavone reductase like (AHRD V3.3 *** A0A0B2PWE9_GLYSO)				G3DSA:3.90.25.10 (GENE3D); IPR00	0,100	0,152	0,000	0,022	0,046									
Solyc06g066170	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_LUPAL)				G3DSA:3.40.50.720 (GENE3D); G3DS	4,867	2,798	2,401	3,630	1,717									
Solyc06g066180	Myb family transcription factor family protein (AHRD V3.3 *** B9GZU3_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (PFAM G2-like	3,649	1,983	0,783	0,590	0,919									
Solyc06g066190	50S ribosomal protein L35 (AHRD V3.3 *** A0A151QY68_CAJCA)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:2.40.50.530 (GENE3D); IPR0	17,681	16,390	33,473	34,240	31,198									
Solyc06g066200	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)		F:GO:0046872	F:metal ion binding	PTHR33304:SF2 (PANTHER); PTHR3	0,115	0,380	0,000	0,025	0,000									
Solyc06g066210	LOW QUALITY:ARF-GAP domain 15 (AHRD V3.3 --* AT3G17660.3)					10,426	9,908	10,411	10,344	9,240									
Solyc06g066220	LOW QUALITY:WRKY DNA-binding protein 74 (AHRD V3.3 --* AT5G28650.1)					0,239	0,194	0,246	0,097	0,095									
Solyc06g066230	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS); IPR002401 (PF	0,000	0,018	0,046	0,164	0,024									
Solyc06g066240	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR002401 (PRINTS); IPR001128 (PF	0,021	0,203	0,000	0,000	0,000									

Solyc06g066270	Cytochrome P450, putative (AHRD V3.3 *** A0A061G7Z4_THECC)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,079	0,000	0,074	0,325	0,000									
Solyc06g066280	Cytochrome P450, putative (AHRD V3.3 *** A0A061G7Z4_THECC)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,313	0,133	0,069	0,120	0,188									
Solyc06g066290	cystic fibrosis transmembrane conductance regulator (AHRD V3.3 *** AT1G31940.1)						PTHR34196:SF2 (PANTHER): PTHR3	1,656	1,498	2,731	2,765	2,875									
Solyc06g066295	telomeric repeat binding protein 1 (AHRD V3.3 --* AT5G59430.5)							0,000	0,000	0,000	0,025	0,000									
Solyc06g066310	Phosphomevalonate kinase (AHRD V3.3 *** A0A0X9ZV04_9ROSI)		F:GO:0004631; F:GC	F:phosphomevalona	EC:2.7.4.2	Phosphomevalonate	IPR016005 (PIRSF): IPR006204 (PFA	13,977	14,081	9,862	10,001	11,920									
Solyc06g066320	Transcription factor IWS1, putative (AHRD V3.3 *** B9S1I4_RICCO)		C:GO:0005634	C:nucleus			IPR017923 (PFAM): IPR035441 (G3D	177,927	196,800	203,687	210,890	197,087									
Solyc06g066330	Poly [ADP-ribose] polymerase (AHRD V3.3 *** A0A0V0IXP4_SOLCH)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylt	IPR022003 (PFAM): G3DSA:3.90.228	62,691	64,317	104,093	124,663	106,051									
Solyc06g066340	Myb family transcription factor family protein (AHRD V3.3 *** U5GMY7_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGR: G2-like	2,972	3,532	3,471	4,222	3,171									
Solyc06g066360	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)		F:GO:0046872	F:metal ion binding			PTHR33304:SF2 (PANTHER): PTHR3	0,021	0,139	0,068	0,000	0,023									
Solyc06g066370	WRKY transcription factor 31	WRKY31	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	197,680	99,679	59,690	199,693	108,540			0,860	0,000	1,744	0,000		up	up
Solyc06g066380	LOW QUALITY:Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RE94_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	43,102	36,846	15,945	19,014	16,794									
Solyc06g066400	Dolichol phosphate-mannose biosynthesis regulatory family protein (AHRD V3.3 *** B9MU62_POPTR)		P:GO:0019348; C:GC	P:dolichol metabolic process; C:integral component of endoplas			IPR009914 (PFAM): IPR009914 (PAN	1,297	1,362	2,007	2,698	1,657									
Solyc06g066410	Profilin (AHRD V3.3 *** K4C7R7_SOLLC)		F:GO:0003785; C:GC	F:actin monomer binding; C:cytoskeleton; C:cell cortex; P:seque			IPR005455 (PRINTS): IPR005455 (PF	0,019	0,018	0,510	0,830	0,519									
Solyc06g066420	Oxidative stress 3, putative isoform 1 (AHRD V3.3 *** A0A061GC09_THECC)						mobidb-lite (MOBIDB_LITE): PTHR331	0,195	0,493	1,087	1,577	1,867									
Solyc06g066430	SUN-like protein 18	SUN18	F:GO:0005515	F:protein binding			IPR000048 (SMART): G3DSA:1.20.5.1	11,143	10,069	17,843	12,142	13,898					-0,551	0,013			down
Solyc06g066440	hexokinase 2	hxk2	P:GO:0001678; F:GC	P:cellular glucose h	EC:2.7.1.1	Hexokinase	PR00475 (PRINTS): IPR022673 (PFA	16,330	18,076	16,317	14,813	18,532									
Solyc06g066460	Poly(A) polymerase (AHRD V3.3 *-* A0A0B2Q923_GLYSO)		F:GO:0004652; C:GC	F:polynucleotide ad	EC:2.7.7.19	Polynucleotide aden	mobidb-lite (MOBIDB_LITE): mobidb-lit	41,271	58,335	44,290	51,267	46,580									
Solyc06g066470	Poly(A) polymerase (AHRD V3.3 *-* W9RV28_9ROSA)		F:GO:0004652; C:GC	F:polynucleotide ad	EC:2.7.7.19	Polynucleotide aden	G3DSA:1.10.1410.10 (GENE3D): IPR	13,012	15,480	12,318	16,109	13,526									
Solyc06g066473	Poly(A) polymerase (AHRD V3.3 *-* W9RV28_9ROSA)		F:GO:0004652; C:GC	F:polynucleotide ad	EC:2.7.7.19	Polynucleotide aden	G3DSA:3.30.460.10 (GENE3D): PTHF	9,673	12,580	10,015	10,729	9,194									
Solyc06g066477	Poly (A) polymerase (AHRD V3.3 *-* A0A0B0PIP1_GOSAR)		F:GO:0004652; C:GC	F:polynucleotide ad	EC:2.7.7.19	Polynucleotide aden	IPR007012 (PFAM): IPR014492 (PAN	10,831	13,834	11,102	12,817	12,490									
Solyc06g066490	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *-* G7II06_MEDTR)						IPR008480 (PFAM): PTHR33265 (PAN	0,000	0,043	0,025	0,025	0,046									
Solyc06g066500	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)						IPR008480 (PFAM): PTHR33265 (PAN	0,690	0,265	0,248	0,528	0,235									
Solyc06g066510	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *-* G7II06_MEDTR)						IPR008480 (PFAM): PTHR33265:SF8	0,000	0,036	0,047	0,098	0,117									
Solyc06g066520	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 146 (AHRD V3.3 *** Q9FQZ6_TOBAC)						IPR008480 (PFAM): PTHR33265 (PAN	0,544	0,259	0,243	0,146	0,096									
Solyc06g066530	LOW QUALITY:DUF1677 family protein (AHRD V3.3 *** G7LFY6_MEDTR)						IPR012876 (PFAM): mobidb-lite (MOB	0,037	0,019	0,000	0,000	0,000									
Solyc06g066540	Ethylene-responsive transcription factor TINY (AHRD V3.3 *** TINY_ARATH)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	3,937	4,684	0,971	1,080	1,240									
Solyc06g066550	LETM1 and EF-hand domain-containing protein anon-60Da isoform 1 (AHRD V3.3 *** A0A061GCJ8_THECC		C:GO:0016021	C:integral component of membrane			IPR011685 (PFAM): mobidb-lite (MOB	34,297	22,115	87,992	94,654	83,862	-0,605	0,013					down		
Solyc06g066560	tonoplast intrinsic protein 2.5	TIP2.5	F:GO:0015267; C:GC	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,000	0,037	0,000	0,000	0,000									
Solyc06g066570	Peroxisome biogenesis protein 2 (AHRD V3.3 *** W9REG8_9ROSA)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR018957 (PF	29,726	27,347	35,069	31,747	32,409									
Solyc06g066580	bHLH transcription factor137	bHLH137	F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DSA:4.10.280.GENE3	4,342	3,148	0,834	0,875	0,921									
Solyc06g066590	Plant cadmium resistance 2 (AHRD V3.3 *** A0A0K9NVT8_ZOSMR)						IPR006461 (PFAM): IPR006461 (TIGF	0,955	5,235	0,489	1,112	1,646	2,468	0,000	1,743	0,001			up	up	
Solyc06g066600	plastidic glucose translocator 2	pGlcT2	C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	102,965	89,870	74,226	83,435	93,305									
Solyc06g066610	Golgin candidate 5 (AHRD V3.3 *** GOGC5_ARATH)		C:GO:0005634; C:GC	C:nucleus; C:Golgi apparatus			IPR022092 (PFAM): IPR022091 (PFA	100,830	92,741	106,507	105,284	105,458									
Solyc06g066620	Thylakoid membrane phosphoprotein, chloroplastic (AHRD V3.3 *** A0A1D1ZKM1_9ARAE)		C:GO:0009579	C:thylakoid			IPR025564 (PFAM): IPR033344 (PAN	39,614	68,785	43,929	45,139	61,602	0,824	0,000	0,486	0,003			up	up	
Solyc06g066630	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55350.1)		F:GO:0008374	F:O-acyltransferase activity			IPR017088 (PIRSF): IPR032805 (PFA	2,784	7,452	0,911	1,730	1,624	1,445	0,003					up		
Solyc06g066640	Photosystem I reaction center subunit VI (AHRD V3.3 *** B7FN63_MEDTR)		C:GO:0009538; P:GC	C:photosystem I reaction center; P:photosynthesis			IPR004928 (PFAM): IPR023833 (TIGF	2,113	11,860	1,699	3,569	8,845	2,506	0,000	2,364	0,000	1,068	0,021	up	up	up
Solyc06g066650	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 *** AT1G52240.1)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.1310 (GENE3D): IPR	0,390	0,682	0,075	0,047	0,070									
Solyc06g066660	Ribosomal protein L37 (AHRD V3.3 *** M1BDD8_SOLTU)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR011331 (G3DSA:2.20.25.GENE3D	96,400	103,497	98,214	81,829	91,048									
Solyc06g066670	RNA helicase DEAH-box20	DEAH20	F:GO:0003677; F:GC	F:DNA binding; F:A'	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR006555 (SMART): IPR006554 (SM	2,226	1,762	1,117	0,772	1,292									
Solyc06g066680	Mitochondrial carrier protein (AHRD V3.3 *** A0A0K9PC13_ZOSMR)		F:GO:0022857; F:GC	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR023395 (G3	2,943	3,571	3,486	4,214	4,438									
Solyc06g066730	Coatomer beta subunit, putative (AHRD V3.3 *** B9SQC0_RICCO)		F:GO:0005198; F:GC	F:structural molecule activity; F:protein binding; P:intracellular p			IPR020472 (PRINTS): IPR001680 (SM	78,678	81,551	47,842	42,164	48,531									
Solyc06g066740	Ran-binding protein 1 domain-containing (AHRD V3.3 *** B9GEK5_POPTR)		C:GO:0005643; P:GC	C:nuclear pore; P:intracellular transport			IPR000156 (SMART): IPR011993 (G3	27,923	25,887	19,194	23,871	25,452			0,402	0,042				up	
Solyc06g066750	thionin-like protein (AHRD V3.3 *** AT1G12663.1)		C:GO:0016021	C:integral component of membrane			PTHR36312:SF1 (PANTHER): IPR038	0,124	0,134	0,022	0,000	0,000									
Solyc06g066760	Protein-tyrosine phosphatase mitochondrial 1-like protein (AHRD V3.3 *** W9SEA4_9ROSA)		P:GO:0006470; F:GC	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR003595 (SM	20,670	17,051	27,615	24,199	22,175									
Solyc06g066770	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9GEJ8_POPTR)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR006652 (PF	11,199	4,156	12,571	27,681	20,260	-1,401	0,000	0,685	0,006	1,139	0,000	down	up	up
Solyc06g066780	DNA-repair protein xrcc1, putative (AHRD V3.3 *** B9RUV1_RICCO)		P:GO:0006266; P:GC	P:DNA ligation; P:double-strand break repair via nonhomologous			IPR001357 (SMART): IPR036420 (G3	11,469	10,412	12,303	12,074	11,304									
Solyc06g066790	N-alpha-acetyltransferase 16, NatA auxiliary subunit (AHRD V3.3 *** A0A0B2P106_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13414 (PFAM	73,417	68,104	59,184	56,094	58,843									
Solyc06g066795	vacuolar protein sorting-associated protein, putative (DUF1162) (AHRD V3.3 --* AT5G24740.6)							0,019	0,000	0,000	0,000	0,000									
Solyc06g066800	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 *** AT1G64980.2)						PTHR35105 (PANTHER): PTHR35105	71,698	108,777	28,120	17,227	27,290									
Solyc06g066810	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4C7V5_SOLLC)		F:GO:0005524; F:GC	F:ATP binding; F:mi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003959 (PF	36,278	35,457	31,984	31,410	30,285									
Solyc06g066820	Le3OH-13b-hydroxylase	3oh1	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,634	2,123	0,788	0,324	0,354	1,753	0,001					up		
Solyc06g066830	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,750	0,795	0,354	0,293	0,406									
Solyc06g067870	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** H9AY17_SALMI)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,094	0,000	0,000	0,000									
Solyc06g067880	V-type proton ATPase proteolipid subunit (AHRD V3.3 *** A0A1D1XX18_9ARAE)		F:GO:0015078; P:GC	F:proton transmembrane transporter activity; P:ATP hydrolysis c			IPR000245 (PRINTS): G3DSA:1.20.12	66,306	51,830	66,377	62,381	60,602									
Solyc06g067890	Alpha/beta hydrolase-like (AHRD V3.3 *** A0A0K9P0U5_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR000073 (PFAM): IPR029058 (G3D	7,192	8,431	6,884	7,611	6,563									
Solyc06g067900	Boron transporter, putative (AHRD V3.3 *-* A0A061G9M0_THECC)		F:GO:0005452; P:GC	F:inorganic anion exchanger activity; P:anion transport; C:integ			IPR011531 (PFAM): IPR003020 (PAN	0,021	0,021	0,000	0,075	0,000									
Solyc06g067910	transmembrane protein, putative (Protein of unknown function, DUF642) (AHRD V3.3 *** AT5G11420.1)						IPR006946 (PFAM): PTHR31265:SF9	0,318	0,349	0,074	0,222	0,141									
Solyc06g067920	Cytochrome c1, heme protein (AHRD V3.3 *** G7KN99_MEDTR)		F:GO:0009055; F:GC	F:electron transfer activity; F:heme binding			IPR002326 (PRINTS): IPR036909 (G3	38,653	36,363	43,705	41,173	44,709									
Solyc06g067940	Cytochrome c oxidase subunit 5b (AHRD V3.3 *** Q1EMP4_PLAMJ)		F:GO:0004129; C:GC	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR002124 (PFAM): IPR036972 (G3D	30,518	39,698	41,071	38,879	39,417									
Solyc06g067950	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A0B0PZC3_GOSAR)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,078	0,199	0,169	0,262	0,214									
Solyc06g067960	Glutaredoxin (AHRD V3.3 *** A0A103XX44_CYNCS)		F:GO:0009055; F:GC	F:electron transfer activity; F:protein disulfide oxidoreductase a			G3DSA:3.40.30.10 (GENE3D): IPR0	14,549	16,045	29,992	30,387	28,711									
Solyc06g067970	DUF1644 family protein (AHRD V3.3 *** G7LIM9_MEDTR)						IPR012866 (PFAM): mobidb-lite (MOB	34,554	25,845	43,383	35,388	37,901									
Solyc06g067975	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT1G64670.3)							2,471	1,920	2,896	2,491	2,744									
Solyc06g067980	Late embryogenesis abundant protein (AHRD V3.3 --* Q2QKE8_CATRO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,925	1,932	7,245	7,868	6,460									
Solyc06g067990	Mov34/MPN/PAD-1 family protein (AHRD V3.3 *** G7IMH2_MEDTR)		F:GO:0004843; F:GC	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR000555 (SMART): G3DSA:3.40.14	24,209	20,708	23,057	21,786	20,655									
Solyc06g068010	Biotin carboxyl carrier protein (AHRD V3.3 *** A0A0H5BV69_PEA)		C:GO:0016021	C:integral component of membrane			G3DSA:2.40.50.100 (GENE3D): IPR0	17,757	21,793	34,292	39,476	38,807									
Solyc06g068030	Trafficking protein particle complex subunit 2 (AHRD V3.3 *-* A0A0B2R9I4_GLYSO)		C:GO:0005622; P:GC	C:intracellular; P:endoplasmic reticulum to Golgi vesicle-mediate			G3DSA:3.30.450.70 (GENE3D): IPR0	12,830	10,388	10,976	13,394	11,069									
Solyc06g068040	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G80170.1)	PG17-2	F:GO:0004650; P:GC	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR012334 (G3	0,095	0,057	0,050	0,050	0,024									
Solyc06g068050	Alba DNA/RNA-binding protein (AHRD V3.3 *** AT2G34160.1)		F:GO:0003676	F:nucleic acid binding			IPR036882 (G3DSA:3.30.110.GENE3	8,091	7,106	3,700	4,349	5,072									
Solyc06g068060	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2PCJ8_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion			IPR002999 (SMART): G3DSA:2.30.30	42,144	35,333	35,822	31,773	34,740									
Solyc06g068065	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT5G08305.1)							0,000	0,019	0,044	0,050	0,070									
Solyc06g068070	LOW QUALITY:BTB/POZ domain-containing protein (AHRD V3.3 --* AT1G63850.1)							0,038	0,000	0,022	0,025	0,023									
Solyc06g068080	Coatomer subunit zeta-3 (AHRD V3.3 *** A0A1D1YYD5_9ARAE)		P:GO:0006890; C:GC	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			G3DSA:3.30.450.60 (GENE3D): IPR0	21,364	24,497	17,390	14,939	15,970									
Solyc06g068090	phospholipase PLDa1	plda1	F:GO:0004630; F:GC	F:phospholipase D	EC:3.1.4.4	Phospholipase D	IPR001736 (SMART): IPR000008 (SM	214,846	339,309	246,702	227,438	234,486									
Solyc06g068120	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR335	14,845	12,528	19,969	18,066	18,971									
Solyc06g068130	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT5G20190.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,444	5,324	0,000	0,022	0,000									
Solyc06g068140	Methyl-CpG binding domain containing protein, expressed (AHRD V3.3 *** Q2QM23_ORYSJ)		F:GO:0003677; C:GC	F:DNA binding; C:nucleus			G3DSA:3.30.890.10 (GENE3D): IPR0	87,763	60,338	72,962	89,537	75,765									
Solyc06g068150	Phosphatidylcholine:diacylglycerol cholinephosphotransferase 1 (AHRD V3.3 *** PDCT1_ARATH)		F:GO:0004142; P:GC	F:diacylglycerol cho	EC:2.7.8.2	Diacylglycerol cholin	IPR026841 (PFAM): mobidb-lite (MOB	1,225	0,806	0,286	0,242	0,140									
Solyc06g068160	SNF4	snf4	F:GO:0016301; P:GC	F:kinase activity; P:phosphorylation			IPR000644 (SMART): IPR000644 (PF	9,868	6,428	11,563	16,372	11,497					0,504	0,039			up
Solyc06g068170	U11/U12 small nuclear ribonucleoprotein 25 kDa (AHRD V3.3 *** A0A0B0MCU7_GOSAR)		P:GO:0000398; C:GC	P:mRNA splicing, via spliceosome; C:U12-type spliceosomal co			G3DSA:3.10.20.90 (GENE3D): PF180	0,525	0,346	0,165	0,139	0,187									
Solyc06g068180	Ubiquitin system component Cue protein (AHRD V3.3 *-* AT5G32440.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,972	0,458	0,934	1,244	0,709									
Solyc06g068190	Ubiquitin system component Cue protein, putative (AHRD V3.3 *-* A0A061GFQ5_THECC)						PTHR31245:SF12 (PANTHER): PTHR	1,815	0,746	1,205	1,201	1,199									
Solyc06g068200	Far1-related sequence 6 (AHRD V3.3 *** A0A061G8J5_THECC)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR004330 (PFAM FAR1	0,080	0,186	0,144	0,119	0,258									
Solyc06g068210	Protein FAR1-RELATED SEQUENCE 8 (AHRD V3.3 *** W9RSB0_9ROSA)		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	14,190	8,034	11,202	10,491	11,227	-0,793	0,025					down		
Solyc06g068215	Myosin heavy chain-like protein (AHRD V3.3 --* A0A072UED1_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,824	0,738	1,131	0,801	0,868									
Solyc06g068220	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G52510.1)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS): IPR000073 (PF	24,958	44,175	43,412	49,318	54,390	0,850	0,001					up		
Solyc06g068230	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G15290.1)		F:GO:0005515	F:protein binding			IPR019734 (SMART): PF13424 (PFAM	111,090	147,090	83,576	99,321	132,166			0,658	0,000				up	
Solyc06g068240	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)		F:GO:0004427; F:GC	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (TIGRFAM): IPR004131 (F	10,378	8,172	7,061	7,876	7,690									
Solyc06g068250	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G49390.2)		F:GO:0046872; F:GC	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			PTHR10209 (PANTHER): PTHR10209	0,019	0,000	0,025	0,122	0,023									
Solyc06g068260	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,059	0,021	0,071	0,292	0,284									
Solyc06g068270	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	2,045	5,096	14,114	30,887	22,730	1,334	0,013			1,133	0,000	up		up
Solyc06g068280	RNA helicase DEAD20	DEAD20	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding; F:zinc ion binding			IPR014001 (SMART): IPR001878 (SM	23,767	21,891	35,650	33,634	33,491									
Solyc06g068310	LOW QUALITY:Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT1G80520.1)						G3DSA:1.10.150.50 (GENE3D): PTHF	0,183	0,254	0,044	0,072	0,070									
Solyc06g068320	tRNA synthetase-related family protein (AHRD V3.3 *** B9GTA1_POPTR)		F:GO:0004827; F:GC	F:proline-tRNA ligas	EC:6.1.1.15	Proline--tRNA ligase	IPR002316 (PRINTS): IPR016061 (SM	172,599	212,538	150,155	143,203	145,654									
Solyc06g068330	LOW QUALITY:serine-rich protein-like protein (AHRD V3.3 *** AT5G25280.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,669	4,201	7,141	5,983	5,328									
Solyc06g068340	transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G02645.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN	0,021	0,037	0,000	0,000	0,023									
Solyc06g068350	Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE)	0,415	0,520	0,099	0,226	0,000									
Solyc06g068360	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RS58_9ROSA)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,121	0,214	0,046	0,025	0,047									
Solyc06g068370	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT2G17050.3)							4,401	3,778	7,850	6,824	7,831									
Solyc06g068390	LOW QUALITY:Zinc finger protein, putative (AHRD V3.3 *** B9SMU5_RICCO)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	5,573	5,403	0,240	0,151	0,093									
Solyc06g068400	60S ribosomal protein L7 (AHRD V3.3 *** B9GMC3_POPTR)		P:GO:0000463; F:GC	P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU			IPR005998 (TIGRFAM): IPR012988 (F	21,307	23,100	16,304	14,989	14,552									
Solyc06g068410	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT2G32070.1)		F:GO:0003676; F:GC	F:nucleic acid bindi	EC:3.1.13; EC:3.1.1:	Acting on ester bond	IPR036397 (G3DSA:3.30.420.GENE3	24,728	28,906	25,716	23,537	23,333									
Solyc06g068435	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2RCM4_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion			IPR002999 (SMART): G3DSA:2.30.30	8,622	6,969	12,324	15,193	11,631									
Solyc06g068440	cinnamoyl-CoA reductase	ccr1	F:GO:0003824; F:GC	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	14,948	17,801	133,927	146,622	120,307									
Solyc06g068450	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C820_SOLLC)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	32,822	35,169	47,900	38,739	40,055									
Solyc06g068460	WRKY transcription factor 40	WRKY40	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	200,002	92,636	38,226	113,746	48,012	-1,087	0,002			1,575	0,000	down		up
Solyc06g068470	phospholipid N-methyltransferase (AHRD V3.3 *** AT1G80860.2)		P:GO:0006656; F:GC	P:phosphatidylcholine biosynthetic process; F:S-adenosylmethi			IPR007318 (PFAM): G3DSA:1.20.120	8,444	6,183	4,877	5,306	5,034									
Solyc06g068480	Low PSII Accumulation 3 isoform 3 (AHRD V3.3 *** A0A061G863_THECC)		C:GO:0009570; P:GC	C:chloroplast stroma; P:response to cytokinin; P:photosystem II			IPR018962 (PFAM): PTHR34051:SF2	21,980	28,975	32,225	28,640	44,101			0,450	0,011				up	
Solyc06g068490	Magnesium transporter MRS2-like protein (AHRD V3.3 *** G7ZYX9_MEDTR)		C:GO:0016020; P:GC	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:1.20.58.340 (GENE3D): G3DS	25,596	18,693	43,403	53,054	43,413									
Solyc06g068500	Chaperone DnaJ domain protein (AHRD V3.3 *** B7FGF7_MEDTR)		C:GO:0005737; C:GC	C:cytoplasm; C:integral component of membrane			IPR001623 (PRINTS): IPR001623 (SM	36,702	33,220	221,890	136,564	174,436					-0,697	0,000			down
Solyc06g068510	LOW QUALITY:MAP kinase kinase kinase 38	MAPKKK38	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	2,184	2,059	11,160	10,750	8,742									
Solyc06g068520	Hydroxyproline-rich systemin (AHRD V3.3 *** HSY1_SOLLC)		F:GO:0005179; C:GC	F:hormone activity; C:extracellular region; P:defense response;			mobidb-lite (MOBIDB_LITE): mobidb-lit	52,040	30,140	14,915	9,039	16,933	-0,761	0,000			-0,720	0,027	down		down
Solyc06g068530	LOW QUALITY:S-locus lectin protein kinase family protein (AHRD V3.3 --* AT4G21390.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,022	0,000	0,023									
Solyc06g068540	ATP-dependent DNA helicase (AHRD V3.3 *** AT2G24100.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,697	8,798	32,404	32,958	33,290									
Solyc06g068550	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061GAK7_THECC)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR021109 (G3D	0,061	0,074	0,000	0,000	0,000									
Solyc06g068560	Major facilitator superfamily protein (AHRD V3.3 *** AT1G79710.2)		C:GO:0016021	C:integral component of membrane			IPR039309 (PFAM): G3DSA:1.20.125	7,970	9,738	8,382	7,731	9,373									
Solyc06g068570	AP2-like ethylene-responsive transcription factor		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' AP2	0,655	1,938	0,075	0,122	0,376	1,575	0,017					up		
Solyc06g068590	Kinase (AHRD V3.3 *** D7KWK7_ARALL)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,000	0,000	0,000	0,022	0,000									
Solyc06g068600	ABC transporter family protein (AHRD V3.3 *** A0A097P9R8_HEVBR)	ABCI7	F:GO:0005315; F:GC	F:inorganic phosph	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	2,513	0,899	3,157	4,102	2,524	-1,449	0,006					down		
Solyc06g068610	Transcriptional adapter 1 (AHRD V3.3 *** A0A0B0NYM8_GOSAR)		C:GO:0070461	C:SAGA-type complex			IPR024738 (PFAM): mobidb-lite (MOB	4,350	4,730	5,132	4,662	4,591									
Solyc06g068615	root meristem growth factor (AHRD V3.3 --* AT5G64770.1)							0,232	0,174	0,262	0,339	0,186									
Solyc06g068620	Negative regulator of sporulation MDS3 (AHRD V3.3 *-* A0A0B0N6H6_GOSAR)						PTHR33181 (PANTHER): PTHR33181	7,754	15,663	1,751	0,510	1,219	1,045	0,002					up		
Solyc06g068630	F-box protein SKIP23 (AHRD V3.3 *-* A0A1D1YYW2_9ARAE)						PTHR33110:SF20 (PANTHER): PTHR	9,029	8,214	3,674	3,274	3,364									
Solyc06g068640	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GE38_THECC)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR002867 (SMART): IPR002867 (PF	0,000	0,041	0,000	0,000	0,000									
Solyc06g068650	4-coumarate--CoA ligase	4CL	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.30.300	6,914	16,341	1,295	1,418	1,809	1,266	0,001					up		
Solyc06g068660	F-box/RNI superfamily protein (AHRD V3.3 *** AT1G73120.1)		P:GO:0006979	P:response to oxidative stress			PTHR35109 (PANTHER): PTHR35109	0,137	0,117	0,188	0,439	0,662									
Solyc06g068670	ACT domain-containing protein		C:GO:0009535; C:GC	C:chloroplast thylakoid membrane; C:chloroplast stroma			IPR040217 (PANTHER): PTHR31096:	75,960	124,679	76,277	82,231	129,627	0,742	0,003	0,762	0,000			up	up	
Solyc06g068680	Respiratory burst oxidase homolog (AHRD V3.3 *** Q84KK7_NICBE)		F:GO:0004601; F:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000778 (PRINTS): IPR039261 (G3	3,323	4,394	0,713	0,988	1,035									
Solyc06g068690	Glutamyl-tRNA(Gln) amidotransferase subunit A (AHRD V3.3 *** A0A151S2E8_CAJCA)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR023631 (PFAM): IPR036928 (G3D	0,392	0,627	0,222	0,655	0,094									
Solyc06g068710	40S ribosomal protein S27 (AHRD V3.3 *** K4C845_SOLLC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.20.25.640 (GENE3D): IPR0	7,857	8,765	7,980	7,469	7,940									
Solyc06g068720	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G51050.1)		F:GO:0005509; F:GC	F:calcium ion binding; F:transmembrane transporter activity; P:t			IPR002067 (PRINTS): IPR002048 (SM	22,937	33,423	20,519	19,942	21,673	0,569	0,048					up		
Solyc06g068740	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT5G61830.2)		F:GO:0016829; P:GC	F:lyase activity; P:protein-phycocyanobilin linkage			IPR002347 (PRINTS): IPR002347 (PF	22,100	23,561	35,028	34,701	31,034									
Solyc06g068750	Transferase, transferring glycosyl groups, putative (AHRD V3.3 *** B9RG20_RICCO)						PTHR33880:SF3 (PANTHER): IPR038	1,115	1,611	0,248	0,210	0,304									
Solyc06g068760	Chromophore lyase CpcT/CpeT 3 (AHRD V3.3 *** A0A0B0NHE8_GOSAR)	CRL	F:GO:0016829; P:GC	F:lyase activity; P:protein-phycocyanobilin linkage			IPR010404 (PFAM): IPR038672 (G3D	2,175	1,864	1,894	1,989	2,072									
Solyc06g068770	DB279		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM): PTHR11062:SF1	0,504	0,212	0,194	0,045	0,047									
Solyc06g068780	Protein kish (AHRD V3.3 *** M1CEH5_SOLTU)		C:GO:0005623; P:GC	C:cell; P:protein secretion; C:integral component of membrane;			IPR009653 (PFAM): IPR009653 (PAN	8,104	8,446	8,159	9,175	7,430									
Solyc06g068790	Linoleate 9S-lipoxygenase (AHRD V3.3 --* LOX1_LENCU)							0,606	0,721	0,489	0,660	0,422									
Solyc06g068800	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G01630.1)						IPR001251 (SMART): IPR011074 (SM	9,362	8,530	4,131	4,354	5,182									
Solyc06g068810	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XWD4_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR011990 (G3D	1,782	0,772	0,500	0,357	0,353	-1,169	0,040					down		
Solyc06g068820	Mitochondrial import inner membrane translocase subunit TIM16 (AHRD V3.3 *** A0A0K9Q5B1_ZOSMR)		C:GO:0005744; P:GC	C:TIM23 mitochondrial import inner membrane translocase com			IPR036869 (G3DSA:1.10.287.GENE3	5,231	6,041	12,652	13,001	10,756									
Solyc06g068830	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9S0J2_9ROSA)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	0,040	0,112	0,068	0,097	0,023									

Solyc06g068840	Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 *** AT5G61900.3)		F:GO:0005544; P:GC	F:calcium-dependent phospholipid binding; P:negative regulation			IPR000008 (SMART); IPR002035 (SM	28,520	38,165	38,237	39,736	39,767								
Solyc06g068850	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT5G61910.5)		F:GO:0005544; P:GC	F:calcium-dependent phospholipid binding; P:negative regulation			IPR013989 (SMART); IPR013989 (PF	30,418	40,464	39,000	35,701	40,853								
Solyc06g068860	Alpha-mannosidase (AHRD V3.3 *** E0XN34_SOLLC)		F:GO:0004559; P:GC	F:alpha-mannosidas	EC:3.2.1.24	Alpha-mannosidase	IPR015341 (SMART); G3DSA:2.70.98	119,381	113,292	85,845	74,401	89,240								
Solyc06g068870	bHLH transcription factor 087		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	120,871	109,762	139,425	146,541	153,659								
Solyc06g068880	Carboxypeptidase (AHRD V3.3 *** M1CT34_SOLTU)		F:GO:0004185; P:GC	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	17,264	9,733	28,576	33,592	25,518	-0,797	0,008					down		
Solyc06g068890	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT5G63760.4)						PTHR34780 (PANTHER); PTHR34780	0,042	0,118	0,441	1,062	0,356								
Solyc06g068900	Nudix hydrolase (AHRD V3.3 *** A0A061E9N4_THECC)		F:GO:0016787	F:hydrolase activity			IPR000086 (PFAM); G3DSA:3.90.79.1	3,211	2,721	80,364	100,588	57,906								
Solyc06g068910	receptor-like kinase 1 (AHRD V3.3 *** AT1G48480.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM); G3DSA:3.30.200	2,137	1,288	0,653	0,725	0,847								
Solyc06g068920	Kinase, putative (AHRD V3.3 *** B9T5A7_RICCO)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); G3DSA:1.10.51	92,530	73,019	108,248	110,920	109,921								
Solyc06g068930	Jasmonate ZIM domain protein g (AHRD V3.3 *** I3WTA5_NICAT)		C:GO:0005634; P:GC	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (SMART); IPR010399 (PF	0,098	0,060	0,000	0,000	0,000								
Solyc06g068940	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G17980.1)						IPR000008 (SMART); IPR000008 (PF	0,152	1,722	0,097	0,050	0,071	3,399	0,000					up		
Solyc06g068950	Phosphoethanolamine N-methyltransferase (AHRD V3.3 *** PEAMT_SPIOL)		F:GO:0000234; P:GC	F:phosphoethanolar	EC:2.1.1.13	Phosphoethanolamin	IPR013216 (PFAM); G3DSA:3.40.50.1	34,105	36,239	4,037	3,863	4,059								
Solyc06g068960	Calcium binding protein (AHRD V3.3 *** Q93YA8_SESRO)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); IPR002048 (PF	9,455	43,458	4,759	3,268	4,923	2,224	0,000					up		
Solyc06g068970	3-oxo-5-alpha-steroid 4-dehydrogenase (AHRD V3.3 *** G7LDB8_MEDTR)		P:GO:0006629; F:GC	P:lipid metabolic process; F:oxidoreductase activity, acting on t			IPR010721 (PFAM); G3DSA:1.20.120	4,940	7,170	5,806	7,631	9,723			0,735	0,014				up	
Solyc06g068980	MAP kinase kinase kinase 39	MAPKKK39	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:3.30.20	16,993	15,884	12,042	11,449	11,934								
Solyc06g068985	Kinase family protein (AHRD V3.3 *-* B9IEA9_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PF14381 (PFAM); mobidb-lite (MOBID	5,847	4,602	3,983	3,517	4,365								
Solyc06g068990	Mitogen-activated protein kinase (AHRD V3.3 *** A0A022QA30_ERYGU)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF	0,857	2,636	6,764	11,404	7,402	1,635	0,001			0,760	0,023	up		up
Solyc06g069000	Uncharacterized GPI-anchored protein At4g28100 (AHRD V1 ***- UGPI7_ARATH)		C:GO:0016021	C:integral component of membrane			PTHR34056:SF1 (PANTHER); IPR040	4,877	2,797	0,158	0,097	0,353								
Solyc06g069010	LeArcA1 protein	arca1	F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	286,841	322,858	224,603	217,559	228,204								
Solyc06g069020	Elongation factor 1 alpha (AHRD V3.3 *** A0A1B2LUN9_9CARY)		F:GO:0005525	F:GTP binding			IPR004160 (PFAM); IPR004161 (PFAI	108,756	109,757	139,184	131,639	122,713								
Solyc06g069030	PAP fibrillin domain protein,expressed protein (AHRD V3.3 *** G7LD88_MEDTR)		C:GO:0009507	C:chloroplast			PTHR35690 (PANTHER)	8,706	11,846	15,433	16,322	21,481			0,474	0,039				up	
Solyc06g069045	Glutathione-S-transferase (AHRD V3.3 *** K9P0S3_IPOBA)		F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D); IPR00	0,565	0,876	2,346	5,745	4,214					1,295	0,000			up
Solyc06g069070	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)		P:GO:0006869	P:lipid transport			IPR016140 (SMART); IPR016140 (PF	1,382	1,072	0,175	0,454	0,259								
Solyc06g069080	Tetratricopeptide repeat protein 7A (AHRD V3.3 *** A0A0B2PS28_GLYSO)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR011990 (G3	6,702	6,160	6,331	11,564	7,281					0,873	0,000			up
Solyc06g069090	40S ribosomal protein S7-like protein (AHRD V3.3 *** Q3HRX6_SOLTU)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000554 (PFAM); PTHR11278:SF1	180,738	215,527	153,381	145,119	139,887								
Solyc06g069100	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	NAC058	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,000	0,000	0,000	0,025	0,024								
Solyc06g069110	Lipid transfer protein (AHRD V3.3 *** A0A072UZK3_MEDTR)		C:GO:0016020	C:membrane			IPR016140 (PFAM); G3DSA:1.10.110	0,407	0,636	0,144	0,124	0,141								
Solyc06g069120	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)						PTHR33384:SF1 (PANTHER); PTHR3	1073,199	819,231	612,897	639,749	585,426								
Solyc06g069130	Kinesin-like protein (AHRD V3.3 *** K4C886_SOLLC)		F:GO:0003777; F:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (SM	0,226	0,638	0,219	0,397	0,330								
Solyc06g069140	Ribosomal RNA small subunit methyltransferase NEP1 (AHRD V3.3 *** A0A0B0N413_GOSAR)		F:GO:0008168	F:methyltransferase activity			IPR029026 (G3DSA:3.40.1280.GENE	0,132	0,080	0,000	0,000	0,000								
Solyc06g069150	LOW QUALITY:Zinc finger BED domain-containing protein DAYSLEEPER (AHRD V3.3 --* DSLE_ARATH)						mobidb-lite (MOBIDB_LITE); PTHR345	13,210	11,312	3,368	1,478	1,714					-1,185	0,005			down
Solyc06g069170	AT-rich interactive domain protein (AHRD V3.3 *** AT1G73885.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	120,069	137,642	138,116	144,428	209,271			0,597	0,000				up	
Solyc06g069180	protein phosphatase 2A subunit A		C:GO:0000159; F:GC	C:protein phosphata	EC:3.1.3.16	Protein-serine/threor	PF13646 (PFAM); IPR032878 (PFAM)	77,342	74,262	141,827	141,320	132,594								
Solyc06g069190	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G49050.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS); IPR032799 (PF	49,685	66,278	11,082	15,573	17,034			0,617	0,013				up	
Solyc06g069210	CASP-like protein		P:GO:0006891; C:GC	P:intra-Golgi vesicle-mediated transport; C:integral component c			IPR012955 (PFAM); mobidb-lite (MOB	75,271	80,316	114,963	126,192	110,721								
Solyc06g069220	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G18490.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	31,807	14,409	3,190	4,227	3,564								
Solyc06g069230	DNA mismatch repair protein (AHRD V3.3 *** Q6DQL7_PETHY)		F:GO:0005524; P:GC	F:ATP binding; P:mismatch repair; F:mismatched DNA binding; C			IPR007696 (SMART); IPR000432 (SM	3,954	3,733	4,651	3,059	3,414								
Solyc06g069240	branched1b	TCP8					IPR017887 (PFAN TCP	0,000	0,060	0,000	0,000	0,023								
Solyc06g069250	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7JT03_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33237 (PANTHER); PTHR33237	0,019	0,019	0,000	0,000	0,000								
Solyc06g069260	LOW QUALITY:Oleosin family protein (AHRD V3.3 *** A0A061FVM3_THECC)		C:GO:0012511; C:GC	C:monolayer-surrounded lipid storage body; C:integral compone			IPR000136 (PFAM); IPR000136 (PAN	5,149	3,848	0,025	0,251	0,046								
Solyc06g069270	LOW QUALITY:Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *-* AT1G48960.1)						IPR006016 (PFAM); PTHR31964:SF1	0,766	0,485	0,094	0,047	0,094								
Solyc06g069280	Binding-like protein isoform 5 (AHRD V3.3 *** A0A061G1J2_THECC)						IPR025609 (SMART); IPR019050 (SM	36,333	30,966	74,017	79,989	71,830								
Solyc06g069290	Leucine-rich repeat receptor-like protein kinase family protein, putative (AHRD V3.3 *-* A0A061E290_THEC		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,040	0,039	0,000	0,000	0,000								
Solyc06g069300	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G23100.1)						IPR006460 (PFAM); IPR006460 (TIGF	0,397	0,277	0,000	0,025	0,047								
Solyc06g069310	Nuclear transcription factor Y protein (AHRD V3.3 *** G7JT12_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAN NF-YB	30,947	39,229	33,321	31,252	31,442								
Solyc06g069320	Tetraspanin family protein (AHRD V3.3 *** A0A072V357_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR018499 (PFAM); PTHR32191:SF2	0,019	0,019	0,025	0,073	0,120								
Solyc06g069330	serine/threonine protein kinase 3 (AHRD V3.3 *** AT5G08160.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	20,287	19,324	27,387	26,460	24,381								
Solyc06g069350	Low-affinity inorganic phosphate transporter (AHRD V3.3 *** A0A0B0NPY8_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,875	2,873	3,939	4,695	4,148								
Solyc06g069355	root meristem growth factor (AHRD V3.3 --* AT2G04025.2)							3,805	1,972	0,000	0,047	0,000								
Solyc06g069360	RING/U-box protein (AHRD V3.3 *-* AT3G05670.3)		F:GO:0046872	F:metal ion binding			IPR001965 (SMART); IPR001841 (SM	10,218	10,093	12,085	11,325	11,983								
Solyc06g069370	bHLH transcription factor 046		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIL bHLH	8,781	8,695	7,418	7,762	8,923								
Solyc06g069375	Transcription factor BIM2-like protein (AHRD V3.3 *** G7JZB3_MEDTR)		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE); mobidb-lit	8,083	8,635	6,847	6,974	8,440								
Solyc06g069380	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G15740.1)		C:GO:0005737; P:GC	C:cytoplasm; P:fucose metabolic process; C:integral componen			IPR024709 (PIRSF); IPR019378 (PFA	5,712	5,396	2,156	2,128	2,051								
Solyc06g069385	Dof zinc finger protein (AHRD V3.3 *** W9RP28_9ROSA)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM); mobidb-lite (MOB	69,723	111,279	47,353	24,734	35,464	0,703	0,016	-0,421	0,043	-0,933	0,000	up	down	down
Solyc06g069390	D-aminoacyl-tRNA deacylase (AHRD V3.3 *-* AT2G03800.2)		F:GO:0051499	F:D-aminoacyl-tRN	EC:3.1.1.96; EC:3.1.	D-aminoacyl-tRNA de	G3DSA:3.40.630.50 (GENE3D); IPR0	16,812	17,464	11,947	10,712	13,172								
Solyc06g069395	LOW QUALITY:Rhodanese-like/PpiC domain-containing protein 12, chloroplastic (AHRD V3.3 --* STR12_ARATH)						IPR008581 (PFAM)	0,177	0,197	0,050	0,119	0,142								
Solyc06g069400	Isoaspartyl peptidase/L-asparaginase (AHRD V3.3 *** ASPG_LUPLU)		F:GO:0004867; P:GC	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS); IPR000864 (PF	2,153	1,295	0,044	0,045	0,023								
Solyc06g069410	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 *** ADT_ORYSJ)		C:GO:0005743; F:GC	C:mitochondrial inner membrane; F:transmembrane transporter			IPR002113 (PRINTS); IPR002067 (PF	9,004	7,666	17,333	16,237	15,366								
Solyc06g069420	Adenine nucleotide alpha hydrolases-like superfamily protein, putative (AHRD V3.3 *** A0A061FX93_THECC)						IPR006016 (PFAM); IPR014729 (G3D	7,576	10,876	11,787	15,804	11,659								
Solyc06g069430	FRUITFULL-like MADS-box 1	FUL1	F:GO:0000977; F:GC	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	167,896	182,190	844,701	899,454	817,765								
Solyc06g069440	Zinc finger transcription factor 45	C3H45	F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	84,138	73,850	181,247	201,565	175,419								
Solyc06g069445	DEAD-box ATP-dependent RNA helicase 25 (AHRD V3.3 --* RH25_ARATH)							0,019	0,018	0,022	0,025	0,047								
Solyc06g069450	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *-* AT4G26190.5)						IPR004274 (SMART); IPR004274 (PF	6,247	5,500	13,238	15,055	14,822								
Solyc06g069460	TCP transcription factor 6	TCP6	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAN TCP	0,042	0,000	0,044	0,022	0,047								
Solyc06g069470	Glycerophosphoryl diester phosphodiesterase family protein (AHRD V3.3 *** A0A072URQ0_MEDTR)		P:GO:0006629; F:GC	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR017946 (G3DSA:3.20.20.GENE3D	44,053	42,367	25,634	24,716	27,013								
Solyc06g069480	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *** AT5G61140.2)		F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding			IPR004179 (SMART); IPR003593 (SM	93,437	72,890	120,064	128,794	125,952								
Solyc06g069490	Transmembrane adipocyte-associated 1 (AHRD V3.3 *** A0A0B0NBD1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR018781 (PFAM); mobidb-lite (MOB	30,209	21,926	69,683	65,171	55,736								
Solyc06g069500	Dentin sialophosphoprotein-related, putative (AHRD V3.3 *** A0A061FY91_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	50,840	45,024	51,883	57,484	53,400								
Solyc06g069510	Cyclin-dependent kinase 2-interacting protein (AHRD V3.3 *** A0A1D1Y958_9ARAE)						mobidb-lite (MOBIDB_LITE); PTHR158	10,758	11,264	11,915	11,228	11,576								
Solyc06g069520	asterix-like protein (AHRD V3.3 *** AT5G07960.1)		C:GO:0016021	C:integral component of membrane			IPR005351 (PFAM); mobidb-lite (MOB	62,097	67,662	78,659	76,313	71,985								
Solyc06g069530	Biotin carboxyl carrier acetyl-CoA carboxylase (AHRD V3.3 *** G7KMP4_MEDTR)		F:GO:0003989; P:GC	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR001249 (PRINTS); IPR001249 (TI	28,451	33,787	20,799	20,352	22,094								
Solyc06g069540	ATP-binding cassette sub-family D member 4, putative (AHRD V3.3 *** A0A061FY60_THECC)							0,000	0,037	0,000	0,000	0,000								
Solyc06g069545	2-methylene-furan-3-one reductase (AHRD V3.3 --* ENOX_SOLLC)							0,019	0,021	0,000	0,000	0,000								
Solyc06g069550	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT3G29360.2)		F:GO:0003979; F:GC	F:UDP-glucose 6-de	EC:1.1.1.22	UDP-glucose 6-dehy	IPR014027 (SMART); IPR001732 (PF	0,763	0,973	0,293	0,267	0,212								
Solyc06g069560	AT-rich interactive domain-containing protein 2 (AHRD V3.3 *** A0A0B2QRH4_GLYSO)						mobidb-lite (MOBIL MYB_related	44,933	42,772	42,966	38,900	44,487								
Solyc06g069565	staurosporin and temperature sensitive 3-like A (AHRD V3.3 --* AT5G19690.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	5,087	6,257	3,159	3,165	3,678								
Solyc06g069570	Soluble N-ethylmaleimide-sensitive factor adaptor protein (AHRD V3.3 *** A0A072UQP3_MEDTR)		C:GO:0005886	C:plasma membrane			IPR000727 (SMART); G3DSA:1.20.5.1	74,152	131,143	57,995	90,143	76,650			0,400	0,043	0,639	0,000		up	up
Solyc06g069580	Heparanase (AHRD V3.3 *** C9E7B7_ORYSI)		C:GO:0016020; F:GC	C:membrane; F:hydrolase activity, acting on glycosyl bonds			G3DSA:3.20.20.80 (GENE3D); IPR00	8,080	7,802	2,428	3,010	3,245								
Solyc06g069590	Remorin family protein (AHRD V3.3 *** D7MUJ3_ARALL)						IPR005516 (PFAM); PTHR31471 (PAN	0,019	0,079	0,000	0,000	0,024								
Solyc06g069600	bHLH transcription factor 047	PIF7b	P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,000	0,018	0,000	0,000	0,000								
Solyc06g069635	T-box transcription factor, putative (DUF863) (AHRD V3.3 *-* AT1G13940.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	9,682	8,863	4,162	5,044	4,944								
Solyc06g069640	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A151SL49_CAJCA)		P:GO:0009143; F:GC	P:nucleoside tripho	EC:3.6.1.19	Acting on acid anhyd	IPR025984 (PIRSF); G3DSA:1.10.287	1,305	1,039	0,214	0,268	0,332								
Solyc06g069650	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT1G74360.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART); IPR000719 (SM	0,619	2,651	0,384	0,514	0,518								
Solyc06g069660	Formin-like protein (AHRD V3.3 *-* A0A068VCP1_COFCA)						IPR014020 (SMART); G3DSA:2.60.40	0,421	0,310	0,798	1,569	1,175								
Solyc06g069665	Formin-like protein (AHRD V3.3 *-* K4C8E0_SOLLC)						PR01217 (PRINTS); IPR015425 (SMA	5,175	5,968	7,306	7,960	8,669								
Solyc06g069670	Formin-like protein (AHRD V3.3 *** K4C8E0_SOLLC)						IPR015425 (SMART); G3DSA:1.20.58	0,000	0,037	0,025	0,072	0,117								
Solyc06g069700	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061G4F9_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	1,714	2,425	1,808	2,001	1,977								
Solyc06g069710	NAC domain protein, (AHRD V3.3 *** A0A061FWI7_THECC)	ORE1S06	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAN NAC	2,715	3,348	0,284	0,291	0,212								
Solyc06g069720	Thioredoxin-like protein (AHRD V3.3 *** T2DNK5_PHAVU)		C:GO:0005623; P:GC	C:cell; P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D); PTHR4	0,173	0,132	0,218	0,249	0,210								
Solyc06g069723	Nitrate reductase [NADH] 1 (AHRD V3.3 --* NIA1_ORYSJ)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,000	0,000	0,022	0,000								
Solyc06g069727	Thioredoxin-like protein (AHRD V3.3 *-* T2DNK5_PHAVU)		C:GO:0005623; P:GC	C:cell; P:cell redox homeostasis			PTHR43601 (PANTHER); PTHR43601	0,489	0,399	0,266	0,343	0,259								
Solyc06g069730	chlorophyll a-b binding protein Cab12		P:GO:0009765; C:GC	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM); IPR023329 (G3D	3,225	32,103	0,146	0,581	0,847	3,336	0,000					up		
Solyc06g069740	EF hand calcium-binding family protein (AHRD V3.3 *** G7K424_MEDTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,546	2,779	0,383	0,288	0,285	2,360	0,000					up		
Solyc06g069760	Dof zinc finger protein 22		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAN Dof	34,768	34,001	26,349	22,770	32,475								
Solyc06g069770	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* G7KER5_MEDTR)		C:GO:0005634; P:GC	C:nucleus; P:nucleologenesis			G3DSA:3.10.450.40 (GENE3D); PF11	46,814	38,359	43,758	40,375	38,035								
Solyc06g069780	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT3G47550.6)		F:GO:0008270; C:GC	F:zinc ion binding; C:integral component of membrane			IPR022143 (PFAM); mobidb-lite (MOB	12,945	16,368	22,155	21,629	19,580								
Solyc06g069790	Gibberellin-regulated protein (AHRD V3.3 *** B4UW77_ARAHY)						IPR003854 (PFAM); PTHR23201:SF2	4,348	4,912	4,198	3,492	3,530								
Solyc06g069820	DUF674 family protein (AHRD V3.3 *** A0A072TP22_MEDTR)						IPR007750 (PFAM); IPR007750 (PAN	20,236	15,928	14,111	14,276	13,471								
Solyc06g069850	R2R3MYB transcription factor 30	R2R3MYB30	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	12,040	17,066	1,205	0,811	1,477								
Solyc06g069860	60S ribosomal protein L34 (AHRD V3.3 *** RL34_TOBAC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR008195 (PRINTS); IPR008195 (PF	265,642	279,097	141,008	112,214	125,078								
Solyc06g069870	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G26850.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	0,533	0,401	0,075	0,000	0,024								
Solyc06g069880	LOW QUALITY:Phytochrome kinase substrate-related family protein (AHRD V3.3 *** B9N4C0_POPTR)		P:GO:0009638	P:phototropism			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,038	0,039	0,000	0,000	0,000								
Solyc06g069890	Nucleosome assembly protein family (AHRD V3.3 *** A9RDJ7_PHYPA)		C:GO:0005634; P:GC	C:nucleus; P:nucleosome assembly			G3DSA:3.30.1120.90 (GENE3D); IPR	36,424	40,018	33,084	29,452	27,342								
Solyc06g070900	TCP transcription factor 17	TCP17	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAN TCP	0,142	0,019	0,025	0,000	0,000								
Solyc06g070940	ABC transporter A family protein (AHRD V3.3 *** A0A072UVK2_MEDTR)	ABCA5	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); G3DSA:3.40.50	0,021	0,019	0,025	0,050	0,023								
Solyc06g070950	ABC transporter A family protein (AHRD V3.3 *** A0A072UUA7_MEDTR)	ABCA6	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); G3DSA:3.40.50	5,047	3,553	0,407	0,314	0,259								
Solyc06g070960	ABC transporter family protein (AHRD V3.3 *** A0A097P9Q6_HEVBR)	ABCA7	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); G3DSA:3.40.50	4,559	3,452	0,352	0,265	0,329								
Solyc06g070970	Serine/threonine-protein kinase atr (AHRD V3.3 *** A0A0B0N9L0_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,915	0,996	0,264	0,119	0,119								
Solyc06g070980	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A072TRF9_MEDTR)		P:GO:0000209; F:GC	P:protein polyubiquitination; F:ATP binding; P:DNA repair; F:liga			SM00212 (SMART); IPR016135 (G3D	2,144	2,224	2,335	1,629	1,699								
Solyc06g070985	Tubulin beta-1 chain (AHRD V3.3 --* W9SPB5_9ROSA)							0,000	0,000	0,000	0,025	0,000								
Solyc06g070990	WRKY transcription factor 74		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,470	0,383	0,143	0,025	0,093								
Solyc06g071000	aldehyde dehydrogenase 12A1 (AHRD V3.3 *** AT5G62530.1)		F:GO:0016620; P:GC	F:oxidoreductase activity, acting on the aldehyde or oxo group c			IPR015590 (PFAM); IPR016163 (G3D	112,237	99,139	163,793	148,299	157,714								
Solyc06g071010	F6A14.6 protein, putative (AHRD V3.3 *** A0A061FY10_THECC)		C:GO:0005730; P:GC	C:nucleolus; P:rRNA processing			PTHR37181 (PANTHER)	17,456	20,246	31,798	31,476	27,887								
Solyc06g071020	Pectate lyase (AHRD V3.3 *** K4C8H5_SOLLC)		F:GO:0030570	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS); IPR002022 (SM	0,000	0,021	0,000	0,000	0,024								
Solyc06g071030	isochorismate synthase	ICS	F:GO:0008909; P:GC	F:isochorismate syi	EC:5.4.4.2	Isochorismate syntha	IPR004561 (TIGRFAM); IPR015890 (F	1,615	3,854	1,229	1,764	1,903	1,275	0,011					up		
Solyc06g071040	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT5G62760.3)		C:GO:0005634	C:nucleus			G3DSA:3.40.50.300 (GENE3D); mobic	48,639	47,856	62,599	62,311	60,332								
Solyc06g071050	Hypersensitive-induced response protein (AHRD V3.3 *** A6YGE4_CARPA)						IPR001107 (SMART); G3DSA:3.30.47	52,054	80,732	15,835	18,843	19,364								
Solyc06g071060	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G03980.1),Pfam:PF13561		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	2,016	3,635	1,927	1,560	1,597								
Solyc06g071070	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G03980.1),Pfam:PF13561		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	12,134	33,374	6,314	6,590	10,289	1,486	0,000					up		
Solyc06g071080	Major facilitator superfamily protein, putative (AHRD V3.3 *** A0A061FWT4_THECC)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D); IPR	0,415	0,252	0,706	1,142	0,992								
Solyc06g071090	Major facilitator superfamily protein (AHRD V3.3 *-* A0A061EEJ1_THECC)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM); G3DSA:1.20.125	0,119	0,197	0,465	0,776	0,521								
Solyc06g071100	Plasma membrane ATPase (AHRD V3.3 *** M1D6E0_SOLTU)	lha2	F:GO:0000166; F:GC	F:nucleotide binding	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS); IPR001757 (PRIN	374,880	411,705	495,189	477,031	477,065								
Solyc06g071110	DnaJ like protein (AHRD V3.3 *** Q9FEW7_SOLLC)		P:GO:0006457; F:GC	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS); IPR001623 (SM	11,064	10,815	13,584	11,408	11,129								
Solyc06g071120	Ubiquitin carboxyl-terminal hydrolase-related protein (AHRD V3.3 *** AT3G47910.2)		F:GO:0005515; P:GC	F:protein binding; P	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D); IPR00	112,733	84,434	106,896	113,369	107,455								
Solyc06g071130	Zinc finger protein, putative (AHRD V3.3 *** B9R926_RICCO)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART); IPR012312 (PF	0,096	0,103	0,218	0,095	0,096								
Solyc06g071140	WW domain-binding protein 11 (AHRD V3.3 *** A0A0B2SUN7_GLYSO)		P:GO:0006396	P:RNA processing			PF12622 (PFAM); IPR019007 (PFAM)	77,295	70,301	82,249	77,325	77,032								
Solyc06g071150	HIPL1-like protein (AHRD V3.3 *** A0A0B0MLG6_GOSAR)		F:GO:0003824	F:catalytic activity			IPR012938 (PFAM); IPR011042 (G3D	0,271	0,702	0,047	0,095	0,095								
Solyc06g071160	Galactosyltransferase family protein (AHRD V3.3 *** AT5G62620.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR001079 (SMART); IPR001079 (PF	32,871	29,454	22,191	20,528	20,065								
Solyc06g071170	tRNA (Ile)-lysidine synthase (AHRD V3.3 *** A0A0B0MZ94_GOSAR)		C:GO:0009507	C:chloroplast			mobidb-lite (MOBIDB_LITE); mobidb-lit	64,709	48,716	99,592	82,455	89,397								
Solyc06g071180	Dynein light chain (AHRD V3.3 *** W9QNT0_9ROSA)		P:GO:0007017; C:GC	P:microtubule-based process; C:dynein complex			IPR001372 (SMART); IPR001372 (PF	9,159	6,941	15,253	13,512	13,668								
Solyc06g071190	myosin-binding protein, putative (Protein of unknown function, DUF593) (AHRD V3.3 *** AT1G74830.1)		F:GO:0017022	F:myosin binding			IPR007656 (PFAM); mobidb-lite (MOB	0,000	0,635	0,000	0,025	0,024								
Solyc06g071200	Transportin-3 (AHRD V3.3 *** A0A0B2QFE0_GLYSO)		P:GO:0006886; F:GC	P:intracellular protein transport; F:Ran GTPase binding			IPR001494 (SMART); IPR001494 (PF	77,554	89,037	117,987	118,927	114,259								
Solyc06g071210	Serine/threonine-protein kinase (AHRD V3.3 *** X5D770_TOBAC)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART); IPR000961 (SM	63,629	69,706	147,663	166,964	136,910								
Solyc06g071220	LOW QUALITY:Peptidase S41 family protein (AHRD V3.3 --* AT5G46390.2)							0,229	0,357	0,000	0,025	0,072								
Solyc06g071230	MYB transcription factor (AHRD V3.3 *** A1DR86_CATRO)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	150,824	124,197	124,050	128,356	118,117								
Solyc06g071240	Glutamine-dependent NAD(+) synthetase (AHRD V3.3 *-* NADE_ARATH)		F:GO:0003952; F:GC	F:NAD+ synthase (c	EC:6.3.5.1	NAD(+) synthase (glu	IPR003694 (PANTHER); PTHR23090:	0,763	1,644	0,150	0,529	0,376								
Solyc06g071250	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G40910.9)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	11,530	11,302	13,556	14,066	12,596								
Solyc06g071260	Transmembrane protein, putative (AHRD V3.3 *** A0A072US49_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR38525 (PANTHER)	5,706	6,012	9,214	8,852	8,787								
Solyc06g071270	RING/U-box superfamily protein (AHRD V3.3 *** AT5G62910.2)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			IPR013083 (G3DSA:3.30.40.GENE3D	11,937	12,508	28,104	23,726	21,710								
Solyc06g071280	protein EDS1		P:GO:0006629	P:lipid metabolic process			PF18117 (PFAM); IPR002921 (PFAM)	38,729	125,167	7,770	16,179	16,667	1,714	0,001	1,100	0,000	1,060	0,001	up	up	up
Solyc06g071285	SMAD/FHA domain-containing protein (AHRD V3.3 --* AT3G07260.1)							0,119	0,080	0,025	0,049	0,000								

Solyc06g071290	putative betaine aldehyde dehyrogenase		F:GO:0016620: P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR015590 (PFAM): IPR016162 (G3D	58,390	59,222	44,936	45,631	42,396									
Solyc06g071300	MADS-box transcription factor family protein (AHRD V3.3 --* AT5G27944.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity	IPR036879 (G3DS M-type_MADS	0,810	0,843	5,481	4,057	3,680									
Solyc06g071310	Pollen-specific protein SF3, putative (AHRD V3.3 *** Q53J16_SOLLC)		F:GO:0046872	F:metal ion binding	IPR001781 (SMART): IPR001781 (PF	10,356	11,869	5,265	4,844	5,532									
Solyc06g071320	D-ribose-binding periplasmic protein (AHRD V3.3 *** AT1G60010.1)				IPR025322 (PFAM): PTHR33413 (PAN	0,096	0,442	0,044	0,047	0,094									
Solyc06g071330	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** A0A072VA43_MEDTR)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR006043 (PFAM): PTHR11119 (PAN	29,404	23,505	2,541	1,587	1,929									
Solyc06g071333	ABC transporter G family member 53 (AHRD V3.3 --* AB53G_ORYSJ)					0,197	0,152	0,000	0,050	0,000									
Solyc06g071337	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 --* AT4G14920.3)					0,599	0,577	0,508	0,412	0,283									
Solyc06g071340	RING-box protein (AHRD V3.3 --* Q2PYP4_ARAHY)				SSF57850 (SUPERFAMILY)	0,245	0,341	0,196	0,169	0,166									
Solyc06g071350	BAH domain-containing protein, putative (AHRD V3.3 *** Q53J12_SOLLC)		F:GO:0003682: C:G(	F:chromatin binding; C:nucleus	IPR003617 (SMART): IPR001025 (SM	189,317	145,765	154,821	184,413	185,755									
Solyc06g071370	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 *-* A0A061EBN2_THECC)				PTHR13833 (PANTHER): PTHR13833	15,006	9,572	23,674	24,358	22,902									
Solyc06g071380	1-deoxy-D-xylulose-5-phosphate synthase (AHRD V3.3 *** A0A0B0N5A7_GOSAR)		C:GO:0016021	C:integral component of membrane	PTHR38543 (PANTHER)	9,014	6,526	14,381	14,321	12,583									
Solyc06g071390	Deleted in split hand/splt foot protein 1 (AHRD V3.3 *** D2XQ35_IPOBA)		P:GO:0006406: C:G(	P:mRNA export from nucleus; C:proteasome regulatory particle,	IPR007834 (SMART): IPR007834 (PF	4,130	5,677	2,156	1,595	2,029									
Solyc06g071410	MAP kinase kinase kinase 40	MAPKKK40	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PRINTS): IPR000719 (SM	29,810	29,769	8,631	8,147	9,962									
Solyc06g071420	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G61180.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART): IPR013083 (G3	11,878	7,957	18,851	18,957	20,918									
Solyc06g071430	Protein EXECUTER 1, chloroplastic (AHRD V3.3 *** A0A1D1XJU0_9ARAE)		F:GO:0005515	F:protein binding	IPR021894 (PFAM): IPR001943 (PFA	73,216	81,398	134,638	131,477	141,128									
Solyc06g071440	CASP-like protein (AHRD V3.3 *** K4C8L6_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM): mobidb-lite (MOB	8,760	6,755	9,010	7,548	7,090									
Solyc06g071450	General transcription factor IIH subunit, putative (AHRD V3.3 *** G7J304_MEDTR)		C:GO:0000439: P:G(	C:transcription factor TFIIH core complex; P:nucleotide-excision	IPR004600 (PFAM): IPR036465 (G3D	7,163	6,339	11,317	10,902	11,352									
Solyc06g071460	Exosome complex exonuclease RRP40 (AHRD V3.3 *** B7FLI0_MEDTR)		C:GO:0000178: F:G(	C:exosome (RNase complex); F:RNA binding	IPR004088 (PFAM): IPR036612 (G3D	1,057	1,441	1,015	0,885	1,158									
Solyc06g071470	Peroxisomal membrane protein PEX14 (AHRD V3.3 *** W9RQB1_9ROSA)		F:GO:0003723: F:G(	F:RNA binding; F:protein binding; C:peroxisomal membrane; P:p	IPR004088 (PFAM): IPR006785 (PFA	133,489	134,813	275,114	279,629	281,229									
Solyc06g071480	Dof zinc finger protein (AHRD V3.3 *** A0A0B6VJP1_TOBAC)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM Dof	0,338	0,376	0,025	0,000	0,047									
Solyc06g071490	Serine/threonine-protein kinase ATM (AHRD V3.3 *-* A0A0B0NJM8_GOSAR)		F:GO:0003676	F:nucleic acid binding	IPR000313 (PFAM): G3DSA:2.30.30.1	83,529	74,918	191,700	172,384	173,953									
Solyc06g071500	Boron transporter, putative (AHRD V3.3 *** B9RB14_RICCO)		F:GO:0005452: P:G(	F:inorganic anion exchanger activity; P:anion transport; C:integ	IPR011531 (PFAM): mobidb-lite (MOB	134,993	93,052	78,481	57,873	68,033									
Solyc06g071510	GDSL esterase/lipase (AHRD V3.3 *** A0A1D1YN85_9ARAE)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	13,168	14,204	12,491	12,975	12,687									
Solyc06g071530	60S ribosomal protein L44 (AHRD V3.3 *** RL44_GOSHI)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:3.10.450.80 (GENE3D): IPR0(	78,754	91,624	85,020	79,507	76,630									
Solyc06g071540	Transmembrane protein, putative (AHRD V3.3 *** A0A072UQ63_MEDTR)		F:GO:0005524: C:G(	F:ATP binding; C:integral component of membrane	PTHR12242:SF8 (PANTHER): PTHR1:	0,624	1,089	0,187	0,313	0,214									
Solyc06g071550	Anthranilate phosphoribosyltransferase (AHRD V3.3 *** F1BPW3_SOLPN)	APT	P:GO:0000162: F:G(	P:tryptophan biosyr EC:2.4.2.18 Anthranilate phospho	G3DSA:1.20.970.10 (GENE3D): IPR0	12,265	17,950	3,456	2,757	4,176									
Solyc06g071560	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B (AHRD V3.3 *** K4C8M8_SOLLC)		C:GO:0000159: F:G(	C:protein phosphatase type 2A complex; F:protein binding; F:pr	IPR000009 (PRINTS): IPR001680 (SM	0,098	0,139	0,137	0,219	0,117									
Solyc06g071570	Major facilitator superfamily protein (AHRD V3.3 *** AT5G62680.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): PTHR11654:SF5	0,194	0,138	0,118	0,172	0,048									
Solyc06g071580	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0PTV2_GOSAR)				IPR036890 (G3DSA:3.30.565.GENE3	2,216	1,663	4,512	4,605	2,384			-0,918	0,015				down	
Solyc06g071590	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)		C:GO:0016021	C:integral component of membrane	IPR025521 (PFAM): IPR004314 (PFA	0,676	0,531	0,197	0,311	0,117									
Solyc06g071600	Kinetochore protein spc25, putative (AHRD V3.3 *** A0A061FUW7_THECC)		C:GO:0000777: P:G(	C:condensed chromosome kinetochore; P:chromosome segrega	IPR013255 (PFAM): G3DSA:3.30.457	3,366	2,952	1,594	1,205	1,367									
Solyc06g071610	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G50130.1)		C:GO:0016021	C:integral component of membrane	IPR002347 (PRINTS): IPR002347 (PF	0,042	0,119	0,050	0,048	0,023									
Solyc06g071620	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *** AT1G20960.2)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding	IPR004179 (SMART): IPR003593 (SM	11,177	10,447	9,565	12,090	11,663									
Solyc06g071630	Integrator complex subunit 3 (AHRD V3.3 *** A0A103XQR6_CYNCS)				IPR019333 (PFAM): IPR019333 (PAN	7,857	5,847	8,149	7,931	7,121									
Solyc06g071640	tryptophan aminotransferase related 2 (AHRD V3.3 *** AT4G24670.2)		F:GO:0016846	F:carbon-sulfur lyase activity	IPR006948 (PFAM): IPR015422 (G3D	0,218	0,536	0,000	0,000	0,048									
Solyc06g071660	LOB domain-containing protein, putative (AHRD V3.3 *** B9S640_RICCO)				IPR004883 (PFAM LBD	0,021	0,000	0,000	0,000	0,000									
Solyc06g071670	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein (AHRD V3.3 *** Q9FML3_ARATH)				G3DSA:3.40.50.150 (GENE3D): PTHR	13,185	14,565	10,869	10,987	12,399									
Solyc06g071680	Histone deacetylase (AHRD V3.3 *** K4C8P0_SOLLC)		F:GO:0004407: P:G(	F:histone deacetyla EC:3.5.1.98 Histone deacetylase	IPR000286 (PRINTS): IPR003084 (PF	67,654	66,762	109,115	93,522	95,977									
Solyc06g071690	R2R3MYB transcription factor 50	R2R3MYB50	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	3,909	3,944	0,455	0,412	0,617									
Solyc06g071700	LOW QUALITY:Amine oxidase (AHRD V3.3 *** K4C8P2_SOLLC)		F:GO:0005507: F:G(	F:copper ion bindin EC:1.4.3.21 Primary-amine oxida	IPR015802 (PFAM): G3DSA:3.10.450.	0,264	0,366	0,091	0,076	0,000									
Solyc06g071720	60S ribosomal protein L27A (AHRD V3.3 *** B6VC54_VERFO)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:large ribos	G3DSA:3.100.10.10 (GENE3D): IPR0:	613,785	607,071	381,038	380,065	351,001									
Solyc06g071725	U-box domain-containing protein 33 (AHRD V3.3 *** W9RIP2_9ROSA)				IPR014729 (G3DSA:3.40.50.GENE3D	1,206	1,709	0,673	0,777	0,616									
Solyc06g071730	U-box domain-containing protein kinase family protein (AHRD V3.3 --* AT2G19410.3)				PTHR31964:SF53 (PANTHER): IPR00	0,174	0,099	0,068	0,145	0,071									
Solyc06g071750	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *** A0A0K9NT10_ZOSMR)		F:GO:0005515	F:protein binding	IPR000270 (SMART): G3DSA:3.10.20	13,828	11,526	46,744	63,861	39,538					0,455	0,031			up
Solyc06g071770	Ubiquitin-associated/TS-N domain protein, putative (AHRD V3.3 *-* A0A072UPL1_MEDTR)		F:GO:0008270: P:G(	F:zinc ion binding; P:macroautophagy; F:ubiquitin binding	IPR000433 (SMART): IPR000433 (PF	116,226	118,483	220,576	231,177	212,580									
Solyc06g071780	Dehydration-induced 19-like protein (AHRD V3.3 *** E3T7S4_GOSHI)				IPR027935 (PFAM): IPR008598 (PFA	78,000	67,951	32,423	40,761	31,701									
Solyc06g071805	Kinase family protein (AHRD V3.3 *-* B9I3F6_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	6,439	5,611	7,657	8,275	7,403									
Solyc06g071810	Leucine-rich repeat receptor-like kinase (AHRD V3.3 *** K4C8Q3_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	54,257	88,675	11,929	26,195	26,244			1,134	0,000	1,134	0,000		up	up
Solyc06g071820	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)		F:GO:0003712: F:G(	F:transcription core EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	IPR000197 (SMART): IPR000210 (SM	343,469	140,201	190,852	157,935	163,953	-1,263	0,000					down		
Solyc06g071830	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)		F:GO:0003712: F:G(	F:transcription core EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	IPR000210 (SMART): IPR000197 (SM	0,098	0,195	0,075	0,022	0,024									
Solyc06g071840	Pectate lyase (AHRD V3.3 *-* M1CKT3_SOLTU)		F:GO:0030570: P:G(	F:pectate lyase act EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS): IPR002022 (SM	0,212	0,079	0,000	0,000	0,000									
Solyc06g071850	Tetratricopeptide repeat-containing family protein (AHRD V3.3 *** B9I3K1_POPTR)		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR011990 (G3	31,023	20,902	16,968	18,669	19,135	-0,541	0,038					down		
Solyc06g071860	Zinc finger transcription factor 46	C3H46	F:GO:0046872	F:metal ion binding	IPR000571 (SMAF C3H	76,779	63,262	74,336	70,735	71,656									
Solyc06g071870	Ribosomal protein (AHRD V3.3 *** Q947H2_PETHY)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:large ribos	IPR005721 (TIGRFAM): IPR036394 ((	51,782	56,411	47,386	44,198	47,497									
Solyc06g071880	60S ribosomal protein L17 (AHRD V3.3 *** A0A0D3QSL6_TOBAC)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:large ribos	IPR005721 (TIGRFAM): IPR036394 ((	62,800	74,225	54,806	47,285	51,519									
Solyc06g071890	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4C8R1_SOLLC)		C:GO:0005743: P:G(	C:mitochondrial inner membrane; P:mitochondrial pyruvate trans	IPR005336 (PFAM): PTHR14154 (PAN	15,691	13,253	8,674	9,684	9,250									
Solyc06g071900	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JW05_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM): IPR002885 (F	13,945	14,395	16,071	16,122	15,286									
Solyc06g071910	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G24360.1)		F:GO:0004316: P:G(	F:3-oxoacyl-[acyl-c: EC:2.3.1.85; EC:1.1. Fatty-acid synthase:	IPR002347 (PRINTS): IPR002347 (PF	61,248	71,892	33,423	33,507	38,888									
Solyc06g071920	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** C9DRQ8_SOLCH)		P:GO:0006006: F:G(	P:glucose metabolic process; F:oxidoreductase activity, acting	IPR020831 (PRINTS): IPR020828 (SM	687,672	645,039	1576,396	1345,830	1458,960									
Solyc06g071950	GDP-mannose transporter, putative (AHRD V3.3 *** B9RMI4_RICCO)		C:GO:0005794: P:G(	C:Golgi apparatus; P:nucleotide-sugar transmembrane transpor	IPR004853 (PFAM): mobidb-lite (MOB	0,160	0,122	0,236	0,193	0,118									
Solyc06g071960	Nucleoside diphosphate kinase (AHRD V3.3 *** K4C8R8_SOLLC)		F:GO:0004550: P:G(	F:nucleoside diphos EC:2.7.4.6 Nucleoside-diphosph	IPR001564 (PRINTS): IPR034907 (SM	14,767	28,621	20,886	22,974	34,731	0,983	0,001	0,731	0,000			up	up	
Solyc06g071980	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G24860.4)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): G3DSA:1.10.8.6	10,105	8,904	11,462	11,099	10,607									
Solyc06g071990	ATPase family AAA domain-containing protein 1 (AHRD V3.3 *-* A0A0B0PMY4_GOSAR)		F:GO:0005524	F:ATP binding	mobidb-lite (MOBIDB_LITE): PTHR230	94,118	109,655	49,593	37,948	40,315									
Solyc06g072000	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G24860.4)		F:GO:0005524	F:ATP binding	IPR003593 (SMART): IPR003959 (PF	0,400	0,317	0,076	0,000	0,000									
Solyc06g072010	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT4G24860.4)		F:GO:0005524	F:ATP binding	G3DSA:1.10.8.60 (GENE3D): PTHR2:	0,240	0,328	0,965	1,247	0,971									
Solyc06g072012	ATPase family AAA domain-containing protein 1-A (AHRD V3.3 --* W9RQR6_9ROSA)				mobidb-lite (MOBIDB_LITE)	1,982	1,274	2,368	2,304	2,698									
Solyc06g072014	Pyrroline-5-carboxylate reductase (AHRD V3.3 --* P5CR1_ARATH)					1,684	1,537	2,651	2,527	2,631									
Solyc06g072016	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT4G24860.4)		F:GO:0000166	F:nucleotide binding	G3DSA:1.10.8.60 (GENE3D): PTHR23	2,926	2,998	5,743	5,271	6,002									
Solyc06g072018	Protein transport protein Sec61 subunit gamma (AHRD V3.3 *** SC61G_ORYSJ)		P:GO:0006605: F:G(	P:protein targeting; F:P-P-bond-hydrolysis-driven protein transm	IPR023391 (G3DSA:1.20.5.GENE3D):	56,248	69,931	82,055	91,599	74,128									
Solyc06g072030	disease resistance protein (TIR-NBS class) (AHRD V3.3 --* AT4G16990.9)					12,127	16,947	16,947	17,303	15,239									
Solyc06g072040	CONSTANS interacting protein 2a	CIP2a	F:GO:0046982	F:protein heterodimerization activity	IPR003958 (PFAM NF-YC	64,515	55,558	45,769	36,502	42,670									
Solyc06g072050	CBS domain-containing protein (AHRD V3.3 *** W9QLL8_9ROSA)		F:GO:0005515	F:protein binding	IPR000644 (SMART): IPR000270 (SM	41,343	36,528	41,122	38,489	39,389									
Solyc06g072060	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT5G08391.1)		C:GO:0016021	C:integral component of membrane	IPR021775 (PFAM): IPR021775 (PAN	0,097	0,019	0,000	0,000	0,000									
Solyc06g072070	transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT3G48660.1)		C:GO:0016021	C:integral component of membrane	IPR021775 (PFAM): IPR021775 (PAN	3,855	4,010	2,168	2,347	2,536									
Solyc06g072080	ubiquitin activating enzyme	AJ011418				2,034	1,703	1,138	1,108	0,844									
Solyc06g072100	ABC transporter G family member (AHRD V3.3 *** A0A0K9NYG1_ZOSMR)	ABCG16	F:GO:0005524: C:G(	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	0,019	0,059	0,000	0,000	0,000									
Solyc06g072110	Testis-expressed sequence 2 protein (AHRD V3.3 *** A0A0B2Q462_GLYSO)		F:GO:0008289	F:lipid binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	49,444	62,278	36,618	32,542	40,571									
Solyc06g072120	40S ribosomal protein SA (AHRD V3.3 *** K4C8T4_SOLLC)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:small ribos	IPR001865 (PRINTS): G3DSA:3.40.50	208,533	254,353	257,315	230,702	229,056									
Solyc06g072130	tonoplast intrinsic protein 3.1	TIP3.1	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR000425 (TI(	32,573	28,289	1,720	4,942	0,393									
Solyc06g072135	ankyrin repeat protein (AHRD V3.3 *** AT1G73350.7)				mobidb-lite (MOBIDB_LITE): mobidb-lit	7,086	6,044	6,764	6,735	5,323									
Solyc06g072140	phytochrome-associated serine/threonine-protein phosphatase 3-like		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding; F:hydrolase activity	IPR006186 (PRINTS): IPR000270 (SM	41,699	40,174	51,524	50,022	52,290									
Solyc06g072160	Alcohol dehydrogenase family protein (AHRD V3.3 *** B9H299_POPTR)		P:GO:0055114	P:oxidation-reduction process	IPR013149 (PFAM): IPR013154 (PFA	7,716	8,490	12,375	13,409	12,487									
Solyc06g072165	Coiled-coil domain-containing 12 (AHRD V3.3 *** A0A0B0PPQ1_GOSAR)				IPR013169 (PFAM): mobidb-lite (MOB	0,320	0,423	0,485	0,365	0,261									
Solyc06g072170	Coiled-coil domain-containing 12 (AHRD V3.3 *** A0A0B0PPQ1_GOSAR)				IPR013169 (PFAM): mobidb-lite (MOB	0,366	0,791	0,751	0,584	0,750									
Solyc06g072220	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity	IPR002160 (PRINTS): IPR002160 (SM	1,376	1,524	0,000	0,070	0,000									
Solyc06g072230	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)		F:GO:0004866	F:endopeptidase inhibitor activity	IPR002160 (PRINTS): IPR002160 (SM	0,799	0,712	0,025	0,000	0,093									
Solyc06g072240	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein heterodimerization activity	IPR001951 (PRINTS): IPR001951 (SM	0,699	0,946	0,121	0,025	0,023									
Solyc06g072250	S-adenosyl-L-methionine-dependent methyltransferase (AHRD V3.3 *** G7JUC5_MEDTR)		F:GO:0016435: P:G(	F:rRNA (guanine) methyltransferase activity; P:rRNA (guanine-N	IPR022238 (PFAM): IPR013216 (PFA	21,533	22,280	16,001	14,257	13,047									
Solyc06g072260	E3 ubiquitin-protein ligase RING1 (AHRD V3.3 *** RING1_GOSHI)		F:GO:0061630	F:ubiquitin protein ligase activity	IPR039525 (PFAM): mobidb-lite (MOB	0,040	0,018	0,000	0,025	0,023									
Solyc06g072270	RING/U-box superfamily protein (AHRD V3.3 *** AT3G19950.3)		F:GO:0061630	F:ubiquitin protein ligase activity	IPR001841 (SMART): IPR039525 (PF	0,337	0,117	0,047	0,119	0,000									
Solyc06g072273	Homeodomain-like superfamily protein, putative isoform 3 (AHRD V3.3 *-* A0A061GHU4_THECC)		P:GO:0015986: C:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	13,248	12,142	14,818	14,621	14,553									
Solyc06g072277	Homeodomain-like superfamily protein, putative isoform 3 (AHRD V3.3 *-* A0A061GHU4_THECC)		P:GO:0015986: C:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	8,660	7,171	9,511	10,002	10,324									
Solyc06g072280	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT2G18740.1)		P:GO:0000398: C:G(	P:mRNA splicing, via spliceosome; C:spliceosomal complex	IPR001163 (SMART): G3DSA:2.30.30	12,778	13,735	10,729	10,336	11,070									
Solyc06g072290	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** A0A072UM28_MEDTR)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): PTHR32258 (PAN	0,094	0,039	0,000	0,000	0,000									
Solyc06g072300	Argonaute 1		F:GO:0003676: F:G(	F:nucleic acid binding; F:protein binding	IPR003100 (SMART): IPR014811 (SM	203,729	182,939	138,547	126,998	154,029									
Solyc06g072310	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9N3B2_POPTR)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding	IPR001356 (SMAF HD-ZIP	1,007	0,977	0,621	0,645	0,703									
Solyc06g072320	Serine palmitoyltransferase (AHRD V3.3 *** B3Y000_NICBE)		F:GO:0003824: P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	IPR015422 (G3DSA:3.90.1150.GENE	0,021	0,039	0,000	0,000	0,000									
Solyc06g072335	Peroxidase (AHRD V3.3 --* G7JMV9_MEDTR)					0,019	0,000	0,000	0,000	0,000									
Solyc06g072340	Kinase family protein (AHRD V3.3 *** B9I4W2_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	6,259	6,404	4,582	7,014	5,496					0,621	0,028			up
Solyc06g072350	CASP-like protein (AHRD V3.3 *** K4C8V5_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane	IPR006702 (PFAM): PTHR33573 (PAN	1,592	2,099	0,654	1,552	0,895									
Solyc06g072360	Zinc finger family protein (AHRD V3.3 *** B9HJL4_POPTR)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	0,260	0,135	0,050	0,096	0,117									
Solyc06g072370	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN93_SOLLC)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR010409 (SMAF BBR-BPC	4,014	3,324	3,561	2,765	3,078									
Solyc06g072380	3,4-dihydroxy-2-butanone kinase	dhbk	F:GO:0004371: F:G(	F:glycerone kinase EC:2.7.1.29 Glycerone kinase	IPR004007 (SMART): IPR004006 (PF	24,865	29,132	23,642	23,086	28,388									
Solyc06g072407	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *-* A0A0B2QZK8_GLYSO)		F:GO:0016787: P:G(	F:hydrolase activity; P:phosphatidylinositol dephosphorylation	PTHR11200:SF190 (PANTHER): PTHI	0,000	0,019	0,000	0,000	0,000									
Solyc06g072410	DUF674 family protein (AHRD V3.3 *-* A0A072TP22_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR007750 (PFAM): mobidb-lite (MOB	0,021	0,099	0,047	0,000	0,048									
Solyc06g072430	BAG family molecular chaperone regulator 5 (AHRD V3.3 *-* W9QTU5_9ROSA)		F:GO:0051087	F:chaperone binding	IPR000048 (SMART): IPR003103 (SM	22,616	12,700	53,263	57,481	43,031									
Solyc06g072440	B-cell receptor-associated-like protein (AHRD V3.3 *** G7JZ88_MEDTR)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte	IPR040463 (PFAM): IPR008417 (PAN	12,617	11,956	13,958	15,063	14,624									
Solyc06g072460	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *-* AT2G27660.1)				IPR004146 (PFAM): PTHR13871 (PAN	0,019	0,078	0,000	0,025	0,000									
Solyc06g072465	50S ribosomal protein L29 (AHRD V3.3 *** F4YFA4_CAMSI)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001854 (TIGRFAM): IPR001854 (F	17,628	26,720	14,078	13,411	19,158	0,627	0,038					up		
Solyc06g072490	40S ribosomal protein S3a (AHRD V3.3 *** RS3A_TOBAC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001593 (SMART): IPR001593 (PF	178,842	213,315	163,709	136,408	144,262									
Solyc06g072500	N-acetyltransferase, putative (AHRD V3.3 *** B9T667_RICCO)		F:GO:0010485: F:G(	F:H4 histone acetyl EC:2.3.1.5; EC:2.3.1 Arylamine N-acetyltra	IPR000182 (PFAM): G3DSA:3.40.630.	0,353	0,302	0,312	0,415	0,638									
Solyc06g072510	Phosphate carrier, mitochondrial (AHRD V3.3 *** A0A0B0NBL8_GOSAR)		F:GO:0022857	F:transmembrane transporter activity	IPR018108 (PFAM): IPR023395 (G3D	0,140	0,064	0,165	0,263	0,141									
Solyc06g072520	bHLH transcription factor GBOF-1	bHLH048	P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,081	0,039	0,618	2,147	0,399					1,761	0,000			up
Solyc06g072530	CASP-like protein (AHRD V3.3 *** K4C8X3_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM): IPR006459 (TIGF	0,213	0,142	1,252	3,514	1,731					1,484	0,000			up
Solyc06g072540	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_NICTO)		F:GO:0005524: C:G(	F:ATP binding; C:ch EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.12240 (GENE3D): PT	0,370	1,146	0,096	0,270	0,400									
Solyc06g072550	CASP-like protein (AHRD V3.3 *** K4C8X5_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006702 (PFAM): IPR006459 (TIGF	0,000	0,091	0,022	0,022	0,071									
Solyc06g072570	ubiquitin conjugating enzyme	ubc	F:GO:0005515	F:protein binding	SM00212 (SMART): IPR015940 (SMA	30,226	28,504	32,902	35,274	35,119									
Solyc06g072580	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** B6T6H3_MAIZE)		F:GO:0004739: P:G(	F:pyruvate dehydro EC:1.2.4.1 Pyruvate dehydroger	IPR005475 (SMART): IPR005475 (PF	36,878	35,199	49,300	50,090	50,124									
Solyc06g072600	Mitochondrial import inner membrane translocase subunit (AHRD V3.3 *** F2VPS7_SOLNI)		C:GO:0005758: P:G(	C:mitochondrial intermembrane space; P:chaperone-mediated p	IPR004217 (PFAM): IPR035427 (G3D	9,503	10,908	14,643	13,527	13,688									
Solyc06g072610	S-acyltransferase (AHRD V3.3 *** K4C8Y1_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic retic EC:2.3.1.225 Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	14,885	19,743	14,698	13,903	14,509									
Solyc06g072620	Bidirectional sugar transporter SWEET (AHRD V3.3 *-* K4C8Y2_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004316 (PFAM): G3DSA:1.20.128	0,019	0,018	0,000	0,000	0,000									
Solyc06g072660	Protein DEK (AHRD V3.3 *** A0A0B2QBX5_GLYSO)		C:GO:0005634: F:G(	C:nucleus; F:histone binding; P:regulation of double-strand brea	IPR014876 (PFAM): G3DSA:1.10.10.6	16,650	15,193	2,347	2,091	1,907									
Solyc06g072670	hydroxysteroid dehydrogenase 1 (AHRD V3.3 *** AT5G50700.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; F	IPR002347 (PRINTS): IPR002347 (PF	11,114	21,372	4,832	9,442	3,131									
Solyc06g072680	HVA22-like protein (AHRD V3.3 *-* K4C8Y8_SOLLC)		C:GO:0016021	C:integral component of membrane		0,295	0,875	5,299	6,451	5,591									
Solyc06g072690	Mitotic-spindle organizing 1B-like protein (AHRD V3.3 *** A0A072VE60_MEDTR)		C:GO:0008274: P:G(	C:gamma-tubulin ring complex; P:gamma-tubulin complex localiz	IPR022214 (PFAM): PTHR28520:SF5	2,718	2,752	0,719	0,341	0,469									
Solyc06g072700	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G50740.5)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D): G3DS	70,549	56,877	13,284	8,377	11,182					-0,665	0,009			down
Solyc06g072710	Sigma factor (AHRD V3.3 *** Q9SLX3_TOBAC)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra	IPR000943 (PRINTS): IPR014284 (TI(	10,005	15,934	13,956	11,147	19,035									
Solyc06g072720	Zinc finger transcription factor 47	C3H47	F:GO:0046872	F:metal ion binding	IPR000571 (SMAF C3H	18,770	20,656	21,312	23,232	20,402									
Solyc06g072730	WEB family protein, chloroplastic (AHRD V3.3 *** A0A0B2RLR4_GLYSO)		P:GO:0000160: P:G(	P:phosphorelay signal transduction system; P:reciprocal meiotic	IPR008545 (PFAM): mobidb-lite (MOB	0,465	0,393	0,046	0,050	0,166									
Solyc06g072740	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4C8Z4_SOLLC)		F:GO:0000287: F:G(	F:magnesium ion bi EC:2.7.1.134; EC:2.: Inositol-tetrakisphosp	IPR040464 (PFAM): G3DSA:3.40.50.1	5,415	10,520	7,332	5,678	5,912	0,987	0,004					up		
Solyc06g072750	SolycHsfA1e	HSF-08	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	7,669	9,576	11,510	14,823	14,253									
Solyc06g072760	Syntaxin family protein (AHRD V3.3 *** B9MU58_POPTR)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport	IPR006011 (SMART): IPR000727 (SM	0,175	0,158	1,456	4,058	2,621					1,482	0,000			up
Solyc06g072770	RNA-binding family protein isoform 1 (AHRD V3.3 *** A0A061G6K6_THECC)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	4,535	8,928	13,525	17,506	17,297	1,001	0,024					up		
Solyc06g072780	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 (AHRD V3.3 --* GLO5_ORYSJ)					0,412	0,215	1,173	1,091	1,013									
Solyc06g072785	DUF399 family protein, putative (DUF399 and DUF3411) (AHRD V3.3 --* AT3G56140.3)					1,745	1,505	1,439	1,330	1,557									
Solyc06g072790	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GUW0_THECC)		C:GO:0016021: F:G(	C:integral component of membrane; F:ligase activity	IPR001841 (SMART): IPR001841 (PF	19,750	18,808	26,070	26,546	25,456									
Solyc06g072800	ADP-ribosylation factor (AHRD V3.3 *** Q5FYS3_DAUCA)		F:GO:0005525	F:GTP binding	IPR006689 (PRINTS): SM00178 (SMA	7,757	6,323	12,095	11,894	11,197									
Solyc06g072810	aspartic/glutamic acid-rich protein (AHRD V3.3 *-* AT5G17160.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,465	0,737	0,075	0,025	0,000									
Solyc06g072820	Tudor/PWWP/MBT superfamily protein (AHRD V3.3 *** G7JRQ8_MEDTR)		C:GO:0005634: C:G(	C:nucleus; C:plasmodesma; P:vegetative to reproductive phase	IPR000313 (PFAM): G3DSA:2.30.30.1	10,792	12,585	14,538	13,254	13,425									
Solyc06g072830	WD40 repeat-containing protein (AHRD V3.3 *** A0A103YEC3_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:anaphase-promoting complex binding; F:ubi(	IPR001680 (SMART): IPR015943 (G3	2,037	2,009	0,556	0,311	0,493									
Solyc06g072840	Hydrogen peroxide induced protein 1 (AHRD V3.3 *** J7F198_CAMSI)				PTHR35122:SF2 (PANTHER): IPR039	332,750	200,810	385,465	250,525	317,393	-0,701	0,022			-0,618	0,000	down		down

Solyc06g072845	Hydrogen peroxide-induced 1 (AHRD V3.3 *** B8Y3H9_TOBAC)				IPR039291 (PANTHER): PTHR35122::	1524,949	1067,985	2939,004	2303,990	2725,605									
Solyc06g072850	LOW QUALITY:Calpain-type cysteine protease DEK1 (AHRD V3.3 --* DEK1_MAIZE)					0,186	0,250	0,265	0,126	0,213									
Solyc06g072860	Glycosyltransferase (AHRD V3.3 *** M1DB11_SOLTU)		C:GO:0043231; F:G(	C:intracellular membrane-bounded organelle; F:quercetin 3-O-gl	G3DSA:3.40.50.2000 (GENE3D): G3D	0,121	0,076	0,000	0,000	0,000									
Solyc06g072865	Protein phosphatase 2C family protein (AHRD V3.3 --* AT2G46920.4)					0,057	0,037	0,000	0,025	0,047									
Solyc06g072880	Glycosyltransferase (AHRD V3.3 *** K4C908_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): IPR(	0,021	0,181	0,172	0,268	0,212									
Solyc06g072890	WUSCHEL-related homeobox (AHRD V3.3 *-* A0A0K9P0R2_ZOSMR)		F:GO:0003677	F:DNA binding	IPR001356 (SMAF WOX	0,183	0,290	0,050	0,000	0,118									
Solyc06g072900	60S ribosomal protein L13 (AHRD V3.3 *** A0A067JD82_JATCU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001380 (PFAM): PTHR11722:SF3	0,279	0,334	0,000	0,076	0,000									
Solyc06g072930	uncharacterized protein with two transmembrane helix		C:GO:0016021	C:integral component of membrane	PTHR34370:SF1 (PANTHER): PTHR3	10,068	10,332	9,527	7,996	9,017									
Solyc06g072940	auxin canalization protein (DUF828) (AHRD V3.3 *-* AT5G57770.1)				IPR013666 (PFAM): IPR008546 (PFA	0,061	0,060	0,000	0,025	0,000									
Solyc06g072950	ABC transporter B family protein (AHRD V3.3 *** G7J9Q4_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:int EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF	1,033	0,844	1,137	1,610	1,156									
Solyc06g072970	Zinc finger with UFM1-specific peptidase domain protein (AHRD V3.3 *** A0A0B2SPL0_GLYSO)				IPR012462 (PFAM): G3DSA:3.90.70.1	4,534	3,740	5,736	5,138	5,712									
Solyc06g072980	Autophagy-related protein 13 (AHRD V3.3 *** A0A103XD03_CYNCS)		P:GO:0000045; C:G(	P:autophagosome assembly; C:Atg1/ULK1 kinase complex	IPR036570 (G3DSA:3.30.900.GENE3	21,382	26,438	40,621	42,171	39,951									
Solyc06g072990	LOW QUALITY:Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)		P:GO:0098869	P:cellular oxidant detoxification	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,038	0,101	0,175	0,293	0,188									
Solyc06g073010	PGPS/D3 (AHRD V3.3 *** Q9ZTN4_PETHY)		P:GO:0044237	P:cellular metabolic process	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc06g073020	Serine protease inhibitor, Kazal-type family protein (AHRD V3.3 *** D7LSR6_ARALL)		C:GO:0016021	C:integral component of membrane	G3DSA:3.30.60.30 (GENE3D): PTHR3	3,819	3,677	4,481	5,251	3,960									
Solyc06g073030	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT5G54100.1)		C:GO:0016020	C:membrane	IPR001972 (PRINTS): G3DSA:3.30.47	0,042	0,000	0,000	0,000	0,047									
Solyc06g073037	Ovate family protein 5 (AHRD V3.3 *** A0A061G3I6_THECC)		P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (PFAM): IPR038933 (PAN	0,000	0,265	0,000	0,000	0,000									
Solyc06g073050	NAC domain-containing protein	NAC060	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM NAC	193,973	138,231	77,938	142,011	126,353			0,694	0,003	0,867	0,000		up	up
Solyc06g073055	LOW QUALITY:DNA repair protein reca, putative (AHRD V3.3 --* B9SVD4_RICCO)					0,118	0,119	0,000	0,149	0,116									
Solyc06g073060	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9S5P0_RICCO)		F:GO:0016787	F:hydrolase activity	IPR002933 (PFAM): IPR017439 (PIRS	4,369	4,180	14,800	12,122	13,127									
Solyc06g073070	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G24580.4)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding	IPR006121 (PFAM): G3DSA:3.30.70.1	0,021	0,018	0,075	0,100	0,000									
Solyc06g073080	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G24530.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR027443 (G3D	0,238	1,040	0,288	1,190	0,990									
Solyc06g073090	chloroplast-specific ribosomal protein chloroplast-specific ribosomal protein		P:GO:0044238	P:primary metabolic process	IPR038416 (G3DSA:3.30.505.GENE3	22,143	34,028	31,446	37,069	49,639	0,648	0,024	0,656	0,000			up	up	
Solyc06g073110	DUF936 family protein (AHRD V3.3 *** G7JEV5_MEDTR)				IPR010341 (PFAM): mobidb-lite (MOB	36,891	37,883	26,900	28,245	24,953									
Solyc06g073120	Ribosomal RNA processing protein 36 like (AHRD V3.3 *** A0A0B2PAC6_GLYSO)		P:GO:0000469	P:cleavage involved in rRNA processing	IPR009292 (PFAM): mobidb-lite (MOB	28,662	32,754	20,168	22,756	19,169									
Solyc06g073130	RNA-binding ASCH domain protein (AHRD V3.3 *-* AT2G43465.1)				PTHR34204 (PANTHER)	0,905	0,872	1,006	1,402	1,344									
Solyc06g073133	RNA-binding ASCH domain protein (AHRD V3.3 *-* AT2G43465.6)				G3DSA:2.30.130.30 (GENE3D): PTHF	1,511	1,528	0,920	0,933	1,198									
Solyc06g073137	RNA-binding ASCH domain protein (AHRD V3.3 *** A0A072VD16_MEDTR)				IPR007374 (PFAM): G3DSA:2.30.130	4,659	4,935	3,549	3,559	4,209									
Solyc06g073140	Transmembrane protein, putative (AHRD V3.3 *** A0A072VMY8_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR31414:SF1 (PANTHER): IPR040	0,040	0,000	0,025	0,095	0,024									
Solyc06g073150	COP9 signalosome complex subunit 5b-like protein (AHRD V3.3 *** A0A0B0P622_GOSAR)		F:GO:0005515	F:protein binding	IPR000555 (SMART): IPR000555 (PF	1,776	2,350	2,981	2,367	1,619									
Solyc06g073160	COP9 signalosome complex subunit 5b-like protein (AHRD V3.3 *-* A0A0B0P622_GOSAR)		F:GO:0005515	F:protein binding	IPR000555 (SMART): IPR000555 (PF	7,375	6,416	5,104	5,972	5,111									
Solyc06g073165	LOW QUALITY:BURP domain-containing protein (AHRD V3.3 *-* AT1G23760.1)				IPR004873 (SMART): IPR004873 (PF	0,670	0,633	1,071	1,307	1,201									
Solyc06g073170	Armadillo repeat-containing protein 2 (AHRD V3.3 *** A0A1D1YSE7_9ARAE)		C:GO:0016021	C:integral component of membrane	PTHR36743 (PANTHER)	13,860	9,267	25,558	23,873	22,143									
Solyc06g073180	CONSTANS interacting protein 1	BBX24	F:GO:0008270	F:zinc ion binding	IPR000315 (SMAF DBB	38,102	31,131	33,973	38,907	40,914									
Solyc06g073190	fructokinase 2	frk2	F:GO:0016301	F:kinase activity	IPR002139 (PRINTS): IPR029056 (G3	270,051	297,204	125,160	126,846	146,956									
Solyc06g073200	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 *** AT3G59470.2)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR004330 (PFAM FAR1	0,042	0,021	0,025	0,051	0,046									
Solyc06g073210	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 *** AT3G59470.2)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR004330 (PFAM FAR1	4,101	4,001	2,362	1,555	2,228									
Solyc06g073230	tRNA-dihydrouridine synthase (AHRD V3.3 *** A0A061DPF2_THECC)		P:GO:0008033; F:G(	P:tRNA processing; F:tRNA dihydrouridine synthase activity; F:1	IPR001269 (PFAM): IPR013785 (G3D	14,431	14,954	13,648	13,303	13,395									
Solyc06g073240	Carbohydrate esterase plant-like protein (AHRD V3.3 *** A0A072W1E8_MEDTR)				IPR036514 (G3DSA:3.40.50.GENE3D	23,994	22,797	22,804	24,019	21,402									
Solyc06g073245	Calcium-binding protein (AHRD V3.3 *** Q9SCA1_LOTJA)		F:GO:0005509	F:calcium ion binding	PR01697 (PRINTS): IPR002048 (SMA	20,559	14,585	26,142	80,675	43,589			0,735	0,012	1,627	0,000		up	up
Solyc06g073250	LOW QUALITY:callose synthase 1 (AHRD V3.3 --* AT1G05570.4)					0,000	0,043	0,096	0,222	0,047									
Solyc06g073260	chloroplast RNA binding protein (AHRD V3.3 *** AT1G09340.1)		F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding	IPR001509 (PFAM): G3DSA:3.40.50.7	16,364	44,246	4,327	4,786	14,136	1,462	0,000	1,694	0,000			up	up	
Solyc06g073270	Golgi apparatus membrane protein TVP23 (AHRD V3.3 *** K4C946_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR008564 (PFAM): PTHR13019:SF1	33,569	30,424	35,978	31,447	29,943									
Solyc06g073280	Aminotransferase (AHRD V3.3 *** C1FDC5_MICCC)		F:GO:0008483; P:G(	F:transaminase activity; P:biosynthetic process; F:pyridoxal pho	IPR004839 (PFAM): IPR015421 (G3D	112,459	124,229	183,803	160,710	188,222									
Solyc06g073290	Tetrapyrrole-binding family protein (AHRD V3.3 *** B9HH58_POPTR)	GUN4	C:GO:0009507; P:G(	C:chloroplast; P:chloroplast-nucleus signaling pathway; F:tetrap	G3DSA:1.25.40.620 (GENE3D): G3DS	6,817	24,250	2,770	4,051	7,147	1,858	0,000	1,355	0,000			up	up	
Solyc06g073300	60S ribosomal protein L27 (AHRD V3.3 *** A0A0V0HNB9_SOLCH)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001141 (PFAM): IPR038655 (G3D	646,349	675,293	394,308	331,471	337,777									
Solyc06g073310	60S ribosomal protein l9 (AHRD V3.3 *** E5GBD5_CUCME)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR036789 (G3DSA:3.90.930.GENE3	312,142	345,882	265,532	234,570	236,310									
Solyc06g073320	GDP-L-galactose phosphorylase 1 (AHRD V3.3 *** AT4G26850.1)	GGP1	F:GO:0080048	F:GDP-D-glucose p EC:2.4.1.1; EC:2.7.7 Glycogen phosphoryl	mobidb-lite (MOBIDB_LITE): IPR0265(	577,442	640,925	703,760	722,800	728,180									
Solyc06g073330	Lysine--tRNA ligase (AHRD V3.3 *** K4C952_SOLLC)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:6.1.1.6 Lysine--tRNA ligase	IPR018149 (PRINTS): IPR004364 (PF	150,127	152,058	131,898	126,110	130,862									
Solyc06g073340	RING/U-box superfamily protein (AHRD V3.3 *** AT1G05890.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (SMART): G3DSA:1.20.12	41,430	35,870	50,742	46,588	44,588									
Solyc06g073350	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9T5K7_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR002048 (SMART): IPR000719 (SM	0,482	0,578	0,190	0,237	0,165									
Solyc06g073360	succinate dehydrogenase subunit (AHRD V3.3 *** AT5G62575.2)		C:GO:0005749	C:mitochondrial respiratory chain complex II, succinate dehydro	IPR034573 (PANTHER)	47,459	44,951	76,460	67,911	64,167									
Solyc06g073370	Ribosomal protein S13 (AHRD V3.3 *** A0A103XPA4_CYNCS)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR027437 (G3DSA:4.10.910.GENE3	120,122	145,086	133,598	115,170	116,504									
Solyc06g073380	Histidine protein methyltransferase (AHRD V3.3 *** A0A199VXX2_ANACO)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	PTHR14614 (PANTHER): PTHR14614	11,403	12,785	7,084	6,842	7,190									
Solyc06g073390	farnesyl protein transferase subunit A	fta	F:GO:0008318; P:G(	F:protein prenyltransferase activity; P:protein prenylation	G3DSA:1.25.40.120 (GENE3D): IPR0(	17,872	17,592	18,550	16,554	14,928									
Solyc06g073395	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G32430.2)					0,566	0,345	0,529	0,343	0,472									
Solyc06g073400	Endonuclease III homolog (AHRD V3.3 *** K4C959_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-(apurinic or apyrimidinic site) endonuclea	IPR003265 (SMART): IPR003651 (SM	9,150	9,911	9,183	9,546	8,995									
Solyc06g073410	gamma-secretase subunit APH1-like protein (AHRD V3.3 *** AT2G31440.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein processing; P:pos	IPR009294 (PFAM): IPR009294 (PAN	7,816	7,153	8,274	8,200	8,831									
Solyc06g073420	Inositol transporter 1	INT1	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): IPR005828 (PF	14,012	11,959	27,006	27,021	26,115									
Solyc06g073430	Ribosomal protein S3 (AHRD V3.3 --* A0A0K1ZDA3_9SOLA)		F:GO:0003735; F:G(	F:structural constituent of ribosome; F:zinc ion binding	G3DSA:4.10.830.10 (GENE3D): PTHF	357,066	370,361	256,817	280,942	256,009									
Solyc06g073450	DUF1685 family protein (AHRD V3.3 *** G7IB02_MEDTR)				IPR012881 (PFAM): mobidb-lite (MOB	44,251	51,158	46,234	41,475	41,099									
Solyc06g073455	RNA-binding CRS1 / YhbY (CRM) domain-containing protein (AHRD V3.3 --* AT4G31010.2)					0,021	0,000	0,025	0,047	0,047									
Solyc06g073460	phospholipid hydroperoxide glutathione peroxidase		F:GO:0004602; P:G(	F:glutathione peroxi EC:1.11.1.9; EC:1.1 Glutathione peroxida	IPR000889 (PRINTS): IPR000889 (PF	69,433	66,473	291,882	276,716	241,486									
Solyc06g073470	Biotin synthase (AHRD V3.3 *** BIOB_ARATH)		F:GO:0004076; P:G(	F:biotin synthase a EC:2.8.1.6 Biotin synthase	IPR006638 (SMART): IPR010722 (SM	23,176	25,727	37,796	38,748	40,969									
Solyc06g073480	Phototropic-responsive NPH3 family protein, putative (AHRD V3.3 *** A0A061EZT3_THECC)		F:GO:0005515	F:protein binding	IPR000210 (SMART): IPR027356 (PF	0,136	0,059	0,047	0,148	0,164									
Solyc06g073490	LOW QUALITY:Chaperone protein ClpB 2 (AHRD V3.3 *** A0A1D1YLY8_9ARAE)				mobidb-lite (MOBIDB_LITE): PTHR360	9,998	11,007	17,680	15,900	15,055									
Solyc06g073500	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT3G59300.1)				IPR037119 (G3DSA:3.20.180.GENE3	21,627	23,373	45,105	43,812	41,370									
Solyc06g073510	Origin recognition complex subunit 2 family protein (AHRD V3.3 *** U5GMP7_POPTR)		C:GO:0000808; C:G(	C:origin recognition complex; C:nucleus; P:DNA replication	IPR007220 (PFAM): IPR007220 (PAN	0,479	0,462	0,779	0,918	0,611									
Solyc06g073520	Solute carrier family 35 protein (AHRD V3.3 *** G7KWQ4_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR009262 (PFAM): mobidb-lite (MOB	6,504	5,895	12,921	17,796	14,555									
Solyc06g073530	Argonaute4c	AGO4c	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding	IPR014811 (SMART): IPR003165 (SM	0,000	0,021	0,000	0,000	0,000									
Solyc06g073540	Argonaute4b	AGO4b	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding	IPR003165 (SMART): IPR014811 (SM	212,739	190,597	120,761	125,808	140,040									
Solyc06g073550	La-related protein (AHRD V3.3 *** A0A0B2S1Z3_GLYSO)		F:GO:0003723	F:RNA binding	IPR006630 (SMART): IPR006607 (SM	74,679	70,709	63,871	63,211	66,284									
Solyc06g073560	Acyl-CoA dehydrogenase, putative (AHRD V3.3 *** B9SK49_RICCO)		F:GO:0003995; F:G(	F:acyl-CoA dehydrc EC:1.3.99.3 Acting on the CH-CH	IPR013786 (PFAM): G3DSA:2.40.110	0,040	0,043	0,000	0,000	0,000									
Solyc06g073580	1-aminocyclopropane-1-carboxylate oxidase1	ACCO1	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM): IPR026992 (PFA	0,019	0,000	0,000	0,000	0,000									
Solyc06g073600	Ubiquitin-associated/translation elongation factor EF1B protein (AHRD V3.3 *** A0A061GSV5_THECC)		F:GO:0005515; F:G(	F:protein binding; F:channel activity; C:membrane; P:transmemb	IPR000425 (PRINTS): IPR015940 (SM	71,892	82,006	84,178	77,435	77,762									
Solyc06g073610	cyclin B1	cycb1	C:GO:0005634	C:nucleus	IPR004367 (SMART): IPR013763 (SM	1,274	1,170	1,294	1,045	1,106									
Solyc06g073620	Molybdopterin synthase catalytic subunit (AHRD V3.3 *** K4C981_SOLLC)		C:GO:0005829; P:G(	C:cytosol; P:Mo-mc EC:2.8.1.12 Molybdopterin syntha	IPR003448 (PFAM): IPR036563 (G3D	0,000	0,021	0,022	0,000	0,000									
Solyc06g073630	cyclin-dependent kinase C-1 (AHRD V3.3 *** AT5G10270.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	58,943	51,987	96,099	86,756	85,169									
Solyc06g073640	GAMYB-like2	R2R3MYB33	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	2,388	3,311	1,244	1,282	1,271									
Solyc06g073650	F-box/WD-40 repeat-containing protein (AHRD V3.3 *** W9R2N4_9ROSA)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR001810 (SM	11,368	12,165	15,775	14,130	15,284									
Solyc06g073660	Lipid transfer protein (AHRD V3.3 *** B7FFE5_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding; C:integral component of membra	IPR016140 (SMART): IPR016140 (PF	5,363	5,384	1,744	0,972	1,599									
Solyc06g073670	Protein FAR1-RELATED SEQUENCE 3 (AHRD V3.3 *** W9R5U7_9ROSA)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding	IPR006564 (SMAF FAR1	43,633	36,940	54,204	53,821	50,463									
Solyc06g073680	Transducin/WD40 repeat protein (AHRD V3.3 *** G7KFW3_MEDTR)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR001680 (PF	8,400	9,137	5,140	5,332	5,157									
Solyc06g073700	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT1G65700.2)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U6 snRNP; C:U4/U6 x U5	IPR001163 (SMART): IPR001163 (PF	36,026	35,354	47,267	41,235	43,711									
Solyc06g073710	Glucan endo-1,3-beta-glucosidase 14 (AHRD V3.3 *** A0A151SPX1_CAJCA)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D): IPR00(	2,692	2,667	3,748	3,226	2,774									
Solyc06g073720	EIL1	EIL1	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus	IPR023278 (G3DS EIL	169,355	143,290	112,718	110,474	108,902									
Solyc06g073730	LeEIL4EIN3-like	EIL4	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus	IPR006957 (PFAM EIL	181,415	199,803	138,006	141,438	124,292									
Solyc06g073740	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001764 (PRINTS): IPR036881 (G3	121,674	105,783	172,440	190,176	152,493									
Solyc06g073760	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001764 (PRINTS): IPR036962 (G3	3,861	5,685	4,587	5,286	6,995									
Solyc06g073770	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 --* A0A0E0EUK8_9ORYZ)					0,000	0,000	0,000	0,000	0,023									
Solyc06g073780	SMC3	SMC3	F:GO:0005515; F:G(	F:protein binding; F:ATP binding; C:chromosome; P:chromosom	IPR010935 (SMART): IPR010935 (PF	137,168	113,265	104,370	98,070	102,173									
Solyc06g073790	40s ribosomal protein S11 (AHRD V3.3 *** K7XKQ3_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000266 (PRINTS): IPR028333 (TI(	70,991	71,169	61,914	53,748	56,382									
Solyc06g073800	40s ribosomal protein S11 (AHRD V3.3 *** K7XKQ3_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000266 (PRINTS): IPR028333 (TI(	0,038	0,062	0,171	0,050	0,071									
Solyc06g073810	40s ribosomal protein S11 (AHRD V3.3 *-* K7XKQ3_SOLTU)		F:GO:0003676; F:G(	F:nucleic acid binding; F:structural constituent of ribosome; C:ril	IPR000266 (PRINTS): IPR001878 (SM	19,694	21,928	24,579	23,062	22,203									
Solyc06g073820	Ubiquitin carboxyl-terminal hydrolase 12-like protein (AHRD V3.3 *** A0A0B0PTR8_GOSAR)		F:GO:0005515; P:G(	F:protein binding; P EC:3.4.19.12 Ubiquitinyl hydrolase	IPR002083 (SMART): IPR001394 (PF	0,920	1,009	0,762	0,807	1,161									
Solyc06g073830	Calcium-binding protein (AHRD V3.3 *** A0A199V9T9_ANACO)		F:GO:0005509	F:calcium ion binding	IPR002048 (SMART): IPR002048 (PF	3,517	11,028	2,276	0,617	1,312	1,672	0,002					up		
Solyc06g073840	Peptidyl-prolyl cis-trans isomerase, FKBP-type (AHRD V3.3 *** A0A103YFM3_CYNCS)		F:GO:0005515	F:protein binding	IPR019734 (SMART): IPR001440 (PF	66,583	89,319	84,217	101,564	83,858									
Solyc06g073860	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G02290.6)		F:GO:0016874	F:ligase activity	IPR001841 (SMART): IPR013083 (G3	36,930	49,057	40,720	48,306	45,120									
Solyc06g073870	DNA-directed RNA polymerase II subunit RPB4 (AHRD V3.3 *** A0A0B2RF86_GLYSO)		F:GO:0000166; F:G(	F:nucleotide binding; F:catalytic activity; P:DNA-templated trans	IPR006590 (SMART): IPR005574 (PF	53,088	54,731	91,774	81,499	81,023									
Solyc06g073880	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G15790.4)		F:GO:0016874	F:ligase activity	IPR001841 (SMART): IPR001841 (PF	19,246	22,980	25,400	27,037	26,512									
Solyc06g073890	E3 ubiquitin-protein ligase RHF2A (AHRD V3.3 *-* RHF2A_ARATH)		F:GO:0016874	F:ligase activity	mobidb-lite (MOBIDB_LITE): mobidb-lit	7,569	9,241	11,358	10,986	9,375									
Solyc06g073900	Succinate dehydrogenase subunit 6, mitochondrial (AHRD V3.3 *** SDH6_ARATH)		C:GO:0005749	C:mitochondrial respiratory chain complex II, succinate dehydro	IPR034574 (PANTHER)	135,917	116,680	230,472	184,680	197,307									
Solyc06g073910	Strictosidine synthase, putative (AHRD V3.3 *** B9RJ21_RICCO)		P:GO:0009058; F:G(	P:biosynthetic proc EC:4.3.3.2 Strictosidine synthas	IPR018119 (PFAM): IPR011042 (G3D	9,986	9,498	5,185	4,209	5,109									
Solyc06g073920	CRABS CLAW-like protein 2a	YABBY2a	P:GO:0007275	P:multicellular organism development	IPR036910 (G3DS YABBY	155,535	116,367	187,394	208,365	177,868									
Solyc06g073930	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9RQ57_RICCO)		P:GO:0016579; F:G(	P:protein deubiquiti EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	16,325	14,409	21,790	23,091	20,460									
Solyc06g073940	Protein FAF-like, chloroplastic (AHRD V3.3 *** A0A0B2RVL4_GLYSO)				IPR021410 (PFAM): mobidb-lite (MOB	18,726	12,916	4,402	4,668	4,548									
Solyc06g073950	DnaJ domain containing protein, expressed (AHRD V3.3 *** Q10NS2_ORYSJ)				IPR001623 (PRINTS): IPR001623 (SM	4,015	2,975	6,234	4,998	4,668									
Solyc06g073960	Serine/threonine-protein phosphatase (AHRD V3.3 *** K4C9B4_SOLLC)		F:GO:0004721; F:G(	F:phosphoprotein pl EC:3.1.3.16 Protein-serine/threor	IPR006186 (PRINTS): IPR006186 (SM	31,641	30,186	37,190	36,062	36,093									
Solyc06g073970	core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT3G52060.1)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM): PTHR31042 (PAI	80,069	66,193	120,088	83,237	96,943					-0,526	0,003			down
Solyc06g073980	B3 domain-containing protein (AHRD V3.3 *-* A0A199VRZ0_ANACO)		F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	3,537	3,169	1,829	1,579	1,507									
Solyc06g073990	Gb:AAF02129.1, putative (AHRD V3.3 *** A0A061GVZ4_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,929	1,384	1,634	1,366	0,959									
Solyc06g074000	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G52500.1)		F:GO:0004190; P:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	20,736	13,494	0,177	0,228	0,142									
Solyc06g074010	Transcription factor (E2F) (AHRD V3.3 *** Q9FNS0_OXYRB)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:transcription facto	IPR003316 (SMAF E2F/DP	13,616	9,708	8,920	8,213	7,512									
Solyc06g074020	LOW QUALITY:ovate family protein12	OFP12	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (PFAM): IPR006458 (TIGF	0,040	0,000	0,000	0,000	0,000									
Solyc06g074030	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT3G44260.1)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.13; EC:3.1.1! Acting on ester bonds	IPR006941 (PFAM): IPR036397 (G3D	232,033	70,547	48,876	182,644	68,166	-1,694	0,000			1,905	0,000	down		up
Solyc06g074040	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G44220.1)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore	IPR004864 (PFAM): PTHR31415:SF2	0,391	0,554	0,025	0,162	0,189									
Solyc06g074050	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *-* AT2G27260.1)		C:GO:0016021	C:integral component of membrane	IPR004864 (PFAM): PTHR31852:SF2	16,080	13,864	10,534	12,351	10,983									
Solyc06g074070	Receptor-kinase-like protein (AHRD V3.3 *** A0A072U3D4_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR003591 (SMART): IPR000719 (SM	43,680	44,989	1,311	1,842	1,975									
Solyc06g074080	Histone deacetylase, putative (AHRD V3.3 *** B9SD06_RICCO)		C:GO:0005634; F:G(	C:nucleus; F:NAD-d EC:3.5.1.98 Histone deacetylase	IPR000286 (PRINTS): IPR023801 (PF	24,595	19,481	25,193	24,537	25,347									
Solyc06g074090	Sterol delta-7 reductase (AHRD V3.3 *** Q6S5A3_TROMA)		C:GO:0016020	C:membrane	IPR001171 (PFAM): PTHR21257:SF3	19,651	22,829	9,760	8,943	11,442									
Solyc06g074110	BHLH transcription factor-like protein (AHRD V3.3 *-* A0A072UK41_MEDTR)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR025610 (PFAM): mobidb-lite (MOB	9,810	10,308	4,075	4,179	3,759									
Solyc06g074120	bell-like homeodomain protein 2	bl2	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR001356 (SMAF TALE	121,381	96,578	194,997	211,638	182,432									
Solyc06g074130	Growth inhibition and differentiation-related protein 88 like (AHRD V3.3 *** A0A0B2QEC7_GLYSO)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	10,340	11,453	15,360	14,373	13,226									
Solyc06g074140	LOW QUALITY:U-box domain-containing family protein (AHRD V3.3 *** B9IIL0_POPTR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR003613 (SMART): IPR011989 (G3	0,061	0,524	0,100	0,050	0,000									
Solyc06g074150	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PTR8_ZOSMR)		F:GO:0005515	F:protein binding	IPR013210 (PFAM): IPR032675 (G3D	0,019	0,043	0,000	0,000	0,024									
Solyc06g074160	B3 domain-containing protein (AHRD V3.3 *** M8CP43_AEGTA)		F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	0,019	0,021	0,000	0,000	0,000									
Solyc06g074170	NAC domain protein, (AHRD V3.3 *** A0A061GVZ7_THECC)	NAC061	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	0,909	1,283	1,272	1,522	1,434									
Solyc06g074190	Plant/F24K9-26 protein (AHRD V3.3 *** A0A072UED0_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	16,189	13,169	8,040	12,521	12,064					0,639	0,025			up
Solyc06g074200	photosystem I subunit O (AHRD V3.3 *** AT1G08380.1)		C:GO:0009507; C:G(	C:chloroplast; C:photosystem I; P:photosynthetic electron trans	IPR017498 (TIGRFAM): IPR017498 (F	119,637	305,698	39,820	71,930	133,700	1,381	0,001	1,744	0,000	0,857	0,000	up	up	up
Solyc06g074210	mRNA-decapping enzyme-like protein (AHRD V3.3 *** A0A0B2REC5_GLYSO)		P:GO:0000290; F:G(	P:deadenylation-dependent decapping of nuclear-transcribed ml	IPR011993 (G3DSA:2.30.29.GENE3D	147,349	103,704	86,130	76,674	78,226									
Solyc06g074220	OTU-like cysteine protease family protein (AHRD V3.3 *** B9HQ41_POPTR)		F:GO:0004843; F:G(	F:thiol-dependent ul EC:3.4.19.12 Ubiquitinyl hydrolase	IPR003323 (PFAM): G3DSA:3.90.70.8	60,877	59,166	63,400	60,060	61,377									
Solyc06g074230	CASP-like protein (AHRD V3.3 *** K4C9E1_SOLLC)		C:GO:0005886; P:G(	C:plasma membrane; P:cell-cell junction assembly; C:integral co	IPR006459 (TIGRFAM): IPR006702 (F	0,000	0,000	0,000	0,000	0,024									
Solyc06g074240	Beta-carotene	CYCβ	C:GO:0016021; P:G(	C:integral component of membrane; P:carotenoid biosynthetic p	IPR010908 (SMART): IPR001388 (PF	5,528	4,585	2,424	3,576	3,199									
Solyc06g074250	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9SCW7_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS): IPR010908 (SM	3,011	2,654	4,570	4,735	4,048									
Solyc06g074260	pollen proteins Ole e I-like				PF01190 (PFAM): PTHR33083 (PANT	1956,459	967,000	5,122	2,292	4,500	-0,988	0,018			-1,154	0,022	down		down
Solyc06g074300	5'-3' exonuclease family protein (AHRD V3.3 --* AT3G28030.4)					2,469	2,895	2,970	3,037	1,917									
Solyc06g074310	Transmembrane 9 superfamily member (AHRD V3.3 *** K4C9E9_SOLLC)		F:GO:0009055; C:G(	F:electron transfer activity; C:integral component of membrane;	IPR028364 (PFAM): IPR004240 (PFA	13,948	12,224	8,709	8,309	9,605									
Solyc06g074320	BZIP family transcription factor family protein (AHRD V3.3 *** B9HQ02_POPTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc	IPR004827 (SMAF bZIP	0,618	0,661	0,654	0,672	0,632									
Solyc06g074330	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G44510.2)				IPR029058 (G3DSA:3.40.50.GENE3D	4,035	3,537	4,463	4,105	4,379									
Solyc06g074360	TRANSPARENT TESTA 1 protein, putative (AHRD V3.3 *** B9SCR9_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	0,119	0,240	0,096	0,076	0,143									
Solyc06g074370	Sialyltransferase, putative (AHRD V3.3 *** A0A061GVE5_THECC)		P:GO:0006486; F:G(	P:protein glycosylat EC:2.4.99 Glycosyltransferases	IPR038578 (G3DSA:3.90.1480.GENE	5,250	3,465	2,264	1,448	1,939									

Solyc06g074380	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G27590.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,779	14,116	13,893	12,343	12,779									
Solyc06g074390	Fatty acyl-CoA reductase (AHRD V3.3 *** K4C9F7_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			IPR033640 (PFAM): IPR013120 (PFA	1,098	1,591	0,337	0,419	0,376									
Solyc06g074400	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** W9R5G8_9ROSA)		F:GO:0005515	F:protein binding			G3DSA:3.40.50.11980 (GENE3D): IPF	21,284	21,382	19,787	16,443	17,488									
Solyc06g074420	Cytochrome P450 family protein (AHRD V3.3 *** B9HQW0_POPTR)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,599	0,998	0,215	0,125	0,048									
Solyc06g074430	60s acidic ribosomal protein-like protein (AHRD V3.3 *** Q3HVP0_SOLTU)		F:GO:0003735: C:G(	F:structural constituent of ribosome: C:ribosome: P:translationa			IPR038716 (G3DSA:1.10.10.GENE3D	96,129	111,458	80,315	73,725	73,643									
Solyc06g074450	Protein FRIGIDA-like protein (AHRD V3.3 *** A0A0B0P3W9_GOSAR)		P:GO:0032502	P:developmental process			IPR012474 (PFAM): mobidb-lite (MOB	10,124	10,418	10,607	10,474	10,180									
Solyc06g074463	Peroxisome biogenesis protein 16 (AHRD V3.3 *-* A0A0B2P914_GLYSO)		C:GO:0005778: P:G(	C:peroxisomal membrane; P:peroxisome organization; C:integral			component of membrane	0,805	1,324	1,125	1,207	1,274									
Solyc06g074467	Peroxisome biogenesis 16-like protein (AHRD V3.3 *** A0A0B0MSZ8_GOSAR)		C:GO:0005778: P:G(	C:peroxisomal membrane: P:peroxisome organization: C:integra			IPR013919 (PFAM): mobidb-lite (MOB	5,710	4,682	5,825	6,336	6,432									
Solyc06g074470	B-block-binding subunit of tfiiic protein, putative (AHRD V3.3 --* A0A072USI4_MEDTR)							0,258	0,188	0,072	0,143	0,142									
Solyc06g074480	Protein kinase (AHRD V3.3 *-* A0A0K9NMI8_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	21,175	24,032	22,837	22,259	21,612									
Solyc06g074500	DUF868 family protein (AHRD V3.3 *** G7JKY7_MEDTR)						IPR008586 (PFAM): IPR008586 (PAN	0,021	0,081	0,000	0,000	0,000									
Solyc06g074510	Phosphoglycerate mutase, putative (AHRD V3.3 *** B9T5T3_RICCO)		F:GO:0003824: C:G(	F:catalytic activity; C:cytoplasm			IPR013078 (SMART): IPR013078 (PF.	7,206	15,192	8,061	9,173	14,898	1,102	0,000	0,880	0,000			up	up	
Solyc06g074530	Arogenate dehydratase (AHRD V3.3 *** K4C9H1_SOLLC)		F:GO:0004664: P:G(	F:prephenate dehyc	EC:4.2.1.51	Prephenate dehydrat	IPR001086 (PFAM): G3DSA:3.30.70.2	170,271	156,453	30,044	33,102	38,256									
Solyc06g074540	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)		C:GO:0005576: F:G(	C:extracellular region: F:growth factor activity: P:cell population			IPR009438 (PFAM): IPR009438 (PAN	1,340	0,922	0,093	0,000	0,000									
Solyc06g074550	LOW QUALITY:Histone-lysine N-methyltransferase ATX5 (AHRD V3.3 --* ATX5_ARATH)							4,313	3,896	0,729	0,951	1,037									
Solyc06g074560	LOW QUALITY:GATA transcription factor 19 (AHRD V3.3 --* AT4G36620.1)						mobidb-lite (MOBIDB_LITE)	0,236	0,280	0,075	0,170	0,072									
Solyc06g074570	LOW QUALITY:ATP synthase subunit alpha (AHRD V3.3 --* A8VRN0_9SPER)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR331	0,058	0,018	0,022	0,073	0,024									
Solyc06g074580	LOW QUALITY:Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT2G43700.5)							0,000	0,064	0,000	0,050	0,000									
Solyc06g074600	LOW QUALITY:DNA-directed RNA polymerase subunit beta" (AHRD V3.3 *-* RPOC2_SOLLC)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.6	DNA-directed RNA polymerase		0,019	0,083	0,000	0,099	0,023									
Solyc06g074620	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT4G29930.2)						PTHR33270:SF3 (PANTHER): IPR040	72,907	38,168	33,249	60,070	32,664	-0,909	0,011			0,854	0,000	down		up
Solyc06g074630	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)		C:GO:0016021: F:G(	C:integral component of membrane: F:transferase activity, trans			IPR029044 (G3DSA:3.90.550.GENE3I	25,944	22,993	3,939	3,043	3,373									
Solyc06g074640	PHD finger family protein (AHRD V3.3 *** AT5G22760.1)		F:GO:0046872	F:metal ion binding			IPR018501 (SMART): IPR001965 (SM	0,816	0,869	0,093	0,245	0,283									
Solyc06g074650	AP-2 complex subunit alpha-1 (AHRD V3.3 *** AP2A1_ARATH)		P:GO:0006886: C:G(	P:intracellular protein transport: C:AP-2 adaptor complex: F:clatl			IPR008152 (SMART): IPR012295 (G3	51,890	50,032	44,085	48,822	45,378									
Solyc06g074670	UDP-apiose/xylose synthase (AHRD V3.3 *** Q2I2N3_SOLTU)		F:GO:0003824: F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	127,908	157,787	27,000	34,178	55,572			1,038	0,015				up	
Solyc06g074680	phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** AT5G13640.1)		P:GO:0006629: F:G(	P:lipid metabolic process; F:O-acyltransferase activity			IPR029058 (G3DSA:3.40.50.GENE3D	1,317	1,547	0,292	0,493	0,729									
Solyc06g074690	ARM repeat superfamily protein (AHRD V3.3 *** AT5G22820.3)						IPR011989 (G3DSA:1.25.10.GENE3D	16,471	14,503	14,716	15,515	15,050									
Solyc06g074700	Kinase family protein (AHRD V3.3 *** B9MYL8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	54,343	51,343	51,468	49,286	48,841									
Solyc06g074710	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (AHRD V3.	HCT	F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3I	18,907	24,461	216,078	287,577	189,608					0,416	0,031			up
Solyc06g074720	RNA binding protein-like protein (AHRD V3.3 *** Q2VCH8_SOLTU)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	481,482	429,193	378,398	362,029	331,281									
Solyc06g074730	Argonaute 5	AGO.5	F:GO:0003676: F:G(	F:nucleic acid binding; F:protein binding			IPR003165 (SMART): IPR003100 (SM	23,392	21,276	1,689	1,589	4,185									
Solyc06g074740	LEU86662_VPS41	tvps41	F:GO:0005515: P:G(	F:protein binding: P:intracellular protein transport: P:vesicle-mec			IPR000547 (SMART): IPR001680 (SM	46,369	43,022	56,278	53,470	55,577									
Solyc06g074760	Ring/U-Box superfamily protein (AHRD V3.3 *** AT2G27950.3)						PF13920 (PFAM): IPR013083 (G3DS/	0,637	0,575	0,806	0,727	0,801									
Solyc06g074770	U-box domain-containing protein (AHRD V3.3 *** AT5G15400.1)		C:GO:0000151: P:G(	C:ubiquitin ligase complex: P:ubiquitin-dependent protein catabo			IPR003613 (SMART): IPR013083 (G3	1,207	1,294	1,234	0,919	1,176									
Solyc06g074780	Histone H2B (AHRD V3.3 *** K4C9J5_SOLLC)		C:GO:0000786: F:G(	C:nucleosome: F:DNA binding: F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	42,776	40,069	71,294	57,698	50,666			-0,495	0,010				down	
Solyc06g074790	Histone H2B (AHRD V3.3 *** M1AAN4_SOLTU)		C:GO:0000786: F:G(	C:nucleosome: F:DNA binding: F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	25,598	27,074	8,350	3,933	5,255					-1,077	0,000			down
Solyc06g074800	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HQP7_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,676	0,726	0,454	0,432	0,329									
Solyc06g074810	Protein SMG8 (AHRD V3.3 *** A0A0B0MQ28_GOSAR)		P:GO:0000184	P:nuclear-transcribed mRNA catabolic process, nonsense-medi			IPR019354 (PFAM): mobidb-lite (MOB	15,714	12,069	14,952	15,951	15,502									
Solyc06g074820	tonoplast intrinsic protein 1.1	TIP1.1	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	181,293	173,390	35,496	42,011	49,265									
Solyc06g074840	Vacuolar protein sorting-associated protein 24 like 1 (AHRD V3.3 *** A0A0B2QEZ9_GLYSO)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): mobidb-lite (MOB	31,220	52,453	23,917	23,226	24,008									
Solyc06g074850	Carboxypeptidase (AHRD V3.3 *** K4C9K1_SOLLC)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR029058 (G3	0,257	0,263	0,197	0,050	0,024									
Solyc06g074855	Sister chromatid cohesion 1 protein 1 (AHRD V3.3 *-* SCC11_ARATH)		F:GO:0005515: P:G(	F:protein binding: P:sister chromatid cohesion: C:cohesin comp			IPR006910 (PFAM): mobidb-lite (MOB	0,000	0,142	0,022	0,000	0,000									
Solyc06g074870	Sister chromatid cohesion 1 protein 1 (AHRD V3.3 *** A0A0B2RVU6_GLYSO)		P:GO:0006457: P:G(	P:protein folding: P:sister chromatid cohesion: C:cohesin compl			IPR036611 (G3DSA:3.30.70.GENE3D	7,293	12,465	1,774	1,908	4,304			1,264	0,018				up	
Solyc06g074900	Trigger factor (AHRD V3.3 *** A0A0B0P5P6_GOSAR)		P:GO:0006457: P:G(	P:protein folding; P:protein transport			IPR036611 (G3DSA:3.30.70.GENE3D	4,142	5,036	2,683	2,609	3,644									
Solyc06g074905	26S proteasome regulatory subunit Rpn7 (AHRD V3.3 --* AT4G24820.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane				1,385	1,632	0,719	0,750	1,079									
Solyc06g074930	LOW QUALITY:Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G60800.1)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	0,021	0,000	0,000	0,000	0,000									
Solyc06g074940	ABC transporter family protein (AHRD V3.3 *** AT5G60790.1)	ABCF2	F:GO:0005524: F:G(	F:ATP binding: F:AT	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	34,201	47,752	73,662	69,311	70,859									
Solyc06g074950	Small auxin up-regulated RNA62	SAUR62	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF1(	0,000	0,061	0,000	0,000	0,000									
Solyc06g074960	ABC transporter family protein (AHRD V3.3 *** A0A097P9Q7_HEVBR)		F:GO:0005524: C:G(	F:ATP binding: C:m(	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	26,657	22,011	14,025	13,989	15,008									
Solyc06g074980	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524: F:G(	F:ATP binding; F:hydrolase activity			IPR003593 (SMART): IPR004201 (SM	564,521	475,559	519,637	480,945	501,227									
Solyc06g074990	putative high affinity nitrate transporter 2	nrt2c2	C:GO:0016021: P:G(	C:integral component of membrane: P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,084	0,107	0,000	0,025	0,047									
Solyc06g075000	(R)-specific enoyl-CoA hydratase (AHRD V3.3 *** W9RN50_9ROSA)		C:GO:0005739: P:G(	C:mitochondrion: P:	EC:4.2.1.59	3-hydroxyacyl-[acyl-(	IPR002539 (PFAM): G3DSA:3.10.129	1,470	1,367	2,063	1,721	1,818									
Solyc06g075010	Chaperonin 60 alpha subunit (AHRD V3.3 *** Q9ZTV1_CANLI)		F:GO:0005524: C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR027413 (G3	27,376	25,756	11,385	6,407	8,604					-0,829	0,004			down
Solyc06g075020	ABC transporter G family-like protein (AHRD V3.3 *** A0A072UJT7_MEDTR)	ABCG60	F:GO:0005524: F:G(	F:ATP binding: F:AT	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	0,000	0,000	0,050	0,025	0,024									
Solyc06g075030	LOW QUALITY:Kinase family protein (AHRD V3.3 *** A9P9S2_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	9,351	9,730	7,638	5,968	7,082									
Solyc06g075040	Auxin efflux carrier family protein (AHRD V3.3 --* AT1G23080.4)						mobidb-lite (MOBIDB_LITE): PS51257	0,165	0,085	0,000	0,070	0,000									
Solyc06g075070	Carbonic anhydrase (AHRD V3.3 *** B6T9W3_MAIZE)		F:GO:0004089: F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001148 (SMART): IPR001148 (PF.	1,843	2,546	0,288	0,172	0,308									
Solyc06g075080	Nudix family hydrolase (AHRD V3.3 *** A0A072V814_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR020476 (PRINTS): G3DSA:3.90.79	57,651	63,218	44,995	43,767	57,933									
Solyc06g075090	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** I0IUQ4_SOLLC)		C:GO:0005634: C:G(	C:nucleus: C:cytosol: P:cytokinin biosynthetic process: F:hydro			IPR005269 (TIGRFAM): G3DSA:3.40.!	0,019	0,000	0,000	0,025	0,000									
Solyc06g075100	Glycosyl transferase, family 2 (AHRD V3.3 *** A0A124SHF0_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR029044 (G3DSA:3.90.550.GENE3I	0,433	0,156	0,364	0,614	0,306									
Solyc06g075110	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		C:GO:0016021	C:integral component of membrane			IPR007877 (PFAM): PTHR31210:SF3(	39,335	36,793	45,496	45,154	42,460									
Solyc06g075130	Pleckstrin-like (PH) and lipid-binding START domain protein (AHRD V3.3 *** G7IRU5_MEDTR)		F:GO:0008289	F:lipid binding			IPR002913 (SMART): IPR001849 (SM	5,823	7,117	1,182	0,366	1,178									
Solyc06g075140	GATA transcription factor (AHRD V3.3 *-* A0A0J8C2J7_BETVU)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of transc			IPR000679 (SMAF GATA	0,255	0,200	0,000	0,000	0,000									
Solyc06g075150	Auxin Response Factor 10B	ARF10B	F:GO:0003677: F:G(	F:DNA binding: F:protein binding: C:nucleus: P:regulation of tran			IPR003340 (SMAF ARF	15,425	12,673	26,694	22,384	24,743									
Solyc06g075160	SIT4 phosphatase-associated family protein (AHRD V3.3 *** B9HQ89_POPTR)						IPR007587 (PFAM): mobidb-lite (MOB	36,330	33,077	25,512	30,126	29,739									
Solyc06g075170	Senescence regulator (AHRD V3.3 *** A0A103XHC6_CYNCS)						IPR007608 (PFAM): mobidb-lite (MOB	5,468	6,754	7,675	4,810	6,711									
Solyc06g075180	60S ribosomal protein L12 (AHRD V3.3 *** K7WTX4_SOLTU)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000911 (SMART): IPR020783 (PF.	219,154	210,724	48,425	39,031	48,412									
Solyc06g075190	LOW QUALITY:Methyltransferase-related protein (AHRD V3.3 *** AT5G18150.1)		F:GO:0008168: F:G(	F:methyltransferase activity: F:transferase activity: P:methylatio			mobidb-lite (MOBIDB_LITE): mobidb-lit	26,082	20,148	10,826	14,444	12,320									
Solyc06g075210	Protein disulfide-isomerase (AHRD V3.3 *** M1AE79_SOLTU)		F:GO:0003756: P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	IPR005792 (TIGRFAM): G3DSA:3.40.:	0,040	0,043	0,025	0,076	0,046									
Solyc06g075220	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7L2R9_MEDTR)		C:GO:0005886: P:G(	C:plasma membrane: P:response to salt stress: P:response to a			IPR000782 (SMART): IPR036378 (G3	0,646	0,922	0,025	0,025	0,024									
Solyc06g075250	Zinc finger family protein (AHRD V3.3 *** S8C619_9LAMI)		F:GO:0003676: F:G(	F:nucleic acid binding: F:DNA-binding transcription factor activit			IPR013087 (SMAF C2H2	79,593	78,706	52,009	58,511	58,961									
Solyc06g075260	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** A0A0B0PUP3_GOSAR)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR014710 (G3	0,019	0,043	0,000	0,000	0,000									
Solyc06g075270	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** W9SCA8_9ROSA)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR014710 (G3	0,590	0,353	0,115	0,050	0,305									
Solyc06g075280	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** W9SCA8_9ROSA)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR006045 (PF.	0,019	0,039	0,000	0,000	0,000									
Solyc06g075290	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** W9SCA8_9ROSA)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR006045 (PF.	0,251	0,246	0,075	0,025	0,096									
Solyc06g075310	Adenylate kinase isoenzyme 6 homolog (AHRD V3.3 *** M1ABZ6_SOLTU)		F:GO:0004017: F:G(	F:adenylate kinase	EC:2.7.4.4: EC:2.7.4	Nucleoside-phosphat	G3DSA:3.40.50.300 (GENE3D): PF13	1,072	1,679	1,165	1,650	1,834									
Solyc06g075320	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** W9SCA8_9ROSA)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (SMART): IPR006045 (PF.	0,211	0,328	0,068	0,413	0,141									
Solyc06g075330	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)						IPR004883 (PFAM LBD	0,042	0,082	0,000	0,000	0,000									
Solyc06g075335	LOB domain-containing protein, putative (AHRD V3.3 *-* B9SK21_RICCO)						IPR004883 (PFAM): PTHR31301:SF1.	0,019	0,021	0,000	0,000	0,000									
Solyc06g075340	Carbamoyl-phosphate synthase large chain (AHRD V3.3 *** A0A0B0PI12_GOSAR)		F:GO:0005524: P:G(	F:ATP binding: P:nitrogen compound metabolic process: F:meta			IPR005483 (PRINTS): IPR011607 (SM	135,770	121,938	164,606	141,070	169,251									
Solyc06g075345	Unknown protein (AHRD V3.3)							0,118	0,120	0,172	0,290	0,308									
Solyc06g075350	tRNA-splicing endonuclease subunit Sen2 (AHRD V3.3 *** A2Q3E8_MEDTR)		F:GO:0000213: F:G(	F:tRNA-intron endo	EC:3.1.27.9: EC:3.1.	Acting on ester bonds	IPR006678 (PFAM): IPR011856 (G3D	4,282	3,784	5,769	5,842	5,606									
Solyc06g075360	Tetraspanin (AHRD V3.3 *** A0A103XGG0_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	84,778	64,021	30,015	29,226	31,460									
Solyc06g075370	Dof zinc finger protein (AHRD V3.3 *** W9RMR9_9ROSA)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	15,840	16,214	5,320	7,033	6,760									
Solyc06g075390	Exosome complex component RRP43 (AHRD V3.3 *** A0A0B2Q2J1_GLYSO)		C:GO:0005829	C:cytosol			IPR027408 (G3DSA:3.30.230.GENE3I	54,955	46,959	34,674	35,198	33,190									
Solyc06g075400	V-type proton ATPase subunit a (AHRD V3.3 *** K4C9Q5_SOLLC)		C:GO:0000220: F:G(	C:vacuolar proton-transporting V-type ATPase, V0 domain: F:pr			IPR002490 (PFAM): IPR026028 (PIRS	12,342	14,357	10,438	14,819	12,907					0,507	0,017			up
Solyc06g075410	D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein (AHRD V3.3 --* AT5G57850.2)						PTHR33737 (PANTHER): PTHR33737	0,059	0,141	0,022	0,123	0,023									
Solyc06g075420	LOW QUALITY:phosphoglycerate/bisphosphoglycerate mutase family protein (AHRD V3.3 --* AT5G22620.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,404	1,244	0,336	0,415	0,378									
Solyc06g075440	Major Facilitator Superfamily protein (AHRD V3.3 *** Q6L3J2_SOLDE)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,262	0,132	1,374	0,889	0,937									
Solyc06g075470	Major facilitator superfamily protein (AHRD V3.3 *-* AT3G45690.1)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			IPR034907 (SMART): IPR000109 (PF.	1,080	0,827	1,627	1,191	1,336									
Solyc06g075490	Major facilitator superfamily protein (AHRD V3.3 *** AT3G45660.2)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,040	0,077	0,025	0,000	0,024									
Solyc06g075510	APETALA2e	AP2e	F:GO:0003677: F:G(	F:DNA binding: F:DNA-binding transcription factor activity: P:reg			IPR001471 (PRINT AP2	1,864	3,302	0,885	0,486	1,035									
Solyc06g075513	Dehydroascorbate reductase (AHRD V3.3 *-* Q1G0W3_SOLLC)		P:GO:0010731: F:G(	P:protein glutathion	EC:1.8.5.1	Glutathione dehydroc	G3DSA:1.20.1050.10 (GENE3D): PTH	0,342	0,403	0,100	0,216	0,326									
Solyc06g075517	aluminum activated malate transporter family protein (AHRD V3.3 --* AT3G11680.2)							0,000	0,018	0,025	0,000	0,023									
Solyc06g075520	Dehydroascorbate reductase (AHRD V3.3 *-* Q1G0W3_SOLLC),Pfam:PF13410	DHAR3	P:GO:0010731: F:G(	P:protein glutathion	EC:1.8.5.1	Glutathione dehydroc	G3DSA:1.20.1050.10 (GENE3D): PTH	0,159	0,346	0,046	0,192	0,260									
Solyc06g075540	hydrolase family protein / HAD-superfamily protein (AHRD V3.3 *** AT3G45740.1)		F:GO:0005507: C:G(	F:copper ion binding: C:mitochondrion: F:zinc ion binding: F:tran			IPR006353 (TIGRFAM): IPR006357 (F	35,348	32,583	35,648	36,650	37,611									
Solyc06g075550	Protein kinase-like protein (AHRD V3.3 *** Q6TKQ5_VITAE)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	33,511	30,856	27,339	29,870	33,639									
Solyc06g075555	Germacrene A oxidase (AHRD V3.3 --* GAO_LACSA)							0,203	0,282	0,194	0,392	0,235									
Solyc06g075570	Respiratory burst oxidase-like protein (AHRD V3.3 *** G7L3G1_MEDTR)		F:GO:0004601: F:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000778 (PRINTS): G3DSA:2.40.3(	0,141	0,097	0,000	0,022	0,118									
Solyc06g075580	Kinesin-like protein (AHRD V3.3 *** A0A0V0IXV7_SOLCH)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	42,378	40,975	5,371	2,749	6,543									
Solyc06g075590	CCR4-NOT transcription complex subunit 2 (AHRD V3.3 *** G7IUA4_MEDTR)		C:GO:0005634: P:G(	C:nucleus: P:regulation of transcription, DNA-templated: C:CCR			IPR038635 (G3DSA:2.30.30.GENE3D	99,317	87,251	116,559	122,118	118,638									
Solyc06g075610	LOW QUALITY:Exocyst subunit exo70 family protein (AHRD V3.3 *** G7JTM6_MEDTR)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): G3DSA:1.20.128(	53,306	46,674	5,532	11,178	7,284					1,017	0,000			up
Solyc06g075620	60S ribosomal protein L35 (AHRD V3.3 *** RL35_EUPES)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.287.310 (GENE3D): IPR(	17,330	17,648	19,419	18,106	17,999									
Solyc06g075630	Dirigent protein (AHRD V3.3 *** K4C9S8_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAN	0,058	0,039	0,000	0,025	0,000									
Solyc06g075640	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT4G20900.2)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	0,119	0,101	0,000	0,075	0,000									
Solyc06g075650	tonoplast intrinsic protein 1.2	TIP1.2	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,038	0,161	0,090	0,117	0,117									
Solyc06g075660	MYB family protein (AHRD V3.3 *** A0A067L6V8_JATCU)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,352	0,980	0,234	0,315	0,542									
Solyc06g075665	Myb/SANT-like domain-containing protein (AHRD V3.3 *-* A0A103Y2K4_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,057	0,000	0,025	0,050	0,000									
Solyc06g075667	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103Y4I4_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,047	0,072									
Solyc06g075670	MYB-related transcription factor (AHRD V3.3 *-* A0A059PRS8_SALMI)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB_related	0,000	0,036	0,000	0,000	0,000									
Solyc06g075690	auxin-regulated protein AF416289						IPR021182 (PIRSF): IPR010369 (PFA	180,793	343,557	46,719	43,922	54,493									
Solyc06g075700	Protein yippee-like (AHRD V3.3 *** K4C9V4_SOLLC)		C:GO:0016020	C:membrane			IPR038841 (PANTHER): IPR034751 (I	0,019	0,000	0,000	0,000	0,000									
Solyc06g075720	Protein yippee-like (AHRD V3.3 *-* K4C9V4_SOLLC)		F:GO:0046872	F:metal ion binding			IPR004910 (PFAM): mobidb-lite (MOB	0,098	0,057	4,373	0,886	0,711			-2,602	0,000	-2,289	0,005		down	down
Solyc06g075730	Ribosomal protein S3 family protein (AHRD V3.3 --* AT3G53870.1)							0,000	0,000	0,072	0,000	0,023									
Solyc06g075770	Protein yippee-like (AHRD V3.3 *** K4C9V4_SOLLC)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,023									
Solyc06g075780	Zinc finger, C2H2 (AHRD V3.3 *** A0A103Y6U7_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	41,310	29,962	11,119	37,895	17,143					1,766	0,000			up
Solyc06g075790	DNA-binding protein (AHRD V3.3 *** AT5G59830.3)						IPR032308 (PFAM): mobidb-lite (MOB	46,513	39,881	43,418	43,513	42,241									
Solyc06g075800	Histone H2B (AHRD V3.3 *** K4C9U5_SOLLC)		C:GO:0000786: F:G(	C:nucleosome: F:DNA binding: F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	37,481	42,675	16,954	13,291	14,152									
Solyc06g075810	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 (AHRD V3.3 *** A0A0B2Q420_GLYSO)		C:GO:0005747	C:mitochondrial respiratory chain complex I			IPR007741 (SMART): IPR007741 (PF.	96,166	91,254	170,446	133,992	151,961									
Solyc06g075820	LOW QUALITY:Protein yippee-like (AHRD V3.3 *** K4C9V4_SOLLC)						IPR004910 (PFAM): IPR038841 (PAN	0,000	0,057	0,000	0,000	0,000									
Solyc06g075830	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	51,077	57,664	62,470	47,828	56,613					-0,382	0,031			down
Solyc06g075860	LOW QUALITY:Protein yippee-like (AHRD V3.3 *-* M1DX18_SOLTU)		F:GO:0046872	F:metal ion binding			IPR004910 (PFAM): IPR038841 (PAN	0,019	0,000	0,000	0,000	0,023									
Solyc06g075920	LOW QUALITY:Protein yippee-like (AHRD V3.3 *-* K4C9V4_SOLLC)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,100	0,163	0,047	0,095	0,304									
Solyc06g075930	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	17,838	18,020	6,125	4,727	6,021									
Solyc06g075950	Protein yippee-like (AHRD V3.3 *** M1DX18_SOLTU)		C:GO:0016020: C:G(	C:membrane: C:integral component of membrane: F:metal ion bi			IPR004910 (PFAM): mobidb-lite (MOB	0,019	0,000	0,022	0,000	0,000									
Solyc06g075960	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G(	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR001951 (SM	84,888	93,180	47,162	29,775	40,231					-0,660	0,000			down
Solyc06g075980	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein (AHRD V3.3 *** AT3G46450		C:GO:0016021	C:integral component of membrane			IPR001251 (SMART): IPR001251 (PF.	14,665	13,226	11,554	12,024	11,985									
Solyc06g075990	dessication-induced 1VOC superfamily protein (AHRD V3.3 *** AT1G07645.1)						PF18029 (PFAM): IPR029068 (G3DS/	1,051	2,393	1,263	2,011	1,365									
Solyc06g076000	WUSCHEL-related homeobox 2 (AHRD V3.3 *** A0A0B2RJI5_GLYSO)		F:GO:0003677	F:DNA binding			IPR001356 (SMAF WOX	0,000	0,021	0,000	0,000	0,000									
Solyc06g076010	Cysteine alpha-hairpin motif superfamily (AHRD V3.3 *** A0A103YFL5_CYNCS)		F:GO:0003735: P:G(	F:structural constituent of ribosome: P:mitochondrial translation			IPR031731 (PFAM): IPR017264 (PAN	4,817	3,515	7,789	7,500	7,803									
Solyc06g076020	heat shock protein 70 kD	hsc1	F:GO:0005524: C:G(	F:ATP binding: C:cy	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS): IPR029048 (G3	334,024	526,994	148,917	288,527	208,087					0,956	0,000			up
Solyc06g076030	Dof zinc finger protein (AHRD V3.3 *** Q9M4G1_SOLTU)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,534	0,578	0,125	0,147	0,400									
Solyc06g076035	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 --* AT1G20960.2)							0,000	0,000	0,000	0,000	0,024									
Solyc06g076040	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PZF9_ZOSMR)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity: F:protein binding: P:cell :			IPR003613 (SMART): IPR000225 (SM	559,079	686,099	88,738	133,592	146,500			0,720	0,039				up	
Solyc06g076050	Ankyrin repeat family protein (AHRD V3.3 *** B9GJP4_POPTR)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR002110 (PF.	218,821	279,851	55,343	88,954	83,060					0,685	0,005			up
Solyc06g076060	LOW QUALITY:Cyclin-dependent protein kinase inhibitor SMR3 (AHRD V3.3 *-* M5W251_PRUPE)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,062	0,022	0,100	0,070									
Solyc06g076080	Cell division cycle protein 48-related / CDC48-related isoform 1 (AHRD V3.3 --* A0A061ERQ8_THECC)							7,794	11,054	1,610	4,030	3,594			1,150	0,001	1,316	0,000		up	up
Solyc06g076090	Actin (AHRD V3.3 *** ACT1_TOBAC)		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): IPR004000 (SM	0,670	2,563	0,174	0,347	0,470	1,947	0,014					up		
Solyc06g076100	Phosphatase 2C family protein (AHRD V3.3 *** B9GJN9_POPTR)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF.	47,322	46,158	27,416	36,011	35,107									
Solyc06g076110	Fasciclin-like arabinogalactan family protein (AHRD V3.3 *-* A0A061GX88_THECC)		P:GO:0009738: P:G(	P:abscisic acid-activated signaling pathway: P:multidimensional			IPR000782 (SMART): IPR000782 (PF.	7,686	5,722	3,572	3,887	3,128									
Solyc06g076120	Fasciclin-like arabinogalactan protein (AHRD V3.3 *-* A0A072V7M5_MEDTR)		P:GO:0009738: P:G(	P:abscisic acid-activated signaling pathway: P:multidimensional			IPR036378 (G3DSA:2.30.180.GENE3I	10,476	6,866	5,413	5,836	4,731									
Solyc06g076130	GTP-binding protein Obg/CgtA protein (AHRD V3.3 *** A0A072VCX1_MEDTR)						IPR025486 (PFAM): mobidb-lite (MOB	6,200	10,472	2,330	3,789	4,771			1,026	0,002				up	

Solyc06g076150	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *** K4C9X5_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in	IPR000717 (SMART): SM00753 (SMA	77,181	85,686	129,852	117,234	112,100									
Solyc06g076160	Cytochrome P450 (AHRD V3.3 *-* C5NM77_TOBAC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,042	0,422	9,226	15,291	10,701									
Solyc06g076170	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9T3M9_RICCO)		F:GO:0004553; F:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; F:iron i	IPR002401 (PRINTS): IPR012946 (SM	8,408	7,354	7,346	14,114	10,728					0,947	0,004			up
Solyc06g076200	XH/XS domain-containing family protein (AHRD V3.3 *** U5G4S7_POPTR)		P:GO:0031047	P:gene silencing by RNA	IPR005380 (PFAM): IPR038588 (G3D	0,176	0,174	0,122	0,050	0,072									
Solyc06g076210	XH/XS domain-containing family protein (AHRD V3.3 *** U5G4S7_POPTR)		P:GO:0031047	P:gene silencing by RNA	IPR038588 (G3DSA:3.30.70.GENE3D	0,499	0,439	0,387	0,437	0,661									
Solyc06g076220	expansin18	EXPA18	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization	IPR007118 (PRINTS): IPR002963 (PF	18,541	15,669	0,834	0,696	1,794									
Solyc06g076250	PGR5-like protein 1B, chloroplastic (AHRD V3.3 *** A0A0B0MIW0_GOSAR)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:photosynthetic electron tra	PTHR31032:SF2 (PANTHER): IPR039	12,715	15,297	14,440	13,533	14,715									
Solyc06g076257	Vetispiradiene synthase 1 (AHRD V3.3 --* VTSS1_HYOMU)					0,097	0,099	0,022	0,000	0,047									
Solyc06g076265	Nuclear transcription factor Y subunit A-3 (AHRD V3.3 --* A0A151T593_CAJCA)					0,663	0,615	0,546	0,754	0,679									
Solyc06g076270	Telomere-binding family protein (AHRD V3.3 *** B9HPG4_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	26,673	25,546	44,423	38,973	37,219									
Solyc06g076280	Transcription factor GRAS (AHRD V3.3 *** A0A118K209_CYNCS)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM GRAS	57,548	51,768	22,125	38,568	28,569					0,803	0,000			up
Solyc06g076300	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JUV7_MEDTR)		F:GO:0016787	F:hydrolase activity	IPR006439 (TIGRFAM): IPR010237 (T	14,179	33,068	5,796	6,086	7,739	1,246	0,000					up		
Solyc06g076310	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 *** AT5G02220.1)		P:GO:0032875	P:regulation of DNA endoreduplication	mobidb-lite (MOBIDB_LITE): IPR0403	0,199	0,525	0,317	0,522	0,212									
Solyc06g076320	LOW QUALITY:Rotundifolia-like protein (AHRD V3.3 *** G7JUW7_MEDTR)		P:GO:0048367	P:shoot system development	IPR012552 (PFAM): mobidb-lite (MOB	0,728	1,177	16,142	15,986	11,196									
Solyc06g076340	Pumilio-like protein (AHRD V3.3 *** A0A0B0PMB1_GOSAR)		F:GO:0003723	F:RNA binding	IPR001313 (SMART): IPR011989 (G3	88,821	74,971	127,563	120,871	117,609									
Solyc06g076350	LePCL1	pcl1	F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 G2-like	12,025	9,432	14,473	14,502	14,880									
Solyc06g076360	outer envelope membrane protein		P:GO:0006886; F:G(	P:intracellular protein transport; F:P-P-bond-hydrolysis-driven pr	G3DSA:3.10.20.310 (GENE3D): IPR0(	189,262	221,863	212,682	185,332	213,054									
Solyc06g076370	low-temperature-induced protein (AHRD V3.3 *** AT3G46750.1)		P:GO:0009737	P:response to abscisic acid	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc06g076380	LOW QUALITY:intracellular protein transporter USO1-like protein (AHRD V3.3 --* AT5G41620.2)				IPR040381 (PTHR33912:PANTHER):	0,000	0,018	0,000	0,000	0,000									
Solyc06g076390	Transcription initiation factor IIA subunit 1 (AHRD V3.3 *** A0A061GWZ2_THECC)		C:GO:0005672; P:G(	C:transcription factor TFIIA complex; P:transcription initiation fro	IPR004855 (SMART): G3DSA:1.10.28	74,214	70,074	79,952	70,170	70,382									
Solyc06g076400	Protein phosphatase 2C (AHRD V3.3 *** A0A103XPQ7_CYNCS)		F:GO:0004722; P:G(	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	55,456	33,642	25,516	30,488	32,199	-0,695	0,002					down		
Solyc06g076410	sterol 4-alpha-methyl-oxidase 2-1 (AHRD V3.3 *** AT1G07420.1)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas	IPR006694 (PFAM): PTHR11863 (PAN	59,954	49,955	91,297	79,401	98,103									
Solyc06g076420	LOW QUALITY:Repetitive proline-rich cell wall protein 2 (AHRD V3.3 -** PRP2_MEDTR)				PR01217 (PRINTS): mobidb-lite (MOB	4,596	12,539	0,884	1,780	0,327									
Solyc06g076430	Serine/threonine-protein phosphatase (AHRD V3.3 *** A0A0V0I8D9_SOLCH)		F:GO:0016787	F:hydrolase activity	IPR006186 (PRINTS): IPR006186 (SM	43,320	33,573	42,116	43,806	41,371									
Solyc06g076440	Metal tolerance protein (AHRD V3.3 *** D5G3Q0_ARAHH)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;	IPR002524 (PFAM): IPR027469 (G3D	7,700	7,395	6,882	5,134	6,789									
Solyc06g076450	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	11,930	15,744	12,174	10,110	8,590									
Solyc06g076460	Transcription elongation factor B polypeptide 1 (AHRD V3.3 *** A0A199VJ64_ANACO)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process	IPR001232 (SMART): G3DSA:3.30.71	21,323	19,399	25,364	23,777	22,599									
Solyc06g076470	Plant/T7H20-70 protein (AHRD V3.3 *** G7L5L0_MEDTR)				PTHR33738 (PANTHER)	2,309	1,542	0,756	0,863	1,108									
Solyc06g076480	Thylakoid lumenal 15 kDa protein (AHRD V3.3 *** A0A072V034_MEDTR)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast thylakoid lumer	IPR001646 (PFAM): G3DSA:2.160.20	14,706	18,535	21,511	23,351	27,960									
Solyc06g076490	G patch domain-containing 3 (AHRD V3.3 *** A0A0B0MID7_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	6,325	4,710	6,002	7,893	6,004									
Solyc06g076510	Phosphoserine phosphatase, putative (AHRD V3.3 *** B9RLN8_RICCO),Pfam:PF00702		F:GO:0004647; P:G(	F:phosphoserine ph EC:3.1.3.3 Phosphoserine phosp	PF00702 (PFAM): IPR023190 (G3DSA	17,083	16,329	34,524	23,800	29,702					-0,534	0,033			down
Solyc06g076540	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	Hsp17.6A	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;	IPR002068 (PFAM): IPR008978 (G3D	8,480	50,175	17,697	243,301	473,114	2,593	0,004	4,735	0,000	3,785	0,000	up	up	up
Solyc06g076550	UDP-glycosyltransferase (AHRD V3.3 *** A0A164TMY6_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	0,312	0,502	0,262	0,120	0,355									
Solyc06g076560	17.6 kD class I small heat shock protein	Hsp17.6B	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;	IPR002068 (PFAM): IPR008978 (G3D	265,187	131,291	3171,785	1735,691	1037,550	-0,992	0,048	-1,616	0,000	-0,866	0,000	down	down	down
Solyc06g076570	class I small heat shock protein	Hsp17.6C	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;	IPR002068 (PFAM): IPR008978 (G3D	339,170	237,485	1674,314	1552,508	1644,037									
Solyc06g076580	Minichromosome maintenance (MCM2/3/5) family protein (AHRD V3.3 --* AT5G46280.4)					0,403	0,103	0,661	0,855	0,638									
Solyc06g076590	DUF3527 domain protein (AHRD V3.3 *** G7IRZ2_MEDTR)				IPR021916 (PFAM): mobidb-lite (MOB	37,819	32,327	15,907	17,413	18,527									
Solyc06g076600	Kinase family protein (AHRD V3.3 *** B9HPA3_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR011990 (G3DSA:1.25.40.GENE3D	0,792	0,996	0,192	0,321	0,446									
Solyc06g076610	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT5G05830.1)		F:GO:0008270	F:zinc ion binding	IPR011016 (SMART): IPR011016 (PF	4,537	3,818	1,641	1,698	1,694									
Solyc06g076620	28S ribosomal S34, mitochondrial (AHRD V3.3 *** A0A0B0MVM1_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:mitochondrion	IPR032053 (PFAM): mobidb-lite (MOB	9,190	11,622	11,365	11,354	10,401									
Solyc06g076630	Peroxidase (AHRD V3.3 *** K4CA23_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	18,415	12,854	5,018	3,567	5,709									
Solyc06g076640	Tubulin beta chain (AHRD V3.3 *** M1CZM0_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	124,087	140,635	41,420	29,882	36,804									
Solyc06g076650	Enolase, putative (AHRD V3.3 *-* B9S376_RICCO)		C:GO:0000015; F:G(	C:phosphopyruvate EC:4.2.1.11 Phosphopyruvate hy	IPR000941 (PRINTS): IPR020811 (SM	10,812	11,972	9,177	9,746	10,224									
Solyc06g076655	Enolase family protein (AHRD V3.3 *-* U5G5W8_POPTR)		C:GO:0000015; F:G(	C:phosphopyruvate EC:4.2.1.11 Phosphopyruvate hy	IPR000941 (PRINTS): IPR020810 (SM	3,310	2,981	2,495	2,248	2,324									
Solyc06g076660	proliferating cell nuclear antigen	pcna	F:GO:0003677; P:G(	F:DNA binding; P:regulation of DNA replication; F:DNA polymera	IPR000730 (PRINTS): IPR022649 (PF	13,852	14,741	6,463	3,637	4,525					-0,824	0,031			down
Solyc06g076670	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G07350.1)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR012677 (G3	219,929	141,099	360,684	341,194	320,304	-0,614	0,019					down		
Solyc06g076700	LOW QUALITY:UPF0503 protein, chloroplastic (AHRD V3.3 *** A0A0B2P4J5_GLYSO)				IPR008004 (PFAM): mobidb-lite (MOB	9,593	11,974	28,989	25,785	27,531									
Solyc06g076710	LOW QUALITY:AT-rich interactive domain protein (AHRD V3.3 *-* Q2HUC6_MEDTR)				mobidb-lite (MOBIDB_LITE): PTHR229	0,139	0,200	1,630	1,211	1,177									
Solyc06g076740	AT-rich interactive domain protein (AHRD V3.3 *-* Q2HUC6_MEDTR)				IPR000949 (SMART): mobidb-lite (MO	0,102	0,395	0,022	0,000	0,024									
Solyc06g076750	Peptide transporter, putative (AHRD V3.3 *** B9S358_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR000109 (PFAM): PTHR11654:SF2	66,533	72,993	113,328	116,866	104,125									
Solyc06g076760	Laccase 1a		F:GO:0005507; P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR008972 (G3DSA:2.60.40.GENE3D	0,021	0,021	0,068	0,073	0,024									
Solyc06g076770	Myb family transcription factor family protein (AHRD V3.3 *** B9HCK2_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	23,166	19,969	14,329	16,999	13,643									
Solyc06g076780	Glycosyl hydrolase family protein (AHRD V3.3 *** AT3G47000.1)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001764 (PRINTS): IPR002772 (PF	54,506	58,995	71,023	62,012	60,265									
Solyc06g076790	LOW QUALITY:Thylakoid soluble phosphoprotein (AHRD V3.3 *** Q8GT36_SPIOL)		C:GO:0009507	C:chloroplast	IPR021584 (PFAM): mobidb-lite (MOB	10,093	21,155	15,901	16,770	26,227	1,095	0,002	0,720	0,000			up	up	
Solyc06g076800	Cytochrome P450, putative (AHRD V3.3 *** B9SHY9_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,182	0,209	0,500	1,083	0,798									
Solyc06g076820	Zinc finger (C2H2 type) family protein		F:GO:0003676	F:nucleic acid binding	IPR013087 (SMAF C2H2	37,431	35,829	7,708	8,644	9,404									
Solyc06g076830	GDP-mannose transporter, putative (AHRD V3.3 *** B9SHZ3_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:GDP-mannose transmem	IPR004853 (PFAM): PTHR44371:SF2	1,056	0,950	0,187	0,072	0,165									
Solyc06g076840	R2R3MYB transcription factor 119	R2R3MYB119	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,229	0,100	0,000	0,000	0,000									
Solyc06g076850	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT2G29670.2)		F:GO:0005515	F:protein binding	PF14559 (PFAM): IPR011990 (G3DSA	67,454	85,663	20,422	23,083	29,690			0,536	0,024				up	
Solyc06g076860	cell division control 6 (AHRD V3.3 *** AT2G29680.2)		P:GO:0006270; P:G(	P:DNA replication initiation; P:cell division	IPR015163 (SMART): IPR016314 (PIF	2,770	3,379	0,698	0,327	0,677									
Solyc06g076870	60S acidic ribosomal protein P0 (AHRD V3.3 *** K4CA45_SOLLC)		C:GO:0005622; P:G(	C:intracellular; P:ribosome biogenesis	IPR001790 (PFAM): PF00428 (PFAM)	0,056	0,000	0,000	0,000	0,000									
Solyc06g076880	Flavoprotein wrbA, putative (AHRD V3.3 *** B9SI05_RICCO)		F:GO:0003955; F:G(	F:NAD(P)H dehydro EC:1.6.5.2 NAD(P)H dehydroger	IPR010089 (TIGRFAM): IPR029039 ((	24,960	23,969	28,675	26,191	25,578									
Solyc06g076890	Pleckstrin homology domain-containing protein 1 (AHRD V3.3 *** PH1_ARATH)		F:GO:0032266	F:phosphatidylinositol-3-phosphate binding	IPR001849 (SMART): IPR001849 (PF	33,925	31,319	36,940	32,787	32,233									
Solyc06g076910	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): IPR003591 (SM	0,081	0,137	0,147	0,322	0,166									
Solyc06g076930	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TSU1_ACAMN)	ABCG43	F:GO:0005524; C:G(	F:ATP binding; C:m(EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	0,210	0,193	0,000	0,000	0,000									
Solyc06g076940	NudC domain-containing protein 2 (AHRD V3.3 *** A0A0B2PF32_GLYSO)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding; P:developmental process; F:unfo	IPR008978 (G3DSA:2.60.40.GENE3D	43,875	46,613	77,313	76,605	74,920									
Solyc06g076950	PfkB-like carbohydrate kinase family protein (AHRD V3.3 *** A0A061GZW1_THECC)		F:GO:0005524; P:G(	F:ATP binding; P:my EC:2.7.1.64 Inositol 3-kinase	IPR029056 (G3DSA:3.40.1190.GENE	17,349	15,537	28,310	27,617	25,266									
Solyc06g076960	ELF4-like 4 (AHRD V3.3 *** AT1G17455.2)		P:GO:0042753	P:positive regulation of circadian rhythm	IPR009741 (PFAM): PTHR33469:SF1	12,030	8,345	13,020	11,500	10,461									
Solyc06g076970	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4CA55_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-pr EC:5.2.1.8 Peptidylprolyl isomera	IPR002130 (PRINTS): IPR002130 (PF	477,296	401,653	790,563	679,578	656,965									
Solyc06g081980	Pyridoxal biosynthesis protein PDX1-like protein (AHRD V3.3 *** T2DNB9_PHAVU)		F:GO:0003824; P:G(	F:catalytic activity; P:pyridoxal phosphate biosynthetic process	IPR001852 (PIRSF): IPR001852 (TIGI	72,984	115,574	179,046	151,694	167,963	0,689	0,007					up		
Solyc06g081990	LOW QUALITY:Dynein light chain type 1 family protein (AHRD V3.3 --* AT4G27360.1)					0,000	0,000	0,000	0,025	0,000									
Solyc06g082000	PI-phospholipase C6		F:GO:0004435; P:G(	F:phosphatidylinosit EC:3.1.4.11; EC:3.1. Phosphoinositide pho	IPR001192 (PRINTS): IPR000909 (SM	0,436	0,433	0,365	0,531	0,285									
Solyc06g082010	Zinc finger transcription factor 48	C3H48	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding	IPR000571 (SMAF C3H	112,233	149,993	41,829	41,179	50,743									
Solyc06g082030	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G58660.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS): IPR026992 (PFA	0,641	0,332	0,426	0,474	0,468									
Solyc06g082040	PHD finger transcription factor (AHRD V3.3 *-* AT5G58610.3)		F:GO:0003677	F:DNA binding	IPR017956 (PRINTS): IPR014002 (SM	5,141	2,990	1,738	1,804	2,097									
Solyc06g082060	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT5G42120.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	2,364	3,049	1,438	1,969	1,877									
Solyc06g082070	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR025846 (PFAM): IPR026057 (PFA	16,072	11,586	1,609	2,334	1,547									
Solyc06g082080	Protein phosphatase 2C (AHRD V3.3 *** Q3V656_SOLTU)		F:GO:0004722; P:G(	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR001932 (SM	20,880	12,511	10,079	32,632	16,399			0,699	0,010	1,695	0,000		up	up
Solyc06g082090	Methionine aminopeptidase,related (AHRD V3.3 *** A0A0K9Q0L8_ZOSMR)		P:GO:0001558; F:G(	P:regulation of cell growth; F:RNA binding; C:nucleolus; C:cytop	IPR001714 (PRINTS): IPR036388 (G3	111,783	120,131	99,287	86,364	93,089									
Solyc06g082100	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *** AT1G20960.2)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR001650 (SMART): IPR014001 (SM	204,069	172,318	184,108	176,261	178,180									
Solyc06g082120	RAN binding protein 1 (AHRD V3.3 *-* AT5G58590.1)		P:GO:0046907	P:intracellular transport	IPR004179 (SMART): IPR000156 (SM	67,852	75,416	115,208	115,581	96,822									
Solyc06g082130	Pyruvate decarboxylase (AHRD V3.3 *** A0A068LJB0_HEVBR)		F:GO:0000287; F:G(	F:magnesium ion binding; F:carboxy-lyase activity; F:thiamine p	G3DSA:3.40.50.970 (GENE3D): IPR0	0,038	0,000	0,000	0,000	0,000									
Solyc06g082140	autoinhibited Ca2+-ATPase 1 (AHRD V3.3 --* AT1G27770.4)					119,064	128,748	91,503	82,717	87,296									
Solyc06g082150	Fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase (AHRD V3.3 *** Q93XR7_BRUGY)		F:GO:0003824; F:G(	F:catalytic activity; F:ATP binding; P:fructose 2,6-bisphosphate	IPR002044 (SMART): IPR002044 (PF	7,998	8,280	12,889	14,180	15,021									
Solyc06g082155	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (AHRD V3.3 *-* F26_ARATH)		F:GO:0003824; F:G(	F:catalytic activity; F:ATP binding; P:fructose 2,6-bisphosphate	IPR003094 (PRINTS): IPR013078 (SM	7,530	8,146	11,305	12,100	13,683									
Solyc06g082160	SAGA-associated factor 11 (AHRD V3.3 *** K4CA75_SOLLC)		C:GO:0005634	C:nucleus	IPR013246 (PFAM): G3DSA:3.30.160	10,917	11,164	19,467	18,446	17,136									
Solyc06g082170	LOW QUALITY:Glutaredoxin family protein, putative (AHRD V3.3 *** A0A061GYL6_THECC)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bonds	IPR002156 (PFAM): IPR002109 (PFA	1,059	1,682	2,242	1,635	1,576									
Solyc06g082180	Glutaredoxin family protein, putative (AHRD V3.3 *** A0A061GYL6_THECC)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR002109 (PFAM): G3DSA:3.40.30.1	10,941	10,420	10,285	8,186	8,503									
Solyc06g082190	Protein kinase, putative (AHRD V3.3 *** B9SKV0_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): PIRS	11,207	14,860	41,669	41,592	41,043									
Solyc06g082200	Rab3 GTPase-activating protein catalytic subunit (AHRD V3.3 *** A0A072UXW3_MEDTR)		F:GO:0005096	F:GTPase activator activity	IPR026147 (PFAM): mobidb-lite (MOB	32,149	27,008	37,931	41,121	38,542									
Solyc06g082210	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT1G07090.1)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus	IPR006936 (PFAM): mobidb-lite (MOB	13,728	17,895	28,271	24,929	24,826									
Solyc06g082220	RNA binding protein, putative (AHRD V3.3 *** B9S5B9_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR001876 (SMART): IPR012677 (G3	80,787	97,544	128,185	117,365	117,122									
Solyc06g082230	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NPK0_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR038770 (G3DSA:1.20.1530.GENE	1,320	1,424	1,645	1,211	1,695									
Solyc06g082260	Laccase (AHRD V3.3 *** A0A1B0YZD2_DAUCA)		F:GO:0005507; P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR011707 (PFAM): IPR008972 (G3D	1,095	1,408	0,918	1,146	1,436									
Solyc06g082280	Serine-threonine protein phosphatase, putative, expressed (AHRD V3.3 *** Q8L676_ORYSJ)		F:GO:0016787	F:hydrolase activity	IPR004843 (PFAM): mobidb-lite (MOB	22,898	21,885	49,006	46,643	50,679									
Solyc06g082290	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT1G07030.1)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS): IPR023395 (G3	8,947	11,350	9,896	10,058	10,053									
Solyc06g082300	UDP-glycosyltransferase (AHRD V3.3 *** A0A067XTI9_CICAR)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	0,558	1,523	0,074	0,145	0,446									
Solyc06g082320	Pentatricopeptide repeat-containing protein At5g12100, mitochondrial (AHRD V3.3 *** A0A1D1Z416_9ARAE)				PTHR37176 (PANTHER)	0,851	1,383	0,370	0,573	0,352									
Solyc06g082340	F-box family protein (AHRD V3.3 *** AT3G06240.1)		F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D): IPR(	0,040	0,021	0,000	0,000	0,000									
Solyc06g082350	Biotin carboxyl carrier acetyl-CoA carboxylase (AHRD V3.3 --* G7KRK6_MEDTR)				mobidb-lite (MOBIDB_LITE)	0,421	0,317	0,449	0,580	0,305									
Solyc06g082360	U1 small nuclear ribonucleoprotein (AHRD V3.3 *** G7K5T4_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR000504 (SMART): IPR000504 (PF	27,523	29,632	25,239	26,450	23,789									
Solyc06g082370	mitochondrial 28S ribosomal protein S29-like protein (AHRD V3.3 *** AT1G16870.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:mitochondrial small ribos	IPR019368 (PFAM): mobidb-lite (MOB	15,657	14,075	23,374	20,030	19,293									
Solyc06g082380	Protein LURP-one-related 7 (AHRD V3.3 *** A0A0B2QBY8_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR038595 (G3DSA:3.20.90.GENE3D	2,171	3,090	1,485	1,800	1,723									
Solyc06g082390	RNA-directed DNA methylation 4 (AHRD V3.3 *** AT2G30280.1)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:DNA methylation; I	IPR013883 (PFAM): mobidb-lite (MOB	65,741	51,711	57,558	51,120	49,885									
Solyc06g082410	Major facilitator superfamily protein (AHRD V3.3 *-* AT2G30300.1)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1250.20 (GENE3D): PTH	0,203	0,041	1,038	0,339	0,753									
Solyc06g082420	Peroxidase (AHRD V3.3 *-* K4CAA1_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	1,245	1,184	5,204	4,421	5,935									
Solyc06g082430	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4B8_RICCO)				IPR004883 (PFAM LBD	0,117	0,490	0,187	0,099	0,212									
Solyc06g082440	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CAA3_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	32,259	32,478	13,412	19,669	15,169									
Solyc06g082460	LOW QUALITY:ovate family protein 14	OFP14	F:GO:0003677; P:G(	F:DNA binding; P:negative regulation of transcription, DNA-temp	IPR006458 (TIGRFAM): IPR006458 (F	4,881	5,629	0,071	0,075	0,047									
Solyc06g082470	MAP kinase kinase kinase 42	MAPKKK42	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	17,873	16,980	29,588	34,780	31,395									
Solyc06g082480	Nucleotidyltransferase domain containing protein, expressed (AHRD V3.3 *-* A0A0K9PR62_ZOSMR)				G3DSA:3.30.460.10 (GENE3D): PTHR	6,860	7,170	4,167	4,153	4,127									
Solyc06g082490	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 *** AT1G78800.1)		F:GO:0004378; P:G(	F:GDP-Man:Man1G EC:2.4.1.132 GDP-Man:Man(1)Glc	G3DSA:3.40.50.2000 (GENE3D): G3D	14,808	18,131	19,403	22,872	21,474									
Solyc06g082500	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT2G30460.2)		C:GO:0016021	C:integral component of membrane	IPR004853 (PFAM): PTHR44159 (PAN	20,388	16,387	5,637	4,882	4,437									
Solyc06g082510	Telomeric repeat-binding factor 1 (AHRD V3.3 *** A0A1D1YNQ3_9ARAE)		F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB_related	19,194	17,571	21,233	18,220	18,615									
Solyc06g082520	B3 domain-containing protein (AHRD V3.3 *** W9SAB7_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding	IPR003340 (SMAF B3	22,723	28,043	29,369	26,263	27,214									
Solyc06g082530	cinnamate-4-hydroxylase (AHRD V3.3 *-* AT2G30490.1)	C4H	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRIN GRAS	38,518	31,495	199,633	239,756	186,825									
Solyc06g082535	cinnamate-4-hydroxylase (AHRD V3.3 *** AT2G30490.1)	C4H	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	25,576	19,970	61,211	67,763	65,069									
Solyc06g082560	Chaperone protein (AHRD V3.3 *** W9RSC3_9ROSA)		F:GO:0005524; P:G(	F:ATP binding; P:protein metabolic process	IPR001270 (PRINTS): IPR003593 (SM	1,444	0,832	1,614	1,874	1,711									
Solyc06g082570	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *-* G7K0U4_MEDTR)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): mobidb-lite (MOB	2,490	6,881	0,501	1,619	0,658	1,491	0,005			1,665	0,001	up		up
Solyc06g082580	Eukaryotic translation initiation factor 2 beta subunit-like (AHRD V3.3 *** Q2V9B2_SOLTU)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation	IPR002735 (SMART): G3DSA:3.30.70	117,537	130,202	136,794	116,984	121,838									
Solyc06g082590	DNA-binding protein Pti6	CRF1	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	35,366	37,015	5,943	7,981	8,242									
Solyc06g082600	Ubiquitin-conjugating enzyme E2-like protein (AHRD V3.3 *** Q2PYY4_SOLTU)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e	SM00212 (SMART): IPR000608 (PFA	55,618	54,252	94,202	84,423	80,966									
Solyc06g082610	Receptor-like kinase (AHRD V3.3 *** G7K0V8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001611 (PFAM): IPR013210 (PFA	33,555	22,109	25,578	28,572	28,307									
Solyc06g082620	LOW QUALITY:RNA-binding KH domain-containing protein (AHRD V3.3 *** AT3G13230.2)		F:GO:0003723	F:RNA binding	IPR004087 (SMART): IPR036612 (G3	497,979	400,317	252,314	207,998	209,458									
Solyc06g082630	26S protease regulatory subunit 6B homolog (AHRD V3.3 *** PRS6B_SOLTU)		F:GO:0005524; C:G(	F:ATP binding; C:cy EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): PF17862 (PFAM	114,954	109,488	219,644	209,808	198,477									
Solyc06g082640	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR000719 (PF	1,248	0,732	0,782	0,971	0,754									
Solyc06g082650	60S ribosomal protein L10 (AHRD V3.3 *** RL10_SOLME)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	G3DSA:2.20.25.330 (GENE3D): IPR0(	99,570	119,700	110,370	97,188	99,994									
Solyc06g082660	26S protease regulatory subunit 6B homolog (AHRD V3.3 *** PRS6B_SOLTU)		F:GO:0005524; C:G(	F:ATP binding; C:cy EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): PF17862 (PFAM	98,637	94,575	164,393	166,313	154,226									
Solyc06g082670	60S ribosomal protein L10 (AHRD V3.3 *** RL10_SOLME)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001197 (TIGRFAM): IPR001197 (F	25,674	27,665	21,549	16,643	17,301									
Solyc06g082680	Cytochrome b-c1 complex subunit 8 (AHRD V3.3 *** QCR8_SOLTU)		C:GO:0005743; P:G(	C:mitochondrial inner membrane; P:electron transport chain; C:r	IPR020101 (PFAM): IPR020101 (PAN	64,844	57,712	95,339	84,932	88,262									
Solyc06g082690	LOW QUALITY:Protein phosphatase 2C family protein (AHRD V3.3 --* AT3G63320.1)		F:GO:0004722; P:G(	F:protein serine/thre EC:3.1.3.16 Protein-serine/threonine phosphatase		0,176	0,238	0,099	0,070	0,144									
Solyc06g082700	LOW QUALITY:Protein phosphatase 2C family protein (AHRD V3.3 *-* AT3G63320.2)		F:GO:0004722; P:G(	F:protein serine/thre EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	0,576	0,851	0,320	0,120	0,235									
Solyc06g082710	KH domain-containing protein (AHRD V3.3 *** A0A0B2S8I8_GLYSO)		F:GO:0003723	F:RNA binding	IPR004088 (PFAM): IPR036612 (G3D	24,036	25,351	47,970	51,216	42,439									
Solyc06g082720	GTP-binding nuclear protein (AHRD V3.3 *** M1CZU9_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR002041 (PRINTS): SM00175 (SMA	0,000	0,000	0,000	0,025	0,000									
Solyc06g082730	Cytochrome P450 (AHRD V3.3 *** A0A061H0G3_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR001128 (PRINTS): IPR002401 (PF	0,098	0,043	0,141	0,145	0,070									
Solyc06g082740	Reticulon-like protein (AHRD V3.3 *** K4CAC9_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me	IPR003388 (PFAM): mobidb-lite (MOB	0,019	0,021	0,122	0,025	0,117									
Solyc06g082750	50S ribosomal protein L17 (AHRD V3.3 *** A0A072UXJ8_MEDTR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000456 (PFAM): IPR000456 (TIGF	6,212	10,359	5,361	7,997	10,963			1,021	0,001				up	
Solyc06g082760	50S ribosomal protein L17 (AHRD V3.3 *** W9R5S7_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000456 (TIGRFAM): IPR036373 ((	4,197	5,561	4,131	4,423	5,045									
Solyc06g082770	LOB domain family protein				IPR004883 (PFAM LBD	0,222	0,220	0,212	0,271	0,166									
Solyc06g082780	Calcium uniporter, mitochondrial (AHRD V3.3 *** A0A0B0N729_GOSAR)		P:GO:0051560	P:mitochondrial calcium ion homeostasis	IPR006769 (PFAM): IPR039055 (PAN	19,158	18,852	17,562	26,691	22,668					0,605	0,023			up
Solyc06g082790	LOW QUALITY:Pentatricopeptide repeat-containing family protein (AHRD V3.3 *-* B9H1W8_POPTR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,061	0,025	0,000	0,071									

Solyc06g082800	Mitochondrial import receptor subunit tom40, putative (AHRD V3.3 *** B9RGH8_RICCO)		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:protein transmembrane tran			IPR027246 (PFAM); IPR023614 (G3D	40,203	43,307	36,491	35,915	33,649									
Solyc06g082810	Oligoribonuclease (AHRD V3.3 *** A0A151U1P3_CAJCA)		F:GO:0000175; F:G(	F:3'-5'-exoribonucle	EC:3.1.13; EC:3.1.1!	Acting on ester bond:	IPR013520 (SMART); IPR013520 (PF	9,232	10,781	3,230	3,942	3,600									
Solyc06g082830	Iron-stress related protein (AHRD V3.3 *** B4FBU5_MAIZE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	152,424	144,904	138,934	139,447	137,851									
Solyc06g082840	DnaJ domain-containing protein (AHRD V3.3 *** A0A118JVJ0_CYNCS)		C:GO:0005737; F:G(	C:cytoplasm; F:clathrin binding; C:vesicle; C:intracellular membr			IPR036869 (G3DSA:1.10.287.GENE3I	162,263	149,237	142,183	140,189	136,444									
Solyc06g082850	High mobility group B 6-like protein (AHRD V3.3 *-* A0A0B0N3I4_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,075	0,115	0,000	0,000	0,000									
Solyc06g082860	Cytochrome b561/ferric reductase transmembrane with DOMON related domain-containing protein (AHRD V:		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART); IPR005018 (SM	0,511	0,570	0,000	0,000	0,000									
Solyc06g082870	60S ribosomal protein L5-like protein (AHRD V3.3 *** T2DN67_PHAVU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR005485 (PRINTS); IPR005485 (PF	366,528	361,884	207,708	180,470	195,184									
Solyc06g082880	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T5G9_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	5,102	4,035	1,756	2,496	1,691									
Solyc06g082890	S-like ribonuclease (AHRD V3.3 *** A0A142F3E4_CAMSI)		F:GO:0003723; F:G(	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bond:	IPR036430 (G3DSA:3.90.730.GENE3I	15,445	14,036	27,248	27,091	27,541									
Solyc06g082900	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT5G19480.4)		F:GO:0008134; C:G(	F:transcription factor binding; C:mediator complex; P:positive re			mobidb-lite (MOBIDB_LITE); mobidb-lit	3,373	3,111	4,117	3,956	4,216									
Solyc06g082910	Formin-like protein (AHRD V3.3 *** K4CAE6_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (SMART); G3DSA:1.20.58	27,258	33,809	3,150	1,665	3,398									
Solyc06g082920	Receptor-like kinase (AHRD V3.3 *** D4QD70_DIACA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR032675 (G3DSA:3.80.10.GENE3D	33,537	88,600	36,822	40,911	42,132	1,425	0,001					up		
Solyc06g082930	Protein FRIGIDA-like protein (AHRD V3.3 *** A0A0B0PA17_GOSAR)		P:GO:0009908; P:G(	P:flower development; P:cell differentiation			IPR012474 (PFAM); mobidb-lite (MOB	157,669	131,853	122,728	119,624	119,357									
Solyc06g082940	Photosystem I reaction center subunit XI (AHRD V3.3 *** A0A061DNS9_THECC)		C:GO:0009538; P:G(	C:photosystem I reaction center; P:photosynthesis			IPR036592 (G3DSA:1.20.1240.GENE	143,688	362,036	47,006	67,051	149,539	1,361	0,000	1,666	0,000	0,516	0,040	up	up	up
Solyc06g082950	Photosystem I reaction center subunit XI (AHRD V3.3 *** A0A061DNS9_THECC)		C:GO:0009538; P:G(	C:photosystem I reaction center; P:photosynthesis			IPR036592 (G3DSA:1.20.1240.GENE	95,042	216,768	57,975	74,510	133,700	1,217	0,001	1,202	0,000			up	up	
Solyc06g082960	maternal effect embryo arrest protein (AHRD V3.3 *** AT3G07510.3)		C:GO:0016021	C:integral component of membrane			PTHR33430:SF4 (PANTHER); PTHR3:	0,063	0,081	0,000	0,000	0,000									
Solyc06g082970	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *** A0A0F7H181_9ROSI)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:NAD(P)H dehydrogenase (			IPR001623 (PFAM); IPR036869 (G3D	4,775	9,269	1,462	1,835	3,721	0,986	0,005	1,333	0,000			up	up	
Solyc06g082980	Sterol-8,7-isomerase (AHRD V3.3 *** Q2TU57_MAIZE)		C:GO:0016021; P:G(	C:integral compone	EC:5.3.3.5	Cholestenol Delta-isc	IPR007905 (PFAM); PTHR14207:SF0	85,750	79,379	57,026	47,657	53,850									
Solyc06g082990	RNA-binding CRS1 / YhbY (CRM) domain protein (AHRD V3.3 *** AT3G25440.1)		F:GO:0003723; F:G(	F:RNA binding; F:calcium ion binding			IPR002048 (SMART); IPR001890 (SM	28,994	21,374	21,675	18,920	19,388									
Solyc06g082995	2Fe-2S ferredoxin-like protein (AHRD V3.3 *** Q9SRR8_ARATH)		F:GO:0009055; F:G(	F:electron transfer activity; F:iron-sulfur cluster binding			IPR012675 (G3DSA:3.10.20.GENE3D	49,116	43,018	83,924	67,998	73,695									
Solyc06g083000	Calcium-binding protein (AHRD V3.3 *** Q9SCA1_LOTJA)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART); G3DSA:1.10.23	0,000	0,021	0,050	0,000	0,023									
Solyc06g083020	Carboxypeptidase (AHRD V3.3 *** K4CAF7_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); G3DSA:3.40.5C	0,690	2,216	0,000	0,025	0,000									
Solyc06g083030	Carboxypeptidase (AHRD V3.3 *** K4CAF8_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	11,003	28,808	0,837	0,670	1,011									
Solyc06g083040	wound-inducible carboxypeptidase		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	2,392	2,305	0,097	0,092	0,427									
Solyc06g083050	Carboxypeptidase (AHRD V3.3 *** K4CAG0_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); G3DSA:3.40.5C	0,000	0,019	0,000	0,000	0,000									
Solyc06g083060	MIP18 family protein (AHRD V3.3 *** A0A0B2S844_GLYSO)		P:GO:0016226	P:iron-sulfur cluster assembly			IPR002744 (PFAM); IPR034904 (G3D	5,262	5,523	7,873	9,324	8,192									
Solyc06g083070	Fimbrin, putative (AHRD V3.3 *** B9SMN8_RICCO)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly			IPR001715 (SMART); IPR036872 (G3	76,631	51,402	2,673	1,189	1,900									
Solyc06g083080	Pathogenic type III effector avirulence factor Avr cleavage site-containing protein (AHRD V3.3 *** A0A118J\		P:GO:0080167	P:response to karrikin			PTHR33699:SF2 (PANTHER); PTHR3:	5,785	7,602	0,575	0,541	0,636									
Solyc06g083085	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G10840.4)							0,100	0,077	0,022	0,098	0,000									
Solyc06g083090	HAUS augmin-like complex subunit 3 (AHRD V3.3 *** A0A0B0MQB3_GOSAR)		P:GO:0051225; C:G(	P:spindle assembly; C:HAUS complex			IPR032733 (PFAM); IPR026206 (PAN	13,972	10,956	11,618	12,075	10,865									
Solyc06g083100	HAUS augmin-like complex subunit (AHRD V3.3 *** AT5G48520.1)		P:GO:0051225; C:G(	P:spindle assembly; C:HAUS complex			IPR032733 (PFAM); IPR026206 (PAN	0,182	0,157	0,025	0,048	0,047									
Solyc06g083110	YGGT family protein (AHRD V3.3 *** AT4G27990.1)		C:GO:0016020	C:membrane			IPR003425 (PFAM); PTHR33219:SF1(	39,885	57,852	59,294	57,841	66,891	0,563	0,029					up		
Solyc06g083120	LOW QUALITY:ARGONAUTE 3 (AHRD V3.3 --* AT1G31290.3)							0,180	0,117	0,025	0,164	0,141									
Solyc06g083130	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A151QMJ8_CAJCA)		P:GO:0009143; F:G(	P:nucleoside tripho:	EC:3.6.1.19	Acting on acid anhyd	IPR025984 (PFAM); IPR025984 (PIRS	0,539	1,000	0,424	0,885	0,708									
Solyc06g083140	Auxin induced-like protein (AHRD V3.3 *-* E0Z5V6_PICSI)		C:GO:0016021	C:integral component of membrane			IPR005018 (PFAM); mobidb-lite (MOB	2,454	4,726	0,072	0,072	0,047									
Solyc06g083150	U-box domain protein (AHRD V3.3 *** A0A0K9NUT8_ZOSMR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR003613 (SMART); IPR019734 (SM	48,435	60,289	23,605	21,950	26,512									
Solyc06g083160	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)						IPR006502 (PFAM); IPR006502 (TIGF	0,078	0,019	0,000	0,000	0,000									
Solyc06g083170	bHLH transcription factor 049		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	4,739	4,990	0,334	0,410	0,424									
Solyc06g083180	40S ribosomal protein S8 (AHRD V3.3 *** K4CAH3_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022309 (PFAM); G3DSA:1.10.168.	82,469	97,526	79,889	68,764	69,587									
Solyc06g083190	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NXQ5_ZOSMR)		F:GO:0005515	F:protein binding			IPR019734 (SMART); G3DSA:3.10.50	469,502	436,161	728,878	725,000	719,490									
Solyc06g083200	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T7Z0_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	7,797	7,282	10,538	10,908	9,899									
Solyc06g083210	Protein kinase superfamily protein (AHRD V3.3 *** AT4G13020.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); PIRSF000654 (	30,308	30,991	50,388	53,226	49,406									
Solyc06g083220	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061D		F:GO:0005525; C:G(	F:GTP binding; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR142	28,620	25,287	37,173	38,295	36,042									
Solyc06g083230	GTP cyclohydrolase 1		F:GO:0003934; C:G(	F:GTP cyclohydrola	EC:3.5.4.16	GTP cyclohydrolase	IPR020602 (PFAM); G3DSA:1.10.286.	1,925	3,162	0,836	0,564	0,985									
Solyc06g083250	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT5G63710.4)							6,189	5,778	6,649	6,802	6,475									
Solyc06g083260	cyclin1_1	CycC1_1	F:GO:0016538; C:G(	F:cyclin-dependent protein serine/threonine kinase regulator act			IPR013763 (SMART); G3DSA:1.10.47	26,166	23,415	49,544	51,910	48,432									
Solyc06g083270	ER lumen retaining receptor family-like protein (AHRD V3.3 *** Q38JH5_SOLTU)		P:GO:0006621; C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS); IPR000133 (PF	5,003	5,496	15,010	24,840	16,230					0,729	0,000			up
Solyc06g083280	ER lumen retaining receptor family-like protein (AHRD V3.3 *** Q38JH5_SOLTU)		P:GO:0006621; C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS); IPR000133 (PF	0,101	0,076	0,244	0,222	0,166									
Solyc06g083300	Nuclear transport factor 2 family protein with RNA binding domain, putative isoform 2 (AHRD V3.3 *** A0A06		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR002075 (PF.	577,494	461,702	291,004	225,368	246,714					-0,365	0,032			down
Solyc06g083310	Hexosyltransferase (AHRD V3.3 *** K4CAI6_SOLLC)	GAUT8	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM); IPR029044 (G3D	311,917	377,691	137,967	165,906	168,742									
Solyc06g083320	LOW QUALITY:Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 --* AT2G17850.1)						mobidb-lite (MOBIDB_LITE)	0,000	0,041	0,000	0,000	0,000									
Solyc06g083330	LOW QUALITY:acidic leucine-rich nuclear phosphoprotein 32 family B protein (AHRD V3.3 *-* AT3G25130.1		C:GO:0016020	C:membrane			PTHR36760 (PANTHER)	0,452	0,361	0,315	0,485	0,189									
Solyc06g083340	Wound-induced basic protein (AHRD V3.3 *** PR4_PHAVU)		C:GO:0005829; P:G(	C:cytosol; P:response to cytokinin			IPR012643 (PFAM); mobidb-lite (MOB	67,831	71,287	100,273	85,349	88,972									
Solyc06g083350	Forkhead-associated (FHA) domain-containing protein (AHRD V3.3 *** A0A103Y779_CYNCS)		F:GO:0005515	F:protein binding			IPR000253 (SMART); IPR000253 (PF.	19,721	22,203	42,615	43,625	32,980									
Solyc06g083360	DNA-directed RNA polymerase II, subunit n, putative (AHRD V3.3 *** B9T3C0_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR000268 (PIRSF); IPR000268 (PFA	51,226	43,739	56,572	52,150	54,244									
Solyc06g083370	Trypsin-like cysteine/serine peptidase domain-containing protein (AHRD V3.3 *** A0A103YNC2_CYNCS)						mobidb-lite (MOBIDB_LITE); mobidb-lit	10,808	8,877	0,639	0,568	0,912									
Solyc06g083380	Acyl-[acyl-carrier-protein] hydrolase (AHRD V3.3 *** K4CAJ3_SOLLC)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:thiolester hydrolase activity			IPR002864 (PFAM); G3DSA:3.10.129.	26,982	28,127	40,238	39,956	38,432									
Solyc06g083390	RPM1-interacting protein 4 (AHRD V3.3 *** B9GQK9_POPTR)		C:GO:0005886; P:G(	C:plasma membrane; P:defense response signaling pathway, re			IPR008700 (PFAM); mobidb-lite (MOB	76,458	203,725	73,306	100,761	109,300	1,434	0,042	0,574	0,001	0,462	0,042	up	up	up
Solyc06g083400	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CAJ5_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucc	IPR010713 (PFAM); G3DSA:2.60.120.	0,000	0,000	0,000	0,025	0,000									
Solyc06g083410	Protein XRI1-like protein (AHRD V3.3 *** A0A0B0NEL0_GOSAR)		P:GO:0007140; P:G(	P:male meiotic nuclear division; P:female meiotic nuclear divisic			mobidb-lite (MOBIDB_LITE); mobidb-lit	10,387	10,748	19,278	24,962	22,504									
Solyc06g083415	3-ketoacyl-CoA synthase 17 (AHRD V3.3 --* AT4G34510.1)							0,081	0,100	0,000	0,000	0,000									
Solyc06g083420	Helicase/SANT-associated, DNA binding protein (AHRD V3.3 *** AT3G24880.3)						IPR014012 (SMART); IPR001005 (SM	70,660	60,033	74,290	79,359	78,981									
Solyc06g083425	JmjC domain protein JMJ24 (AHRD V3.3 --* AT1G09060.4)							2,352	2,476	2,436	2,794	2,679									
Solyc06g083430	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *** B9S517_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:response to osmotic stress; P:hormone-mediated			IPR006578 (SMAF Trihelix	7,864	8,360	12,486	12,452	12,137									
Solyc06g083440	Cytochrome b5 (AHRD V3.3 *** CYB5_TOBAC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR001199 (PRINTS); IPR001199 (SM	20,387	15,413	9,678	8,374	10,090									
Solyc06g083450	Caffeic acid O-methyltransferase (AHRD V3.3 *** G3FDY0_SALMI)		F:GO:0008171	F:O-methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	0,019	0,000	0,000	0,000	0,000									
Solyc06g083460	Transcriptional corepressor LEUNIG (AHRD V3.3 *-* W9S398_9ROSA)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	69,624	61,323	113,540	105,553	101,273									
Solyc06g083465	Transcriptional corepressor LEUNIG-like protein (AHRD V3.3 *** A0A0B0NJ14_GOSAR)		F:GO:0005515	F:protein binding			IPR006594 (SMART); IPR006594 (PF.	73,859	59,858	112,800	108,279	107,480									
Solyc06g083470	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		C:GO:0005829; F:G(	C:cytosol; F:oxidoreductase activity; P:oxidation-reduction proc			IPR002347 (PRINTS); IPR002347 (PF	0,019	0,159	0,075	0,022	0,000									
Solyc06g083480	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1)		C:GO:0005829; F:G(	C:cytosol; F:oxidoreductase activity; P:oxidation-reduction proc			IPR002347 (PRINTS); IPR002347 (PF	0,000	0,000	0,123	0,072	0,000									
Solyc06g083490	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		C:GO:0005829; F:G(	C:cytosol; F:oxidoreductase activity; P:oxidation-reduction proc			IPR002347 (PRINTS); IPR002347 (PF	0,038	0,082	0,429	0,438	0,143									
Solyc06g083500	Kinase family protein (AHRD V3.3 *** D7L628_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); PIRSF000615 (	0,600	0,444	0,699	0,659	0,612									
Solyc06g083510	DNA-directed RNA polymerase III subunit (AHRD V3.3 *** AT4G01590.3)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA p(	mobidb-lite (MOBIDB_LITE); mobidb-lit	12,214	10,696	23,353	21,267	17,953									
Solyc06g083520	GTP-binding family protein (AHRD V3.3 *** A0A061DNE0_THECC)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS); G3DSA:3.40.5C	15,202	14,544	14,398	13,044	12,992									
Solyc06g083530	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9S543_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			IPR001388 (PRINTS); IPR010908 (SM	114,649	109,420	112,572	107,508	95,289									
Solyc06g083535	multidrug resistance-associated protein 11 (AHRD V3.3 --* AT2G07680.6)							0,000	0,021	0,000	0,000	0,000									
Solyc06g083540	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT3G07030.5)		F:GO:0003676	F:nucleic acid binding			IPR036882 (G3DSA:3.30.110.GENE3I	22,894	24,718	32,530	27,116	27,786									
Solyc06g083550	F-box/kelch-repeat protein (AHRD V3.3 *** W9QCT4_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR015915 (G3	1,566	1,990	1,152	0,949	0,852									
Solyc06g083570	Thioredoxin-like protein 4B (AHRD V3.3 *** A0A0B0MT12_GOSAR)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			IPR004123 (SMART); G3DSA:3.40.30	3,427	2,939	3,869	3,158	2,952									
Solyc06g083580	Pectate lyase (AHRD V3.3 *** A0A022QXK5_ERYGU)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:U4/U6 x U5 tri-snRNP con			IPR018082 (PRINTS); IPR004123 (SM	28,084	15,036	2,863	1,586	1,862	-0,870	0,013					down		
Solyc06g083590	ABI3	abi3	F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	0,764	0,521	0,025	0,424	0,096									
Solyc06g083600	B3 domain-containing transcription factor ABI3-like protein (AHRD V3.3 *** A0A0B0MR68_GOSAR)		F:GO:0003677	F:DNA binding			IPR003340 (SMAF B3	2,081	2,139	0,148	0,427	0,000									
Solyc06g083610	Late embryogenesis abundant protein family protein, putative (AHRD V3.3 *** A0A061EZ48_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc06g083620	26S protease regulatory subunit (AHRD V3.3 *** A0A199VGJ0_ANACO)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata			IPR003593 (SMART); IPR032501 (PF.	239,563	239,948	293,703	273,486	265,051									
Solyc06g083630	Integral membrane HRF1 family protein (AHRD V3.3 *** AT1G30890.2)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR005578 (PFAM); IPR005578 (PAN	29,276	31,887	40,260	36,690	34,412									
Solyc06g083640	Leucine-rich repeat, ribonuclease inhibitor subtype (AHRD V3.3 *** A0A124SID0_CYNCS)		F:GO:0005515	F:protein binding			SM00368 (SMART); IPR032675 (G3D	21,814	18,440	13,740	16,349	14,400									
Solyc06g083650	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SFU0_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	0,770	1,037	0,000	0,000	0,000									
Solyc06g083660	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741) (AHRD V3.3 *** AT4G28760.2)						IPR022212 (PFAM); IPR032795 (PFA	134,775	114,791	42,128	26,719	40,851					-0,654	0,002			down
Solyc06g083670	RAC-like 10 (AHRD V3.3 --* AT5G62880.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	16,866	23,202	9,471	9,829	11,842									
Solyc06g083690	Glutaredoxin family protein (AHRD V3.3 *** AT4G28730.1)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR014025 (PRINTS); IPR011899 (TI(	18,194	25,036	30,193	28,365	33,000									
Solyc06g083700	Flavin-containing monooxygenase (AHRD V3.3 *** D2IGV4_SOLLC)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.	Flavin-containing mo	PR00368 (PRINTS); IPR000103 (PRI	0,158	0,246	0,000	0,000	0,000									
Solyc06g083710	DENN domain-containing protein 5B (AHRD V3.3 *** A0A0B2PJ42_GLYSO)						IPR001194 (SMART); IPR001194 (PF.	0,795	0,825	0,282	0,624	0,589									
Solyc06g083730	Nuclear transport factor 2 family protein with RNA binding domain (AHRD V3.3 *** A0A061DNP4_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART); IPR000504 (PF.	73,379	75,184	83,376	74,481	78,281									
Solyc06g083750	Cysteine-rich repeat secretory protein (AHRD V3.3 *** A0A0K9P487_ZOSMR)		C:GO:0009505; C:G(	C:plant-type cell wall; C:plasmodesma; P:plasmodesmata-media			IPR002902 (PFAM); IPR038408 (G3D	18,159	13,186	10,356	10,763	10,758									
Solyc06g083760	Histone-lysine N-methyltransferase (AHRD V3.3 *-* W9QWZ0_9ROSA)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR001214 (SMART); IPR007728 (SM	47,416	38,154	29,822	26,798	27,981									
Solyc06g083770	Glutathione S-transferase family protein (AHRD V3.3 *** AT5G44000.1)	GHR2	F:GO:0004364; F:G(	F:glutathione transf	EC:2.5.1.18	Glutathione transfera	PF13410 (PFAM); G3DSA:1.20.1050.'	3,961	3,391	6,121	6,230	6,845									
Solyc06g083780	50S ribosomal protein L14 (AHRD V3.3 *** A0A0K9PMD0_ZOSMR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000218 (SMART); IPR000218 (PF.	194,908	219,371	165,569	143,793	148,913									
Solyc06g083790	succinyl CoA ligase beta subunit		F:GO:0003824; F:G(	F:catalytic activity; F:ATP binding; P:tricarboxylic acid cycle; F:i			IPR005811 (PFAM); IPR005809 (TIGF	130,684	144,318	172,828	149,420	151,996									
Solyc06g083800	ROP-interactive CRIB motif protein (AHRD V3.3 *-* A0A072U2K9_MEDTR)						IPR000095 (SMART); IPR000095 (PF.	6,483	4,397	7,078	5,052	5,833									
Solyc06g083810	Glycolipid transfer protein domain-containing protein (AHRD V3.3 *** A0A103Y7C8_CYNCS)		C:GO:0005737; P:G(	C:cytoplasm; P:intermembrane lipid transfer; F:intermembrane li			IPR014830 (PFAM); IPR036497 (G3D	85,208	85,112	87,922	77,925	78,865									
Solyc06g083820	60S ribosomal protein L14, putative (AHRD V3.3 *** B9SS61_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR014722 (G3DSA:2.30.30.GENE3D	0,839	0,920	1,497	1,555	1,321									
Solyc06g083830	Casein kinase, putative (AHRD V3.3 *** B9SS69_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR000719 (PF.	16,219	21,278	35,717	36,436	34,401									
Solyc06g083850	NAC domain protein, (AHRD V3.3 *** A0A061DNM9_THECC)	NAC063	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,019	0,080	0,181	0,870	0,843									
Solyc06g083860	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G31160.1)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM); mobidb-lite (MOB	11,449	12,028	3,113	2,976	3,128									
Solyc06g083870	structural maintenance of chromosomes 1	smc1	F:GO:0003682; F:G(	F:chromatin binding; F:ATP binding; P:mitotic sister chromatid c			IPR010935 (SMART); G3DSA:3.30.70	82,749	69,437	70,819	71,262	69,247									
Solyc06g083890	Pre-mRNA-splicing factor SLU7 (AHRD V3.3 *** SLU7_ORYSI)		F:GO:0000386; P:G(	F:second spliceosomal transesterification activity; P:mRNA spli			IPR021715 (PFAM); mobidb-lite (MOB	31,253	21,544	36,212	30,669	32,551									
Solyc06g083900	R2R3MYB transcription factor 13	R2R3MYB13	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,019	0,340	0,097	0,000	0,000									
Solyc06g083920	Sn1-specific diacylglycerol lipase alpha (AHRD V3.3 *-* W9S987_9ROSA)		P:GO:0006629; F:G(	P:lipid metabolic process; F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	6,257	5,354	6,779	7,178	7,003									
Solyc06g083930	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4L6_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:positive regulation of transcription, DNA-templated			IPR004883 (PFAM LBD	0,000	0,085	0,000	0,000	0,000									
Solyc06g083950	SIN3-like 2 (AHRD V3.3 --* AT5G15020.2)							0,058	0,019	0,000	0,000	0,000									
Solyc06g083960	Myosin (AHRD V3.3 *** W6A1M7_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:(	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS); IPR001609 (SM	0,172	0,081	0,000	0,000	0,047									
Solyc06g083980	bHLH transcription factor138		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	27,398	36,432	39,679	50,981	40,090					0,365	0,020			up
Solyc06g083990	Cytosolic Fe-S cluster assembly factor NBP35 (AHRD V3.3 *** A0A0K9P2A2_ZOSMR)		F:GO:0005524; C:G(	F:ATP binding; C:mitochondrion; P:iron-sulfur cluster assembly;			G3DSA:3.40.50.300 (GENE3D); IPR0:	7,695	9,490	9,474	10,591	10,152									
Solyc06g084000	Poly(RC)-binding protein, putative (AHRD V3.3 *** B9S7H6_RICCO)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR036612 (G3	51,250	54,262	57,187	50,860	53,606									
Solyc06g084005	RNA-binding KH domain-containing protein (AHRD V3.3 *-* AT3G04610.2)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR004088 (PF.	32,115	31,251	33,940	31,152	31,046									
Solyc06g084020	histone H1	h1	C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR005819 (PRINTS); IPR005818 (SM	426,816	392,731	694,308	594,687	577,082									
Solyc06g084030	Methyltransferase-like protein (AHRD V3.3 *** G7KGP9_MEDTR)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0'	8,268	8,041	5,662	4,858	6,773									
Solyc06g084035	LOW QUALITY:Agenet domain-containing protein, putative (AHRD V3.3 *** A0A061ER75_THECC)						IPR014002 (SMART); IPR008395 (PF.	0,000	0,058	0,000	0,000	0,000									
Solyc06g084040	E3 ubiquitin ligase DRIP2-like protein (AHRD V3.3 *** A0A0B0N1B0_GOSAR)		F:GO:0016874	F:ligase activity			IPR001841 (SMART); IPR013083 (G3	3,667	3,920	4,120	4,278	3,937									
Solyc06g084060	F-box family protein (AHRD V3.3 *** B9GS69_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	13,234	13,333	17,859	21,257	19,482									
Solyc06g084080	Guanylate-binding family protein (AHRD V3.3 *** AT2G38840.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR015894 (PFAM); G3DSA:1.20.100(	0,991	0,930	0,358	0,426	0,585									
Solyc06g084090	Histone H2A (AHRD V3.3 *** K4CAR4_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimei			IPR002119 (PRINTS); IPR002119 (SM	1,258	1,437	0,265	0,142	0,239									
Solyc06g084100	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G63320.2)		F:GO:0004722; P:G(	F:protein serine/thr(	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART); IPR001932 (PF.	5,741	5,566	8,404	7,502	7,720									
Solyc06g084110	kinase superfamily protein (AHRD V3.3 *-* AT3G63340.8)		F:GO:0004722; P:G(	F:protein serine/thr(	EC:3.1.3.16	Protein-serine/threor	IPR015655 (PANTHER); PTHR13832:	1,066	1,074	0,899	1,174	1,087									
Solyc06g084120	BIG SEEDS 1 (AHRD V3.3 *** K4CAR7_SOLLC)		C:GO:0005634; P:G(	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (SMART); IPR018467 (PF.	3,220	3,016	0,352	0,370	0,350									
Solyc06g084130	Bax inhibitor (AHRD V3.3 *** A0A0K1ETI6_TECGR)		C:GO:0016021	C:integral component of membrane			IPR006214 (PFAM); PTHR23291:SF3	0,589	0,508	0,421	0,576	0,305									
Solyc06g084140	Sulfate transporter (AHRD V3.3 *** D7LTZ8_ARALL)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR011547 (PFAM); IPR001902 (TIGF	2,928	1,997	0,047	0,122	0,047									
Solyc06g084150	Harbinger transposase-derived nuclease (AHRD V3.3 *** A0A103XPB0_CYNCS)						IPR027806 (PFAM); mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc06g084155	Sulfate transporter, putative (AHRD V3.3 *-* B9SFG4_RICCO)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR002645 (PFAM); IPR036513 (G3D	6,803	4,560	0,176	0,192	0,187									
Solyc06g084160	probable serine/threonine-protein kinase BUD32 homolog		F:GO:0004674; F:G(	F:protein serine/thr(	EC:2.7.11	Transferring phospho	IPR000719 (SMART); G3DSA:3.30.20	36,540	38,614	48,550	48,276	48,490									
Solyc06g084170	low-molecular-weight cysteine-rich 56 (AHRD V3.3 -** AT3G20993.1)							0,822	0,681	0,194	0,417	0,305									
Solyc06g084180	Plant thionin family protein (AHRD V3.3 -** AT2G20619.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:oxidoreduct			IPR036466 (G3DSA:1.10.287.GENE3I	0,623	0,568	0,413	0,593	0,282									
Solyc06g084190	Lipid transfer protein (AHRD V3.3 *** B7FGM2_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS); IPR016140 (SM	21,490	19,825	19,178	17,653	15,712									
Solyc06g084210	Protein transport protein Sec24-like family (AHRD V3.3 *** A0A151TQ51_CAJCA)		P:GO:0006886; P:G(	P:intracellular protein transport; P:endoplasmic reticulum to Gol(			PR01217 (PRINTS); IPR006896 (PFA	213,435	193,052	227,222	220,307	226,515									
Solyc06g084220	Heat shock 22 kDa protein (AHRD V3.3 *** A0A072VPF4_MEDTR)						PTHR33879 (PANTHER); PTHR33879	10,011	7,983	10,092	9,869	8,958									
Solyc06g084230	40S ribosomal protein S24 (AHRD V3.3 *** K4CUG0_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001976 (PFAM); G3DSA:3.30.70.3	133,532	150,259	90,966	86,718	82,204									
Solyc06g084240	copalyl diphosphate synthase	cps1	F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM); IPR008949 (G3D	6,302	4,762	0,520	0,421	0,591									
Solyc06g084250	ARM repeat protein interacting with ABF2 (AHRD V3.3 *** AT5G19330.1)		F:GO:0005515	F:protein binding			IPR000225 (SMART); IPR000210 (SM	38,899	32,097	11,875	7,485	9,890									
Solyc06g084260	Chalcone--flavonone isomerase (AHRD V3.3 *** A0A1D1YAB8_9ARAE)	CHI	F:GO:0016872	F:intramolecular lyase activity			IPR016088 (G3DSA:3.50.70.GENE3D	10,766	16,358	12,006	11,673	15,215	0,631	0,041					up		
Solyc06g084270	GTP-binding family protein (AHRD V3.3 *** AT4G02790.1)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS); IPR019991 (TI(	24,811	28,267	54,985	53,659	58,035									
Solyc06g084280	LOW QUALITY:FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT5G19260.1)						IPR021410 (PFAM); mobidb-lite (MOB	0,782	0,462	0,821	1,262	0,547									

Solyc06g084290	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G06080.2)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR026057 (PFAM); IPR025846 (PFA	15,720	17,039	34,198	44,144	37,344								
Solyc06g084300	Outer envelope membrane family protein (AHRD V3.3 *-* B9H870_POPTR)		C:GO:0031359	C:integral component of chloroplast outer membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,915	2,537	5,778	6,573	5,186								
Solyc06g084310	Small nuclear ribonucleoprotein Sm D1 (AHRD V3.3 *-* A0A199VU58_ANACO)		P:GO:0006396	P:RNA processing	IPR001163 (PFAM); G3DSA:2.30.30.1	22,646	22,031	16,969	12,258	15,808								
Solyc06g084320	EID1-like F-box protein 2 (AHRD V3.3 *** A0A0B2SV68_GLYSO)				IPR040267 (PANTHER); PTHR31348:	11,175	9,208	19,909	18,427	17,535								
Solyc06g084330	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G02900.4)		C:GO:0016020	C:membrane	IPR003864 (PFAM); IPR027815 (PFA	0,246	0,502	0,465	0,583	0,659								
Solyc06g084340	LOW QUALITY:Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT4G23882.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding	IPR006121 (PFAM); G3DSA:3.30.70.1	0,000	0,000	0,000	0,073	0,023								
Solyc06g084350	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT1G03330.1)		P:GO:0006397	P:mRNA processing	IPR001163 (SMART); G3DSA:2.30.30	15,823	17,308	15,928	16,412	16,306								
Solyc06g084360	E3 Ubiquitin ligase family protein (AHRD V3.3 *** AT1G63900.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:organelle organization	IPR022170 (PFAM); PTHR12183 (PAN	56,363	62,306	112,290	100,977	108,939								
Solyc06g084370	LOW QUALITY:sodium hydrogen exchanger 4 (AHRD V3.3 --* AT3G06370.4)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,473	0,759	2,864	5,887	3,442					1,049	0,003			up
Solyc06g084380	2OG-Fe(II) oxygenase family oxidoreductase (AHRD V3.3 *** A0A072VPE6_MEDTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR037151 (G3DSA:2.60.120.GENE3I	0,038	0,146	0,074	0,149	0,095								
Solyc06g084390	ER auxin binding 1	erabp1	F:GO:0010011	F:auxin binding	IPR000526 (PRINTS); IPR014710 (G3	42,682	34,489	138,316	138,526	137,570								
Solyc06g084400	Methyl-CpG-binding domain-containing family protein (AHRD V3.3 *** A9PE20_POPTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; F:zinc ion binding	IPR001739 (SMART); IPR011124 (PF.	18,513	17,730	15,573	11,992	12,931								
Solyc06g084410	Histidine phosphotransfer protein (AHRD V3.3 *** A0A0A1WCB7_NICAT)		P:GO:0000160	P:phosphorelay signal transduction system	IPR036641 (G3DSA:1.20.120.GENE3I	17,002	17,706	27,903	28,090	23,278								
Solyc06g084420	Leucine-rich repeat receptor-like kinase (AHRD V3.3 *** A0A0K9PKL2_ZOSMR)		F:GO:0005515	F:protein binding	PR00019 (PRINTS); IPR001611 (PFA	2,348	1,901	0,451	0,288	0,541								
Solyc06g084430	Cupredoxin superfamily protein (AHRD V3.3 --* AT4G39830.1)					9,313	3,942	2,454	4,188	4,769	-1,212	0,001	0,960	0,018			down	up	
Solyc06g084440	NPL4 family protein (AHRD V3.3 *** A9PCA9_POPTR)		C:GO:0005634; P:G(	C:nucleus; P:ubiquitin-dependent protein catabolic process; F:ul	G3DSA:3.10.20.90 (GENE3D); IPR00	51,481	54,980	89,384	81,196	77,864								
Solyc06g084450	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9PZI3_ZOSMR)		P:GO:0007165	P:signal transduction	IPR000198 (SMART); IPR000095 (SM	0,159	0,195	0,051	0,000	0,000								
Solyc06g084460	Shikimate dehydrogenase, 3-dehydroquinate dehydratase (AHRD V3.3 *** A0A0K9F	SDH/DHQ2	F:GO:0003855; F:G(	F:3-dehydroquinate EC:1.1.1.25; EC:4.2. Shikimate dehydroge	PF18317 (PFAM); G3DSA:3.40.50.10	25,246	23,575	6,767	4,683	6,781								
Solyc06g084470	atypical CYS HIS rich thioredoxin 4 (AHRD V3.3 --* AT1G08570.4)				PTHR36776 (PANTHER); PTHR36776	2,132	3,373	1,484	1,906	2,756								
Solyc06g084480	Protease Do-like 2, chloroplastic (AHRD V3.3 *** DEGP2_ARATH)		F:GO:0004252; F:G(	F:serine-type endor EC:3.4.21 Acting on peptide bor	IPR001940 (PRINTS); PF17815 (PFAI	5,257	6,806	2,422	3,476	3,953								
Solyc06g084483	rRNA-processing protein (AHRD V3.3 *** AT4G03180.1)				IPR013730 (PFAM); mobidb-lite (MOB	0,180	0,280	0,190	0,119	0,117								
Solyc06g084487	Transport inhibitor response 1 (AHRD V3.3 *-* C7E4R3_TOBAC)		F:GO:0005488; P:G(	F:binding; P:cell communication; P:response to auxin; P:post-en	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,000	0,024								
Solyc06g084500	rRNA-processing protein (AHRD V3.3 *** AT4G03180.1)				IPR013730 (PFAM); mobidb-lite (MOB	0,077	0,039	0,072	0,000	0,071								
Solyc06g084510	CHY zinc finger family protein, expressed (AHRD V3.3 *** Q2QP88_ORYSJ)		F:GO:0008270; P:G(	F:zinc ion binding; P:protein ubiquitination	IPR001841 (SMART); IPR001841 (PF.	31,919	27,149	65,859	62,729	64,469								
Solyc06g084520	Cul1		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot	IPR016158 (SMART); IPR019559 (SM	103,267	89,783	123,739	121,795	119,902								
Solyc06g084530	ATPase family AAA domain-containing protein 1 (AHRD V3.3 *** A0A0B0NTB1_GOSAR)		F:GO:0005515; F:G(	F:protein binding; F:ATP binding	IPR003593 (SMART); G3DSA:1.10.8.6	175,427	125,770	145,915	147,626	142,106								
Solyc06g084540	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** A0A061DQR0_THECC)				IPR006015 (PRINTS); IPR006016 (PF	54,819	47,808	466,081	464,874	418,736								
Solyc06g084550	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion comple:	PF02466 (PFAM); IPR039175 (PANTH	16,895	14,326	15,198	14,196	14,374								
Solyc06g084570	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G02405.1)		F:GO:0018423; P:G(	F:protein C-terminal leucine carboxyl O-methyltransferase activi	IPR007213 (PFAM); G3DSA:3.40.50.1	13,224	13,321	21,582	19,150	18,942								
Solyc06g084590	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *** A0A199USB3_ANACO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans	IPR032176 (PFAM); PTHR31061 (PAI	41,323	36,089	64,464	65,969	59,713								
Solyc06g084615	beta-carotene isomerase D27 (AHRD V3.3 *** AT4G01995.1)		F:GO:0016853	F:isomerase activity	IPR025114 (PFAM); IPR038938 (PAN	5,846	7,586	3,593	3,966	4,727								
Solyc06g084620	Pectinesterase (AHRD V3.3 *** K4CAW7_SOLLC)		F:GO:0004857; F:G(	F:enzyme inhibitor a EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR006501 (SMART); IPR006501 (PF.	0,356	0,313	0,557	0,546	0,382								
Solyc06g084621	zinc ion binding/nucleic acid binding/hydrolase (AHRD V3.3 --* AT1G48360.6)				G3DSA:3.20.170.20 (GENE3D); IPR0(	7,745	6,467	5,742	4,032	4,991								
Solyc06g084624	DWNN domain, a CCHC-type zinc finger (AHRD V3.3 --* AT5G47430.5)					0,000	0,000	0,000	0,022	0,000								
Solyc06g084626	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic (AHRD V3.3 --* DXR_ORYSJ)					0,019	0,041	0,025	0,000	0,023								
Solyc06g084760	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS); IPR036396 (G3	82,694	33,111	74,564	64,020	64,567	-1,294	0,000					down		
Solyc07g004993	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-like protein (AHRD V3.3 --* AT2G45900.3)					0,021	0,000	0,025	0,000	0,000								
Solyc07g004997	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT1G01800.2)					0,000	0,000	0,000	0,025	0,000								
Solyc07g005000	Pleckstrin-like (PH) and lipid-binding START domain protein (AHRD V3.3 *** A0A072V208_MEDTR)		F:GO:0008289	F:lipid binding	IPR009769 (PFAM); IPR023393 (G3D	38,454	37,779	63,193	67,768	62,021								
Solyc07g005010	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A068USB4_COFCA)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART); IPR013210 (PF.	13,277	10,080	2,586	3,095	3,106								
Solyc07g005020	DNA helicase (AHRD V3.3 *** K4CAX4_SOLLC)		F:GO:0003688; F:G(	F:DNA replication origin binding; F:ATP binding; C:nucleus; P:DI	IPR001208 (PRINTS); IPR008048 (PF	4,222	4,171	8,350	6,659	6,932								
Solyc07g005030	Dicer-like 4	DCL4	F:GO:0003677; F:G(	F:DNA binding; F:rit EC:3.1.3; EC:3.1.26; Acting on ester bond:	IPR014001 (SMART); IPR001650 (SM	40,599	34,871	33,777	39,487	37,746								
Solyc07g005035	LOW QUALITY:CC-NBS-LRR type resistance protein (AHRD V3.3 --* E3W9R9_CAPCH)				IPR025558 (PFAM); PTHR34427 (PAI	0,140	0,218	0,146	0,189	0,188								
Solyc07g005040	Plasma membrane ATPase (AHRD V3.3 *-* M1AUY5_SOLTU)		C:GO:0016021	C:integral component of membrane	PR00119 (PRINTS); IPR004014 (SMA	0,038	0,043	0,000	0,051	0,000								
Solyc07g005050	60S ribosomal protein L39 (AHRD V3.3 *** RL39_MAIZE)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR023626 (G3DSA:1.10.1620.GENE:	182,985	181,635	117,967	102,914	104,910								
Solyc07g005060	Defective in cullin neddylation protein (AHRD V3.3 *** K4CAX8_SOLLC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:ubiquitin conjugating enzyme bindir	IPR005176 (PFAM); G3DSA:1.10.238	17,852	16,028	19,157	22,561	19,512								
Solyc07g005090	Chitinase, putative (AHRD V3.3 *** B9SC02_RICCO)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:chitin binding	IPR011583 (SMART); G3DSA:3.20.20	0,037	0,059	0,000	0,000	0,000								
Solyc07g005100	Chitinase/lysozyme (AHRD V3.3 *** Q43591_TOBAC)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:chitin binding	IPR011583 (SMART); IPR001223 (PF.	1,139	1,601	15,004	9,200	12,643								
Solyc07g005110	Receptor-like kinase CHRK1 (AHRD V3.3 *** Q9SWX8_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:carbohydrate metabc	IPR011583 (SMART); IPR000719 (SN	0,000	0,021	0,000	0,000	0,000								
Solyc07g005120	Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** AT5G58200.2)		F:GO:0016787	F:hydrolase activity	IPR029052 (G3DSA:3.60.21.GENE3D	23,574	17,468	10,737	10,252	11,285								
Solyc07g005130	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G31020.2)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	4,080	3,107	2,548	2,733	3,224								
Solyc07g005140	Two-component response regulator (AHRD V3.3 *** W9RL08_9ROSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding; F:D	IPR001789 (SMAF ARR-B	15,835	15,881	10,478	10,293	11,694								
Solyc07g005150	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding	PR00019 (PRINTS); IPR003591 (SMA	0,040	0,021	0,000	0,094	0,024								
Solyc07g005170	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S4A9_RICCO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,817	0,511	0,644	0,750	0,898								
Solyc07g005180	ubiquitin-associated protein (DUF1068) (AHRD V3.3 *** AT2G24290.1)		C:GO:0016021	C:integral component of membrane	IPR010471 (PFAM); PTHR32254 (PAI	35,447	37,641	9,452	8,321	8,870								
Solyc07g005190	Lysosomal Pro-X carboxypeptidase (AHRD V3.3 *** A0A0B0PYF0_GOSAR)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity	IPR008758 (PFAM); IPR029058 (G3D	2,368	3,511	0,074	0,272	0,000								
Solyc07g005200	VAMP-like protein YKT61 (AHRD V3.3 *** YKT61_ARATH)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS); IPR010908 (SN	35,942	39,649	39,161	43,859	40,281								
Solyc07g005210	Temperature-induced lipocalin (AHRD V3.3 *** Q38JE1_SOLLC)		F:GO:0005215	F:transporter activity	IPR002446 (PRINTS); IPR000566 (PF	71,594	72,102	45,320	49,489	76,597			0,754	0,031				up	
Solyc07g005215	SIGNAL PEPTIDE PEPTIDASE-LIKE 2 (AHRD V3.3 --* AT1G63690.1)					5,100	4,372	2,014	2,353	2,111								
Solyc07g005220	LOW QUALITY:TLC ATP/ADP transporter (AHRD V3.3 --* AT5G05310.9)					0,000	0,061	0,047	0,000	0,071								
Solyc07g005230	Respiratory burst oxidase-B-like protein (AHRD V3.3 --* M8CH43_AEGTA)					1,285	1,606	0,609	0,879	0,684								
Solyc07g005240	FAD-dependent oxidoreductase family protein (AHRD V3.3 *** AT2G22650.3)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	G3DSA:3.30.9.10 (GENE3D); IPR006	13,731	11,183	6,237	5,454	7,361								
Solyc07g005250	Auxin response factor 6 (AHRD V3.3 --* ARFF_ORYSI)					0,155	0,041	0,094	0,095	0,023								
Solyc07g005280	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain-containing protein (AHRD V3.3 --* AT5G03700.1)					3,315	2,409	2,138	1,962	2,239								
Solyc07g005300	LOW QUALITY:RING-finger, DEAD-like helicase, PHD and SNF2 domain-containing protein (AHRD V3.3 --* AT2G40770.3)					3,169	3,022	1,728	1,343	1,248								
Solyc07g005310	Quinoprotein amine dehydrogenase, beta chain-like, RIC1-like guanyl-nucleotide exchange factor (AHRD V3.3 --* AT3G61480.2)				mobidb-lite (MOBIDB_LITE)	1,828	0,713	1,124	1,399	1,318								
Solyc07g005320	Pre-mRNA polyadenylation factor Fip1 (AHRD V3.3 *** A0A103XMV0_CYNCS)		F:GO:0003723; F:G(	F:RNA binding; F:identical protein binding	IPR007854 (PFAM); mobidb-lite (MOB	83,967	73,734	78,167	75,834	77,631								
Solyc07g005330	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SXY3_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012946 (SMART); G3DSA:3.20.20	96,988	168,423	76,244	93,892	96,460	0,821	0,019					up		
Solyc07g005340	UPF0549 protein C20orf43 (AHRD V3.3 *** A0A1D1YCW9_9ARAE)		F:GO:0005515; P:G(	F:protein binding; P:mitotic DNA replication termination	IPR027799 (PFAM); IPR006735 (PAN	81,734	83,384	128,639	119,582	111,946								
Solyc07g005345	Single hybrid motif superfamily protein (AHRD V3.3 --* AT3G15690.3)					0,000	0,000	0,000	0,025	0,023								
Solyc07g005350	filament-like protein (DUF869) (AHRD V3.3 --* AT1G19835.6)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,040	0,039	0,000	0,000	0,000								
Solyc07g005360	Hexosyltransferase (AHRD V3.3 *** K4CB08_SOLLC)	GAUT5	F:GO:0047262	F:polygalacturonate EC:2.4.1.43 Polygalacturonate 4-	IPR002495 (PFAM); IPR029044 (G3D	18,899	14,075	43,541	47,215	43,260								
Solyc07g005370	Pathogenesis-related (PR)-10-related norcoclaurine synthase-like protein (AHRD V3.3 *** C3SBS5_ESCCA		P:GO:0006952	P:defense response	IPR000916 (PFAM); IPR023393 (G3D	0,282	1,326	18,784	25,295	17,556								
Solyc07g005380	Pathogenesis-related (PR)-10-related norcoclaurine synthase-like protein (AHRD V3.3 *** C3SBS5_ESCCA		P:GO:0006952	P:defense response	IPR000916 (PFAM); IPR023393 (G3D	0,084	1,671	0,150	0,444	0,331								
Solyc07g005390	aldehyde dehydrogenase 11A3 (AHRD V3.3 *** AT2G24270.3)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (	IPR016163 (G3DSA:3.40.309.GENE3I	104,371	120,255	52,234	48,051	70,326			0,425	0,036				up	
Solyc07g005400	bHLH transcription factor 050	bHLH050	F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	19,901	46,403	12,528	15,031	14,351	1,246	0,000					up		
Solyc07g005410	Cytochrome C oxidase, subunit VIb family protein (AHRD V3.3 *** I3SUN3_MEDTR)		C:GO:0005739	C:mitochondrion	IPR003213 (PFAM); IPR003213 (PAN	0,061	0,156	0,584	0,642	0,730								
Solyc07g005420	Thiamin diphosphate-binding fold (THDP-binding) superfamily protein (AHRD V3.3 --* AT1G21400.5)					0,019	0,037	0,000	0,076	0,023								
Solyc07g005430	SH3/FCH domain protein (AHRD V3.3 *** AT1G68680.1)		C:GO:0005747; C:G(	C:mitochondrial respiratory chain complex I; C:chloroplast; C:int	PTHR37713 (PANTHER)	27,118	29,946	27,171	27,627	27,142								
Solyc07g005440	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CB16_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART); G3DSA:3.30.31	21,475	56,189	4,604	5,862	6,008	1,415	0,000					up		
Solyc07g005450	RNA polymerase II C-terminal domain phosphatase-like protein (AHRD V3.3 *** A0A0K9Q1D5_ZOSMR)		C:GO:0005634; F:G(	C:nucleus; F:RNA p EC:3.1.3.16 Protein-serine/threor	IPR004274 (SMART); IPR001357 (SN	9,422	11,424	9,198	8,901	8,389								
Solyc07g005460	RNA polymerase II C-terminal domain phosphatase-like protein (AHRD V3.3 *** A0A0K9Q1D5_ZOSMR)		C:GO:0005634; F:G(	C:nucleus; F:RNA p EC:3.1.3.16 Protein-serine/threor	IPR001357 (SMART); IPR004274 (SN	7,690	7,729	8,942	9,288	8,015								
Solyc07g005470	Reticulon-like protein (AHRD V3.3 *** K4CB19_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me	IPR003388 (PFAM); mobidb-lite (MOB	0,314	0,267	0,000	0,000	0,000								
Solyc07g005480	Formin-like protein (AHRD V3.3 *** K4CB20_SOLLC)				IPR015425 (SMART); G3DSA:1.20.58	74,816	55,862	104,427	99,753	95,904								
Solyc07g005490	MATH domain and coiled-coil domain-containing protein At3g58260 (AHRD V3.3 --* MCC20_ARATH)					0,677	0,486	0,898	0,773	0,776								
Solyc07g005500	Formin-like protein (AHRD V3.3 *-* F6I7A3_VITVI)				IPR014020 (SMART); IPR014020 (PF.	11,520	7,269	14,450	15,268	13,783								
Solyc07g005510	Omega-6 fatty acid desaturase (AHRD V3.3 *** U3MY72_SOLAC)		P:GO:0006629	P:lipid metabolic process	IPR005804 (PFAM); PTHR32100 (PAI	81,600	111,182	83,089	89,788	111,598			0,423	0,011				up	
Solyc07g005520	BTB/POZ domain-containing protein (AHRD V3.3 *** W9QLB4_9ROSA)		F:GO:0005515; P:G(	F:protein binding; P:protein homooligomerization	IPR000210 (SMART); G3DSA:3.30.71	4,353	8,124	4,316	2,402	3,369					-0,831	0,044			down
Solyc07g005530	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** A0A061GR07_THECC)		P:GO:0016579; F:G(	P:protein deubiquitii EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D); IPR00	1116,027	972,022	790,442	729,507	721,439								
Solyc07g005540	LRR receptor-like kinase family protein (AHRD V3.3 *** G7JGQ5_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	PR00019 (PRINTS); SM00365 (SMAR	2,415	2,147	0,679	0,665	0,655								
Solyc07g005550	Transmembrane protein, putative (AHRD V3.3 *** A0A072UTY2_MEDTR)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane	PTHR36356 (PANTHER)	28,761	37,843	88,477	84,054	89,462								
Solyc07g005560	Eukaryotic translation initiation factor 5A (AHRD V3.3 *** A0A0V0HTA2_SOLCH)		F:GO:0003746; P:G(	F:translation elongation factor activity; P:translational frameshif	IPR020189 (SMART); IPR014722 (G3	595,189	600,840	579,453	496,488	531,182								
Solyc07g005570	APO protein 2 (AHRD V3.3 *** W9S368_9ROSA)		F:GO:0003723	F:RNA binding	IPR023342 (PFAM); mobidb-lite (MOB	19,163	22,588	38,381	34,410	41,598								
Solyc07g005580	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** K4CB29_SOLLC)		F:GO:0003841; P:G(	F:1-acylglycerol-3-p EC:2.3.1.51 1-acylglycerol-3-phos	IPR002123 (SMART); IPR002123 (PF.	11,194	14,066	30,573	31,951	29,393								
Solyc07g005583	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* AT1G48700.3)					0,000	0,000	0,000	0,025	0,000								
Solyc07g005587	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)					0,000	0,025	0,025	0,000	0,000								
Solyc07g005590	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9STR6_RICCO)		F:GO:0005249; F:G(	F:voltage-gated potassium channel activity; F:protein binding; P	IPR003938 (PRINTS); IPR000595 (SN	36,308	31,662	32,078	34,006	29,976								
Solyc07g005600	Transmembrane 9 superfamily member (AHRD V3.3 *** M1AS65_SOLTU)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM); PTHR10766:SF3	132,243	136,066	121,898	136,704	123,429								
Solyc07g005610	DNAse I-like superfamily protein (AHRD V3.3 *** AT4G30900.3)		C:GO:0005886	C:plasma membrane	IPR036691 (G3DSA:3.60.10.GENE3D	15,310	18,839	25,111	27,064	24,419								
Solyc07g005640	26S proteasome non-ATPase regulatory subunit-like protein (AHRD V3.3 *** A0A072V9K9_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:proteasome regulatory particle assembly	IPR001478 (SMART); IPR001478 (PF.	5,904	5,731	6,870	6,444	5,626								
Solyc07g005650	WRKY transcription factor 32	WRKY32	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	11,074	9,429	19,587	19,270	17,857								
Solyc07g005660	Purine permease-related family protein (AHRD V3.3 *** B9HB18_POPTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane	PF16913 (PFAM); IPR030182 (PANTH	24,982	21,227	30,819	29,697	28,002								
Solyc07g005670	Integral membrane HRF1 family protein (AHRD V3.3 *** A0A061GI14_THECC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G	IPR005578 (PFAM); PTHR14083:SF3	0,056	0,106	0,000	0,000	0,000								
Solyc07g005685	Carboxypeptidase (AHRD V3.3 *-* M1ARY0_SOLTU)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor	IPR001563 (PFAM); G3DSA:3.40.50.1	0,000	0,019	0,000	0,000	0,000								
Solyc07g005690	Ribosomal RNA small subunit methyltransferase G (AHRD V3.3 *** A0A0B0NU00_GOSAR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	PTHR34807 (PANTHER); PTHR34807	63,864	66,461	86,881	92,349	84,931								
Solyc07g005700	Zinc finger protein 385D (AHRD V3.3 *** A0A0B2SEZ1_GLYSO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding	IPR003604 (SMART); G3DSA:3.30.16	39,391	39,336	32,073	26,612	29,048								
Solyc07g005710	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 --* NDHI_ANGEV)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	29,619	25,049	35,131	30,174	30,499								
Solyc07g005720	Low temperature and salt responsive protein family (AHRD V3.3 *** AT4G30660.2)		C:GO:0016021	C:integral component of membrane	IPR000612 (PFAM); PTHR21659:SF3	0,120	0,181	0,240	0,167	0,165								
Solyc07g005730	Low temperature and salt responsive protein family (AHRD V3.3 *** AT4G30660.2)		C:GO:0016021	C:integral component of membrane	IPR000612 (PFAM); PTHR21659:SF3	48,494	41,596	34,886	38,246	33,756								
Solyc07g005740	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061DRG0_THECC)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	2,283	3,400	2,617	2,401	2,230								
Solyc07g005750	F-box family protein (AHRD V3.3 *** A0A061GK25_THECC)		F:GO:0005515	F:protein binding	IPR006553 (SMART); G3DSA:1.20.12	8,703	13,266	9,423	14,256	13,652								
Solyc07g005760	hydroxycinnamoyl CoA quinate transferase	hqt	F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR023213 (G3DSA:3.30.559.GENE3I	20,260	19,473	120,012	144,255	97,798								
Solyc07g005765	Ferredoxin-1, chloroplastic (AHRD V3.3 --* FER1_ORYSI)				mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,075	0,000								
Solyc07g005770	LOW QUALITY:Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	5,233	4,259	2,347	1,808	2,212								
Solyc07g005780	Eukaryotic translation initiation factor 4G (AHRD V3.3 *-* W9QJ22_9ROSA)		F:GO:0003723; F:G(	F:RNA binding; F:protein binding	IPR003890 (SMART); IPR016021 (G3	0,792	0,641	0,284	0,210	0,496								
Solyc07g005790	Multipolar spindle 1, putative isoform 1 (AHRD V3.3 *** A0A061GPW9_THECC)		P:GO:0000212; P:G(	P:meiotic spindle organization; P:meiotic DNA double-strand bre	mobidb-lite (MOBIDB_LITE); IPR0375(	5,989	5,796	6,102	6,094	5,726								
Solyc07g005810	translation initiation factor eIF(iso)4G		F:GO:0003723; F:G(	F:RNA binding; F:protein binding	IPR003891 (SMART); IPR003890 (SN	424,908	379,339	366,339	308,885	315,427								
Solyc07g005820	heat shock protein 70 (AHRD V3.3 *** AT3G12580.1)		F:GO:0005524; C:G(	F:ATP binding; C:cy EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR013126 (PRINTS); G3DSA:3.90.64	0,360	2,443	3,355	6,557	0,582								
Solyc07g005830	Translation initiation factor IF-3 (AHRD V3.3 *** K4CB54_SOLLC)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation	IPR036788 (G3DSA:3.30.110.GENE3I	15,358	22,997	31,847	31,809	39,256	0,610	0,028					up		
Solyc07g005840	Cellulose synthase (AHRD V3.3 *** M1ARZ5_SOLTU)		C:GO:0016020; F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (l	IPR005150 (PFAM); IPR029044 (G3D	0,465	0,409	0,051	0,048	0,093								
Solyc07g005850	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** A0A061GNM9_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR032867 (PFAM); IPR011990 (G3D	2,638	2,480	2,284	2,745	2,425								
Solyc07g005860	QWRF motif protein (DUF566) (AHRD V3.3 *** AT4G30710.3)		C:GO:0005737; C:G(	C:cytoplasm; C:centrosome; C:nuclear microtubule; P:centrosor	IPR007573 (PFAM); mobidb-lite (MOB	11,377	7,742	15,467	15,847	14,801								
Solyc07g005870	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT4G30720.1)		F:GO:0071949	F:FAD binding	IPR036188 (G3DSA:3.50.50.GENE3D	4,088	5,619	7,140	6,677	8,584								
Solyc07g005880	Replication factor C subunit 1 (AHRD V3.3 *** A0A061FPV6_THECC)		F:GO:0003689; F:G(	F:DNA clamp loader EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR001357 (SMART); IPR003593 (SN	80,299	63,224	67,210	64,050	64,528								
Solyc07g005890	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9T3L1_RICCO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR014001 (SMART); IPR001650 (SN	15,501	10,681	16,012	16,813	15,723								
Solyc07g005895	galactosyltransferase family protein (AHRD V3.3 *-* AT1G30260.1)		P:GO:0009735	P:response to cytokinin	mobidb-lite (MOBIDB_LITE); mobidb-lit	1,760	4,228	0,334	0,075	0,658	1,295	0,009					up		
Solyc07g005900	Calcium-binding EF-hand family protein (AHRD V3.3 *** A0A061GQP8_THECC)		F:GO:0005509	F:calcium ion binding	IPR002048 (SMART); IPR002048 (PF.	2,582	1,576	0,865	0,964	0,843								
Solyc07g005910	zein-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *** AT5G57830.1)				IPR007656 (PFAM); mobidb-lite (MOB	0,279	0,391	0,249	0,319	0,307								
Solyc07g005920	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** AT2G24130.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR000719 (SMART); IPR003591 (SN	0,019	0,000	0,050	0,000	0,047								
Solyc07g005930	DNA-directed RNA polymerase (AHRD V3.3 *** K4CB64_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA p(	IPR029262 (SMART); G3DSA:1.10.15	39,573	39,128	44,230	39,870	41,012								
Solyc07g005940	Vacuolar ATPase subunit H protein (AHRD V3.3 *** B6SIW6_MAIZE)		C:GO:0000221; F:G(	C:vacuolar proton-ti EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR000225 (SMART); IPR038497 (G3	188,814	184,379	218,222	219,066	221,239								
Solyc07g005950	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SQY5_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR011990 ((	10,467	11,719	7,420	7,564	8,863								
Solyc07g005960	Carboxypeptidase (AHRD V3.3 *** K4CB67_SOLLC)		F:GO:0004185; P:G(	F:serine-type carbo EC:3.4.21; EC:3.4.1(Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	26,757	25,675	3,247	2,848	3,591								
Solyc07g005970	Autophagy-related protein 11 (AHRD V3.3 *** W9S712_9ROSA)		P:GO:0000045; P:G(	P:autophagosome assembly; P:autophagy of mitochondrion	IPR019460 (PFAM); mobidb-lite (MOB	19,820	18,240	24,236	23,518	22,339								
Solyc07g005980	RING finger protein (AHRD V3.3 *** G7JDN4_MEDTR)				IPR001841 (SMART); IPR013083 (G3	0,080	0,103	0,517	0,247	0,260								
Solyc07g005990	ATP-dependent DNA helicase (AHRD V3.3 *** AT4G30780.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	71,668	77,405	83,293	86,639	79,572								
Solyc07g006000	50S ribosomal protein L35 (AHRD V3.3 *** K4CB71_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001706 (PRINTS); G3DSA:2.40.50	8,094	14,310	8,217	12,142	15,289	0,852	0,034	0,893	0,000	0,566	0,012	up	up	up
Solyc07g006010	Transducin/WD40 repeat protein (AHRD V3.3 *** G7JFH6_MEDTR)		F:GO:0005515; C:G(	F:protein binding; C:nuclear pore outer ring	IPR001680 (SMART); IPR015943 (G3	15,680	13,964	15,397	12,866	12,779								
Solyc07g006020	ADIPOR-like receptor (AHRD V3.3 *** W9QY38_9ROSA)		C:GO:0016021	C:integral component of membrane	IPR004254 (PFAM); IPR004254 (PAN	0,122	0,310	0,197	0,097	0,260								
Solyc07g006030	F-box family protein (AHRD V3.3 --* AT3G18720.1)					1,315	3,206	2,303	3,427	5,351	1,309	0,003	1,206	0,000			up	up	
Solyc07g006035	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT4G28080.1)		F:GO:0005515	F:protein binding	IPR019734 (SMART); IPR011990 (G3	41,862	80,343	61,361	84,764	147,137	0,966	0,002	1,259	0,000	0,469	0,001	up	up	up

Solyc07g006040	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** AT4G30845.1)		C:GO:0016021	C:integral component of membrane			PTHR38389 (PANTHER)	0,640	0,670	0,097	0,101	0,376									
Solyc07g006045	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9P5Y6_ZOSMR)		C:GO:0005634; F:G(	C:nucleus; F:histon	EC:2.1.1.43	Histone-lysine N-met	IPR001965 (SMART): IPR013083 (G3	0,000	0,000	0,000	0,000	0,023									
Solyc07g006060	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A072THL4_MEDTR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR003616 (SMART): IPR001214 (SM	0,042	0,097	0,025	0,000	0,047									
Solyc07g006070	GDP-mannose 3,5-epimerase 1 (AHRD V3.3 *** GME1_ORYSI)		P:GO:0009226; F:G(	P:nucleotide-sugar biosynthetic process; F:oxidoreductase acti			IPR001509 (PFAM): G3DSA:3.90.25.1	23,483	26,603	33,100	28,223	27,664									
Solyc07g006100	Oxysterol-binding protein (AHRD V3.3 *** A9ZM29_SOYBN)		C:GO:0005829; F:G(	C:cytosol; F:sterol transporter activity; P:sterol transport; C:me			IPR001849 (SMART): G3DSA:2.40.16	0,913	0,859	3,095	3,160	2,782									
Solyc07g006110	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT2G23950.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR032675 (G3	7,767	8,902	4,804	8,665	6,520					0,857	0,008			up
Solyc07g006120	Autophagy-related protein 18 (AHRD V3.3 *** A0A0B2QCI2_GLYSO)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	8,345	8,082	14,350	13,890	12,624									
Solyc07g006130	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *** ERF1X_ARATH)		F:GO:0003747; C:G(	F:translation release factor activity; C:cytoplasm; P:translationa			IPR005140 (SMART): G3DSA:3.30.42	9,320	10,334	37,475	34,061	31,486									
Solyc07g006140	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *-* A0A0A9G2E9_ARUDO)							0,061	0,163	0,050	0,148	0,047									
Solyc07g006145	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	22,885	45,908	9,247	13,323	13,807	1,028	0,016					up		
Solyc07g006150	Transmembrane protein (AHRD V3.3 *** G7JED5_MEDTR)		C:GO:0005773; P:G(	C:vacuole; P:vacuolar protein processing; C:integral component			IPR008506 (PFAM): mobidb-lite (MOB	18,505	20,342	23,760	24,413	23,067									
Solyc07g006160	Lactation elevated protein 1 (AHRD V3.3 *** W9RT81_9ROSA)		F:GO:0005524	F:ATP binding			IPR005654 (PFAM): G3DSA:3.40.50.3	31,619	33,756	54,396	60,803	52,242									
Solyc07g006170	Exostosin family protein (AHRD V3.3 *** A0A061F0X5_THECC)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM): IPR004263 (PAN	0,019	0,094	0,025	0,025	0,095									
Solyc07g006180	Tetratricopeptide repeat protein (AHRD V3.3 *** B6GVA2_SOLLC)	TPR1	F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR001440 (PF	45,743	39,782	100,191	93,316	92,286									
Solyc07g006190	5'-nucleotidase domain-containing protein (AHRD V3.3 *** A0A0B2Q7B7_GLYSO)		F:GO:0008253; P:G(	F:5'-nucleotidase a	EC:3.1.3.5; EC:3.1.3	5'-nucleotidase; Nucl	IPR008380 (PFAM): IPR016695 (PIRS	15,097	13,373	20,165	23,385	20,252									
Solyc07g006200	Metal-dependent phosphohydrolase HD domain-containing protein (AHRD V3.3 *** D7LG30_ARALL)		F:GO:0002953	F:5'-deoxynucleotidase activity			IPR003607 (SMART): IPR006674 (PF	21,466	22,494	33,250	31,661	33,019									
Solyc07g006210	LOW QUALITY:ECA1 gametogenesis family protein (DUF784) (AHRD V3.3 -** AT4G13263.1)						IPR008502 (PFAM): mobidb-lite (MOB	0,040	0,041	0,025	0,000	0,000									
Solyc07g006220	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE1	C:GO:0016021; F:G(	C:integral compone	EC:5.1.3.12	UDP-glucuronate 5'-e	PR01713 (PRINTS): G3DSA:3.40.50.7	487,822	371,622	328,956	429,800	463,686									
Solyc07g006230	LOW QUALITY:NAC domain-containing protein 78 (AHRD V3.3 --* M7YSE5_TRIUA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,292	0,534	0,000	0,025	0,048									
Solyc07g006240	DNA-directed RNA polymerase III subunit rpc8 (AHRD V3.3 *** W9QXR4_9ROSA)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA po	IPR036898 (G3DSA:3.30.1490.GENE	6,739	6,301	6,946	6,926	6,821									
Solyc07g006260	Protein FLX-like 2 (AHRD V3.3 *** A0A199ULF4_ANACO)						mobidb-lite (MOBIDB_LITE): IPR0403	18,300	17,635	19,398	14,652	16,324									
Solyc07g006270	Cytochrome c oxidase subunit 6B (AHRD V3.3 *-* A0A151TZY7_CAJCA)		C:GO:0005739	C:mitochondrion			IPR003213 (PIRSF): IPR036549 (G3D	29,674	32,281	64,156	57,072	55,432									
Solyc07g006280	Tetraspanin family protein (AHRD V3.3 *** A0A072V357_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	940,666	798,329	1216,381	1364,911	1192,682									
Solyc07g006300	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT5G57800.1)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM): G3DSA:3.40.50.7	7,512	5,019	4,239	7,126	4,895					0,745	0,017			up
Solyc07g006310	Basic helix-loop-helix transcription factor (AHRD V3.3 --* A0A0H3Y8Z9_SALMI)		F:GO:0046983	F:protein dimerization activity			PTHR33124 (PANTHER): PTHR33124	0,042	0,037	0,000	0,000	0,000									
Solyc07g006320	auxin canalization protein (DUF828) (AHRD V3.3 *** AT5G57770.1)						IPR008546 (PFAM): IPR013666 (PFA	0,297	0,197	0,101	0,073	0,046									
Solyc07g006330	Mannosyltransferase (AHRD V3.3 *** K4CBA4_SOLLC)		F:GO:0000030; P:G(	F:mannosyltransferase activity; P:GPI anchor biosynthetic proc			IPR005599 (PFAM): mobidb-lite (MOB	2,613	2,091	1,751	1,386	2,189									
Solyc07g006340	Acyl-CoA N-acyltransferase (AHRD V3.3 *** A0A103YMJ3_CYNCS)		C:GO:0009507	C:chloroplast			G3DSA:3.40.630.30 (GENE3D): IPR0	7,813	8,199	42,596	41,710	42,177									
Solyc07g006350	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9T4P9_RICCO)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	9,426	8,458	5,827	7,947	7,219									
Solyc07g006360	RING/U-box superfamily protein (AHRD V3.3 *** AT4G30400.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination; F:u			IPR001841 (SMART): IPR001841 (PF	0,337	0,817	0,025	0,095	0,140									
Solyc07g006370	Cation calcium exchanger (AHRD V3.3 *** A0A072U799_MEDTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004837 (PFAM): G3DSA:1.20.142	10,190	4,466	17,968	13,946	11,313	-1,154	0,013	-0,670	0,011			down	down	
Solyc07g006380	Defensin-like protein (AHRD V3.3 *** DEF_TOBAC)		P:GO:0006952	P:defense response			IPR008176 (PRINTS): IPR003614 (SM	34,210	173,042	0,000	0,000	0,000									
Solyc07g006390	Blight-associated protein p12 (AHRD V3.3 *** B6T987_MAIZE)		C:GO:0005618	C:cell wall			IPR007112 (SMART): IPR009009 (PF	1,355	0,488	0,000	0,000	0,000									
Solyc07g006395	Blight-associated protein P12 (AHRD V3.3 *** B6RN47_CITMA)						IPR036908 (G3DSA:2.40.40.GENE3D	0,019	0,039	0,000	0,000	0,000									
Solyc07g006400	RING/U-box superfamily protein (AHRD V3.3 *** AT4G30370.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	21,478	20,217	27,938	19,689	21,156			-0,405	0,025	-0,502	0,002		down	down
Solyc07g006410	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT4G16850.1)		C:GO:0016021	C:integral component of membrane			PTHR33133 (PANTHER): PTHR33133	0,236	0,314	0,219	0,245	0,307									
Solyc07g006430	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G18490.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR021109 (G3D	0,000	0,039	0,000	0,000	0,000									
Solyc07g006450	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G20015.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR021109 (G3D	0,038	0,019	0,000	0,000	0,000									
Solyc07g006460	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G18490.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,334	0,913	0,000	0,000	0,000									
Solyc07g006480	Receptor-like kinase (AHRD V3.3 *** D4QD70_DIACA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR032675 (G3DSA:3.80.10.GENE3D	3,653	21,909	1,668	2,366	5,451	2,608	0,000	1,705	0,003			up	up	
Solyc07g006490	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 --* C0PRU3_PICSI)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			PTHR37752 (PANTHER)	6,033	8,450	11,043	12,760	13,466									
Solyc07g006500	trehalose-6-phosphate synthase 1	t6ps-1	F:GO:0003824; P:G(	F:catalytic activity; P:trehalose biosynthetic process			IPR006379 (TIGRFAM): G3DSA:3.40.5	10,724	16,376	66,725	101,994	82,934					0,616	0,033			up
Solyc07g006510	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (SMART): IPR014710 (G3	35,851	45,406	53,683	53,030	52,616									
Solyc07g006520	Preprotein translocase subunit SECY, chloroplastic (AHRD V3.3 *** A0A0B2PHE6_GLYSO)		P:GO:0015031; C:G(	P:protein transport; C:membrane			PR00303 (PRINTS): IPR002208 (PFA	17,716	23,729	60,437	68,700	69,094									
Solyc07g006530	Adenylosuccinate lyase (AHRD V3.3 *** K4CBC4_SOLLC)		F:GO:0004018; P:G(	F:N6-(1,2-dicarbox	EC:4.3.2.2	Adenylosuccinate lya	IPR000362 (PRINTS): IPR022761 (PF	28,744	31,439	38,351	40,247	36,241									
Solyc07g006540	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 ***		F:GO:0005524; P:G(	F:ATP binding; P:protein metabolic process			IPR036628 (G3DSA:1.10.1780.GENE	62,357	78,929	88,426	84,237	83,451									
Solyc07g006550	Ribonuclease S-6 (AHRD V3.3 --* RNS6_PYRPY)		F:GO:0003723; C:G(	F:RNA binding; C:e	EC:3.1.31; EC:3.1.2	Acting on ester bonds:	Acting on ester bonds: Ribonuclease	1,294	0,755	0,115	0,273	0,518									
Solyc07g006560	Hypersensitive response assisting protein (AHRD V3.3 *** Q9SWC6_CAPAN)		F:GO:0003723; F:G(	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bond	IPR001568 (PFAM): IPR036430 (G3D	0,793	2,536	0,074	0,297	0,046	1,699	0,037					up		
Solyc07g006570	Ribonuclease (AHRD V3.3 *** Q41722_ZINVI)		F:GO:0003723; F:G(	F:RNA binding; F:rit	EC:3.1.31; EC:3.1.2	Acting on ester bond	IPR036430 (G3DSA:3.90.730.GENE3	33,758	48,091	30,585	42,506	31,492					0,479	0,018			up
Solyc07g006580	Diacylglycerol kinase (AHRD V3.3 *** K4CBC9_SOLLC)		F:GO:0003951; F:G(	F:NAD+ kinase acti	EC:2.7.1.23; EC:2.7.	NAD(+) kinase; Diac	IPR001206 (SMART): IPR000756 (SM	25,490	20,593	22,948	21,801	20,314									
Solyc07g006590	LOW QUALITY:kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing protein (AHRD V3.3 --* AT3G24715.3)						mobidb-lite (MOBIDB_LITE)	1,810	1,739	2,092	2,408	2,590									
Solyc07g006600	glutamine dumper 3 (AHRD V3.3 *** AT5G57685.1)		P:GO:0080143	P:regulation of amino acid export			mobidb-lite (MOBIDB_LITE): mobidb-lit	17,244	28,937	147,210	100,462	120,182					-0,548	0,000			down
Solyc07g006610	Tyrosine kinase family protein (AHRD V3.3 *** G7JD53_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	0,019	0,000	0,000	0,000	0,000									
Solyc07g006620	Receptor-like kinase (AHRD V3.3 *** G7JD52_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,000	0,019	0,000	0,000	0,000									
Solyc07g006630	CONSTANS-like protein (AHRD V3.3 *** B2MW87_SOLLC)	BBX6	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR000315 (SMAF CO-like	1,964	2,220	2,942	2,144	2,610									
Solyc07g006640	ADP-ribosylation factor family protein (AHRD V3.3 *** B9IM33_POPTR)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): SM00178 (SMA	57,343	56,385	49,746	48,287	46,272									
Solyc07g006650	Xylose isomerase (AHRD V3.3 *** A0A0V0IEZ8_SOLCH)		P:GO:0005975; F:G(	P:carbohydrate met	EC:5.3.1.5	Xylose isomerase	IPR001998 (PRINTS): G3DSA:3.20.20	150,218	148,325	290,651	280,845	288,605									
Solyc07g006680	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM): IPR023213 (G3D	13,198	7,908	0,899	0,825	1,079									
Solyc07g006690	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G25770.1)		P:GO:0044255	P:cellular lipid metabolic process			IPR007751 (PFAM): PTHR12482 (PAN	17,516	17,339	26,316	26,306	26,243									
Solyc07g006700	Pathogenesis-related family protein (AHRD V3.3 *** B9IM28_POPTR)		C:GO:0005615	C:extracellular space			IPR002413 (PRINTS): IPR001283 (PF	0,179	0,504	0,075	0,025	0,024									
Solyc07g006710	Pathogenesis-related protein 1 (AHRD V3.3 *** PR1_HORVU)		C:GO:0005615	C:extracellular space			IPR001283 (PRINTS): IPR002413 (PF	0,101	0,076	0,046	0,000	0,000									
Solyc07g006730	Protein DETOXIFICATION (AHRD V3.3 *** K4CBE4_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	23,631	23,484	7,249	5,261	6,114									
Solyc07g006740	Protein DETOXIFICATION (AHRD V3.3 *** K4CBE5_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	0,000	0,019	0,025	0,000	0,047									
Solyc07g006750	blind-like8	R2R3MYB36	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,000	0,018	0,000	0,000	0,000									
Solyc07g006760	MAP kinase kinase kinase 43	MAPKKK43	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PRINTS): IPR000270 (SM	45,462	37,118	46,776	42,795	48,659									
Solyc07g006770	Receptor-like protein kinase (AHRD V3.3 *** RPK1_IPONI)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR000719 (SMA	5,934	26,702	3,213	6,376	5,560	2,191	0,001	0,788	0,007	0,989	0,001	up	up	up
Solyc07g006780	FGGY family of carbohydrate kinase (AHRD V3.3 *** AT4G30310.2)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:phosphotransferase activi			G3DSA:3.30.420.40 (GENE3D): IPR0	38,666	38,177	67,093	77,413	70,516									
Solyc07g006790	Acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4CBF0_SOLLC)		F:GO:0004742; P:G(	F:dihydrolipoyllysine	EC:2.3.1.38; EC:2.3.	[Acyl-carrier-protein]	IPR036625 (G3DSA:4.10.320.GENE3	77,722	78,231	127,624	124,641	116,426									
Solyc07g006810	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (AHRD V3.3 *** W9S907_9ROSA)		F:GO:0008483; F:G(	F:transaminase activity; F:pyridoxal phosphate binding			IPR015422 (G3DSA:3.90.1150.GENE	18,696	17,447	9,874	7,197	9,941									
Solyc07g006820	Transcription initiation factor TFIID subunit 1 (AHRD V3.3 *** A0A1D1Y4I7_9ARAE)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR000626 (SM	74,515	62,231	88,712	91,237	92,220									
Solyc07g006830	Calmodulin-binding protein (AHRD V3.3 *** P93370_TOBAC)		F:GO:0005516	F:calmodulin binding			IPR012416 (PFAM): mobidb-lite (MOB	91,138	80,869	121,128	122,223	117,623									
Solyc07g006850	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *-* K4CBF6_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	G3DSA:2.60.120.200 (GENE3D): IPR	0,000	0,000	0,000	0,000	0,023									
Solyc07g006855	CASP-like protein (AHRD V3.3 *** M1BM50_SOLTU)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 in			IPR006459 (TIGRFAM): IPR006702 (F	0,115	0,099	0,209	0,244	0,371									
Solyc07g006860	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CBF7_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR000757 (PFAM): G3DSA:2.60.120	0,000	0,021	0,000	0,000	0,000									
Solyc07g006870	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CBF8_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR008264 (PRINTS): IPR016455 (PII	0,019	0,021	0,025	0,025	0,000									
Solyc07g006880	Zinc finger protein, putative (AHRD V3.3 *** B9T768_RICCO)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	13,364	12,869	24,473	20,560	18,262									
Solyc07g006890	Cytochrome P450, putative (AHRD V3.3 *** B9S4U5_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	185,384	328,100	31,783	32,582	49,027									
Solyc07g006900	SIPIN2	PIN4	P:GO:0010315; F:G(	P:auxin efflux; F:auxin efflux transmembrane transporter activity			IPR014024 (TIGRFAM): IPR004776 (F	0,019	0,062	0,025	0,050	0,000									
Solyc07g006910	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT5G55950.1)		C:GO:0016021	C:integral component of membrane			IPR004853 (PFAM): mobidb-lite (MOB	24,140	18,213	35,236	49,066	39,358					0,481	0,003			up
Solyc07g006920	TRICHOME BIREFRINGENCE-LIKE 5 (AHRD V3.3 *** AT5G20590.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	10,921	10,167	8,874	6,814	8,217									
Solyc07g006930	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G02645.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): PTHR31549:SF2	0,203	0,240	0,196	0,124	0,212									
Solyc07g006940	Receptor-like kinase (AHRD V3.3 *** G7JT83_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,019	0,126	0,022	0,000	0,047									
Solyc07g006950	peroxisome 1 (AHRD V3.3 --* AT5G08470.4)							4,734	3,559	8,875	8,313	7,786									
Solyc07g006960	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT2G18910.1)						IPR028260 (PFAM): mobidb-lite (MOB	22,317	22,529	12,387	11,180	14,022									
Solyc07g006970	Sugar transporter protein 3	STP3	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI	25,063	22,977	25,844	22,496	26,056									
Solyc07g006980	Trichome birefringence (AHRD V3.3 --* A0A0K9NN56_ZOSMR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR029970 (PTH	0,180	0,132	0,118	0,149	0,163									
Solyc07g006990	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H9D6_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR011990 ((	1,416	1,603	1,770	1,837	1,461									
Solyc07g007000	Protein trichome birefringence (AHRD V3.3 *-* TBR_ARATH)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR029962 (PAN	0,361	0,472	0,692	0,292	0,353									
Solyc07g007010	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G02645.1)		C:GO:0016021	C:integral component of membrane			IPR004158 (PFAM): IPR004158 (PAN	0,019	0,021	0,065	0,050	0,047									
Solyc07g007015	pseudo-response regulator 3 (AHRD V3.3 --* AT5G60100.7)							0,021	0,037	0,123	0,051	0,070									
Solyc07g007020	Kinase family protein (AHRD V3.3 *** B9GLQ0_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR001881 (SMART): IPR000719 (SM	1,372	1,541	0,502	1,156	0,588									
Solyc07g007030	Transmembrane 9 superfamily member (AHRD V3.3 *** A0A0V0IRK7_SOLCH)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): PTHR10766:SF4	119,657	132,152	104,236	120,702	86,904									
Solyc07g007040	G-patch domain-containing protein (AHRD V3.3 *** A0A103XDG0_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR000467 (SMART): IPR000467 (PF	87,939	74,805	126,481	120,661	121,166									
Solyc07g007050	Zinc finger, SWIM-type (AHRD V3.3 *** A0A118JSI3_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,138	2,519	1,540	0,911	1,132									
Solyc07g007060	Metal tolerance protein (AHRD V3.3 *** A7L8D2_CUCSA)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;			IPR027469 (G3DSA:1.20.1510.GENE	27,193	28,115	56,095	65,942	52,907									
Solyc07g007090	LOW QUALITY:xylem cysteine peptidase 1 (AHRD V3.3 --* AT4G35350.2)							0,000	0,021	0,000	0,000	0,000									
Solyc07g007100	LOW QUALITY:Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein isoform 1 (AHRD V3.3 *-* A0A061GPI9_THECC)						mobidb-lite (MOBIDB_LITE): PTHR351	0,000	0,000	0,000	0,000	0,024									
Solyc07g007110	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4CBI2_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR029000 (G3	21,033	21,775	40,939	40,552	39,573									
Solyc07g007120	class II knotted-like homeodomain protein	LeT12	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR005539 (SMAF TALE	138,422	109,023	95,505	89,105	89,906									
Solyc07g007125	embryonic flower 1 (EMF1) (AHRD V3.3 --* AT5G11530.3)							0,693	0,756	0,734	0,884	0,636									
Solyc07g007140	MAP kinase kinase kinase 44	MAPKKK44	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PRINTS): IPR000719 (SM	144,613	68,519	142,133	286,160	151,942	-1,053	0,003			1,012	0,000	down		up
Solyc07g007150	LOW QUALITY:Guanine nucleotide-binding protein subunit beta (AHRD V3.3 --* A0A199VAA6_ANACO)						mobidb-lite (MOBIDB_LITE): PTHR331	29,699	18,983	12,149	7,405	9,481	-0,618	0,042			-0,709	0,021	down		down
Solyc07g007160	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GN77_THECC)		P:GO:0006511; P:G(	P:ubiquitin-dependent protein catabolic process; P:protein ubiqu			IPR001841 (SMART): IPR001841 (PF	31,053	22,090	12,911	10,883	13,238									
Solyc07g007170	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GN77_THECC)		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ligase activit			PTHR14155 (PANTHER): PTHR14155	86,567	112,864	16,517	45,409	35,564			1,103	0,000	1,460	0,000		up	up
Solyc07g007180	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GN77_THECC)		P:GO:0006511; P:G(	P:ubiquitin-dependent protein catabolic process; P:protein ubiqu			IPR001841 (PFAM): IPR013083 (G3D	13,701	11,317	15,257	13,510	14,669									
Solyc07g007190	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 1 (AHRD V3.3 *** A0A061GPH6_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,274	0,326	0,000	0,025	0,000									
Solyc07g007200	Ring finger protein, putative (AHRD V3.3 *** B9T2M9_RICCO)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,006	3,437	6,126	5,908	4,982									
Solyc07g007210	Elongation factor like protein (AHRD V3.3 *** A0A0K9P374_ZOSMR)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR005517 (SM	110,316	96,877	125,437	117,607	121,381									
Solyc07g007220	Protein phosphatase 2c, putative (AHRD V3.3 *** B9T2N5_RICCO)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART): IPR036457 (G3	19,006	19,286	5,480	8,512	10,466			0,926	0,007				up	
Solyc07g007230	DnaJ domain-containing protein (AHRD V3.3 *-* A0A118K6N5_CYNCS)						IPR001623 (SMART): IPR001623 (PF	37,425	38,597	42,119	39,436	40,269									
Solyc07g007240	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** A0A0A0VBW2_SOLTU)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR004231 (PFAM): IPR021142 (PRC	0,040	0,000	0,072	0,197	0,095									
Solyc07g007250	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** MCPI_SOLLC)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR004231 (PFAM): IPR021142 (PRC	152,203	395,489	7,291	3,059	4,830					-1,254	0,000			down
Solyc07g007260	Metallocarboxypeptidase inhibitor-like protein (AHRD V3.3 *** A0A089Q749_SOLHA)		F:GO:0004866	F:endopeptidase inhibitor activity			IPR004231 (PFAM): IPR021142 (PRC	2,100	18,072	0,000	0,025	0,000	3,124	0,004					up		
Solyc07g007270	root meristem growth factor (AHRD V3.3 --* AT5G64770.1)		F:GO:0008083	F:growth factor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,882	3,962	0,022	0,025	0,024									
Solyc07g007280	chlororespiratory reduction 6 (AHRD V3.3 *** AT2G47910.2)		C:GO:0009507; P:G(	C:chloroplast; P:NAD(P)H dehydrogenase complex assembly			IPR014946 (PFAM): PTHR35724:SF1	1,544	3,769	0,457	0,505	1,081	1,309	0,023					up		
Solyc07g007300	Methyltransferase-related family protein (AHRD V3.3 *** B9IMM0_POPTR)		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM): G3DSA:3.40.50.1	8,956	7,546	13,269	15,598	16,398									
Solyc07g007310	Methyltransferase-related family protein (AHRD V3.3 *** B9IMM0_POPTR)		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM): G3DSA:3.40.50.1	18,816	18,835	16,623	15,682	15,983									
Solyc07g007325	Serine-rich protein-related (AHRD V3.3 *-* A0A061GN42_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,212	0,177	0,965	0,875	0,736									
Solyc07g007330	Serine-rich protein-related (AHRD V3.3 *** A0A061GN42_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	13,093	17,884	19,160	14,357	13,745									
Solyc07g007340	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9Q428_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR010658 (PFAM): IPR011701 (PFA	14,344	10,510	10,148	9,881	9,553									
Solyc07g007350	LOW QUALITY:sterile alpha motif (SAM) domain protein (AHRD V3.3 *** AT2G12462.1)		F:GO:0005515	F:protein binding			IPR001660 (PFAM): G3DSA:1.10.150	11,222	6,927	9,294	11,962	9,746									
Solyc07g007360	Harbinger transposase-derived nuclease (AHRD V3.3 *** A0A124SCG9_CYNCS)						IPR027806 (PFAM): mobidb-lite (MOB	22,499	17,890	27,663	26,271	22,863									
Solyc07g007370	NEDD8 ultimate buster 1 (AHRD V3.3 *** A0A0B0NND4_GOSAR)		F:GO:0005515	F:protein binding			IPR015940 (SMART): G3DSA:1.10.8.1	21,316	23,311	27,579	27,178	24,495									
Solyc07g007380	OS-9 (AHRD V3.3 *** A0A061GN28_THECC)		C:GO:0005788; F:G(	C:endoplasmic reticulum lumen; F:carbohydrate binding; P:ubiqu			IPR009011 (G3DSA:2.70.130.GENE3	15,960	16,633	27,730	29,479	26,569									
Solyc07g007390	Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repeat-containing protein (AHRD		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR000270 (SM	62,048	56,557	83,508	92,924	87,861									
Solyc07g007400	Leucine-rich repeat family protein (AHRD V3.3 *-* B9HAJ1_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,119	0,181	0,121	0,050	0,165									
Solyc07g007410	Leucine-rich repeat family protein (AHRD V3.3 *** AT1G15740.1)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR032675 (G3	51,208	34,073	43,373	48,862	58,439									
Solyc07g007420	F-box/LRR-repeat protein, putative (AHRD V3.3 *-* B9RVD1_RICCO)						IPR032675 (G3DSA:3.80.10.GENE3D	36,481	23,996	29,794	32,981	41,738									
Solyc07g007430	S-acyltransferase (AHRD V3.3 *** K4CBL3_SOLLC)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	52,761	69,148	39,586	42,568	44,370									
Solyc07g007440	RING/U-box superfamily protein (AHRD V3.3 *** AT5G05810.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR013083 (G3	1,459	1,429	0,000	0,025	0,070									
Solyc07g007450	Iron-sulfur cluster assembly protein (AHRD V3.3 *** K4CBL5_SOLLC)		F:GO:0005506; P:G(	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl			G3DSA:3.90.1010.10 (GENE3D): IPR	1,301	2,579	1,443	1,510	2,410									
Solyc07g007460	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,078	0,103	0,000	0,072	0,093									
Solyc07g007480	Protein DETOXIFICATION (AHRD V3.3 *-* M1D0T9_SOLTU)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			PTHR11206 (PANTHER): PTHR11206	0,096	0,080	0,025	0,000	0,024									
Solyc07g007490	Protein DETOXIFICATION (AHRD V3.3 *** K4CBE4_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): PTHR11206 (PAN	0,061	0,057	0,000	0,022	0,023									
Solyc07g007500	Protein TIC 214 (AHRD V3.3 --* TI214_PINKO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	42,880	46,622	59,067	57,094	60,516									
Solyc07g007510	Adenylate cyclase (AHRD V3.3 *** G7JGL5_MEDTR)		P:GO:0048364; F:G(	P:root development	EC:3.6.1.25	Triphosphatase	IPR023577 (SMART): IPR023577 (PF	41,070	34,089	40,790	35,315	33,126									
Solyc07g007530	LOW QUALITY:egg cell-secreted-like protein (DUF1278) (AHRD V3.3 -** AT2G14378.1)		C:GO:0005576; P:G(	C:extracellular region; P:double fertilization forming a zygote and			IPR008502 (PFAM)	0,040	0,174	0,000	0,000	0,000									
Solyc07g007550	Heparanase-like protein 3 (AHRD V3.3 *** A0A0B2S006_GLYSO)		C:GO:0016020; F:G(	C:membrane; F:hydrolase activity, acting on glycosyl bonds			G3DSA:3.20.20.80 (GENE3D): IPR00	14,260	9,276	1,312	1,364	2,709			1,015	0,038				up	
Solyc07g007560	phosphate transporter 4-5 (AHRD V3.3 *** AT5G20380.2)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM): G3DSA:1.20.125	6,210	6,025	7,223	8,285	9,842									
Solyc07g007570	LOW QUALITY:Transcription factor PCF6 (AHRD V3.3 --* PCF6_ORYSI)							0,097	0,115	0,000	0,025	0,024									
Solyc07g007580	LOW QUALITY:Actin binding Calponin homology (CH) domain-containing protein (AHRD V3.3 --* AT5G48460.1)							0,154	0,173	0,000	0,000	0,000									

Solyc07g007590	Arogenate dehydrogenase 1 (AHRD V3.3 *** F1BPV5_SOLPN)	ADH1	F:GO:0004665; P:G(	F:prephenate dehyc	EC:1.3.1.12; EC:1.3.	Prephenate dehydroc	IPR003099 (PFAM); G3DSA:3.40.50.7	96,389	52,665	18,798	40,693	28,042	-0,846	0,001			1,114	0,000	down		up
Solyc07g007600	vacuolar-type H+-pyrophosphatase	vp1d1	F:GO:0004427; F:G(	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (PFAM); IPR004131 (PIRS	443,086	455,019	277,591	314,744	306,848									
Solyc07g007610	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GPA7_THECC)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART); IPR013083 (G3	0,236	0,418	0,000	0,223	0,141									
Solyc07g007620	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** A0A087G8S7_ARAAL)		P:GO:0009247; F:G(	P:glycolipid biosynthetic process; F:transferase activity, transfe			IPR009695 (PFAM); IPR007235 (PFA	1,717	1,288	0,483	0,736	0,398									
Solyc07g007630	Actin-related protein 2/3 complex subunit 3 (AHRD V3.3 *** K4CBN3_SOLLC)		C:GO:0005885; P:G(	C:Arp2/3 protein complex; P:Arp2/3 complex-mediated actin nuc			IPR007204 (PFAM); IPR036753 (G3D	16,485	13,677	24,444	23,103	19,608									
Solyc07g007640	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9SXP1_RICCO)		F:GO:0008270; P:G(	F:zinc ion binding; F	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR013083 (G3DSA:3.30.40.GENE3D	8,329	8,532	12,061	12,507	12,379									
Solyc07g007650	Translocase of chloroplast 90, chloroplastic-like protein (AHRD V3.3 *** A0A0B0P4H1_GOSAR)		F:GO:0005525; F:G(	F:GTP binding; F:hydrolase activity, acting on acid anhydrides			G3DSA:3.40.50.300 (GENE3D); IPR0	30,847	30,793	44,569	44,470	42,549									
Solyc07g007660	LOW QUALITY:Mitochondrial group I intron splicing factor CCM1 (AHRD V3.3 *** A0A1D1ZJQ2_9ARAE)						mobidb-lite (MOBIDB_LITE); PTHR358	18,457	17,789	38,707	43,708	31,935									
Solyc07g007670	Purple acid phosphatase (AHRD V3.3 *** K4CBN7_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	24,949	25,466	3,411	2,192	3,843									
Solyc07g007680	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G05500.1)		F:GO:0008289	F:lipid binding			IPR000008 (PRINTS); IPR000008 (SM	48,472	37,398	39,488	37,597	36,418									
Solyc07g007690	Chloride channel protein (AHRD V3.3 *** M1D0Y1_SOLTU)		F:GO:0005247; P:G(	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR001807 (PRINTS); IPR002251 (PF	10,203	7,326	8,019	8,535	7,962									
Solyc07g007700	Protein-s-isoprenylcysteine O-methyltransferase (AHRD V3.3 *** D7MSF6_ARALL)		C:GO:0016021	C:integral component of membrane			IPR007318 (PFAM); G3DSA:1.20.120	11,707	10,835	25,238	25,764	25,963									
Solyc07g007710	Defensin protein (AHRD V3.3 *** B1N680_SOLLC)		P:GO:0006952	P:defense response			IPR008176 (PRINTS); IPR003614 (SM	1,722	6,197	1,037	2,817	0,139									
Solyc07g007730	Defensin protein (AHRD V3.3 *** B1N679_SOLLC)		P:GO:0006952	P:defense response			IPR008176 (PRINTS); IPR003614 (SM	6,154	1,047	0,047	0,000	0,000	-2,510	0,000					down		
Solyc07g007740	LOW QUALITY:Defensin-like protein (AHRD V3.3 *** DEF_TOBAC)		C:GO:0005576; C:G(	C:extracellular region; C:cell wall; C:vacuole; P:defense respons			PF00304 (PFAM); IPR036574 (G3DS/	0,381	0,502	0,823	0,893	0,751									
Solyc07g007745	Defensin-like protein (AHRD V3.3 *** DEF_TOBAC)		C:GO:0005576; C:G(	C:extracellular region; C:cell wall; C:vacuole; P:defense respons			PF00304 (PFAM); IPR036574 (G3DS/	0,194	0,193	0,000	0,000	0,000									
Solyc07g007750	Defensin protein (AHRD V3.3 *** B1N678_SOLLC)		P:GO:0006952	P:defense response			IPR008176 (PRINTS); IPR003614 (SM	856,108	726,378	228,453	89,321	112,460			-1,026	0,000	-1,352	0,000		down	down
Solyc07g007760	defensin-like protein		P:GO:0006952	P:defense response			IPR008176 (PRINTS); IPR003614 (SM	313,519	247,771	276,349	157,760	266,674					-0,806	0,000			down
Solyc07g007770	zinc finger WD40 repeat protein 1 (AHRD V3.3 --* AT4G25440.3)							0,141	0,611	0,072	0,025	0,071									
Solyc07g007775	Protein kinase superfamily protein (AHRD V3.3 --* AT3G57740.2)							0,000	0,021	0,000	0,000	0,000									
Solyc07g007780	Kinase family protein (AHRD V3.3 *** U5G9B2_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); G3DSA:1.10.51	48,235	50,710	90,585	90,122	75,939									
Solyc07g007790	sucrose-phosphate synthase	sps	P:GO:0005985; F:G(	P:sucrose metaboli	EC:2.4.1.14; EC:2.4.	Sucrose-phosphate s	IPR001296 (PFAM); IPR012819 (TIGF	488,844	304,481	678,227	571,732	588,350	-0,656	0,012					down		
Solyc07g007800	ADIPOR-like receptor (AHRD V3.3 *** W9SGZ8_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR004254 (PFAM); mobidb-lite (MOB	9,910	12,922	0,732	0,635	0,656									
Solyc07g007810	N-alpha-acetyltransferase 35, NatC auxiliary subunit (AHRD V3.3 *** A0A0B2Q139_GLYSO)		P:GO:0017196; C:G(	P:N-terminal peptidyl-methionine acetylation; C:NatC complex			IPR007244 (PFAM); mobidb-lite (MOB	16,699	13,708	13,882	15,583	14,672									
Solyc07g007820	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT5G35200.2)		F:GO:0005545; C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART); IPR014712 (G3	35,410	52,174	48,494	54,911	50,287	0,586	0,036					up		
Solyc07g007830	BSD domain-containing family protein (AHRD V3.3 *-* B9IMU0_POPTR)						IPR005607 (SMART); PTHR31923:SF	19,660	16,473	34,472	32,534	27,893									
Solyc07g007835	BSD domain-containing protein, putative (AHRD V3.3 *-* A0A061GVR9_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	27,655	22,975	50,985	46,198	42,123									
Solyc07g007840	SPOC domain / Transcription elongation factor S-II protein (AHRD V3.3 *-* AT2G25640.1)						IPR012921 (PFAM); mobidb-lite (MOB	15,872	14,037	10,612	11,866	11,632									
Solyc07g007850	SPOC domain / Transcription elongation factor S-II protein (AHRD V3.3 *-* AT2G25640.2)						PTHR11477:SF20 (PANTHER); PTHR	0,000	0,000	0,000	0,025	0,000									
Solyc07g007860	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *-* AT2G		C:GO:0009506; C:G(	C:plasmodesma; C:chloroplast thylakoid membrane; C:apoplast			IPR027923 (PFAM); G3DSA:1.10.110	0,042	0,000	0,000	0,000	0,000									
Solyc07g007870	12-oxophytodienoate reductase 3	opr3	F:GO:0010181; F:G(	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR001155 (PFAM); IPR013785 (G3D	120,119	220,053	33,151	23,631	31,457	0,901	0,001			-0,487	0,045	up		down
Solyc07g007890	CCR4-NOT transcription complex subunit 10 (AHRD V3.3 *** A0A0B2P7F1_GLYSO)		F:GO:0005515; C:G(	F:protein binding; C:CCR4-NOT complex			IPR019734 (SMART); IPR011990 (G3	40,631	40,978	52,749	53,972	48,829									
Solyc07g007920	Telomere-associated protein RIF1, putative (AHRD V3.3 *** A0A061GVQ3_THECC)		P:GO:0000723; C:G(	P:telomere maintenance; C:nucleus			IPR022031 (PFAM); mobidb-lite (MOB	0,859	0,464	0,512	0,338	0,448									
Solyc07g007930	Alkaline alpha-galactosidase seed imbibition protein (AHRD V3.3 *** Q8H6N3_SOLLC)		F:GO:0003824	F:catalytic activity			IPR008811 (PFAM); IPR013785 (G3D	0,281	0,115	0,803	0,610	0,472									
Solyc07g007940	Small nuclear RNA activating complex (SNAPc), subunit SNAP43 (AHRD V3.3 *** A0A072US03_MEDTR)		C:GO:0019185; P:G(	C:snRNA-activating protein complex; P:snRNA transcription by I			IPR019188 (PFAM); mobidb-lite (MOB	3,923	3,425	3,553	3,187	3,585									
Solyc07g007945	Cytochrome c oxidase subunit 2 (AHRD V3.3 --* COX2_BETVU)		P:GO:0008152; F:G(	P:metabolic process; F:oxidoreductase activity				0,079	0,041	0,000	0,025	0,119									
Solyc07g007950	Calcium-binding family protein (AHRD V3.3 *** B9HA89_POPTR)		F:GO:0005509	F:calcium ion binding			PR01697 (PRINTS); IPR002048 (SMA	13,403	7,076	4,522	8,700	6,786	-0,898	0,005			0,940	0,000	down		up
Solyc07g007960	Ubiquitin system component Cue protein (AHRD V3.3 *** AT5G32440.3)		F:GO:0005515	F:protein binding			IPR003892 (PFAM); PTHR31245 (PAN	17,151	17,565	28,850	28,897	26,177									
Solyc07g007970	keratin-associated protein, putative (DUF819) (AHRD V3.3 *** AT5G52540.1)		C:GO:0016021	C:integral component of membrane			IPR008537 (PFAM); IPR008537 (PAN	7,473	7,812	8,638	9,224	9,653									
Solyc07g007980	Protein kinase (AHRD V3.3 *** C6ZRY2_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM); PIRSF000615 (P	2,894	3,510	1,214	1,090	1,367									
Solyc07g007990	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT4G32272.1)		C:GO:0005794; P:G(	C:Golgi apparatus; P:carbohydrate transport; F:antiporter activi			IPR004853 (PFAM); PTHR44680:SF1	0,336	0,246	0,147	0,139	0,307									
Solyc07g008000	RabGAP/TBC domain-containing protein (AHRD V3.3 *** AT5G52580.1)		F:GO:0005096; C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (SMART); G3DSA:1.10.8.2	26,520	28,747	32,674	34,974	30,724									
Solyc07g008010	R2R3MYB transcription factor 82	R2R3MYB82	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,380	0,421	0,373	0,295	0,164									
Solyc07g008020	auxin-regulated 35	IAA35	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			IPR033389 (PFAM); G3DSA:3.10.20.9	3,518	15,394	0,116	0,168	0,329	2,152	0,000					up		
Solyc07g008030	Beta-1,4-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061GP08_THECC)		F:GO:0003830; P:G(	F:beta-1,4-mannosy	EC:2.4.1.144	Beta-1,4-mannosyl-g	IPR006813 (PFAM); IPR006813 (PAN	4,054	5,513	2,140	1,483	2,697									
Solyc07g008040	TOPLESS 5	TPL5	F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated			IPR006595 (SMART); IPR001680 (SM	78,911	67,365	77,157	74,350	71,233									
Solyc07g008050	Brca1-associated protein, putative (AHRD V3.3 *** A0A061GNZ4_THECC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:ubiquitin-protein transferase activi			IPR001607 (SMART); IPR001607 (PF	9,628	10,885	13,465	11,803	12,127									
Solyc07g008060	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT4G32285.2)		F:GO:0005545; C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR013809 (SMART); IPR008942 (G3	64,768	95,478	42,827	41,272	49,411									
Solyc07g008070	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** G7I6T6_MED		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR000008 (SMART); IPR000008 (PF	0,647	0,712	0,165	0,123	0,540									
Solyc07g008090	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *-* AT3G33530.4)						IPR039694 (PANTHER)	0,278	0,211	0,047	0,000	0,047									
Solyc07g008095	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *-* AT3G33530.5)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	43,120	32,577	21,715	21,646	19,620									
Solyc07g008100	Histone acetyltransferase (AHRD V3.3 *** A0A0B0NK56_GOSAR)						G3DSA:1.10.246.20 (GENE3D); mobic	9,322	7,079	2,391	1,731	1,809									
Solyc07g008103	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM); IPR008972 (G3D	28,463	42,380	19,706	21,020	28,720			0,538	0,036				up	
Solyc07g008107	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM); IPR008972 (G3D	12,100	18,407	8,812	7,640	11,247									
Solyc07g008130	Blue copper-like protein (AHRD V3.3 *** A0A0B0PL86_GOSAR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM); IPR008972 (G3D	0,021	0,043	0,090	0,025	0,023									
Solyc07g008140	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)		F:GO:0009055	F:electron transfer activity			PR01217 (PRINTS); IPR008972 (G3D	1,083	1,936	1,335	2,332	4,763			1,817	0,000				up	
Solyc07g008150	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RYW1_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM); G3DSA:3.20.20.8	17,536	20,320	9,384	8,659	10,765									
Solyc07g008160	Nuclear pore complex protein Nup155 (AHRD V3.3 *** A0A0B2Q912_GLYSO)		C:GO:0005643; P:G(	C:nuclear pore; P:nucleocytoplasmic transport; F:structural con			IPR014908 (PFAM); G3DSA:1.20.120	85,011	68,166	75,542	72,604	74,914									
Solyc07g008170	Methyl-CpG-binding domain protein (AHRD V3.3 *-* G7JE44_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR001739 (PFAM); G3DSA:3.30.890	12,349	12,818	37,252	36,905	36,048									
Solyc07g008180	CRABS CLAW-like protein 5a	YABBY5a	P:GO:0007275	P:multicellular organism development			IPR036910 (G3DS YABBY	41,891	36,887	22,955	27,279	25,129									
Solyc07g008190	Dedicator of cytokinesis protein 6, putative isoform 1 (AHRD V3.3 *** A0A061GMJ9_THECC)		C:GO:0005635; P:G(	C:nuclear envelope; P:nuclear membrane organization			mobidb-lite (MOBIDB_LITE); mobidb-lit	32,630	32,406	33,159	37,152	33,958									
Solyc07g008200	Equilibrative nucleoside transporter (AHRD V3.3 *** A0A103XNA9_CYNCS)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con			IPR002259 (PFAM); IPR002259 (PIRS	1,151	1,072	0,511	0,095	0,167									
Solyc07g008205	Epidermal patterning factor-like protein (AHRD V3.3 *** G7JE34_MEDTR),Pfam:PF17181		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM); PTHR33109:SF16 (	0,000	0,019	0,000	0,000	0,000									
Solyc07g008210	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT1G80130.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	28,637	6,800	0,068	0,051	0,023	-2,038	0,030					down		
Solyc07g008230	Glycosyltransferase (AHRD V3.3 *** K4CBU2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR(	0,040	0,094	0,000	0,000	0,000									
Solyc07g008240	Non-symbiotic hemoglobin 1 (AHRD V3.3 *** HBL1_GOSHI)		F:GO:0019825; F:G(	F:oxygen binding; F:heme binding			IPR001032 (PRINTS); IPR000971 (PF	29,411	49,513	0,469	0,549	1,032									
Solyc07g008250	EIN3-binding F-box-like protein (AHRD V3.3 *** G7I706_MEDTR)	EBF3	F:GO:0005515	F:protein binding			IPR001810 (SMART); IPR006553 (SM	20,764	30,081	72,241	86,033	64,929									
Solyc07g008260	DUF4050 family protein (AHRD V3.3 *** G7JE31_MEDTR)						IPR025124 (PFAM); PTHR33373:SF3	8,963	7,162	12,412	14,886	13,360									
Solyc07g008270	50S ribosomal protein L36, chloroplastic (AHRD V3.3 *-* RK36_MESVI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000473 (TIGRFAM); IPR000473 (F	14,936	15,648	21,730	19,337	18,726									
Solyc07g008280	Transmembrane protein, putative (AHRD V3.3 *** G7JD04_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33564 (PANTHER); PTHR33564	0,898	1,543	0,337	0,678	0,774									
Solyc07g008290	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G21190.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM); PTHR31288 (PAN	1,932	2,777	0,565	1,429	0,094									
Solyc07g008300	Choline monooxygenase (AHRD V3.3 *** D2DEK9_LYCBA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity; P:cellular metaboli			IPR001663 (PRINTS); G3DSA:3.90.38	0,021	0,128	0,022	0,025	0,000									
Solyc07g008310	Choline monooxygenase (AHRD V3.3 *** D2DEK9_LYCBA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity; P:cellular metaboli			IPR001663 (PRINTS); IPR017941 (PF	0,582	0,283	1,020	0,942	1,088									
Solyc07g008320	Calcium-transporting ATPase (AHRD V3.3 *** B9HAW9_POPTR)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS); IPR001757 (PRIN	113,205	275,321	112,226	122,503	126,343	1,306	0,000					up		
Solyc07g008330	Nucleolar and coiled-body phosphoprotein 1 (AHRD V3.3 *-* A0A1D1XD59_9ARAE)		F:GO:0005515; C:G(	F:protein binding; C:nucleolus			IPR007718 (PFAM); mobidb-lite (MOB	30,113	32,033	30,444	30,662	28,552									
Solyc07g008340	RNase L inhibitor protein 2	ABCE1	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013283 (PRINTS); IPR003593 (SM	111,449	135,390	173,636	174,921	171,155									
Solyc07g008350	voltage-dependent anion channel protein		C:GO:0005741; F:G(	C:mitochondrial outer membrane; F:voltage-gated anion channe			IPR027246 (PFAM); IPR023614 (G3D	34,797	35,638	41,522	43,638	41,801									
Solyc07g008360	ribosomal protein L30/L7 family protein		F:GO:0003824	F:catalytic activity			IPR025110 (PFAM); G3DSA:3.40.50.1	2,137	1,440	0,392	0,220	0,094									
Solyc07g008363	Defensin-like (DEFL) family protein (AHRD V3.3 *** AT4G14276.1)		C:GO:0005576; P:G(	C:extracellular region; P:defense response to fungus			IPR022618 (PFAM); IPR022618 (PAN	0,019	0,019	0,000	0,000	0,000									
Solyc07g008370	60S ribosomal protein L7 (AHRD V3.3 *** A0A072VPV6_MEDTR)		P:GO:0000463; F:G(	P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU			IPR016082 (PFAM); IPR036919 (G3D	159,413	185,111	145,904	125,339	132,488									
Solyc07g008390	Kinase, putative (AHRD V3.3 *-* B9SRU2_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART); IPR023213 (G3	0,209	0,535	0,164	0,248	0,047									
Solyc07g008410	Protein DETOXIFICATION (AHRD V3.3 *** K4CBW0_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM); IPR002528 (F	0,098	0,312	0,150	0,466	0,118									
Solyc07g008430	RING/U-box superfamily protein (AHRD V3.3 --* AT3G56580.3)						PTHR33320 (PANTHER); PTHR33320	11,065	8,497	0,238	0,022	0,094									
Solyc07g008440	Purine permease-like protein (AHRD V3.3 *** G7J4H5_MEDTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); PTHR31376:SF1 (F	0,038	0,082	0,342	0,542	0,637									
Solyc07g008450	ARM repeat superfamily protein (AHRD V3.3 *** AT4G38120.3)						IPR025283 (PFAM); IPR011989 (G3D	41,885	38,387	44,731	47,330	45,968									
Solyc07g008460	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9P7Y1_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR006560 (SMART); IPR001214 (SM	18,412	17,367	25,318	25,977	24,901									
Solyc07g008470	Macrophage migration inhibitory factor family protein (AHRD V3.3 *** D7MMS4_ARALL)						IPR001398 (PFAM); IPR014347 (G3D	1,498	2,521	1,604	1,517	1,837									
Solyc07g008475	Subtilisin-like protease (AHRD V3.3 *-* A0A1D1Z5J1_9ARAE)		F:GO:0004252; P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bonds (peptidases)		4,679	4,493	5,371	5,678	4,293									
Solyc07g008480	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2SVC3_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,335	6,242	7,246	9,039	7,331									
Solyc07g008490	Poly(RC)-binding protein, putative (AHRD V3.3 *-* B9SPR0_RICCO)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR004088 (PF	20,722	23,522	29,821	28,502	29,008									
Solyc07g008495	RNA-binding KH domain-containing protein (AHRD V3.3 *-* AT4G26000.1)		F:GO:0003723	F:RNA binding			IPR004087 (SMART); IPR036612 (G3	10,756	11,131	13,050	14,648	14,150									
Solyc07g008500	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9P7Y1_ZOSMR)		F:GO:0005515	F:protein binding			IPR001214 (SMART); IPR001214 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc07g008520	Peptide transporter (AHRD V3.3 *** W9RPK3_9ROSA)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D); IPR(	3,796	4,552	7,159	11,282	8,122									
Solyc07g008530	Tyrosine--tRNA ligase (AHRD V3.3 *** K4CBX2_SOLLC)		F:GO:0003723; F:G(	F:RNA binding; F:ty	EC:6.1.1.1	Tyrosine--tRNA ligas	IPR002307 (PRINTS); IPR002942 (SM	12,790	12,991	23,199	19,104	23,837									
Solyc07g008540	chloroplast import apparatus 2 (AHRD V3.3 *** AT5G57180.2)		F:GO:0005515	F:protein binding			IPR010402 (PFAM); mobidb-lite (MOB	7,923	12,430	8,706	8,767	11,090	0,675	0,036					up		
Solyc07g008550	Purple acid phosphatase (AHRD V3.3 *** K4CBX4_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR004843 (PFAM); IPR029052 (G3D	0,079	0,231	1,395	1,919	1,832									
Solyc07g008560	Purple acid phosphatase (AHRD V3.3 *** K4CBX4_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	2,808	6,000	12,737	10,554	10,503	1,119	0,005					up		
Solyc07g008570	Purple acid phosphatase (AHRD V3.3 *** K4CBX4_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	0,153	0,359	0,468	0,811	0,707									
Solyc07g008580	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9P7Y1_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR001214 (SMART); IPR006560 (SM	0,021	0,059	0,000	0,000	0,000									
Solyc07g008590	LOW QUALITY:Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** G7K7L1_MEDTR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); SM00364 (SMAR	2,842	20,489	1,420	2,409	4,446	2,871	0,000	1,635	0,000			up	up	
Solyc07g008600	LOW QUALITY:Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** A0A072UGF0_MEDTR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,144	0,952	0,025	0,075	0,119									
Solyc07g008610	(DB142) meloidogyne-induced giant cell protein	ABCF3	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART); IPR003439 (PF	98,923	105,976	154,167	134,990	128,029									
Solyc07g008620	EIX receptor 1	eix1	F:GO:0005515	F:protein binding			PR00019 (PRINTS); SM00365 (SMAR	16,466	34,611	17,535	51,620	35,400			1,011	0,000	1,559	0,000		up	up
Solyc07g008630	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); SM00364 (SMAR	0,297	0,812	0,308	0,687	0,775									
Solyc07g008640	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT2G33170.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR003591 (SMA	0,040	0,041	0,050	0,000	0,095									
Solyc07g008650	Deaminase-related family protein (AHRD V3.3 *** B9HAZ0_POPTR)		F:GO:0003824	F:catalytic activity			IPR002125 (PFAM); G3DSA:3.40.140	2,769	3,796	2,068	2,335	1,532									
Solyc07g008660	30S ribosomal protein S16 (AHRD V3.3 *** B3IWG3_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000307 (PFAM); IPR000307 (TIGF	9,757	11,892	15,692	14,203	14,061									
Solyc07g008670	Protein LONGIFOLIA 1 (AHRD V3.3 *** A0A199VV70_ANACO)		P:GO:0051513	P:regulation of monopolar cell growth			IPR032795 (PFAM); IPR025486 (PFA	10,932	15,042	1,368	0,766	1,529									
Solyc07g008690	Sesquiterpene synthase (AHRD V3.3 *** G8H5N3_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM); IPR008949 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc07g008700	Far1-related sequence 9 (AHRD V3.3 *** A0A061E1V5_THECC)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMART); IPR018289 (PF	17,231	14,027	27,058	27,202	25,387									
Solyc07g008710	Major latex-like protein (AHRD V1 **-- B5THI3_PANGI)		P:GO:0006952	P:defense response			IPR000916 (SMART); IPR023393 (G3	0,098	0,205	0,000	0,050	0,000									
Solyc07g008720	BTF3-like transcription factor		P:GO:0009651	P:response to salt stress			IPR002715 (SMART); IPR002715 (PF	214,656	215,592	222,988	222,164	213,295									
Solyc07g008730	Pathogenesis-related homeodomain protein (AHRD V3.3 *** W9QLT1_9ROSA)		F:GO:0003677	F:DNA binding			IPR001965 (SMAF HB-PHD	7,408	6,519	9,420	10,785	9,441									
Solyc07g008750	Nuclear nucleic acid-binding protein C1D (AHRD V3.3 *** A0A0B0NSY9_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	18,547	17,946	30,980	32,159	28,546									
Solyc07g008755	Protein TIC 214 (AHRD V3.3 --* TI214_SOLLC)							1,845	1,386	2,968	3,365	2,430									
Solyc07g008760	Tetratricopeptide repeat-containing protein (AHRD V3.3 *** D7LWY8_ARALL)		F:GO:0005515	F:protein binding			IPR019734 (SMART); IPR019734 (PF	33,446	29,615	30,929	25,873	26,900									
Solyc07g008770	Serine/arginine repetitive matrix protein 2, putative isoform 1 (AHRD V3.3 *** A0A061G9S9_THECC)						mobidb-lite (MOBIDB_LITE); PTHR339	49,290	47,791	100,719	87,922	91,361									
Solyc07g008780	transmembrane protein (AHRD V3.3 *** AT4G29960.1)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:plasma membrane; C:integral comp(			mobidb-lite (MOBIDB_LITE); mobidb-lit	20,691	20,101	39,018	41,361	37,829									
Solyc07g008790	Protein kinase-like protein (AHRD V3.3 *** A0A087GP50_ARAAL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); G3DS	0,173	0,100	0,075	0,000	0,071									
Solyc07g008800	chaperonin		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding			IPR020818 (PRINTS); IPR020818 (SM	30,016	35,340	31,564	27,775	28,032									
Solyc07g008810	LOW QUALITY:Monovalent Cation:Proton antiporter-2 family (AHRD V3.3 --* C1EH01_MICCC)							0,531	0,586	0,096	0,250	0,233									
Solyc07g008820	TRICHOME BIREFRINGENCE-LIKE 14 (AHRD V3.3 *** AT5G64020.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:acetyl			IPR025846 (PFAM); IPR026057 (PFA	5,227	6,524	1,288	1,037	1,296									
Solyc07g008840	Microtubule-associated protein (AHRD V3.3 *** E1U7Y5_NICBE)		F:GO:0005096; C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (SMART); G3DSA:1.10.47	73,012	94,981	95,650	97,825	96,134									
Solyc07g008850	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (AHRD V3.3 *** A0A072VG88_MEDTR)		F:GO:0008759; P:G(	F:UDP-3-O-[3-hydro	EC:3.5.1.18	UDP-3-O-acyl-N-ace	IPR015870 (G3DSA:3.30.230.GENE3I	8,946	9,037	7,125	6,225	6,852									
Solyc07g008860	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT1G71840.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (SM	22,478	25,958	26,628	24,315	24,418									
Solyc07g008880	Pre-mRNA-processing-splicing factor 8 (AHRD V3.3 *** W9R414_9ROSA)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:protein binding; C:spliceos			IPR000555 (SMART); IPR000555 (PF	541,197	427,493	553,829	540,190	551,067									
Solyc07g008890	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061GRI5_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	4,765	4,459	4,453	3,838	4,333									
Solyc07g008895	Urease accessory protein F (AHRD V3.3 --* UREF_ORYSJ)						mobidb-lite (MOBIDB_LITE)	0,100	0,041	0,047	0,126	0,071									
Solyc07g008900	Subtilisin-like protease (AHRD V3.3 *** A0A151SRS2_CAJCA)		F:GO:0004252; P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bo	IPR015500 (PRINTS); PF17766 (PFAI	367,416	243,703	153,798	126,233	146,217									
Solyc07g008910	Thioredoxin superfamily protein (AHRD V3.3 *** AT5G57230.2)						G3DSA:3.40.30.10 (GENE3D); PTHR3	11,090	10,207	8,881	10,034	8,390									
Solyc07g008920	Oxysterol-binding protein-like (AHRD V3.3 *** A0A0K9NXU5_ZOSMR)		C:GO:0005829; F:G(	C:cytosol; F:sterol transporter activity; P:sterol transport; C:me			IPR000648 (PFAM); G3DSA:1.20.120	0,554	0,792	0,423	0,437	0,613									
Solyc07g008930	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7JUB6_MEDTR)						IPR025322 (PFAM); mobidb-lite (MOB	0,473	1,924	0,547	0,677	0,870									
Solyc07g008940	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT2G19160.2)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM); PTHR31042 (PAN	38,035	32,588	29,479	30,162	29,079									
Solyc07g008950	Methionyl-tRNA synthetase family protein (AHRD V3.3 *** B9N0S4_POPTR)		F:GO:0000049; F:G(	F:tRNA binding; F:m	EC:6.1.1.10	Methionine--tRNA lig	IPR033911 (PRINTS); G3DSA:2.40.50	145,301	139,274	222,130	210,038	207,988									
Solyc07g008970	Myosin heavy chain-related (AHRD V3.3 *** A0A061GI21_THECC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.120.20 (GENE3D); mobic	24,682	21,336	39,724	39,341	36,182									
Solyc07g009050	Defensin-like protein, putative (AHRD V3.3 *** A0A061E6R0_THECC)		P:GO:0006952	P:defense response			IPR036574 (G3DSA:3.30.30.GENE3D	0,156	0,260	0,000	0,050	0,048									
Solyc07g009060	defensin-like protein (AHRD V3.3 *** AT1G19610.1)		P:GO:0006952	P:defense response			IPR036574 (G3DSA:3.30.30.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc07g009130	Heavy metal ATPase (AHRD V3.3 *** T2K0N9_TOBAC)		F:GO:0000166; C:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS); IPR023299 (G3D	33,809	26,318	20,460	22,343	22,458									
Solyc07g009140	26S proteasome regulatory subunit Rpn7 (AHRD V3.3 *** AT4G24820.2)		F:GO:0030234	F:enzyme regulator activity			SM00753 (SMART); IPR000717 (SMA	118,357	110,680	137,643	139,510	128,287									
Solyc07g009150	Protein kinase family protein (AHRD V3.3 *** F4JRQ4_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM); PTHR43173 (PAN	10,031	12,999	8,458	8,142	10,669									
Solyc07g009160	ER membrane protein complex subunit-like protein (AHRD V3.3 *** G7KEJ5_MEDTR)		C:GO:0072546	C:ER membrane protein complex			G3DSA:3.40.140.10 (GENE3D); IPR0(	26,037	29,230	36,904	34,568	34,998									

Solyc07g009170	Nudix hydrolase-like protein (AHRD V3.3 *** G7KNJ9_MEDTR)		F:GO:0016787	F:hydrolase activity	IPR031804 (PFAM): G3DSA:3.30.750	3,909	4,648	4,788	4,780	7,631			0,667	0,011				up	
Solyc07g009180	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	4,444	6,686	0,961	1,471	1,318									
Solyc07g009210	Subtilisin-like protease (AHRD V3.3 *-* A0A1D1YT90_9ARAE)		F:GO:0004252; P:GO	F:serine-type endor EC:3.4.21 Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	0,082	0,041	0,025	0,000	0,023									
Solyc07g009220	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9I405_POPTR)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	2,749	2,830	1,991	2,061	1,718									
Solyc07g009230	Defensin-like protein (AHRD V3.3 -** G7LB12_MEDTR)		C:GO:0005576; P:GO	C:extracellular region; P:defense response	IPR036574 (G3DSA:3.30.30.GENE3D	1,438	1,051	0,966	1,786	1,243									
Solyc07g009235	Defensin-like protein (AHRD V3.3 -** H6SWQ0_DATGL)					0,038	0,233	0,025	0,000	0,000									
Solyc07g009240	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151RA30_CAJCA)		F:GO:0016787	F:hydrolase activity	IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,135	0,199	0,000	0,024									
Solyc07g009270	LOW QUALITY:dentin sialophosphoprotein-like protein (AHRD V3.3 --* AT5G07940.5)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,185	0,117	0,075	0,098	0,237									
Solyc07g009320	metaxin-related protein		C:GO:0001401	C:SAM complex	IPR012336 (PFAM): IPR033468 (PFA	15,577	17,030	26,468	25,483	24,782									
Solyc07g009330	Auxin induced-like protein (AHRD V3.3 *** E0Z5V6_PICSI)		C:GO:0016021; P:GO	C:integral component of membrane; P:oxidation-reduction proce	IPR006593 (SMART): IPR005018 (PF	26,804	34,633	20,655	16,626	18,230									
Solyc07g009333	60S acidic ribosomal protein P3 (AHRD V3.3 *** B9HPG0_POPTR)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:nucleus; P:translational elongation; C:cytosolic ribosome		0,042	0,240	0,097	0,122	0,070									
Solyc07g009350	U3 small nucleolar RNA-associated protein (AHRD V3.3 *** AT1G17690.1)		C:GO:0005634	C:nucleus	IPR010678 (PFAM): mobidb-lite (MOB	43,925	40,831	45,203	43,214	41,691									
Solyc07g009380	xyloglucan endotransglucosylase-hydrolase 2	xth2	F:GO:0004553; C:GO	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucο	IPR000757 (PFAM): IPR010713 (PFA	50,115	62,347	35,078	17,082	27,373									
Solyc07g009410	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9GJS6_POPTR)		F:GO:0005515	F:protein binding	IPR006652 (SMART): IPR001480 (SM	1,775	1,401	0,655	0,349	0,686									
Solyc07g009440	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 *-* M1AFX4_SOLTU)		P:GO:0048544	P:recognition of pollen	IPR001480 (SMART): IPR000858 (PF	0,360	0,308	0,355	0,411	0,401									
Solyc07g009445	Serine/Threonine kinase domain protein (AHRD V3.3 *-* AT1G68830.1)		P:GO:0051260	P:protein homooligomerization	G3DSA:3.30.710.10 (GENE3D): IPR0	0,019	0,019	0,050	0,025	0,000									
Solyc07g009450	LOW QUALITY:BEL1-like homeodomain 10 (AHRD V3.3 --* AT1G19700.5)					0,000	0,000	0,150	0,025	0,071									
Solyc07g009460	purple acid phosphatase 28 (AHRD V3.3 *** AT5G57140.1)		F:GO:0016787	F:hydrolase activity	IPR004843 (PFAM): IPR029052 (G3D	21,700	17,129	11,476	7,381	9,251					-0,632	0,019			down
Solyc07g009470	Actin (AHRD V3.3 *-* ACT_GOSHI)				IPR004000 (PFAM): G3DSA:3.30.420	2,331	2,197	2,387	2,125	2,403									
Solyc07g009490	Ethanolamine-phosphate cytidylyltransferase (AHRD V3.3 *** W9S3K0_9ROSA)		F:GO:0003824; P:GO	F:catalytic activity; P:biosynthetic process	IPR004821 (TIGRFAM): IPR004821 (F	96,207	88,310	64,731	67,306	60,233									
Solyc07g009500	Chitinase (AHRD V3.3 *-* Q9SQF7_BRAJU)		F:GO:0008061	F:chitin binding	IPR001002 (PRINTS): IPR001002 (SM	89,080	110,817	657,744	335,950	351,765									
Solyc07g009510	Chitinase (AHRD V3.3 *-* P93327_MEDTR)		F:GO:0008061	F:chitin binding	IPR001002 (PRINTS): IPR001002 (SM	0,000	0,000	0,225	0,025	0,143									
Solyc07g009520	WEB family protein, chloroplastic (AHRD V3.3 *-* A0A199V6Z9_ANACO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,054	0,098	0,000	0,072									
Solyc07g009530	Chitinase (AHRD V3.3 *-* B8QVJ5_ZEAMP)		F:GO:0008061	F:chitin binding	IPR001002 (PRINTS): IPR001002 (SM	5,438	28,676	151,073	164,898	174,802	2,423	0,029					up		
Solyc07g014580	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061G8N7_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR023213 (G3DSA:3.30.559.GENE3	0,138	0,078	0,000	0,000	0,000									
Solyc07g014590	Isoamylase (AHRD V3.3 *** Q1AJM7_IPOBA)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR006047 (SMART): IPR013780 (G3	32,984	27,839	8,655	6,349	9,176									
Solyc07g014600	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* AT3G16200.1)		C:GO:0005768; C:GO	C:endosome; C:trans-Golgi network; C:integral component of m	PTHR36362 (PANTHER)	0,792	0,702	0,252	0,215	0,538									
Solyc07g014605	Glutamate-1-semialdehyde 2,1-aminomutase 1, chloroplastic (AHRD V3.3 --* GSA1_GSA-AM				mobidb-lite (MOBIDB_LITE)	0,304	0,075	0,638	0,588	0,450									
Solyc07g014610	GPI ethanolamine phosphate transferase 3 (AHRD V3.3 *** A0A0B0NMW8_GOSAR)		P:GO:0006506; F:GO	P:GPI anchor biosynthetic process; F:mannose-ethanolamine p	IPR002591 (PFAM): IPR017849 (G3D	18,751	13,380	25,723	28,081	25,470									
Solyc07g014620	Small auxin up-regulated RNA63	SAUR63	P:GO:0009733	P:response to auxin	IPR003676 (PFAM): mobidb-lite (MOB	1,002	1,856	1,483	0,741	1,526									
Solyc07g014640	Galactokinase, putative (AHRD V3.3 *** B9RKW5_RICCO)		F:GO:0005524; F:GO	F:ATP binding; F:galactose binding; C:cytoplasm; F:kinase activ	PR00959 (PRINTS): IPR013750 (PFA	16,431	14,390	3,077	2,820	3,953									
Solyc07g014650	ADP-ribosylation factor family protein (AHRD V3.3 *** AT2G18390.1)		F:GO:0005525	F:GTP binding	IPR006689 (PRINTS): SM00178 (SMA	63,287	55,061	52,577	42,865	48,944									
Solyc07g014670	Cytochrome P450 (AHRD V3.3 *** C5NM78_TOBAC)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	12,417	11,028	9,772	8,834	11,176									
Solyc07g014680	sodium transporter HKT1,2		P:GO:0006812; F:GO	P:cation transport; F:cation transmembrane transporter activity;	IPR003445 (PFAM): PTHR31064:SF2	0,100	0,041	0,000	0,000	0,000									
Solyc07g014700	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (AHRD V3.3 *** A0A0B2PTB3_GL		P:GO:0006487; C:GO	P:protein N-linked glycosylation; C:oligosaccharyltransferase co	IPR008814 (PFAM): IPR008814 (PAN	70,225	71,713	70,368	69,382	71,073									
Solyc07g014703	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (AHRD V3.3 *-* W9RFI4_9ROSA)		C:GO:0005739; C:GO	C:mitochondrion; C:vacuolar membrane; C:Golgi apparatus; C:plasma membrane; P:protein N-linked gly		10,148	9,539	11,290	11,395	10,481									
Solyc07g014710	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SUT9_CAJCA)		F:GO:0004721; F:GO	F:phosphoprotein phosphatase activity; F:protein serine/threoni	IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,000	0,100	0,025	0,023									
Solyc07g014730	Phospholipase A2 (AHRD V3.3 *** Q5CCT8_TOBAC)		F:GO:0004623; F:GO	F:phospholipase A2 EC:3.1.1.1; EC:3.1.1 Carboxylesterase; Pl	IPR036444 (G3DSA:1.20.90.GENE3D	1,444	2,047	0,642	0,340	0,327									
Solyc07g014740	Sodium Bile acid symporter family (AHRD V3.3 *** AT3G56160.3)		C:GO:0009941; C:GO	C:chloroplast envelope; C:integral component of membrane	IPR016833 (PFAM): IPR038770 (G3D	11,804	15,322	16,126	18,414	19,727									
Solyc07g014750	LOW QUALITY:Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A0B2QEE0_GLYSO)				G3DSA:2.40.50.140 (GENE3D): PTHF	0,000	0,021	0,000	0,050	0,093									
Solyc07g015760	LOW QUALITY:Non-specific serine/threonine protein kinase (AHRD V3.3 --* B0FM67_PERAE)					0,000	0,000	0,000	0,000	0,023									
Solyc07g015800	F-box family protein, putative (AHRD V3.3 *** A0A061F027_THECC)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR001810 (PF	10,102	9,721	6,718	5,582	5,588									
Solyc07g015850	En/Spm transposon protein-like (AHRD V3.3 *-* Q9LH00_ARATH)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,059	0,000	0,000	0,000									
Solyc07g015860	peptide deformylase AF271258		C:GO:0005739; P:GO	C:mitochondrion; P: EC:3.5.1.88 Peptide deformylase	IPR023635 (PRINTS): IPR023635 (PF	19,927	26,841	10,496	7,990	14,611			0,471	0,039				up	
Solyc07g015870	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G10640.1)	PG8	F:GO:0004650; P:GO	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	0,021	0,043	0,000	0,047	0,023									
Solyc07g015910	WAT1-related protein (AHRD V3.3 *** K4CCA8_SOLLC)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM): PTHR31218:SF7	0,772	1,049	0,099	0,346	0,094									
Solyc07g015970	Mitochondrial import receptor subunit TOM7-1 (AHRD V3.3 *** TOM7A_SOLTU)		C:GO:0005742; P:GO	C:mitochondrial outer membrane translocase complex; P:protein	IPR012621 (PFAM): mobidb-lite (MOB	20,141	20,665	28,383	25,207	25,882									
Solyc07g015980	Purple acid phosphatase (AHRD V3.3 *-* A0A0E0D9J4_9ORYZ)		F:GO:0003824	F:catalytic activity	G3DSA:3.90.105.10 (GENE3D): IPR0	4,867	5,082	6,859	6,097	6,803									
Solyc07g015985	Purple acid phosphatase (AHRD V3.3 *-* A0A0D9ZFS8_9ORYZ)		F:GO:0003824; F:GO	F:catalytic activity; F:protein dimerization activity	IPR008906 (PFAM): IPR000310 (PFA	1,615	1,378	1,729	2,041	2,446									
Solyc07g016020	LOW QUALITY:Purple acid phosphatase (AHRD V3.3 *-* A0A0E0GWH3_ORYNI)		F:GO:0003824	F:catalytic activity	IPR015421 (G3DSA:3.40.640.GENE3	0,000	0,019	0,000	0,000	0,000									
Solyc07g016050	LOW QUALITY:Purple acid phosphatase (AHRD V3.3 *-* A0A0E0D9J4_9ORYZ)		F:GO:0003824	F:catalytic activity	IPR000310 (PFAM): IPR008286 (PFA	0,000	0,000	0,022	0,000	0,071									
Solyc07g016080	Purple acid phosphatase (AHRD V3.3 *-* A0A0D9ZFS9_9ORYZ)		F:GO:0003824	F:catalytic activity	IPR015421 (G3DSA:3.40.640.GENE3	0,021	0,000	0,000	0,000	0,000									
Solyc07g016150	Elongation factor 1-beta (AHRD V3.3 *** A0A072UHR3_MEDTR)	ddtfr10	F:GO:0003746; P:GO	F:translation elongation factor activity; P:translational elongatio	IPR014038 (SMART): IPR014038 (PF	248,716	253,366	179,604	156,674	166,313									
Solyc07g016170	L-arabinokinase (AHRD V3.3 *** ARAK_ARATH)		F:GO:0005524; F:GO	F:ATP binding; F:galactose binding	PR00959 (PRINTS): IPR036554 (G3D	50,840	39,125	13,646	12,308	14,421									
Solyc07g016180	Auxin Response Factor 7A	ARF7A	F:GO:0003677; F:GO	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran	IPR003340 (SMAF ARF	3,316	3,007	0,794	0,780	0,820									
Solyc07g016200	Proteasome subunit beta type (AHRD V3.3 *** K4CCD7_SOLLC)		F:GO:0004298; C:GO	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR000243 (PRINTS): IPR029055 (G3	73,273	76,143	98,852	95,063	90,544									
Solyc07g016215	Organ specific protein (AHRD V3.3 *** A0A103YKI8_CYNCS)				IPR024489 (PFAM): mobidb-lite (MOB	0,000	0,174	0,000	0,000	0,000									
Solyc07g017220	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT5G20700.1)				IPR007650 (PFAM): PTHR33059 (PAN	30,449	19,752	14,851	12,707	12,095									
Solyc07g017230	pollen receptor-like protein kinase 2	prk2	F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,036	0,000	0,000	0,000									
Solyc07g017250	tRNA pseudouridine synthase (AHRD V3.3 *** A0A0V0ICE9_SOLCH)		P:GO:0001522; F:GO	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn	IPR020095 (G3DSA:3.30.70.GENE3D	2,238	3,013	3,250	3,345	2,964									
Solyc07g017260	tRNA pseudouridine synthase (AHRD V3.3 *-* A0A0V0ICE9_SOLCH)		P:GO:0001522; F:GO	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn	G3DSA:3.30.70.580 (GENE3D): PTHF	3,171	3,616	3,981	3,608	4,315									
Solyc07g017290	3-phosphoinositide-dependent protein kinase-1 (AHRD V3.3 *** B9HBB3_POPTR)		P:GO:0015919	P:peroxisomal membrane transport	IPR034571 (PANTHER)	6,760	6,854	10,502	11,720	11,084									
Solyc07g017293	3-phosphoinositide-dependent protein kinase-1 (AHRD V3.3 *-* AT3G10572.1)		P:GO:0015919	P:peroxisomal membrane transport	IPR034571 (PANTHER)	1,940	1,713	2,536	2,797	2,356									
Solyc07g017295	cytochrome P450, family 88, subfamily A, polypeptide 3 (AHRD V3.3 --* AT1G05160.2)					0,698	0,477	0,975	1,057	1,247									
Solyc07g017297	basic leucine zipper 24 (AHRD V3.3 --* AT3G51960.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,158	0,214	0,091	0,000	0,072									
Solyc07g017300	LOW QUALITY:RNA recognition motif (RRM)-containing protein (AHRD V3.3 --* AT4G12640.4)					0,042	0,000	0,100	0,000	0,024									
Solyc07g017347	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G14370.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc07g017370	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT2G47240.4)				mobidb-lite (MOBIDB_LITE)	0,061	0,083	0,368	0,361	0,258									
Solyc07g017400	Regulatory particle non-ATPase 13 (AHRD V3.3 *** A0A097PT56_SOLLC)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm	IPR038633 (G3DSA:2.30.29.GENE3D	38,202	36,637	53,224	53,943	46,830									
Solyc07g017410	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT2G41070.4)				PTHR35693 (PANTHER)	22,490	22,148	26,985	22,311	25,114									
Solyc07g017420	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT5G64630.3)					0,038	0,000	0,047	0,047	0,024									
Solyc07g017430	Phosphoinositide phosphatase family protein (AHRD V3.3 *** AT5G20840.1)		P:GO:0007033; P:GO	P:vacuole organization; P:phosphatidylinositol-3-phosphate bios	IPR002013 (PFAM): mobidb-lite (MOB	62,827	65,685	63,003	68,359	64,711									
Solyc07g017437	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 --* AT2G16530.5)					0,124	0,219	0,249	0,201	0,257									
Solyc07g017490	Protein Red (AHRD V3.3 *** A0A0B0MQ48_GOSAR)		C:GO:0005634; P:GO	C:nucleus; P:mitotic spindle assembly checkpoint	IPR012492 (PFAM): IPR012916 (PFA	82,740	76,627	114,603	121,083	120,295									
Solyc07g017495	F-box protein interaction domain protein (AHRD V3.3 --* G7IKC8_MEDTR)					0,080	0,021	0,243	0,145	0,117									
Solyc07g017500	SH3 domain-containing protein (AHRD V3.3 *** W9RVR7_9ROSA)		F:GO:0046872	F:metal ion binding	IPR000306 (SMART): IPR013083 (G3	32,102	27,917	136,884	112,583	100,733			-0,445	0,032				down	
Solyc07g017510	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** W9RVS2_9ROSA)		F:GO:0005524; F:GO	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;	IPR000306 (SMART): IPR002498 (SM	517,585	428,983	630,440	597,581	569,405									
Solyc07g017520	Conserved oligomeric Golgi complex, subunit 3 (AHRD V3.3 *-* A0A103Y6H1_CYNCS)		C:GO:0005801; P:GO	C:cis-Golgi network; P:intracellular protein transport; C:membra	IPR007265 (PANTHER)	15,069	10,865	11,355	11,513	11,805									
Solyc07g017530	Conserved oligomeric Golgi complex subunit 3 (AHRD V3.3 *-* A0A0B2SIZ6_GLYSO)		C:GO:0005801; P:GO	C:cis-Golgi network; P:intracellular protein transport; C:membra	IPR007265 (PFAM): IPR007265 (PAN	4,813	3,132	3,348	3,009	3,641									
Solyc07g017535	Conserved oligomeric Golgi complex, subunit 3 (AHRD V3.3 --* A0A103Y6H1_CYNCS)		C:GO:0005801; C:GO	C:cis-Golgi network; C:cytosol; P:intracellular protein transport;	mobidb-lite (MOBIDB_LITE): mobidb-lit	2,601	2,268	1,731	2,128	2,163									
Solyc07g017540	LEU22441_LeRAD51	rad51	F:GO:0003677; F:GO	F:DNA binding; F:AT EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003593 (SMART): IPR013632 (PF	2,519	3,261	1,763	1,261	1,197									
Solyc07g017570	Defensin protein (AHRD V3.3 -** B1N682_SOLPI)		C:GO:0005576; P:GO	C:extracellular region; P:defense response; F:ion channel inhibi	IPR036574 (G3DSA:3.30.30.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc07g017580	LOW QUALITY:Multidrug resistance-associated protein 14 isoform 2 (AHRD V3.3 --* A0A061G8P0_THECC)					2,038	2,853	0,414	0,293	0,351									
Solyc07g017590	LOW QUALITY:vesicle-associated protein 1-4 (AHRD V3.3 --* AT1G51270.9)		C:GO:0005856	C:cytoskeleton	IPR000299 (PROSITE_PROFILES)	0,040	0,202	0,151	0,000	0,047									
Solyc07g017600	Pectinesterase (AHRD V3.3 *** K4CCH4_SOLLC)		F:GO:0004857; F:GO	F:enzyme inhibitor a EC:3.1.1.11; EC:3.1. Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (PF	172,206	179,417	20,833	20,619	21,741									
Solyc07g017610	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *** G7JS28_MEDTR)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR007698 (SMART): IPR007886 (SM	264,784	176,566	741,100	788,365	687,667	-0,558	0,039					down		
Solyc07g017650	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *-* G7JS28_MEDTR)		F:GO:0004753; C:GO	F:saccharopine dehydrogenase activity; C:cytoplasm; C:integra	IPR007886 (SMART): G3DSA:3.40.50	5,109	3,714	3,916	4,289	4,331									
Solyc07g017660	Lariat debranching enzyme (AHRD V3.3 *** W9RZC5_9ROSA)		P:GO:0006397; F:GO	P:mRNA processing; F:hydrolase activity, acting on ester bonds	IPR007708 (SMART): IPR029052 (G3	15,779	14,313	18,005	19,316	18,596									
Solyc07g017670	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *-* A0A072V2T5_MEDTR)		F:GO:0004753; C:GO	F:saccharopine dehydrogenase activity; C:cytoplasm; C:integra	G3DSA:3.30.360.10 (GENE3D)	2,220	2,216	1,544	1,942	1,514									
Solyc07g017680	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *-* A0A072V2T5_MEDTR)		F:GO:0004753; C:GO	F:saccharopine dehydrogenase activity; C:cytoplasm; C:integra	IPR032095 (PFAM): G3DSA:3.40.50.7	6,238	6,159	4,615	5,506	4,709									
Solyc07g017683	Unknown protein (AHRD V3.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	2,149	2,211	1,509	1,805	1,665									
Solyc07g017687	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 --* PSAB_STAPU)					1,857	2,279	1,861	1,726	1,535									
Solyc07g017700	Haloacid dehalogenase-like hydrolase superfamily protein (AHRD V3.3 *** A0A061GLW4_THECC)		F:GO:0008253; P:GO	F:5'-nucleotidase ac EC:3.1.3.5; EC:3.1.3. 5'-nucleotidase; Nucl	IPR023214 (G3DSA:3.40.50.GENE3D	0,056	0,076	0,000	0,000	0,000									
Solyc07g017730	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RR12_RICCO)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012946 (SMART): IPR012946 (PF	0,630	1,053	0,094	0,073	0,186									
Solyc07g017737	Adagio protein 1 (AHRD V3.3 *-* A0A087GBN2_ARAAL)				G3DSA:3.30.450.20 (GENE3D): mobic	0,000	0,018	0,000	0,022	0,000									
Solyc07g017740	Adagio protein 1 (AHRD V3.3 *-* A0A151SRS3_CAJCA)				G3DSA:3.30.450.20 (GENE3D): mobic	0,080	0,019	0,022	0,139	0,116									
Solyc07g017750	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 *** AT5G57360.1)		F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D): PF1	77,613	79,525	110,262	100,732	98,790									
Solyc07g017760	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K0H2_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (TIGF	11,239	10,502	12,368	13,541	15,073									
Solyc07g017770	Homogentisate phytyltransferase (AHRD V3.3 *** F1BPV8_SOLPN)	VTE2	C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity, trans	G3DSA:1.10.357.140 (GENE3D): IPR(	17,426	18,194	37,022	38,633	37,919									
Solyc07g017773	Fibronectin type III domain-containing protein (AHRD V3.3 --* AT3G24440.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,019	0,100	0,246	0,166									
Solyc07g017777	lateral signaling target-like protein (Protein of unknown function, DUF593) (AHRD V3.3 --* AT2G30690.2)					0,762	0,680	1,399	1,839	1,836									
Solyc07g017780	(DB226) meloidogyne-induced giant cell protein		F:GO:0000166; F:GO	F:nucleotide binding EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRIN	85,306	89,172	110,785	128,325	126,165									
Solyc07g017800	La-related protein 6 isoform 1 (AHRD V3.3 *** A0A061GR72_THECC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	21,310	31,611	40,140	40,075	53,675	0,596	0,016					up		
Solyc07g017820	RING/U-box superfamily protein (AHRD V3.3 --* AT4G19670.7)				mobidb-lite (MOBIDB_LITE): mobidb-lit	4,424	2,843	1,621	2,368	1,719									
Solyc07g017860	Acetyl-coenzyme A synthetase (AHRD V3.3 *** M0ZY55_SOLTU)		F:GO:0003987; F:GO	F:acetate-CoA ligas EC:6.2.1.1 Acetate--CoA ligase	IPR011904 (TIGRFAM): G3DSA:3.40.	25,893	26,691	22,032	21,831	21,887									
Solyc07g017880	Peroxidase (AHRD V3.3 *** K4CCK2_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,000	0,000	0,218	0,309	0,235									
Solyc07g017900	Aldose 1-epimerase family protein (AHRD V3.3 *** G7IN18_MEDTR)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:isomerase activity; F:carb	IPR008183 (PFAM): IPR014718 (G3D	73,775	66,781	82,028	70,681	79,771									
Solyc07g017902	HAT family dimerisation domain containing protein (AHRD V3.3 --* Q2QRD1_ORYSJ)					0,000	0,041	0,000	0,000	0,000									
Solyc07g017925	Ribosomal protein S10 (AHRD V3.3 *-* Q70G82_SOLCO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001848 (PRINTS): IPR036838 (G3	0,000	0,000	0,000	0,051	0,024									
Solyc07g017930	Transcription termination factor MTERF8, chloroplastic (AHRD V3.3 --* MTEF8_ARATH)		C:GO:0005739	C:mitochondrion		0,140	0,252	0,122	0,176	0,189									
Solyc07g017935	DNAse I-like superfamily protein (AHRD V3.3 --* AT1G31500.8)					0,019	0,000	0,000	0,000	0,000									
Solyc07g017940	Ribosomal RNA processing protein 1 like (AHRD V3.3 *** A0A0B2QR80_GLYSO)		P:GO:0006364; C:GO	P:rRNA processing; C:preribosome, small subunit precursor	IPR010301 (PFAM): mobidb-lite (MOB	20,288	26,456	18,819	19,568	19,456									
Solyc07g017950	Ribulose bisphosphate carboxylase small chain (AHRD V3.3 *** K4CCK9_SOLLC)		F:GO:0004497; C:GO	F:monooxygenase a EC:4.1.1.39 Ribulose-bisphospha	IPR024681 (PRINTS): IPR000894 (SM	4,225	4,652	0,292	0,530	0,374									
Solyc07g017955	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G01260.3)					6,368	6,737	7,332	5,991	5,876									
Solyc07g017960	Cofactor-independent phosphoglycerate mutase (AHRD V3.3 --* AT3G30841.2)					46,518	42,914	44,128	35,157	37,939									
Solyc07g017970	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UCR2_MEDTR)				IPR001938 (PRINTS): IPR001938 (SM	0,441	0,923	0,000	0,000	0,000									
Solyc07g017980	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)				mobidb-lite (MOBIDB_LITE): PTHR330	0,059	0,165	0,361	0,521	1,126									
Solyc07g017990	DNA ligase (AHRD V3.3 *** K4CCL3_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI EC:6.5.1.1 DNA ligase (ATP)	IPR012309 (PFAM): IPR012310 (PFA	11,030	10,381	8,677	9,285	9,233									
Solyc07g018000	DNA ligase (AHRD V3.3 *** A0A068V5K0_COFCA)		F:GO:0003677; F:GO	F:DNA binding; F:DI EC:6.5.1.1 DNA ligase (ATP)	IPR001357 (SMART): IPR001357 (PF	11,675	14,294	10,354	11,256	11,147									
Solyc07g018010	bHLH transcription factor139		F:GO:0046983	F:protein dimerization activity	IPR011598 (SMAF bHLH	6,733	43,956	1,504	0,298	1,315	2,730	0,000					up		
Solyc07g018035	3-ketoacyl-CoA synthase 3 (AHRD V3.3 --* AT1G07720.2)					0,779	0,794	0,504	0,583	0,681									
Solyc07g018070	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHRI		P:GO:0019538	P:protein metabolic process	IPR036628 (G3DSA:1.10.1780.GENE	5,657	7,517	0,771	0,386	0,803									
Solyc07g018090	CLEC16A-like protein (AHRD V3.3 *** AT3G28430.1)		P:GO:0001708; C:GO	P:cell fate specification; C:late endosome; C:Golgi apparatus; F	IPR019155 (PFAM): IPR039272 (PAN	22,749	18,021	20,637	24,143	22,035									
Solyc07g018140	Protein kinase family protein (AHRD V3.3 *** C6ZRQ1_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): IPR001245 (PF	16,989	11,060	2,963	2,203	2,541									
Solyc07g018144	DEAD/DEAH box RNA helicase family protein (AHRD V3.3 --* AT1G35530.5)		F:GO:0003677	F:DNA binding	IPR017956 (PRINTS): mobidb-lite (MO	0,171	0,489	0,000	0,000	0,093									
Solyc07g018180	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR003591 (SMA	2,618	2,548	0,804	0,724	0,781									
Solyc07g018190	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): IPR003591 (SM	12,455	10,277	2,020	2,187	2,718									
Solyc07g018200	LOW QUALITY:Hexosyltransferase (AHRD V3.3 *** K4CCN2_SOLLC)		P:GO:0006486; F:GO	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR002659 (PFAM): IPR002659 (PAN	0,000	0,018	0,000	0,025	0,000									
Solyc07g018210	Protein YIPF (AHRD V3.3 *** K4CCN3_SOLLC)		C:GO:0016020	C:membrane	IPR006977 (PFAM): mobidb-lite (MOB	3,691	4,482	5,793	5,449	4,357									
Solyc07g018220	Protein YIPF (AHRD V3.3 *** K4CCN3_SOLLC)		C:GO:0016020	C:membrane	IPR006977 (PFAM): mobidb-lite (MOB	4,857	6,649	8,440	8,637	7,782									
Solyc07g018230	Protein YIPF (AHRD V3.3 *** K4CCN3_SOLLC)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane	PTHR21236 (PANTHER): PTHR21236	4,430	3,766	3,717	3,320	3,675									
Solyc07g018235	Protein YIPF (AHRD V3.3 --* S8CHE2_9LAMI)					2,441	1,999	1,798	1,878	1,903									
Solyc07g018240	LOW QUALITY:GNS1/SUR4 membrane protein (AHRD V3.3 *** A0A103XMP3_CYNCS)		C:GO:0016021	C:integral component of membrane	IPR002076 (PFAM): PTHR11157:SF1	0,021	0,000	0,000	0,000	0,000									
Solyc07g018250	LOW QUALITY:GNS1/SUR4 membrane protein family (AHRD V3.3 *** AT3G06470.1)		C:GO:0016021	C:integral component of membrane	IPR002076 (PFAM): PTHR11157:SF1	0,019	0,077	0,000	0,000	0,000									
Solyc07g018270	Protein VERNALIZATION INSENSITIVE 3 (AHRD V3.3 *** A0A0B2QC33_GLYSO)		F:GO:0005515	F:protein binding	IPR032881 (PFAM): mobidb-lite (MOB	20,204	18,909	25,903	25,820	26,407									
Solyc07g018290	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7JVD9_MEDTR)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN' AP2	1,925	2,525	0,121	0,425	0,023									
Solyc07g018300	Replication protein A subunit (AHRD V3.3 *** A0A1D1Z493_9ARAE)		F:GO:0003677; C:GO	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D	IPR014892 (PFAM): G3DSA:2.40.50.1	3,615	3,301	3,048	2,262	3,011									
Solyc07g018310	OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 *-* AT4G25850.2)				mobidb-lite (MOBIDB_LITE): PTHR332	0,019	0,018	0,000	0,000	0,000									
Solyc07g018340	DNA mismatch repair protein msh6 (AHRD V3.3 *-* G7KNH7_MEDTR)		F:GO:0005524; P:GO	F:ATP binding; P:mismatch repair; F:mismatched DNA binding	IPR007695 (PFAM): IPR016151 (G3D	22,372	17,767	8,430	7,316	9,097									
Solyc07g018350	Mismatch repair protein (AHRD V3.3 *** D6QY21_SOLLC)		F:GO:0005524; P:GO	F:ATP binding; P:mismatch repair; F:mismatched DNA binding	IPR000432 (SMART): IPR007696 (SM	50,939	47,903	20,284	17,290	22,371									
Solyc07g018360	Elongation factor Ts (AHRD V3.3 *** K4CCP7_SOLLC)		F:GO:0003746; F:GO	F:translation elongation factor activity; F:protein binding; P:trans	IPR022967 (SMART): IPR036402 (G3	159,094	264,792	241,049	256,313	386,655	0,762	0,002	0,679	0,000			up	up	

Solyc07g018370	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT4G28840.1)		F:GO:0003700	F:DNA-binding transcription factor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc07g018387	Photosystem II reaction center protein I (AHRD V3.3 *** M9TLF1_SOLCA)		C:GO:0009539: P:G(	C:photosystem II reaction center; P:photosynthesis			IPR003686 (PFAM): PTHR35772:SF1	0,021	0,018	0,025	0,000	0,000									
Solyc07g018390	RING-H2 finger protein 2B (AHRD V3.3 --* AT2G01150.2)							4,662	2,783	6,633	7,771	5,841									
Solyc07g018400	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 --* A0A0B0P093_GOSAR)							1,306	1,106	1,063	1,750	1,159									
Solyc07g018430	F-box family protein (AHRD V3.3 --* AT3G60040.3)						PTHR38396 (PANTHER)	0,000	0,021	0,091	0,050	0,071									
Solyc07g018435	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RDP2_RICCO)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (PFAM): G3DSA:3.40.50.3	0,021	0,018	0,000	0,000	0,000									
Solyc07g019430	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT5G46400.1)							0,061	0,390	0,022	0,000	0,047									
Solyc07g019440	ADP-glucose pyrophosphorylase large subunit 2	AGPase L2	P:GO:0005978: F:G(	P:glycogen biosynth	EC:2.7.7.27	Glucose-1-phosphate	IPR011831 (TIGRFAM): IPR029044 ((	78,725	68,530	110,650	107,994	105,896									
Solyc07g019460	NADPH--cytochrome P450 reductase (AHRD V3.3 *** K4CCQ8_SOLLC)		F:GO:0003958: F:G(	F:NADPH-hemoprot	EC:1.6.2.4	NADPH--hemoprotein	IPR001094 (PRINTS): IPR001709 (PF	348,760	632,711	307,022	346,330	349,377									
Solyc07g019497	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SE46_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAI	1,839	1,597	0,641	0,358	0,637									
Solyc07g019505	Cytochrome c oxidase subunit 1 (AHRD V3.3 *-* K4CCR3_SOLLC)		P:GO:0055114	P:oxidation-reduction process			IPR036927 (G3DSA:1.20.210.GENE3I	0,038	0,043	0,075	0,101	0,000									
Solyc07g019510	Cytochrome c oxidase subunit 1 (AHRD V3.3 *** COX1_SOYBN)		F:GO:0004129: P:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR000883 (PRINTS): IPR036927 (G3	0,158	0,165	0,219	0,623	0,284									
Solyc07g019520	LOW QUALITY:Isocitrate lyase (AHRD V3.3 --* ACEA_RICCO)							0,100	0,369	0,811	0,423	0,495									
Solyc07g019530	Afadin/alpha-actinin-binding protein (AHRD V3.3 *** AT5G57410.3)						IPR021622 (PFAM): mobidb-lite (MOB	31,827	32,042	18,641	17,256	19,500									
Solyc07g019620	Lysine--tRNA ligase (AHRD V3.3 *-* A0A0V0IK21_SOLCH)		F:GO:0000049: F:G(	F:tRNA binding; F:ly	EC:6.1.1.6	Lysine--tRNA ligase	G3DSA:3.30.930.10 (GENE3D): PTHR	0,021	0,055	0,150	0,025	0,024									
Solyc07g019650	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103S9G9_CYNCS)		F:GO:0005515	F:protein binding			G3DSA:3.40.50.11980 (GENE3D): IPF	3,649	8,659	3,375	4,172	5,825	1,275	0,001	0,773	0,018			up	up	
Solyc07g019670	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857: C:G(	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	G3DSA:3.90.226.10 (GENE3D): IPR0(	273,199	293,060	636,037	549,707	560,452									
Solyc07g020710	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 *** A0A061GMK6_THECC)		F:GO:0000977: C:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR033467 (SMAF_CPP	12,877	14,217	15,774	15,364	14,506									
Solyc07g020720	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT3G24240.1		C:GO:0016021: P:G(	C:integral component of membrane; P:defense response to func			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,018	0,025	0,000	0,000									
Solyc07g020730	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT3G24240.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00364 (SMAR	0,059	0,000	0,000	0,000	0,000									
Solyc07g020790	plastidic glucose translocator 3	pGlcT3	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	61,929	45,794	44,562	38,814	38,578									
Solyc07g020800	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	0,982	1,313	0,025	0,050	0,164									
Solyc07g020860	Peroxiredoxin (AHRD V3.3 *** D2D300_GOSHI)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:cell redox homeostasis			IPR013740 (PFAM): G3DSA:3.40.30.1	483,328	421,906	705,792	572,905	643,668									
Solyc07g020870	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061GNL9_THECC)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR003613 (SMART): IPR001680 (SM	2,635	7,042	0,585	0,858	1,812	1,438	0,011					up		
Solyc07g020880	Protein kinase (AHRD V3.3 --* C6ZRX8_SOYBN)		F:GO:0004674: F:G(	F:protein serine/thr	EC:2.7.11	Transferring phosphorus-containing groups		0,058	0,062	0,025	0,000	0,000									
Solyc07g020910	Sister chromatid cohesion protein PDS5 like B-B (AHRD V3.3 *-* A0A0B2PCJ8_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion			IPR039776 (PANTHER): PTHR12663:	0,021	0,000	0,000	0,000	0,023									
Solyc07g020960	bHLH transcription factor140		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	16,457	14,066	10,405	11,692	8,835									
Solyc07g021030	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7LHE4_ARALL)							0,021	0,036	0,000	0,022	0,070									
Solyc07g021035	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7LHE4_ARALL)							0,322	0,385	0,167	0,198	0,423									
Solyc07g021050	Serine/threonine-protein kinase TOR (AHRD V3.3 --* TOR_ARATH)							0,240	0,018	0,096	0,075	0,048									
Solyc07g021120	conserved telomere maintenance component 1 (AHRD V3.3 *** AT4G09680.4)		P:GO:0000723	P:telomere maintenance			IPR028262 (PFAM): mobidb-lite (MOB	11,870	13,410	9,833	11,971	11,279									
Solyc07g021152	Protein SENSITIVITY TO RED LIGHT REDUCED 1 (AHRD V3.3 *-* A0A0B2QIN1_GLYSO)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm; P:microtubule-based process; P:circad			IPR040044 (PANTHER): PTHR28626:	0,021	0,000	0,000	0,000	0,000									
Solyc07g021156	RNA/RNP complex-1-interacting phosphatase (AHRD V3.3 --* AT3G52070.2)							0,664	0,219	0,000	0,047	0,000									
Solyc07g021158	Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *-* AT5G13500.3)						PTHR31485 (PANTHER): PTHR31485	0,417	0,287	0,000	0,047	0,000									
Solyc07g021170	Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *-* AT5G13500.3)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			PTHR31485:SF4 (PANTHER): PTHR3	0,444	0,097	0,022	0,000	0,000									
Solyc07g021180	ATP synthase subunit beta, chloroplastic (AHRD V3.3 *** ATPB_SOLBU)		P:GO:0046034: P:G(	P:ATP metabolic process; P:proton transmembrane transport			IPR004100 (PFAM): G3DSA:2.40.10.1	0,057	0,158	0,000	0,000	0,024									
Solyc07g021200	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_SOLLC)		F:GO:0000287	F:magnesium ion binding			IPR000685 (PFAM): IPR036376 (G3D	0,057	0,447	0,275	0,845	0,424									
Solyc07g021210	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* H6T9H5_PORAR)		F:GO:0016740	F:transferase activity			SSF64484 (SUPERFAMILY)	0,000	0,000	0,025	0,000	0,000									
Solyc07g021220	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* M1CW95_SOLTU)		F:GO:0003677: F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR006592 (SMART): G3DSA:2.40.40	0,000	0,000	0,049	0,048	0,046									
Solyc07g021230	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM): IPR036408 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc07g021240	Photosystem I P700 chlorophyll A apoprotein (AHRD V3.3 *-* C7U1R7_9ASPA)		C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PRINTS): IPR036408 (G3	0,000	0,000	0,000	0,050	0,023									
Solyc07g021280	30S ribosomal protein S2, chloroplastic (AHRD V3.3 *** RR2_SOLLC)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001865 (PRINTS): G3DSA:3.40.50	0,042	0,000	0,000	0,000	0,000									
Solyc07g021290	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLLC)		F:GO:0003677: F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA polymerase		0,021	0,018	0,000	0,000	0,000									
Solyc07g021340	Transmembrane protein, putative (AHRD V3.3 *** A0A072UUM3_MEDTR)						PTHR33474:SF2 (PANTHER): PTHR3	5,784	4,652	1,607	0,523	0,893									
Solyc07g021370	LOW QUALITY:DNA-directed DNA polymerase (AHRD V3.3 --* AT5G67100.2)							0,000	0,000	0,000	0,000	0,023									
Solyc07g021380	ATP synthase subunit b, chloroplastic (AHRD V3.3 *** A0A165BB32_SOLME)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP synthesis c			IPR002146 (PFAM): PTHR34264:SF3	0,119	0,638	0,122	0,320	0,164									
Solyc07g021450	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151SLA5_CAJCA)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR011990 ((	0,040	0,000	0,000	0,000	0,023									
Solyc07g021460	Glutathione s-transferase, putative (AHRD V3.3 *** B9R999_RICCO)	GSTU16	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	0,000	0,021	0,000	0,000	0,000									
Solyc07g021463	mitochondrial ribosomal protein S7 (AHRD V3.3 --* ATMG01270.1)							0,000	0,054	0,000	0,022	0,095									
Solyc07g021490	Protein disulfide-isomerase (AHRD V3.3 *-* M1BHF1_SOLTU)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	0,058	0,206	0,025	1,333	0,024									
Solyc07g021540	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)						IPR004182 (SMART): IPR004182 (PF	51,073	38,134	81,022	76,919	72,400									
Solyc07g021550	Effector of transcription protein (AHRD V3.3 *** G7KJT8_MEDTR)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR038909 (PANT_HRT-like	29,107	27,440	21,101	18,742	21,454									
Solyc07g021610	LOW QUALITY:plasmodesmata callose-binding protein 5 (AHRD V3.3 --* AT3G58100.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,350	11,657	7,046	6,286	7,126									
Solyc07g021620	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2S7U5_GLYSO)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (TIGF	6,959	9,108	12,101	9,094	11,884									
Solyc07g021630	SlBCAT2	BCAT2	F:GO:0004084: P:G(	F:branched-chain-a	EC:2.6.1.42	Branched-chain-amir	IPR005786 (TIGRFAM): IPR001544 (F	0,311	0,251	0,768	1,545	1,344									
Solyc07g021640	Carotenoid isomerase (AHRD V3.3 *-* A0A077EPD5_TOBAC)	CRTISO-Like 2	F:GO:0016491: F:G(	F:oxidoreductase activity; F:isomerase activity; P:oxidation-red			PF13450 (PFAM): IPR036188 (G3DSA	0,000	0,000	0,050	0,000	0,047									
Solyc07g021650	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q53J61_ORYSJ)						IPR029480 (PFAM)	5,057	5,886	5,605	7,328	6,200									
Solyc07g021670	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* A9PAA6_POPTR)		F:GO:0019789	F:SUMO transferase activity			IPR016135 (G3DSA:3.10.110.GENE3I	0,000	0,018	0,000	0,000	0,000									
Solyc07g021700	Pollen-specific SF21-like protein (AHRD V3.3 *** G7LJK8_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004142 (PFAM): IPR029058 (G3D	15,032	14,616	8,056	8,422	7,802									
Solyc07g021710	Inorganic pyrophosphatase 2 (AHRD V3.3 *** A0A199VVZ6_ANACO)		F:GO:0016791	F:phosphatase activity			IPR006384 (TIGRFAM): IPR023214 ((	0,731	1,636	1,960	2,197	1,607									
Solyc07g021730	Transposon protein, putative, Mutator sub-class (AHRD V3.3 *-* Q7XE42_ORYSJ)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,023									
Solyc07g021750	Cytidine deaminase (AHRD V3.3 *** K4CD31_SOLLC)		F:GO:0004126: F:G(	F:cytidine deaminas	EC:3.5.4.5	Cytidine deaminase	IPR013171 (PFAM): IPR002125 (PFAI	48,607	53,133	29,724	44,758	33,153					0,591	0,000			up
Solyc07g022760	pre-mRNA-processing protein 40A (AHRD V3.3 *** AT1G44910.1)		F:GO:0005515: P:G(	F:protein binding; P:mRNA cis splicing, via spliceosome			IPR002713 (SMART): IPR001202 (SM	75,668	73,692	71,095	72,894	74,484									
Solyc07g022790	Calcium-transporting ATPase (AHRD V3.3 *** A0A0V0IZZ4_SOLCH)		F:GO:0005388: F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR004014 (SMA	41,108	42,173	41,408	41,850	39,463									
Solyc07g022830	EXS family protein (AHRD V3.3 *** B9MXW8_POPTR)		C:GO:0016021	C:integral component of membrane			IPR004342 (PFAM): PTHR10783:SF4	18,303	16,104	9,988	10,131	12,096									
Solyc07g022840	LOW QUALITY:DUF620 family protein (DUF620) (AHRD V3.3 *** AT1G75160.1)						IPR006873 (PFAM): PTHR31300:SF4	0,038	0,000	0,000	0,000	0,000									
Solyc07g022860	Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *** A0A072UBV7_MEDTR)		P:GO:0015031	P:protein transport			G3DSA:1.20.1260.60 (GENE3D): IPR(	31,679	31,317	30,555	29,322	30,212									
Solyc07g022880	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *-* G7L900_MEDTR)		F:GO:0003860	F:3-hydroxyisobuty	EC:3.1.2.4	3-hydroxyisobutyryl-(	IPR032259 (PFAM): G3DSA:3.90.226	0,218	0,099	0,146	0,120	0,164									
Solyc07g022900	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4CD46_SOLLC)		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	17,351	45,691	6,754	10,787	25,977	1,424	0,000	1,934	0,000			up	up	
Solyc07g022910	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *** WEB1_ARATH)						IPR027267 (G3DSA:1.20.1270.GENE	72,688	85,121	163,073	185,996	185,616									
Solyc07g022920	BSD domain-containing family protein (AHRD V3.3 *** B9IBP6_POPTR)						IPR005607 (SMART): IPR005607 (PF	20,968	30,291	20,947	20,450	21,169									
Solyc07g023990	AAA-type ATPase family protein (AHRD V3.3 *** B9ILM7_POPTR)		F:GO:0005524	F:ATP binding			IPR000641 (PRINTS): IPR003959 (PF	0,098	0,077	0,000	0,025	0,023									
Solyc07g023995	Ankyrin repeat-containing protein (AHRD V3.3 *-* A0A103Y2F4_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	0,056	0,116	0,025	0,000	0,000									
Solyc07g024000	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G13250.1)		C:GO:0009536: P:G(	C:plastid; P:PSII as	EC:1.1.1.294	Chlorophyll(ide) b rec	IPR002347 (PRINTS): IPR002347 (PF	100,924	94,238	288,578	314,860	255,031									
Solyc07g024010	Protein phosphatase 2C family protein (AHRD V3.3 *-* AT1G47380.1)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR036457 (G3DSA:3.60.40.GENE3D	0,000	0,130	0,000	0,000	0,024									
Solyc07g024020	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G47380.1)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	0,159	0,202	0,000	0,000	0,000									
Solyc07g024040	Photosystem I reaction center subunit VIII (AHRD V3.3 *** K4CD56_SOLLC)		C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis			IPR001302 (TIGRFAM): IPR001302 (F	0,040	0,043	0,046	0,100	0,046									
Solyc07g024070	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* B6UES9_MAIZE)		F:GO:0016740	F:transferase activity			SM00212 (SMART): IPR016135 (G3D	4,823	3,666	0,785	0,454	0,662									
Solyc07g025105	F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	3,093	2,500	2,324	2,458	2,493									
Solyc07g025110	F-box protein (AHRD V3.3 --* W9RLE9_9ROSA)							0,019	0,000	0,000	0,022	0,023									
Solyc07g025170	exocyst complex component sec3A (AHRD V3.3 *** AT1G47550.2)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			IPR028258 (SMART): IPR019160 (PF	26,658	26,549	27,763	27,892	26,913									
Solyc07g025200	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061FBT4_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	8,830	8,783	12,229	10,356	11,601									
Solyc07g025210	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061FBT4_THECC)						PTHR24015:SF515 (PANTHER): PTHI	16,411	15,924	21,682	19,420	20,618									
Solyc07g025220	LOW QUALITY:Zinc finger C-x8-C-x5-C-x3-H type family protein (AHRD V3.3 --* AT2G47850.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,025	0,000	0,000									
Solyc07g025230	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061FBT4_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	8,952	8,414	10,670	9,951	9,799									
Solyc07g025250	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061F1G5_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	7,611	5,439	4,225	4,930	4,024									
Solyc07g025255	magnesium transporter, putative (DUF803) (AHRD V3.3 --* AT1G71900.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,050	0,000									
Solyc07g025370	Cytochrome P450 (AHRD V3.3 *** A0A118JYC4_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	19,778	16,080	9,164	9,581	8,956									
Solyc07g025380	DNA ligase-like protein (AHRD V3.3 *-* AT1G75150.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,372	7,397	0,953	0,650	1,199									
Solyc07g025390	Peptidyl-prolyl cis-trans isomerase-like 3 (AHRD V3.3 *-* A0A0B2PVH2_GLYSO)	EXP	C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane			G3DSA:3.50.4.10 (GENE3D): PTHR33	10,426	10,316	10,571	10,887	11,082									
Solyc07g025400	phloem protein 2-A13 (AHRD V3.3 --* AT3G61060.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,558	7,269	14,867	14,474	11,980									
Solyc07g025490	OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 --* AT4G25850.3)							11,256	7,262	6,536	6,741	7,173									
Solyc07g025500	Ribosomal protein S3 (AHRD V3.3 --* A0A075BNV0_FUNHY)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,022	0,000	0,000									
Solyc07g025510	Tetraspanin family protein (AHRD V3.3 *** G7LJJ7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	35,193	24,664	13,584	11,549	11,638									
Solyc07g025520	Methyltransferase, putative (AHRD V3.3 *** B9RK97_RICCO)		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM): G3DSA:3.40.50.1	6,776	8,334	7,600	6,725	8,469									
Solyc07g025525	U1 small nuclear ribonucleoprotein-70K (AHRD V3.3 --* AT3G50670.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,057	0,114	0,000	0,000	0,023									
Solyc07g025530	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* A0A061GM35		F:GO:0008168: C:G(	F:methyltransferase activity; C:chloroplast; P:methylation				2,719	2,767	2,728	2,624	3,392									
Solyc07g026540	cytokinin oxidase 4 (AHRD V3.3 --* AT4G29740.3)						mobidb-lite (MOBIDB_LITE)	0,019	0,391	0,000	0,022	0,283									
Solyc07g026560	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9N3B2_POPTR)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (SMART): G3DSA:1.10.10	0,040	0,021	0,000	0,025	0,070									
Solyc07g026603	multidrug resistance-associated protein 6 (AHRD V3.3 --* AT3G21250.5)							0,080	0,037	0,000	0,025	0,024									
Solyc07g026607	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 (AHRD V3.3 --* NDUS3_BETTR)							0,000	0,000	0,000	0,000	0,046									
Solyc07g026620	TUBULIN-FOLDING COFACTOR E family protein (AHRD V3.3 --* B9IQ98_POPTR)							20,817	19,763	20,522	20,893	21,779									
Solyc07g026630	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 --* AT1G53340.3)							1,171	0,779	1,224	1,141	1,273									
Solyc07g026640	fanconi anemia group E protein FANCE protein (AHRD V3.3 *** AT4G29560.1)		P:GO:0036297: C:G(	P:interstrand cross-link repair; C:Fanconi anaemia nuclear com			G3DSA:1.25.40.480 (GENE3D): IPR0:	4,091	3,928	2,929	2,800	3,153									
Solyc07g026650	1-aminocyclopropane-1-carboxylate oxidase 5	ACO5	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	5,179	12,498	6,719	3,822	5,226	1,291	0,002					up		
Solyc07g026670	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NUN8_ZOSMR)		P:GO:0006812: F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR006153 (PFAM): IPR038770 (G3D	25,240	21,262	29,200	30,314	28,810									
Solyc07g026675	myb-like transcription factor family protein (AHRD V3.3 *-* AT5G56840.1)		F:GO:0003677	F:DNA binding			IPR001005 (SMART): G3DSA:1.10.10	0,000	0,041	0,000	0,050	0,000									
Solyc07g026680	Myb-like transcription factor family protein, putative (AHRD V3.3 *** A0A061GMU9_THECC)		F:GO:0003677	F:DNA binding			IPR001005 (SMAF_MYB_related	0,059	0,150	0,025	0,025	0,023									
Solyc07g026710	Transposon protein, putative, Mutator sub-class (AHRD V3.3 *-* Q7XE42_ORYSJ)		F:GO:0003677: F:G(	F:DNA binding; F:transposase activity; P:transposition, DNA-me			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,585	2,674	2,531	2,680	2,004									
Solyc07g026720	Calcium-transporting ATPase (AHRD V3.3 *-* M1AEH0_SOLTU)		F:GO:0005388: F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	G3DSA:1.20.1110.10 (GENE3D): IPR(	0,855	1,147	1,042	0,437	0,589									
Solyc07g026730	Calcium-transporting ATPase (AHRD V3.3 *-* K4D2H1_SOLLC)		F:GO:0000166	F:nucleotide binding			PF13246 (PFAM): IPR023299 (G3DSA	0,099	0,059	0,025	0,101	0,023									
Solyc07g026740	Calcium-transporting ATPase (AHRD V3.3 *-* M0SWN7_MUSAM)		F:GO:0005388: F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	G3DSA:1.20.1110.10 (GENE3D): PTH	0,099	0,098	0,025	0,000	0,094									
Solyc07g026770	Mitochondrial ATP synthase subunit G protein (AHRD V3.3 *** AT4G29480.1)		C:GO:0000276: F:G(	C:mitochondrial proton-transporting ATP synthase complex, cou			IPR006808 (PFAM): PTHR12386:SF2	175,727	151,206	154,674	135,736	138,394									
Solyc07g026805	Replication protein A1a (AHRD V3.3 --* A0A059Q228_9POAL)		C:GO:0016020	C:membrane				0,040	0,440	0,000	0,000	0,023									
Solyc07g026810	DnaJ homolog subfamily C member 14 (AHRD V3.3 *** W9RSJ9_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR001623 (PRINTS): IPR001623 (SM	58,102	56,871	85,159	84,783	78,041									
Solyc07g026860	Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q7G3C6_ORYSJ)						IPR004242 (PFAM): mobidb-lite (MOB	0,019	0,021	0,000	0,000	0,000									
Solyc07g026880	LOW QUALITY:Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *-* WEB1		C:GO:0005829: P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			IPR008545 (PFAM): PTHR32054 (PAI	0,000	0,039	0,000	0,022	0,000									
Solyc07g026910	NAD(P)H-quinone oxidoreductase subunit 6, chloroplastic (AHRD V3.3 *** NU6C_SOLLC)		F:GO:0008137: P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001457 (PFAM): G3DSA:1.20.120	0,000	0,228	0,000	0,076	0,046									
Solyc07g026930	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.1)		F:GO:0005215: C:G(	F:transporter activity; C:integral component of membrane; P:tra			IPR001958 (PRINTS): G3DSA:1.20.12	0,079	0,149	3,667	5,857	3,534					0,675	0,045			up
Solyc07g026960	Metallopeptidase M24 family protein (AHRD V3.3 *** AT4G29490.1)		F:GO:0004177: F:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR007865 (SMART): G3DSA:3.90.23	197,844	165,197	285,420	266,479	266,361									
Solyc07g027020	Protein kinase family protein (AHRD V3.3 *-* C6ZRT1_SOYBN)		F:GO:0004713: F:G(	F:protein tyrosine k	EC:2.7.1	Transferring phospho	mobidb-lite (MOBIDB_LITE): mobidb-lit	25,704	26,118	10,203	10,265	10,836									
Solyc07g027025	Protein kinase family protein (AHRD V3.3 *** C6ZRT1_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	0,063	0,000	0,000	0,000	0,000									
Solyc07g032020	DNA-directed RNA polymerase subunit (AHRD V3.3 --* A0A0R0KYG7_SOYBN)							0,241	0,755	0,462	0,744	0,564									
Solyc07g032070	LOW QUALITY:Unknown protein (AHRD V3.3)							0,019	0,037	0,000	0,022	0,000									
Solyc07g032080	V-type proton ATPase subunit a (AHRD V3.3 *** K4CDF2_SOLLC)		C:GO:0000220: F:G(	C:vacuolar proton-transporting V-type ATPase, V0 domain; F:pr			IPR026028 (PIRSF): IPR002490 (PFA	0,564	0,578	0,190	0,241	0,306									
Solyc07g032090	Transcription initiation factor IIF subunit beta (AHRD V3.3 *** A0A0B0MH47_GOSAR)		C:GO:0005674: P:G(	C:transcription factor TFIIF complex; P:transcription initiation fr(			IPR036388 (G3DSA:1.10.10.GENE3D	49,602	43,966	50,929	47,397	48,511									
Solyc07g032100	Coatomer subunit alpha (AHRD V3.3 *** K4CDF4_SOLLC)		F:GO:0005198: F:G(	F:structural molecule activity; F:protein binding; P:intracellular pı			IPR020472 (PRINTS): IPR001680 (SM	131,729	144,043	125,351	126,341	127,697									
Solyc07g032110	SH3 domain-containing protein (AHRD V3.3 *** AT4G34660.1)		F:GO:0005515: C:G(	F:protein binding; C:cytoplasm			IPR001452 (SMART): IPR001452 (PF	17,196	14,982	13,396	11,960	12,765									
Solyc07g032150	Unknown protein (AHRD V3.3)							1,077	0,759	0,939	1,568	1,058									
Solyc07g032170	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT4G24160.2)		F:GO:0004623: F:G(	F:phospholipase A2	EC:3.1.1.1; EC:3.1.1	Carboxylesterase; Pl	IPR029058 (G3DSA:3.40.50.GENE3D	23,251	19,785	19,228	19,046	19,125									
Solyc07g032180	Abhydrolase domain-containing protein 4 (AHRD V3.3 *** A0A0B2SN17_GLYSO)		F:GO:0004623: F:G(	F:phospholipase A2	EC:3.1.1.1; EC:3.1.1	Carboxylesterase; Pl	IPR029058 (G3DSA:3.40.50.GENE3D	22,200	20,639	19,705	17,515	17,799									
Solyc07g032220	Phospholipase A2 (AHRD V3.3 *** Q5CCT9_TOBAC)		F:GO:0004623: F:G(	F:phospholipase A2	EC:3.1.1.1; EC:3.1.1	Carboxylesterase; Pl	IPR036444 (G3DSA:1.20.90.GENE3D	14,942	16,786	15,617	14,853	16,382									
Solyc07g032230	Regulator of Vps4 activity in the MVB pathway protein (AHRD V3.3 *-* AT2G19710.1)		P:GO:0015031	P:protein transport			G3DSA:1.20.1260.60 (GENE3D): IPR(	324,921	213,106	108,236	291,737	208,420			0,942	0,000	1,431	0,000		up	up
Solyc07g032240	arginine methyltransferase 11 (AHRD V3.3 *** AT4G29510.1)		P:GO:0006479: F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:2.70.160.11 (GENE3D): G3DS	8,656	8,724	8,963	8,576	9,835									
Solyc07g032250	AT4G29520-like protein (AHRD V3.3 *** A0A097PSU3_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:plasma membrane; F:protein folding			PTHR36058 (PANTHER)	13,140	14,783	20,128	23,023	19,131									
Solyc07g032260	Activating transcription factor 7-interacting 1 (AHRD V3.3 *** A0A0B0MF55_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	25,139	28,619	22,894	22,773	23,181									
Solyc07g032313	Reverse transcriptase (AHRD V3.3 *-* D5LW17_9POAL)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:2.7.7.49	RNA-directed DNA pc	IPR000477 (PFAM): G3DSA:3.30.70.2	0,042	0,021	0,000	0,000	0,000									
Solyc07g032317	Polyprotein (AHRD V3.3 *-* A0A151R3E4_CAJCA)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:2.7.7.49	RNA-directed DNA pc	G3DSA:3.10.10.10 (GENE3D): IPR0(	0,000	0,000	0,000	0,025	0,023									
Solyc07g032380	DNA LIGASE 6 (AHRD V3.3 --* AT1G66730.1)							0,193	0,262	0,337	0,274	0,421									
Solyc07g032385	Pentatricopeptide repeat-containing-like protein (AHRD V3.3 *** A0A0B0N0N5_GOSAR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	59,052	45,302	31,709	71,058	69,794			1,134	0,000	1,164	0,000		up	up
Solyc07g032390	methyl-CPG-binding domain 3 (AHRD V3.3 --* AT4G00416.1)							0,616	0,512	0,942	1,117	1,087									

Solyc07g032450	LOW QUALITY:Cytochrome b6 (AHRD V3.3 *-* CYB6_LACSA)		F:GO:0005506; C:G(	F:iron ion binding; C:integral component of membrane; F:heme b	IPR027387 (G3DSA:1.20.810.GENE3	0,000	0,000	0,000	0,025	0,000									
Solyc07g032470	LOW QUALITY:F-box family protein (AHRD V3.3 --* AT4G05010.1)					0,347	0,481	0,423	0,596	0,446									
Solyc07g032480	cyclinT1_2	CycT1_2	C:GO:0005634	C:nucleus	IPR013763 (SMART): IPR006671 (PF	19,269	31,846	28,440	28,186	26,491	0,751	0,009					up		
Solyc07g032490	Major facilitator superfamily protein (AHRD V3.3 *** AT2G26690.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmem	IPR000109 (PFAM): PTHR11654:SF8	0,098	0,057	0,075	0,050	0,165									
Solyc07g032510	Forkhead-associated (FHA) domain protein (AHRD V3.3 *** G7J4N3_MEDTR)		F:GO:0002151; F:G(	F:G-quadruplex RNA binding; F:protein binding; C:Ino80 complex	IPR000253 (SMART): G3DSA:2.60.20	3,570	2,966	2,976	3,853	2,634									
Solyc07g032580	LOW QUALITY:Purple acid phosphatase (AHRD V3.3 *-* A0A0D9ZFS8_9ORYZ)		F:GO:0003824	F:catalytic activity	IPR000310 (PFAM): IPR015421 (G3D	0,019	0,000	0,025	0,000	0,000									
Solyc07g032610	Oxygen-evolving enhancer protein 1 (AHRD V3.3 *-* A0A0A0KI32_CUCSA)		C:GO:0009654; P:G(	C:photosystem II oxygen evolving complex; P:photosystem II as	G3DSA:2.40.160.30 (GENE3D): IPR0(	0,000	0,036	0,025	0,025	0,094									
Solyc07g032633	Oxygen-evolving enhancer protein 1 (AHRD V3.3 *** A0A1D3L5W7_SOLLC)		C:GO:0009654; P:G(	C:photosystem II oxygen evolving complex; P:photosystem II as	IPR002628 (PFAM): G3DSA:2.40.160	0,059	0,097	0,044	0,072	0,070									
Solyc07g032640	Oxygen-evolving enhancer protein 1 (AHRD V3.3 *** A0A1D3L5W7_SOLLC)		C:GO:0009654; P:G(	C:photosystem II oxygen evolving complex; P:photosystem II as	G3DSA:3.30.2050.10 (GENE3D): G3D	233,365	372,680	156,862	180,903	351,373			1,160	0,000				up	
Solyc07g032660	LOW QUALITY:Lipoxygenase (AHRD V3.3 *-* K4B0V7_SOLLC)		F:GO:0016702; F:G(	F:oxidoreductase a EC:1.13.11 Acting on single donc	IPR001246 (PRINTS): G3DSA:4.10.37	0,000	0,000	0,046	0,022	0,000									
Solyc07g032670	Unknown protein (AHRD V3.3)					0,000	0,000	0,000	0,000	0,023									
Solyc07g032680	RNA-binding KH domain-containing protein (AHRD V3.3 --* AT4G26000.1)					0,042	0,018	0,000	0,000	0,000									
Solyc07g032700	LOW QUALITY:Histone-lysine N-methyltransferase ATXR7 (AHRD V3.3 --* ATXR7_ARATH)				mobidb-lite (MOBIDB_LITE): PTHR332	0,000	0,019	0,000	0,000	0,000									
Solyc07g032710	Pantothenate synthetase (AHRD V3.3 *-* A0A0B0PGX1_GOSAR)				IPR032795 (PFAM): IPR025486 (PFA	10,973	8,026	3,840	4,249	4,181									
Solyc07g032730	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 *** AT1G52240.1)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity	G3DSA:1.20.58.2010 (GENE3D): G3D	0,000	0,019	0,025	0,000	0,000									
Solyc07g032740	Aspartate aminotransferase (AHRD V3.3 *** M1B9T8_SOLTU)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit	IPR000796 (PRINTS): IPR015421 (G3	157,266	126,492	225,136	144,876	144,754			-0,640	0,000	-0,633	0,000		down	down
Solyc07g032745	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061FID3_THECC)				PTHR23272 (PANTHER): IPR012337 (	0,000	0,000	0,000	0,025	0,000									
Solyc07g032794	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR003653 (PFAM): mobidb-lite (MOB	0,021	0,000	0,074	0,000	0,000									
Solyc07g032798	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9N3B2_POPTR)		F:GO:0005488	F:binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,057	0,208	0,807	0,330									
Solyc07g037910	Homeobox leucine zipper protein (AHRD V3.3 *-* A0A072UAM9_MEDTR)		F:GO:0008289	F:lipid binding	IPR023393 (G3DSA:3.30.530.GENE3	0,000	0,000	0,025	0,312	0,118									
Solyc07g037920	Homeobox leucine zipper protein (AHRD V3.3 *-* A0A072UAM9_MEDTR)		F:GO:0003677	F:DNA binding	PTHR24326 (PANTHER): PTHR24326	0,000	0,000	0,071	0,145	0,116									
Solyc07g037930	LOW QUALITY:alanine:glyoxylate aminotransferase 2 (AHRD V3.3 --* AT4G39660.2)					0,082	0,041	0,069	0,000	0,119									
Solyc07g037940	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)				IPR015410 (PFAM): mobidb-lite (MOB	0,040	0,039	0,050	0,000	0,000									
Solyc07g037950	Ectonucleotide pyrophosphatase/phosphodiesterase, putative (AHRD V3.3 *** B9RK58_RICCO)		F:GO:0003824	F:catalytic activity	IPR002591 (PFAM): G3DSA:3.30.136	6,831	6,277	10,315	9,782	9,388									
Solyc07g037960	Ectonucleotide pyrophosphatase/phosphodiesterase, putative (AHRD V3.3 *** B9RK58_RICCO)		F:GO:0003824	F:catalytic activity	G3DSA:3.30.1360.180 (GENE3D): IPF	30,610	28,658	41,961	40,541	39,840									
Solyc07g038100	acyl-CoA synthetase family protein (AHRD V3.3 *** AT3G60310.2)		C:GO:0016021	C:integral component of membrane		13,608	10,362	20,467	21,693	18,074									
Solyc07g038105	30S ribosomal protein S4, chloroplastic (AHRD V3.3 --* RR4_STIHE)					0,019	0,019	0,121	0,069	0,141									
Solyc07g038110	Beta-galactosidase (AHRD V3.3 *-* V7C958_PHAVU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS): IPR008979 (G3	0,340	0,400	0,316	0,552	0,566									
Solyc07g038130	Beta-galactosidase (AHRD V3.3 *-* A0A103XKB3_CYNCS)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS): G3DSA:3.20.2(	0,040	0,037	0,141	0,380	0,262									
Solyc07g038160	GATA transcription factor (AHRD V3.3 *** A0A0K9PML1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR000679 (SMAF GATA	0,159	0,450	0,123	0,096	0,209									
Solyc07g038190	WAS/WASL-interacting family protein (AHRD V3.3 *** AT1G55160.2)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,005	0,966	0,834	0,629	0,728									
Solyc07g039190	nuclear pore complex protein (DUF3414) (AHRD V3.3 --* AT5G51200.3)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	9,246	13,197	3,524	4,060	6,737			0,924	0,029				up	
Solyc07g039195	Dystrophin-1 (AHRD V3.3 *-* A0A0B0NKV5_GOSAR)		C:GO:0016021	C:integral component of membrane	PTHR36810 (PANTHER)	1,847	2,050	0,601	0,697	1,126									
Solyc07g039200	WD-repeat protein, putative (AHRD V3.3 *** B9SP08_RICCO)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR015943 (G3	65,683	71,068	72,220	61,633	62,261									
Solyc07g039210	PCI domain-containing 2 (AHRD V3.3 *** A0A0B0MN94_GOSAR)		C:GO:0005634; P:G(	C:nucleus; P:ethylene-activated signaling pathway; P:poly(A)+ r	G3DSA:1.25.40.570 (GENE3D): IPR0(	10,965	11,102	20,669	21,074	18,487									
Solyc07g039290	LOW QUALITY:Senescence-associated protein (AHRD V3.3 *-* A0A072TTZ6_MEDTR)				PTHR33047 (PANTHER): PTHR33047	0,077	0,179	0,072	0,148	0,095									
Solyc07g039310	Polyamine oxidase 5 (AHRD V3.3 *** A0A1C8M5K2_MALDO)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	G3DSA:3.90.660.10 (GENE3D): IPR0:	6,050	5,191	0,345	0,239	0,590									
Solyc07g039317	LOW QUALITY:Calmodulin-binding heat-shock protein (AHRD V3.3 *-* Q41251_TOBAC)		P:GO:0016042	P:lipid catabolic process	IPR005592 (PFAM)	0,000	0,000	0,000	0,022	0,000									
Solyc07g039330	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT2G19520.1)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR001680 (PF	165,662	145,523	195,877	187,814	194,222									
Solyc07g039340	Protein kinase (AHRD V3.3 *** A2Q551_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): G3DS	31,957	27,381	31,158	28,769	32,195									
Solyc07g039345	Lycopene beta cyclase, chloroplastic/chromoplastic (AHRD V3.3 --* LCYB_NARPS)				mobidb-lite (MOBIDB_LITE)	1,046	1,534	0,759	0,824	0,705									
Solyc07g039370	cyclin-like protein (AHRD V3.3 --* AT1G70620.8)					0,082	0,062	0,050	0,072	0,000									
Solyc07g039380	cotton fiber protein (AHRD V3.3 *-* AT5G56980.1)		C:GO:0016021	C:integral component of membrane	IPR008480 (PFAM): mobidb-lite (MOB	3,513	5,129	1,831	1,608	1,641									
Solyc07g039410	EDNR2GH3 protein (AHRD V3.3 *** E0Y3V4_9SOLN)		F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,039	0,172	0,319	0,664									
Solyc07g039420	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G38350.1)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): G3DSA:3.40.50.3	0,019	0,039	0,288	0,342	0,689									
Solyc07g039440	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* D1GEE0_BRARP)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	0,915	0,709	0,753	1,171	0,922									
Solyc07g039450	Translation machinery-associated protein 22 (AHRD V3.3 *** K4CDS1_SOLLC)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation	G3DSA:3.30.780.10 (GENE3D): IPR0(	27,997	28,527	30,026	28,977	27,390									
Solyc07g039500	Chloroplastic group IIA intron splicing facilitator CRS1 (AHRD V3.3 *** W9QS67_9ROSA)		F:GO:0003723	F:RNA binding	IPR001890 (SMART): IPR035920 (G3	13,293	12,665	22,685	22,866	24,950									
Solyc07g039505	Beta-glucosidase 3 (AHRD V3.3 --* BGL03_ORYSJ)					1,072	0,876	0,845	1,121	1,086									
Solyc07g039510	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G47560.4)				IPR029058 (G3DSA:3.40.50.GENE3D	10,512	10,455	5,770	4,409	5,307									
Solyc07g039540	LOW QUALITY:Lipid phosphate phosphatase-like protein (AHRD V3.3 --* A0A072VQU9_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		0,059	0,000	0,000	0,000	0,000									
Solyc07g039550	RNA helicase DEAH-box21	DEAH21	F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.6.1.15 Nucleoside-triphosph	IPR014001 (SMART): IPR001650 (SM	35,314	34,807	32,728	29,415	32,001									
Solyc07g039570	bHLH transcription factor 051		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR011598 (SMAF bHLH	0,123	0,746	0,096	0,095	0,190									
Solyc07g039620	cellulose synthase A4 (AHRD V3.3 --* AT5G44030.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,160	0,000	0,000	0,024									
Solyc07g039630	LOW QUALITY:EXORDIUM like 3 (AHRD V3.3 --* AT5G51550.1)					0,019	0,021	0,000	0,000	0,000									
Solyc07g039635	Calmodulin-binding cyclic nucleotide gated channel 15 (AHRD V3.3 --* F5AJX6_HELTU)				mobidb-lite (MOBIDB_LITE)	0,000	0,054	0,000	0,000	0,000									
Solyc07g039660	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151SZ39		C:GO:0000943; F:G(	C:retrotransposon nucleocapsid; F:nucleic acid binding; F:zinc i	PTHR34222 (PANTHER): PTHR34222	0,079	0,295	0,075	0,238	0,213									
Solyc07g040660	golgin Putative 5 (AHRD V3.3 --* AT1G79830.5)				mobidb-lite (MOBIDB_LITE)	3,654	2,727	1,416	1,493	1,229									
Solyc07g040680	SolycHsfA9	HSF-22	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	16,245	10,926	32,449	29,510	28,881									
Solyc07g040685	evolutionarily conserved C-terminal region 10 (AHRD V3.3 --* AT5G58190.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,047	0,022	0,094									
Solyc07g040690	non-inducible immunity 1	nim1	F:GO:0005515	F:protein binding	IPR002110 (SMART): IPR000210 (SM	13,350	22,478	19,838	21,220	20,032	0,777	0,022					up		
Solyc07g040695	LOW QUALITY:Gag-pol polyprotein (AHRD V3.3 --* Q850H5_VITVI)		F:GO:0004497; P:G(	F:monooxygenase activity; P:oxidation-reduction process; F:FAD binding		0,000	0,019	0,000	0,050	0,071									
Solyc07g040700	F-box/RNI-like/FBD-like domains-containing protein (AHRD V3.3 --* AT5G56370.3)					0,000	0,021	0,000	0,022	0,023									
Solyc07g040710	Calmodulin binding protein, putative (AHRD V3.3 *** B9RK85_RICCO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	4,769	13,699	1,949	0,764	2,137									
Solyc07g040720	Casein kinase family protein (AHRD V3.3 *** B9N5F1_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	63,566	89,530	81,853	74,874	82,412									
Solyc07g040730	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 *** I3SBP3_MEDTR)				IPR021899 (PFAM): PTHR33193 (PAN	178,717	122,621	62,395	49,465	52,281					-0,332	0,050			down
Solyc07g040740	O-acyltransferase (AHRD V3.3 *** K4CDV1_SOLLC)		F:GO:0004144; P:G(	F:diacylglycerol O-a EC:2.3.1.2 Diacylglycerol O-acy	IPR014371 (PIRSF): IPR027251 (PIR	4,726	5,369	1,468	1,157	1,693									
Solyc07g040750	RNA helicase DEAD21	DEAD21	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR001650 (SMART): IPR014001 (SM	0,138	0,121	0,220	0,383	0,351									
Solyc07g040770	Unknown protein (AHRD V3.3)				mobidb-lite (MOBIDB_LITE)	0,082	0,154	0,090	0,069	0,048									
Solyc07g040780	WD40 repeat containing protein (AHRD V3.3 *** R9RH89_LINUS)		F:GO:0005515	F:protein binding	IPR001680 (SMART): IPR001680 (PF	10,631	11,209	10,071	10,413	9,686									
Solyc07g040800	LOW QUALITY:Lipoxygenase (AHRD V3.3 *-* K4B0V7_SOLLC)		F:GO:0016702; F:G(	F:oxidoreductase a EC:1.13.11 Acting on single donc	IPR001246 (PRINTS): G3DSA:4.10.37	0,019	0,021	0,025	0,051	0,047									
Solyc07g040840	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT5G61090.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,077	0,081	0,000	0,100	0,023									
Solyc07g040880	Gibberellin receptor GID1, putative (AHRD V3.3 *** B9R9J9_RICCO)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM): IPR029058 (G3D	0,021	0,039	0,046	0,050	0,142									
Solyc07g040890	Gibberellin receptor GID1, putative (AHRD V3.3 *** G7IC52_MEDTR)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM): IPR029058 (G3D	0,165	1,211	0,541	1,326	3,669			2,742	0,000				up	
Solyc07g040900	Gibberellin receptor GID1, putative (AHRD V3.3 *-* B9R9J9_RICCO)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,043	0,000	0,000	0,000									
Solyc07g040910	winged-helix DNA-binding transcription factor family protein (AHRD V3.3 --* AT1G54260.1)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem	mobidb-lite (MOBIDB_LITE): PTHR114	7,493	7,538	8,268	8,001	7,023									
Solyc07g040920	MYB transcription factor (AHRD V3.3 *** E5GB88_CUCME)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem	IPR001005 (SMAF MYB_related	11,980	11,228	11,102	11,567	10,686									
Solyc07g040940	Kinase family protein (AHRD V3.3 *** D7MM98_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity	IPR000719 (SMART): IPR003613 (SM	42,862	31,091	60,916	56,139	60,130									
Solyc07g040950	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT5G57040.1)				IPR004360 (PFAM): IPR029068 (G3D	14,969	20,628	20,251	18,524	25,298									
Solyc07g040960	LOW QUALITY:Harbinger transposase-derived nuclease (AHRD V3.3 *** A0A103Y2W0_CYNCS)				IPR027806 (PFAM): mobidb-lite (MOB	782,474	331,730	170,799	654,091	293,916	-1,215	0,001	0,781	0,048	1,939	0,000	down	up	up
Solyc07g040970	LOW QUALITY:ribosomal protein L5 (AHRD V3.3 *-* ATMG00210.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR022803 (G3DSA:3.30.1440.GENE	0,019	0,019	0,100	0,075	0,023									
Solyc07g040980	Serine/arginine repetitive matrix protein 2 isoform 2 (AHRD V3.3 *** A0A061GLE4_THECC)				IPR019340 (PFAM): mobidb-lite (MOB	65,895	53,732	84,186	82,444	78,137									
Solyc07g040990	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G57050.1)		F:GO:0004722; P:G(	F:protein serine/thr EC:3.1.3.16 Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	53,961	53,096	93,734	97,506	101,291									
Solyc07g041000	Cleavage and polyadenylation specificity factor subunit 5 (AHRD V3.3 *** A0A0B2R9M0_GLYSO)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cleavage factor complex; P:mRNA po	G3DSA:3.90.79.10 (GENE3D): IPR01(	0,472	0,638	0,658	0,687	0,374									
Solyc07g041010	60S ribosomal L18a-like protein (AHRD V3.3 *** AT5G57060.9)		C:GO:0016021	C:integral component of membrane	IPR028877 (PANTHER): PTHR10052:	27,193	28,537	19,884	19,168	18,640									
Solyc07g041020	RNA-binding protein (AHRD V3.3 *** B4FIJ2_MAIZE)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding	IPR003604 (SMART): G3DSA:2.20.28	19,918	17,832	12,428	13,110	11,929									
Solyc07g041070	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G57070.1)		C:GO:0016021	C:integral component of membrane	IPR008480 (PFAM): mobidb-lite (MOB	3,148	4,538	0,442	0,288	0,377									
Solyc07g041080	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G29830.1)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR001680 (SM	15,266	11,770	11,543	8,895	12,263									
Solyc07g041110	LOW QUALITY:Cold shock domain-containing protein e1 (AHRD V3.3 --* A0A061SGP2_9CHLO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,019	0,046	0,000	0,024									
Solyc07g041150	Myosin (AHRD V3.3 *-* W6A1M7_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:/ EC:3.6.1.15 Nucleoside-triphosph	IPR001609 (PRINTS): IPR001609 (SM	84,258	62,677	88,572	108,170	97,506									
Solyc07g041155	Myosin XI (AHRD V3.3 *** Q5R216_TOBAC)		F:GO:0005515; P:G(	F:protein binding; P:actin filament organization	IPR002710 (SMART): IPR002710 (PF	111,147	93,104	130,516	140,110	130,394									
Solyc07g041160	membrane protein (AHRD V3.3 *** AT5G35460.2)		P:GO:0006656; C:G(	P:phosphatidylcholine biosynthetic process; C:integral compone	IPR021261 (PFAM): mobidb-lite (MOB	49,646	63,070	62,692	66,677	58,285									
Solyc07g041170	Endo-1,4-beta-xylanase A (AHRD V3.3 *-* A0A1D1XNF2_9ARAE)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	PTHR31490 (PANTHER): PTHR31490	0,019	0,021	0,071	0,025	0,143									
Solyc07g041180	EEIG1/EHBP1 protein amino-terminal domain protein (AHRD V3.3 *** A0A072V6S3_MEDTR)		P:GO:0009902	P:chloroplast relocation	IPR018392 (SMART): IPR018392 (PF	1,856	1,726	0,436	0,241	0,542									
Solyc07g041190	PHD finger alfin-like protein (AHRD V3.3 *** A0A072V846_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding	IPR001965 (SMART): IPR021998 (PF	17,780	15,235	62,803	71,877	59,227									
Solyc07g041195	Sucrose synthase (AHRD V3.3 --* A0A0D3B255_BRAOL)					0,059	0,054	0,273	0,094	0,188									
Solyc07g041200	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G20520.1)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity	IPR029058 (G3DSA:3.40.50.GENE3D	34,990	35,955	36,342	35,799	36,944									
Solyc07g041210	phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** AT5G13640.1)		P:GO:0006629; F:G(	P:lipid metabolic process; F:O-acyltransferase activity	IPR003386 (PFAM): IPR029058 (G3D	29,430	22,757	41,434	35,536	35,168									
Solyc07g041213	Endonuclease/exonuclease/phosphatase family protein (AHRD V3.3 --* A0A072VES6_MEDTR)				PTHR35218 (PANTHER)	0,000	0,061	0,000	0,025	0,023									
Solyc07g041230	Brevis radix-like protein (AHRD V3.3 *** A0A072TLT2_MEDTR)				IPR027988 (PFAM): IPR013591 (PFA	2,621	2,961	0,596	0,381	0,282									
Solyc07g041240	LOW QUALITY:ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 --* AT1G68710.3)					0,000	0,019	0,025	0,000	0,000									
Solyc07g041245	aldolase like (AHRD V3.3 --* AT4G24080.1)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	mobidb-lite (MOBIDB_LITE)	3,652	3,573	0,827	1,196	1,243									
Solyc07g041280	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (AHRD V3.3 *** AT5G12040		P:GO:0006807	P:nitrogen compound metabolic process	IPR036526 (G3DSA:3.60.110.GENE3	3,172	3,070	1,653	1,299	1,432									
Solyc07g041290	Protein BIG GRAIN 1-like A (AHRD V3.3 *** BIG1A_ARATH)		P:GO:0009734	P:auxin-activated signaling pathway	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,511	0,285	0,000	0,000	0,000									
Solyc07g041300	Spermidine synthase (AHRD V3.3 *** F8WLB6_CITUN)		F:GO:0003824	F:catalytic activity	G3DSA:3.40.50.150 (GENE3D): IPR0:	0,000	0,184	0,139	0,025	0,024									
Solyc07g041310	Ribosomal protein S3 family protein (AHRD V3.3 *** AT5G35530.1)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio	IPR005703 (TIGRFAM): IPR004044 (F	182,555	203,697	135,350	121,161	126,376									
Solyc07g041320	Paired amphipathic helix protein Sin3 (AHRD V3.3 *-* A0A151TFV5_CAJCA)		F:GO:0003714; P:G(	F:transcription corepressor activity; P:regulation of transcriptior	G3DSA:1.20.1160.11 (GENE3D): G3D	0,397	0,349	0,000	0,050	0,000									
Solyc07g041325	Maternal effect embryo arrest 22, putative (AHRD V3.3 *-* A0A061G820_THECC)				mobidb-lite (MOBIDB_LITE): PTHR354	4,315	3,584	3,277	4,790	3,927									
Solyc07g041330	Maternal effect embryo arrest protein (AHRD V3.3 *-* G7IML6_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	6,249	5,168	6,545	7,012	6,465									
Solyc07g041340	Protein ELF4-LIKE 4 (AHRD V3.3 *** A0A0B2QCK9_GLYSO)		P:GO:0042753	P:positive regulation of circadian rhythm	IPR009741 (PFAM): mobidb-lite (MOB	4,349	2,594	3,163	2,742	3,269									
Solyc07g041362	LOW QUALITY:Serine/threonine-protein phosphatase 7 long form (AHRD V3.3 --* A0A1D1YUV9_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,018	0,000	0,000	0,000									
Solyc07g041490	Photosystem II CP43 reaction center protein (AHRD V3.3 --* PSBC_SACOF)				IPR013097 (SMART): G3DSA:3.30.70	56,017	54,251	55,687	48,399	57,424									
Solyc07g041500	Cytochrome P450, putative (AHRD V3.3 *** A0A061GL91_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,057	0,094	0,075	0,000	0,000									
Solyc07g041510	RNA polymerase-associated protein CTR9-like protein (AHRD V3.3 *** W9QUW2_9ROSA)		F:GO:0005515; P:G(	F:protein binding; P:regulation of transcription, DNA-templated; I	IPR019734 (SMART): IPR011990 (G3	66,155	58,757	54,913	51,745	54,260									
Solyc07g041620	LOW QUALITY:Chrysanthemyl diphosphate synthase (AHRD V3.3 --* K7WQ59_9ASTR)					12,451	12,646	3,863	7,352	6,623					0,927	0,003			up
Solyc07g041623	Glycosyltransferase (AHRD V3.3 *-* K4AWL3_SOLLC)		F:GO:0016740	F:transferase activity		0,019	0,000	0,000	0,000	0,000									
Solyc07g041640	Growth-regulating factor-like protein (AHRD V3.3 *** A0A072US13_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten	IPR014978 (SMAF GRF	5,602	6,140	0,600	0,758	0,449									
Solyc07g041660	DENN domain-containing protein (AHRD V3.3 *** A0A103XNL7_CYNCS)		C:GO:0016021	C:integral component of membrane	IPR005113 (SMART): IPR001194 (SM	25,825	25,522	33,337	37,028	36,676									
Solyc07g041680	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0N7CFU2_SOLTU)		C:GO:0016021	C:integral component of membrane	IPR008896 (PANTHER)	0,000	0,021	0,025	0,000	0,000									
Solyc07g041720	Germin-like protein (AHRD V3.3 *** G3F4I5_CAMSI)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS): IPR006045 (SM	1,519	6,979	0,000	0,025	0,023	2,212	0,000					up		
Solyc07g041730	Unknown protein (AHRD V3.3)					0,296	0,159	0,192	0,198	0,189									
Solyc07g041735	MOB kinase activator-like 1A (AHRD V3.3 *** MOB1A_MEDSF)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation	IPR005301 (SMART): IPR005301 (PF	9,248	6,552	4,586	3,784	5,744									
Solyc07g041740	LOW QUALITY:Polynucleotidyl transferase, Ribonuclease H fold (AHRD V3.3 --* Q2HUC4_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bond:	IPR002156 (PFAM): IPR036397 (G3D	0,308	0,491	0,492	0,469	0,800									
Solyc07g041750	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G35570.1)		C:GO:0005794; P:G(	C:Golgi apparatus; P:fucose metabolic process; C:chloroplast; (	G3DSA:3.40.50.11350 (GENE3D): IPF	88,779	135,970	63,897	51,383	95,059									
Solyc07g041760	villin-like 1 (AHRD V3.3 --* AT2G29890.5)					5,386	5,863	3,888	3,703	3,077									
Solyc07g041770	LOW QUALITY:Membrane lipoprotein (AHRD V3.3 *** A0A061GT32_THECC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1110.10 (GENE3D): PTH	0,214	0,302	0,000	0,000	0,000									
Solyc07g041780	OBP3-RESPONSIVE GENE 4 family protein (AHRD V3.3 *** U5FFX8_POPTR)		C:GO:0009536; P:G(	C:plastid; P:response to salicylic acid	PTHR35710 (PANTHER)	3,509	2,693	6,846	5,715	5,791									
Solyc07g041790	LOW QUALITY:Splicing factor 3B subunit 1 (AHRD V3.3 *-* A0A199UTE5_ANACO)		P:GO:0000245; F:G(	P:spliceosomal complex assembly; F:mRNA binding	PTHR38737 (PANTHER)	0,042	0,000	0,044	0,000	0,000									
Solyc07g041830	Damaged dna-binding 2, putative isoform 1 (AHRD V3.3 *** A0A061GM96_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	9,030	11,470	13,702	12,179	13,216									
Solyc07g041840	Bromodomain transcription factor (AHRD V3.3 --* AT5G15570.1)					0,000	0,021	0,047	0,097	0,024									
Solyc07g041870	tubulin-tyrosine ligase (AHRD V3.3 *** AT1G77550.1)		F:GO:0005524; P:G(	F:ATP binding; P:cellular protein modification process	G3DSA:3.30.470.20 (GENE3D): IPR0:	63,009	57,216	70,747	69,504	67,271									
Solyc07g041890	LOW QUALITY:FRIGIDA interacting protein 1 (AHRD V3.3 *-* AT2G06005.6)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	IPR029399 (PANTHER)	0,019	0,000	0,000	0,000	0,000									
Solyc07g041900	cysteine proteinase	cyp3	P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (SM	561,737	383,644	549,807	366,975	461,784					-0,581	0,001			down
Solyc07g041920	Cysteine protease (AHRD V3.3 *** Q9LRI2_TOBAC)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR013201 (SM	0,000	0,060	0,050	0,047	0,000									
Solyc07g041930	Adenylyl cyclase (AHRD V3.3 *** C5MTW3_NICBE)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	25,325	25,726	23,908	23,800	23,890									
Solyc07g041940	Kinase family protein (AHRD V3.3 *** U5GAR5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): PIRSF000654 (P	0,019	0,064	0,072	0,149	0,023									
Solyc07g041960	LOW QUALITY:Histidine decarboxylase (AHRD V3.3 *-* DCHS_SOLLC)		F:GO:0016831; P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F	IPR002129 (PFAM): IPR015421 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc07g041970	Subtilisin-like protease (AHRD V3.3 *** W9R6D5_9ROSA)		F:GO:0004252; P:G(	F:serine-type endor EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	135,088	122,821	44,951	40,572	44,939									
Solyc07g041980	Heterotrimeric G-protein gamma subunit 3 (AHRD V3.3 *** A0A077EST5_CAPAN)		P:GO:0007186	P:G protein-coupled receptor signaling pathway	SM01224 (SMART): IPR015898 (PFAI	2,239	1,893	0,501	0,601	0,868									
Solyc07g042000	Cation calcium exchanger (AHRD V3.3 *** G7L7L8_MEDTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1420.30 (GENE3D): IPR(	13,473	10,843	5,928	6,068	5,917									
Solyc07g042010	RNA helicase DEAH-box22	DEAH22	F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0:	3,292	3,184	4,390	5,196	4,550									

Solyc07g042015	RecQ family ATP-dependent DNA helicase (AHRD V3.3 *-* G7IGG6_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR014001 (SMART): G3DSA:3.40.50	1,753	1,572	2,204	2,923	2,548									
Solyc07g042020	TRICHOME BIREFRINGENCE-LIKE 16 (AHRD V3.3 *** AT5G20680.5)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:acetyl			IPR025846 (PFAM): IPR026057 (PFA	10,930	14,816	16,608	16,465	15,325									
Solyc07g042025	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G17470.4)							5,231	4,033	3,269	3,111	3,313									
Solyc07g042030	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061EC24_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	12,116	10,970	7,935	8,129	8,546									
Solyc07g042080	inter-alpha-trypsin inhibitor heavy chain-like protein (AHRD V3.3 *** AT1G19110.1)						IPR002035 (SMART): IPR036465 (G3	30,286	21,651	50,610	52,622	50,697									
Solyc07g042090	Organic solute transporter ostalpha protein (AHRD V3.3 *** G7IIM9_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): IPR005178 (PAN	0,021	0,142	0,075	0,300	0,047									
Solyc07g042100	Early auxin response protein (AHRD V3.3 *** Q69P88_ORYSJ)						PTHR34045 (PANTHER): PTHR34045	0,278	0,163	0,000	0,000	0,000									
Solyc07g042130	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061FYX7_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (TIGF	11,424	12,814	29,647	40,354	32,224					0,449	0,006			up
Solyc07g042150	ubiquinone biosynthesis COQ9-like protein (AHRD V3.3 *** AT1G19140.1)		P:GO:0006744	P:ubiquinone biosynthetic process			G3DSA:1.10.357.10 (GENE3D): IPR0	24,126	26,182	22,958	19,900	21,945									
Solyc07g042160	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G42950.1)	PG58-2	F:GO:0004650; P:G(	F:polygalacturonas	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF	26,345	18,155	5,724	4,482	5,277									
Solyc07g042170	Jasmonate-zim-domain protein (AHRD V3.3 *** A0A167V6B7_CAMSI)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:response to wounding; P:regulat			IPR010399 (SMART): IPR010399 (PF	74,986	123,385	29,189	28,420	34,602	0,743	0,020					up		
Solyc07g042180	RNA-binding protein (AHRD V3.3 *** A0A0K9PBY9_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	94,464	94,016	129,976	109,683	106,820									
Solyc07g042190	DUF581 family protein (AHRD V3.3 *** B7FN07_MEDTR)						IPR007650 (PFAM): PTHR33059:SF6	88,820	113,703	188,618	118,552	155,244					-0,667	0,000			down
Solyc07g042220	Beta-galactosidase (AHRD V3.3 *** A0A022QEX1_ERYGU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): PF17834 (PFA	0,021	0,039	0,000	0,117	0,093									
Solyc07g042230	Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9P1G2_ZOSMR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	1,193	3,832	0,905	0,722	1,341	1,700	0,002					up		
Solyc07g042250	chaperonin 21 precursor	Cpn21	C:GO:0005737; P:G(	C:cytoplasm; P:protein folding; F:transition metal ion binding; P:			IPR020818 (PRINTS): IPR020818 (SM	248,239	325,435	854,921	795,076	884,056									
Solyc07g042260	Auxin Response Factor 7	ARF7	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR003340 (SMAF ARF	19,267	15,599	8,492	7,757	8,419									
Solyc07g042270	RNA helicase DEAD22	DEAD22	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR025313 (SMART): IPR001650 (SM	42,320	109,282	24,403	21,941	23,255									
Solyc07g042275	DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 *-* A0A072V8B8_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	17,759	40,169	9,310	8,355	8,748									
Solyc07g042290	Protein OBERON 3 (AHRD V3.3 *-* A0A199W341_ANACO)		C:GO:0005634; P:G(	C:nucleus; P:root meristem specification; P:maintenance of roo			IPR004082 (PRINTS): IPR032881 (PF	0,019	0,019	0,068	0,000	0,000									
Solyc07g042293	Protein OBERON 3 (AHRD V3.3 --* A0A0B2R231_GLYSO)							0,021	0,021	0,025	0,000	0,000									
Solyc07g042297	Oberon-like protein (AHRD V3.3 --* G7JTL7_MEDTR)						IPR032535 (PFAM)	0,038	0,059	0,000	0,047	0,000									
Solyc07g042300	Dirigent protein (AHRD V3.3 *** K4CE93_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAN	3,494	4,918	1,481	1,780	1,833									
Solyc07g042313	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061FRD6_THECC)		F:GO:0003824; F:G(	F:catalytic activity; F:protein binding			IPR014031 (PFAM): IPR002885 (TIGF	40,201	43,721	53,873	48,883	53,139									
Solyc07g042317	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151U161_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAN	0,077	0,000	0,000	0,025	0,000									
Solyc07g042330	Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 --* AT4G14060.1)		P:GO:0000462; F:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA); F:RNA				1,534	1,463	1,133	1,137	1,630									
Solyc07g042360	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151TSB4_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,154	0,118	0,000	0,025	0,023									
Solyc07g042380	ARM repeat superfamily protein isoform 2 (AHRD V3.3 *** A0A061GL04_THECC)		C:GO:0016021	C:integral component of membrane			IPR012978 (PFAM): mobidb-lite (MOB	93,785	85,138	68,898	65,296	65,720									
Solyc07g042390	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061GSW0_THECC)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (SMART): IPR006501 (TIG	68,971	74,491	11,943	9,417	18,131									
Solyc07g042400	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT5G20790.2)		C:GO:0016020	C:membrane			PTHR36369 (PANTHER): PTHR36369	3,068	3,357	6,310	7,857	4,692									
Solyc07g042420	Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,000	0,000	0,000									
Solyc07g042430	Flavin-containing monooxygenase family protein (AHRD V3.3 *** B9MT30_POPTR)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.'	Flavin-containing mo	IPR001613 (PRINTS): IPR020946 (PF	0,161	0,188	6,326	10,333	4,929									
Solyc07g042440	Peroxiredoxin (AHRD V3.3 *** A0A0B4SWQ5_9ROSI)		F:GO:0016209; F:G(	F:antioxidant activity; F:oxidoreductase activity; P:cell redox ho			IPR024706 (PIRSF): IPR000866 (PFA	16,123	33,250	32,277	35,842	65,918	1,072	0,001	1,028	0,000			up	up	
Solyc07g042460	Respiratory burst oxidase, putative (AHRD V3.3 *** B9RR53_RICCO)		F:GO:0004601; F:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000778 (PRINTS): IPR013121 (PF	3,760	4,431	4,651	6,558	4,498									
Solyc07g042480	Carotene epsilon-monooxygenase, chloroplastic (AHRD V3.3 --* LUT1_ARATH)							0,205	0,184	0,381	0,244	0,759									
Solyc07g042490	LOW QUALITY:Auxin responsive SAUR protein (AHRD V3.3 *** A0A118K7G8_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): mobidb-lite (MOB	13,978	10,247	51,745	58,567	37,252			-0,477	0,011				down	
Solyc07g042500	Alpha/beta-Hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061GM37_THECC)		C:GO:0016020	C:membrane			IPR003675 (PFAM): IPR029058 (G3D	56,121	45,250	103,711	113,493	108,256									
Solyc07g042520	Sucrose synthase (AHRD V3.3 *** M1B219_SOLTU)	SUS5	P:GO:0005985; F:G(	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	IPR000368 (PFAM): G3DSA:3.40.50.2	2,129	0,864	0,044	0,095	0,142									
Solyc07g042540	LOW QUALITY:DNA mismatch repair protein MutS, type 2 (AHRD V3.3 --* AT1G65070.3)							2,463	2,422	0,863	0,835	0,777									
Solyc07g042550	Sucrose synthase (AHRD V3.3 *** SUS2_SOLTU)	SUS3	P:GO:0005985; F:G(	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	G3DSA:3.40.50.2000 (GENE3D): G3D	132,139	155,823	267,079	306,314	322,130									
Solyc07g042560	Kinesin-like protein (AHRD V3.3 *** K4CEB7_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,705	1,457	0,075	0,145	0,331									
Solyc07g042570	Eukaryotic translation initiation factor 3 subunit K (AHRD V3.3 *** K4CEB8_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			IPR033464 (PFAM): IPR036388 (G3D	40,125	46,161	42,236	41,505	40,614									
Solyc07g042580	Microtubule-associated protein TORTIFOLIA1, putative (AHRD V3.3 *** B9SP95_RICCO)		C:GO:0005874; F:G(	C:microtubule; F:microtubule binding			IPR034085 (SMART): IPR000357 (PF	1,277	1,414	0,186	0,117	0,140									
Solyc07g042590	Kinase family protein (AHRD V3.3 *-* D7M6D0_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	25,084	26,989	13,886	13,279	17,839									
Solyc07g042593	Protein kinase superfamily protein (AHRD V3.3 *-* AT2G07180.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200	17,073	17,488	8,604	9,169	10,858									
Solyc07g042600	Transposon-like element Lyt2-2 DNA (AHRD V3.3 *** D5MNY6_SOLLC)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018289 (PFAM): IPR031052 (PAN	0,080	0,000	0,000	0,073	0,023									
Solyc07g042620	Prefoldin subunit 1 (AHRD V3.3 *** W9RLK5_9ROSA)		P:GO:0006457; C:G(	P:protein folding; C:prefoldin complex; F:unfolded protein bindinc			IPR009053 (G3DSA:1.10.287.GENE3	28,685	30,194	43,614	42,475	39,128									
Solyc07g042630	Terpene cyclase/mutase family member (AHRD V3.3 *** V9LYF2_9SOLA)		F:GO:0016866	F:intramolecular transferase activity			G3DSA:1.50.10.20 (GENE3D): G3DS/	0,913	1,097	1,349	1,677	1,223									
Solyc07g042633	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RDP2_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:A'	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	0,000	0,021	0,000	0,000	0,000									
Solyc07g042680	MAP kinase kinase kinase 46	MAPKKK46	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	83,335	87,540	80,703	83,091	79,007									
Solyc07g042690	Bifunctional dihydrofolate reductase-thymidylate synthase 1 (AHRD V3.3 --* DRTS1_ARATH)							1,703	1,761	0,847	1,023	1,081									
Solyc07g042695	Major facilitator superfamily protein (AHRD V3.3 *** AT3G13050.4)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR005828 (PFAM): G3DSA:1.20.125(	0,255	0,329	0,119	0,095	0,047									
Solyc07g042700	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G58130.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	17,822	18,097	17,568	18,875	17,333									
Solyc07g042710	Cytoplasmic dynein 2 light intermediate chain 1 (AHRD V3.3 *** A0A0B0PF95_GOSAR)						PTHR36008 (PANTHER)	10,221	11,264	21,011	22,214	20,165									
Solyc07g042720	LOW QUALITY:Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061F5B2_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	0,000	0,021	0,000	0,095	0,048									
Solyc07g042740	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G58130.1)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): PTHR230	15,270	13,621	12,991	13,305	13,611									
Solyc07g042750	Pseudouridine synthase family protein (AHRD V3.3 *** AT1G78910.1)		P:GO:0001522; F:G(	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn			IPR006145 (PFAM): G3DSA:3.30.235(	13,718	13,428	14,559	14,363	13,741									
Solyc07g042760	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K4R8_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,813	2,385	1,547	1,788	1,643									
Solyc07g042770	LOW QUALITY:26S protease regulatory subunit 6B homolog (AHRD V3.3 *-* PRS6B_SOLTU)		F:GO:0005524; C:G(	F:ATP binding; C:nu	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,025	0,000									
Solyc07g042780	LOW QUALITY:26S protease regulatory subunit 6B homolog (AHRD V3.3 *-* PRS6B_HELAN)		F:GO:0036402	F:proteasome-activ	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR032501 (PFAM): G3DSA:2.40.50.1	0,000	0,000	0,000	0,000	0,023									
Solyc07g042790	LOW QUALITY:Helicase-like protein (AHRD V3.3 *** Q9AYF0_ORYSJ)		P:GO:0000723; F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	0,000	0,019	0,000	0,000	0,000									
Solyc07g042810	Chloroplast envelope membrane protein, CemA (AHRD V3.3 *** A0A118K0H5_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR004282 (PFAM): IPR004282 (PAN	1,471	1,770	1,608	1,672	2,162									
Solyc07g042820	Chloroplast envelope membrane protein (AHRD V3.3 *-* A0A0B2QY85_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR004282 (PFAM): PTHR33650:SF1	0,582	0,615	1,068	0,872	0,826									
Solyc07g042830	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *** B2ZGM9_SOLLC)		F:GO:0004373	F:glycogen (starch)	EC:2.4.1.11	Glycogen(starch) syn	IPR013534 (PFAM): IPR011835 (TIGF	17,430	18,551	44,920	49,144	43,543									
Solyc07g042840	60S ribosomal protein L14, putative (AHRD V3.3 *** B9SV21_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR014722 (G3DSA:2.30.30.GENE3D	4,477	4,670	2,878	2,097	2,513									
Solyc07g042843	60S ribosomal protein L14 (AHRD V3.3 *-* A9PHC1_POPTR)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR014722 (G3DSA:2.30.30.GENE3D	0,063	0,137	0,025	0,048	0,000									
Solyc07g042847	Gibberellin receptor GID1, putative (AHRD V3.3 --* B9RYG8_RICCO)							0,157	0,226	0,161	0,217	0,190									
Solyc07g042850	aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B (AHRD V3.3 --* AT5G22210.2)							0,558	0,587	0,297	0,406	0,518									
Solyc07g042880	Cytochrome P450 (AHRD V3.3 *** A0A161ABB0_OCIBA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,056	0,021	0,000	0,000	0,000									
Solyc07g042890	MAP kinase kinase kinase 47	MAPKKK47	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR000719 (SM	104,660	150,779	106,778	100,490	111,994									
Solyc07g042900	Transporter-related family protein (AHRD V3.3 *-* B9HG67_POPTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	5,899	5,312	3,618	4,063	4,281									
Solyc07g042905	Transporter-related family protein (AHRD V3.3 *** B9HG67_POPTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	5,367	5,494	3,344	3,675	3,722									
Solyc07g042910	transmembrane protein (AHRD V3.3 *** AT5G58100.2)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:Golgi apparatus; P:pollen exine form			PTHR31515:SF2 (PANTHER): PTHR3'	61,485	56,201	79,174	78,162	73,888									
Solyc07g042930	Rhomboid family protein (AHRD V3.3 *** B9HXC8_POPTR)		F:GO:0004252; C:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001876 (SMART): IPR035952 (G3	9,296	7,835	32,210	31,046	27,328									
Solyc07g042935	Heat shock 70 kDa protein, mitochondrial (AHRD V3.3 --* HSP7M_PHAVU)							0,019	0,000	0,000	0,000	0,070									
Solyc07g042950	Kelch repeat-containing F-box family protein (AHRD V3.3 *** D7KDP2_ARALL)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	2,376	2,173	4,491	3,572	4,279									
Solyc07g042960	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9HXC7_POPTR)		F:GO:0005515	F:protein binding			IPR006652 (SMART): IPR015915 (G3	3,952	3,079	5,133	4,814	4,770									
Solyc07g042970	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *-* AT5G60870.4)		F:GO:0016874	F:ligase activity			IPR000408 (PRINTS): IPR000408 (PF	7,468	5,981	10,005	8,576	8,117									
Solyc07g042980	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G60870.3)		F:GO:0016874	F:ligase activity			IPR000408 (PRINTS): IPR000408 (PF	11,063	8,908	11,984	11,087	11,406									
Solyc07g043000	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *-* AT3G22142.1)						IPR016140 (SMART): IPR027923 (PF	40,367	98,105	5,351	1,496	1,459	1,310	0,048	-1,866	0,004	-1,829	0,020	up	down	down
Solyc07g043030	Glycosyltransferase (AHRD V3.3 *-* M1B232_SOLTU)		F:GO:0008194; C:G(	F:UDP-glycosyltransferase activity; C:integral component of me			G3DSA:3.40.50.2000 (GENE3D): PTH	0,000	0,000	0,000	0,022	0,000									
Solyc07g043050	Glycosyltransferase (AHRD V3.3 *** K4CEG5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	6,949	10,996	3,286	5,334	7,177			1,124	0,001				up	
Solyc07g043060	Glycosyltransferase (AHRD V3.3 *** K4CEG6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,102	0,238	0,025	0,096	0,000									
Solyc07g043070	Rab3 GTPase-activating protein catalytic subunit (AHRD V3.3 --* AT5G55060.3)						PTHR34287 (PANTHER): PTHR34287	0,078	0,043	0,000	0,000	0,000									
Solyc07g043100	Glycosyltransferase (AHRD V3.3 *** K4CEH0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,119	0,018	0,119	0,025	0,070									
Solyc07g043110	Glycosyltransferase (AHRD V3.3 *** K4CEH1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,021	0,060	0,049	0,095	0,093									
Solyc07g043120	Glycosyltransferase (AHRD V3.3 *** K4CEH2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	30,129	36,517	31,209	15,912	26,627					-0,970	0,000			down
Solyc07g043130	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT2G30520.1)		F:GO:0005515; P:G(	F:protein binding; P:phototropism			IPR000210 (SMART): IPR027356 (PF	18,860	12,651	19,571	28,995	27,245									
Solyc07g043137	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SWQ3_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAN	0,097	0,076	0,071	0,025	0,000									
Solyc07g043150	Glycosyltransferase (AHRD V3.3 *** K4CEH5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	3,812	4,714	2,530	2,121	2,234									
Solyc07g043160	Glycosyltransferase (AHRD V3.3 *** K4CEH6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	44,200	47,403	17,526	16,133	30,624			0,801	0,000				up	
Solyc07g043170	Glycosyltransferase (AHRD V3.3 *** K4CEH7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	3,832	2,662	1,840	1,350	2,066									
Solyc07g043180	Glycosyltransferase (AHRD V3.3 *-* D2KY84_FORIN)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): PTH	0,076	0,146	0,096	0,025	0,000									
Solyc07g043190	Glycosyltransferase (AHRD V3.3 *-* M1B8J3_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,539	0,317	0,233	0,075	0,118									
Solyc07g043200	Zinc transporter protein (AHRD V3.3 *** D5LMF9_9FABA)		F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM): IPR003689 (F	0,000	0,000	0,044	0,025	0,000									
Solyc07g043207	Histidine decarboxylase (AHRD V3.3 *-* DCHS_SOLLC)		F:GO:0016831; P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR002129 (PFAM): IPR015421 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc07g043230	Zinc transporter protein (AHRD V3.3 *** D5LMF9_9FABA)		F:GO:0005385; C:G(	F:zinc ion transmembrane transporter activity; C:integral compo			IPR004698 (TIGRFAM): IPR003689 (F	1,955	10,264	1,180	1,499	2,411	2,411	0,001					up		
Solyc07g043240	Pectinesterase (AHRD V3.3 *** K4CEI4_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM): IPR012334 (G3D	0,216	0,558	0,353	0,637	0,424									
Solyc07g043250	LOW QUALITY:VQ motif-containing protein, putative (AHRD V3.3 *-* A0A061DVP3_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	8,217	8,797	4,878	10,181	6,682					1,061	0,000			up
Solyc07g043260	Far1-related sequence 2-like protein (AHRD V3.3 *** A0A0B0NT15_GOSAR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	22,918	21,164	15,797	14,371	16,186									
Solyc07g043270	FAR1 (AHRD V3.3 *** A0A178UYQ0_ARATH)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	146,651	128,865	134,988	137,071	136,406									
Solyc07g043310	Gamma aminobutyrate transaminase isoform 1	GABA-TP1	F:GO:0008483; F:G(	F:transaminase activity; F:pyridoxal phosphate binding			IPR005814 (PFAM): IPR015421 (G3D	92,448	89,482	198,007	251,225	214,747									
Solyc07g043320	myosin heavy chain, embryonic smooth protein (AHRD V3.3 *** AT1G05320.9)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	759,040	856,772	326,917	342,631	352,745									
Solyc07g043330	Transcription factor GRAS (AHRD V3.3 *** A0A103XVP0_CYNCS)	GRAS					IPR005202 (PFAM GRAS	8,225	9,130	13,374	11,441	16,430									
Solyc07g043360	60S ribosomal protein L27 (AHRD V3.3 *** K4CEJ5_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005824 (SMART): IPR038655 (G3	123,464	122,428	112,089	88,799	93,796									
Solyc07g043390	Cellulose synthase (AHRD V3.3 *** A0A118J5T2_CYNCS)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR029044 (G3DSA:3.90.550.GENE3	4,457	2,725	0,000	0,025	0,024									
Solyc07g043395	Cellulose synthase-like protein (AHRD V3.3 *-* A0A072TVD1_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR005150 (PFAM): PTHR13301 (PAN	0,895	0,626	0,000	0,000	0,000									
Solyc07g043400	LOW QUALITY:C2H2 and C2HC zinc fingers superfamily protein (AHRD V3.3 --* AT5G26749.2)							0,000	0,037	0,000	0,000	0,000									
Solyc07g043410	LOW QUALITY:Glycosyltransferase (AHRD V3.3 *** E5L3S0_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,138	0,120	0,000	0,000	0,000									
Solyc07g043420	2-oxoglutarate-dependent dioxygenase 2	gad2	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	94,220	96,041	15,547	11,131	16,940									
Solyc07g043460	Cytochrome P450, putative (AHRD V3.3 *** A0A061E4E7_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	5,783	5,424	1,269	0,959	1,153									
Solyc07g043480	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	1,018	1,483	0,072	0,000	0,024									
Solyc07g043490	UDP-Gal:Tomatidine Galactosyltransferase		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	20,959	26,750	4,350	2,395	3,627									
Solyc07g043500	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	28,698	18,052	2,629	0,583	1,591									
Solyc07g043510	OTU domain-containing (AHRD V3.3 *** A0A0B0PSP5_GOSAR)		F:GO:0004843; C:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.80 (GENE3D): IPR00	52,359	43,170	42,229	67,279	57,539			0,443	0,023	0,674	0,001		up	up
Solyc07g043550	UDP-glucose 4-epimerase, putative (AHRD V3.3 *** B9SV82_RICCO)		F:GO:0003978; P:G(	F:UDP-glucose 4-e	EC:5.1.3.2	UDP-glucose 4-epim	IPR016040 (PFAM): IPR005886 (TIGF	4,602	3,647	4,876	5,293	4,865									
Solyc07g043560	Heat shock 70 kDa protein, putative (AHRD V3.3 *** B9S3M9_RICCO)		F:GO:0005524; C:G(	F:ATP binding; C:endoplasmic reticulum chaperone complex; P:			IPR013126 (PRINTS): G3DSA:3.90.64	80,965	80,115	103,242	112,665	111,102									
Solyc07g043570	NAD(P)-linked oxidoreductase superfamily protein		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR023210 (PF	54,943	73,603	54,152	53,916	71,327			0,394	0,010				up	
Solyc07g043580	bHLH transcription factor 052	PIF4	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	38,476	43,645	3,064	3,190	5,251									
Solyc07g043590	Amine oxidase, putative (AHRD V3.3 *** B9S6G9_RICCO)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001613 (PRINTS): IPR002937 (PF	96,538	69,897	230,517	221,499	217,815									
Solyc07g043600	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T2X9_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	21,478	24,852	30,765	29,802	35,872									
Solyc07g043610	Auxin response factor_SGN-U230670		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D): PTHR3	32,538	27,964	27,152	25,136	25,465									
Solyc07g043620	Auxin Response Factor 6B	ARF6B	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR003340 (SMAF ARF	42,029	30,402	29,355	33,718	31,299									
Solyc07g043630	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.30.300	0,059	0,076	2,121	1,654	1,658									
Solyc07g043640	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity			G3DSA:3.30.300.310 (GENE3D): G3D	0,037	0,000	0,000	0,000	0,000									
Solyc07g043660	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.40.50.1	0,000	0,037	0,260	1,155	0,521									
Solyc07g043710	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	0,000	0,000	0,000	0,097	0,023									
Solyc07g044750	N-acetyl-D-glucosamine kinase (AHRD V3.3 *** A0A0B0P7N8_GOSAR)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			G3DSA:3.30.420.40 (GENE3D): IPR0(	8,617	6,419	4,329	4,784	5,756									
Solyc07g044760	RNA helicase DEAD23	DEAD23	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR001650 (SMART): IPR014001 (SM	334,162	268,742	338,164	297,371	286,047									
Solyc07g044780	RING/U-box superfamily protein (AHRD V3.3 *** AT5G60580.3)		F:GO:0008270	F:zinc ion binding			IPR011016 (SMART): IPR013083 (G3	8,734	7,849	16,679	17,211	15,006									
Solyc07g044790	Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,514	0,527	0,386	0,366	0,472									
Solyc07g044810	Endoplasmic reticulum vesicle transporter protein (AHRD V3.3 *** AT3G22290.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:isomerase activity			IPR012936 (PFAM): IPR039542 (PFA	51,594	45,002	68,382	68,313	63,516									
Solyc07g044820	LOW QUALITY:Hexosyltransferase (AHRD V3.3 *** K4CEP0_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR002659 (PFAM): PTHR11214:SF1	1,352	0,412	0,000	0,000	0,000									
Solyc07g044830	membrane-associated progesterone binding protein 4 (AHRD V3.3 *** AT4G14965.1)		C:GO:0016021	C:integral component of membrane			IPR001199 (SMART): IPR036400 (G3	16,293	17,455	15,118	16,622	15,725									
Solyc07g044840	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (AHRD V3.3 *** PMGI_TOBAC)		F:GO:0004619; C:G(	F:phosphoglycerate	EC:5.4.2.1	Intramolecular transfe	IPR011258 (PFAM): IPR017849 (G3D	622,849	586,742	726,481	651,229	650,402									
Solyc07g044850	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT5G08560.3)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR006595 (SM	77,815	69,238	122,601	120,507	105,693									
Solyc07g044860	psbXphotosystem II 23 kDa protein	psbx	F:GO:0005509; C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR016123 (G3DSA:3.40.1000.GENE	403,255	940,850	351,167	400,345	754,357	1,250	0,000	1,100	0,000			up	up	
Solyc07g044880	Reticulon-like protein (AHRD V3.3 *** A0A0V0HSB2_SOLCH)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994:SF6	8,297	8,269	7,950	7,657	7,864									
Solyc07g044900	LOW QUALITY:AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT5G06250.5)						mobidb-lite (MOBIDB_LITE)	0,154	0,571	0,000	0,022	0,000									
Solyc07g044910	LOW QUALITY:NAC domain containing protein 90 (AHRD V3.3 --* AT5G22380.1)						mobidb-lite (MOBIDB_LITE)	0,019	0,000	0,000	0,000	0,000									
Solyc07g044930	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9S326_RICCO)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (SMART): IPR007502 (SM	18,455	17,654	14,481	13,400	14,331									

Solyc07g044960	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR004263 (PFAM): mobidb-lite (MOB	2,442	6,065	1,114	0,680	1,300	1,339	0,004					up		
Solyc07g044970	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G16790.5),Pfam:PF13671						PF13671 (PFAM): G3DSA:3.40.50.30(	0,138	0,732	0,025	0,566	0,492									
Solyc07g044980	NIM1-like protein 2	nml2	F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR000210 (SM	39,680	78,355	39,943	56,433	48,928	1,004	0,035			0,501	0,004	up		up
Solyc07g044990	Transmembrane protein 56 (AHRD V3.3 *** A0A151U271_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR006634 (SMART): IPR006634 (PF.	8,422	5,292	26,356	34,548	24,522									
Solyc07g045010	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, putative isoform 1 (AHRD V3.3 *** A0A061DK2		P:GO:0007142	P:male meiosis II			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,859	2,902	0,427	0,047	0,281									
Solyc07g045030	NAC domain-containing protein, putative (AHRD V3.3 *** B9RI29_RICCO)	NAC065	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,000	0,018	0,000	0,000	0,046									
Solyc07g045040	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G20400.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,117	0,158	0,194	0,388	0,283									
Solyc07g045050	4-hydroxyphenylpyruvate dioxygenase (AHRD V3.3 *** K4CER3_SOLLC)	HPPD1	F:GO:0003868; P:G(	F:4-hydroxyphenylp	EC:1.13.11; EC:1.13	Acting on single donc	IPR005956 (PIRSF): IPR029068 (G3D	14,433	16,410	34,457	31,200	31,992									
Solyc07g045070	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *** A0A097PSG8_P		F:GO:0003723; F:G(	F:RNA binding; F:methyltransferase activity			IPR023267 (PRINTS): IPR001678 (PF	18,532	17,061	16,825	16,189	16,460									
Solyc07g045080	NADP-dependent alkenal double bond reductase P1 (AHRD V3.3 *** A0A0B2SKR4_GLYSO)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): PF16884 (PFAM)	2,545	2,464	4,266	4,935	3,597									
Solyc07g045090	NADP-dependent alkenal double bond reductase P1 (AHRD V3.3 *** A0A0B2RWA9_GLYSO)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020843 (SMART): IPR013149 (PF.	0,061	0,140	54,744	81,533	55,345					0,578	0,002			up
Solyc07g045120	Exostosin family protein (AHRD V3.3 *** A0A072VBU5_MEDTR)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR004263 (PFAM): IPR004263 (PAN	0,218	0,262	0,291	0,385	0,190									
Solyc07g045140	transmembrane protein (AHRD V3.3 *** AT4G12680.1)		P:GO:0010228; C:G(	P:vegetative to reproductive phase transition of meristem; C:int			PTHR31133:SF2 (PANTHER): IPR040	1,547	1,168	20,149	27,135	17,941									
Solyc07g045145	transmembrane protein (AHRD V3.3 *-* AT4G12680.1)		P:GO:0010228; C:G(	P:vegetative to reproductive phase transition of meristem; C:int			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,442	2,406	40,081	51,518	33,856									
Solyc07g045150	period circadian protein (AHRD V3.3 *** AT3G07640.1)						PTHR37221 (PANTHER)	17,241	20,978	23,577	23,530	21,605									
Solyc07g045160	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** M5W6F1_PRUPE)		F:GO:0003872; F:G(	F:6-phosphofructok	EC:2.7.1.11	6-phosphofructokinas	IPR022953 (PRINTS): IPR012004 (PII	11,919	15,134	22,894	21,682	26,872									
Solyc07g045170	Cytochrome P450 (AHRD V3.3 *** A0A0B0NAE7_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	33,686	28,444	24,796	23,986	26,174									
Solyc07g045180	CONSTANS-like zinc finger protein (AHRD V3.3 *** A0A023GS52_SOYBN)	BBX9	F:GO:0008270	F:zinc ion binding			IPR000315 (SMAF CO-like	6,232	3,294	4,233	5,756	4,215	-0,891	0,018					down		
Solyc07g045185	CONSTANS-like zinc finger protein (AHRD V3.3 *-* A0A023GS52_SOYBN)		F:GO:0005515	F:protein binding			IPR010402 (PFAM): mobidb-lite (MOB	6,372	4,294	5,505	5,411	4,574									
Solyc07g045190	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DMB3_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF.	19,004	72,412	23,288	13,359	18,330	1,955	0,000			-0,799	0,001	up		down
Solyc07g045200	LOW QUALITY:serine-rich protein-like protein (AHRD V3.3 *-* AT5G55980.1)		P:GO:0008150	P:biological_process			PTHR33132:SF29 (PANTHER): PTHR:	0,136	0,199	0,118	0,025	0,047									
Solyc07g045210	calcium ion-binding protein (AHRD V3.3 *** AT2G04280.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane			PTHR31469 (PANTHER): PTHR31469	139,690	126,754	57,388	52,002	50,385									
Solyc07g045220	U-box domain-containing 3-like protein (AHRD V3.3 *** A0A0B0NGP1_GOSAR)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR011989 (G3	3,188	4,135	3,747	2,849	3,427									
Solyc07g045230	Cell wall protein AWA1 isoform 1 (AHRD V3.3 *** A0A061DLI6_THECC)		F:GO:0005515	F:protein binding			IPR009719 (PFAM): mobidb-lite (MOB	67,623	54,748	53,836	52,898	54,726									
Solyc07g045240	RNA-binding family protein (AHRD V3.3 *** A0A061FBT9_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	109,375	116,367	149,298	148,370	136,258									
Solyc07g045250	rho GTPase-activating gacO-like protein (AHRD V3.3 --* AT3G57930.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR340	14,416	19,175	13,435	11,408	12,648									
Solyc07g045260	Cytoplasmic dynein 2 light intermediate chain 1 (AHRD V3.3 *-* A0A0B0PF95_GOSAR)						PTHR36008 (PANTHER)	0,143	0,043	0,118	0,142	0,260									
Solyc07g045270	GPCR-type G protein 2 (AHRD V3.3 *-* AT4G27630.7)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:plasma membrane; P:response to abscisic acid; F:abscisic acid				0,000	0,019	0,000	0,000	0,000									
Solyc07g045290	Long chain acyl-CoA synthetase (AHRD V3.3 *** Q5W6W7_ORYSJ)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D): IPF	87,749	71,091	139,366	131,002	124,269									
Solyc07g045300	transmembrane protein (AHRD V3.3 *** AT2G04360.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR360	4,165	3,855	5,596	5,783	6,174									
Solyc07g045310	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase (AHRD V3.3 *** W9QI		F:GO:0005515	F:protein binding			G3DSA:3.90.1410.10 (GENE3D): IPR(	7,330	8,431	21,319	24,543	24,692									
Solyc07g045315	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase (AHRD V3.3 *-* W9QI		C:GO:0009507; F:G(	C:chloroplast; F:[rib	EC:2.1.1.127	[Ribulose-bisphospha	IPR015353 (PFAM): IPR036464 (G3D	5,133	6,434	17,388	15,908	17,175									
Solyc07g045320	Voltage-dependent calcium channel subunit alpha-2/delta-3 (AHRD V3.3 *** A0A0B0PYX3_GOSAR)		F:GO:0003682	F:chromatin binding			IPR032001 (PFAM): PTHR36384 (PAN	16,118	10,322	34,299	33,368	32,084									
Solyc07g045330	GPCR-type G protein 2 (AHRD V3.3 *** AT4G27630.2)		C:GO:0016020	C:membrane			IPR022535 (PFAM): IPR025969 (PFAI	18,575	14,422	19,333	21,146	18,333									
Solyc07g045340	RPM1-interacting protein 4 family protein (AHRD V3.3 *** A0A061DN91_THECC)		C:GO:0005886; P:G(	C:plasma membrane; P:defense response signaling pathway, re			IPR008700 (PFAM): mobidb-lite (MOB	48,754	33,817	77,479	77,397	67,054									
Solyc07g045350	Acetoacetyl-CoA thiolase (AHRD V3.3 *** F5CLC4_CATRO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR002155 (PIRSF): IPR020617 (PFA	30,091	27,840	44,794	35,450	47,527									
Solyc07g045353	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061DK10_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,475	0,450	0,267	0,291	0,351									
Solyc07g045357	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061DK10_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR025525 (PFAM): IPR008906 (PFAI	0,812	0,799	0,743	0,718	0,587									
Solyc07g045370	Las1-like family protein (AHRD V3.3 *** B9HNI6_POPTR)						IPR007174 (PFAM): mobidb-lite (MOB	13,599	12,196	15,932	15,349	13,911									
Solyc07g045380	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GRQ9_POPTR)		F:GO:0005515; P:G(	F:protein binding; P:intracellular protein transport; P:vesicle-mec			IPR002885 (TIGRFAM): IPR011990 ((	14,657	10,577	15,476	14,236	15,157									
Solyc07g045390	50S ribosomal protein L18 (AHRD V3.3 *** A0A1D1XFY4_9ARAE)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.420.100 (GENE3D): IPR(	9,194	9,771	11,384	10,416	11,404									
Solyc07g045410	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *-* B9IFK4_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,162	0,074	0,076	0,192	0,071									
Solyc07g045420	ABC1 kinase (AHRD V3.3 *** B9DGY1_ARATH)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph			IPR004147 (PFAM): PTHR10566:SF1(	56,719	65,066	54,932	58,155	73,917									
Solyc07g045430	Nudix hydrolase (AHRD V3.3 *** A0A061GGI6_THECC)		F:GO:0016787	F:hydrolase activity			IPR003293 (PRINTS): PF18290 (PFAI	0,021	0,233	0,025	0,171	0,000									
Solyc07g045440	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)		C:GO:0046658	C:anchored component of plasma membrane			IPR000782 (SMART): IPR036378 (G3	401,607	278,074	13,670	8,066	14,046									
Solyc07g045450	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT4G28370.4)		C:GO:0016021	C:integral component of membrane			PTHR35708 (PANTHER): PTHR35708	0,335	0,254	0,075	0,025	0,000									
Solyc07g045460	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** AT4G16360.1)		F:GO:0005515	F:protein binding			IPR006828 (SMART): IPR013783 (G3	12,855	10,742	4,835	3,782	4,667									
Solyc07g045470	Beta 1,2 N-acetylglucosaminyltransferase (AHRD V3.3 *** Q599H9_POPCN)		C:GO:0005795; F:G(	C:Golgi stack; F:alp	EC:2.4.1.143	Alpha-1,6-mannosyl-(	IPR007754 (PFAM): mobidb-lite (MOB	11,502	13,841	10,939	9,187	10,301									
Solyc07g045480	phytochrome F	PHYF	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR001294 (PRINTS): IPR000014 (SM	24,120	23,958	27,302	29,980	28,279									
Solyc07g045490	Cytochrome b561 domain-containing protein (AHRD V3.3 *** A0A199UKZ0_ANACO)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART): IPR006593 (PF.	0,000	0,021	0,025	0,000	0,000									
Solyc07g045500	cell wall invertase 5 (AHRD V3.3 --* AT3G13784.4)							0,019	0,000	0,000	0,000	0,000									
Solyc07g045510	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7M2R8_ARALL)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,538	2,293	1,641	1,608	1,968									
Solyc07g045520	FAR1-related sequence 10 (AHRD V3.3 *** AT5G28530.3)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR006564 (SMAF FAR1	5,195	4,137	3,752	3,570	4,335									
Solyc07g045530	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** I3SMV9_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR34947:SF3 (PANTHER): PTHR3	0,348	1,230	0,298	0,280	0,379									
Solyc07g045540	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** K4CEW0_SOLLC)		F:GO:0004345; P:G(	F:glucose-6-phosph	EC:1.1.1.49	Glucose-6-phosphate	IPR001282 (PRINTS): IPR022675 (PF	37,197	44,021	10,602	14,177	20,672			0,957	0,000				up	
Solyc07g045570	Filament-plant-like protein (AHRD V3.3 *-* A0A072VFI4_MEDTR)						IPR008587 (PFAM): PTHR31580 (PAN	0,672	1,094	0,400	0,122	0,399									
Solyc07g045595	Class I heat shock protein (AHRD V3.3 --* HSP12_SOYBN)						IPR008587 (PFAM): PTHR31580 (PAN	0,000	0,021	0,075	0,073	0,023									
Solyc07g045610	Class I heat shock protein (AHRD V3.3 *-* F4YBC5_SOLNI)	Hsp9.1					IPR008978 (G3DSA:2.60.40.GENE3D	0,000	0,021	0,025	0,070	0,379									
Solyc07g045617	Phosphoinositide phospholipase C (AHRD V3.3 --* A0A178VES8_ARATH)							0,000	0,000	0,000	0,000	0,024									
Solyc07g047610	Transcriptional adapter ADA2 (AHRD V3.3 *** A0A0B0NVH3_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:transcription coactivator activity; F:protein bin			IPR000433 (SMART): IPR001005 (SM	28,044	25,795	22,233	21,448	21,296									
Solyc07g047620	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SW54_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	4,492	5,163	4,069	4,520	5,072									
Solyc07g047625	LOW QUALITY:Cytochrome c biogenesis (AHRD V3.3 *-* Q5U698_BETVU)		C:GO:0005739; F:G(	C:mitochondrion; F:heme transporter activity; P:heme transport; C:integral component of membrane; P:(				0,057	0,021	0,000	0,000	0,000									
Solyc07g047640	LOW QUALITY:F-box protein (AHRD V3.3 *** W9SM54_9ROSA)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): PTHR31790 (	0,654	0,670	0,487	0,143	0,285									
Solyc07g047670	Pescadillo homolog (AHRD V3.3 *** K4CEX3_SOLLC)		C:GO:0005730; P:G(	C:nucleolus; P:ribosome biogenesis			IPR001357 (SMART): IPR036420 (G3	232,095	241,041	195,853	169,307	183,769									
Solyc07g047680	F-box family protein (AHRD V3.3 *** AT5G48170.1)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): PTHR12874 (PAN	1,776	1,702	3,063	4,746	4,645									
Solyc07g047700	UPF0451 protein C17orf61 like (AHRD V3.3 *** A0A0B2S244_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR006696 (PFAM): IPR006696 (PAN	35,268	37,941	54,532	53,926	52,440									
Solyc07g047710	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** G7JMV2_MEDTR)						IPR012946 (SMART): IPR012946 (PF.	2,157	2,140	3,413	3,254	2,950									
Solyc07g047720	Membrin (AHRD V3.3 *** K4CEX8_SOLLC)		F:GO:0005484; C:G(	F:SNAP receptor activity; C:Golgi apparatus; P:vesicle-mediate			IPR027027 (PIRSF): G3DSA:1.20.5.1	9,391	10,229	12,748	11,770	11,472									
Solyc07g047730	LOW QUALITY:Paired amphipathic helix protein Sin3 (AHRD V3.3 *-* A0A0K9PVM9_ZOSMR)		P:GO:0006355	P:regulation of transcription, DNA-templated			G3DSA:1.20.1160.11 (GENE3D): IPR(	0,038	0,000	0,000	0,075	0,000									
Solyc07g047740	TOMTPX2A_peroxidase	tpx2	F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,423	0,199	1,222	1,652	0,943									
Solyc07g047760	F-box protein family (AHRD V3.3 *** A0A151SU61_CAJCA)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF.	0,076	0,079	0,217	0,358	0,142									
Solyc07g047770	Histidine kinase CHK2 (AHRD V3.3 *** A0A0A1WC44_NICAT)		F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR003661 (SM	99,980	64,457	49,088	56,372	57,824									
Solyc07g047780	CONSTANS interacting protein 6	CIP6	C:GO:0005634; P:G(	C:nucleus; P:root meristem specification; P:maintenance of roo			IPR004082 (PRINTS): IPR001965 (SM	40,974	74,543	55,363	54,708	54,851	0,888	0,016					up		
Solyc07g047790	Heat shock protein, putative (AHRD V3.3 *** B9T0C8_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS): IPR003594 (SM	182,032	172,123	223,130	173,776	200,208									
Solyc07g047800	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G01980.4),Pfam:PF13561						IPR002347 (PRINTS): PF13561 (PFAI	166,587	308,613	1882,316	2225,397	1671,732	0,913	0,045					up		
Solyc07g047820	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SF42_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	10,360	10,366	20,581	30,172	19,849					0,554	0,004			up
Solyc07g047830	DUF630 family protein (DUF630 and DUF632) (AHRD V3.3 *** AT2G19090.1)		P:GO:0071249	P:cellular response to nitrate			IPR006868 (PFAM): IPR006867 (PFAI	8,949	8,059	4,817	3,954	5,360									
Solyc07g047850	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** CB23_ORYSI)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE:	198,595	692,243	74,246	90,051	161,084	1,830	0,000	1,114	0,000			up	up	
Solyc07g047860	Nuclear pore complex protein NUP133 (AHRD V3.3 *** NU133_ARATH)		F:GO:0005515; F:G(	F:protein binding; F:structural constituent of nuclear pore			IPR007187 (PFAM): G3DSA:1.25.40.7	35,815	30,852	32,385	30,660	29,363									
Solyc07g047870	nuclear RNA polymerase D1B (AHRD V3.3 --* AT2G40030.2)						mobidb-lite (MOBIDB_LITE)	0,019	0,018	0,000	0,050	0,000									
Solyc07g047880	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT3G07760.5)		F:GO:0005515	F:protein binding			G3DSA:1.10.150.50 (GENE3D): IPR0(	14,532	15,625	9,995	9,300	9,948									
Solyc07g047890	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 --*							0,000	0,021	0,071	0,000	0,000									
Solyc07g047900	CRS1/YhbY (CRM) domain protein (AHRD V3.3 *** A0A072U6I9_MEDTR)		F:GO:0003723	F:RNA binding			IPR001890 (SMART): IPR001890 (PF.	16,277	14,867	15,273	12,864	14,017									
Solyc07g047940	Zinc finger transcription factor 49	C3H49	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (SMART): IPR025605 (PF.	3,590	2,568	0,097	0,246	0,418									
Solyc07g047950	GRAS family transcription factor (AHRD V3.3 *** G7KEQ0_MEDTR)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	21,508	25,611	6,926	8,098	10,708			0,620	0,019				up	
Solyc07g047960	WRKY transcription factor 1	WRKY1	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	18,114	15,771	13,495	14,910	15,294									
Solyc07g047970	Transducin/WD40 repeat-like superfamily protein, putative (AHRD V3.3 *** A0A061E7J2_THECC)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	28,822	31,948	37,684	33,828	35,198									
Solyc07g047980	DGCR14-like protein (AHRD V3.3 *** AT3G07790.1)						IPR019148 (PFAM): mobidb-lite (MOB	162,644	107,891	128,244	208,459	137,475					0,704	0,000			up
Solyc07g048000	Phototropic-responsive NPH3		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0:	0,079	0,058	0,025	0,125	0,094									
Solyc07g048010	Thymidylate kinase (AHRD V3.3 *** ZEUS1_ARATH)		F:GO:0004798; F:G(	F:thymidylate kinas	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR018094 (TIGRFAM): IPR039430 (F	2,940	3,186	1,012	1,390	1,412									
Solyc07g048020	Charged multivesicular body 1 (AHRD V3.3 *-* A0A0B0N7X7_GOSAR)		C:GO:0000815; C:G(	C:ESCRT III complex; C:multivesicular body; P:protein transpor			PTHR10476 (PANTHER): PTHR10476	0,021	0,039	0,065	0,070	0,069									
Solyc07g048030	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding			IPR000504 (SMART): IPR000504 (PF.	33,612	40,497	26,402	22,285	25,940									
Solyc07g048035	Albumin-1 A (AHRD V3.3 --* ALB1A_PEA)							5,892	6,528	4,252	4,061	4,303									
Solyc07g048040	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** G5DXN8_SILLA)						IPR000008 (SMART): IPR000008 (PF.	20,211	23,813	26,536	22,060	26,114									
Solyc07g048050	Auxin-responsive family protein (AHRD V3.3 *** A0A061DLW5_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART): G3DSA:1.20.12	0,411	0,487	0,046	0,048	0,024									
Solyc07g048060	Auxin-induced in root cultures protein 12, putative (AHRD V3.3 *-* B9T181_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR005018 (PFAM): PTHR23130 (PAN	0,422	0,719	0,165	0,443	0,400									
Solyc07g048070	Auxin induced-like protein (AHRD V3.3 *** A0A0K9NX81_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR006593 (SMART): G3DSA:1.20.12	0,121	0,460	0,169	0,343	0,426									
Solyc07g048080	Threonyl-tRNA synthetase (AHRD V3.3 *** D9ZHD6_HYPPE)		F:GO:0004829; F:G(	F:threonine-tRNA lic	EC:6.1.1.3	Threonine--tRNA liga	IPR002320 (PRINTS): IPR012947 (SM	26,940	28,919	34,279	40,218	49,720			0,533	0,000				up	
Solyc07g048085	Fasciclin-like arabinogalactan protein (AHRD V3.3 *-* G7K503_MEDTR)		P:GO:0009834; C:G(	P:plant-type secondary cell wall biogenesis; C:integral compone			IPR036378 (G3DSA:2.30.180.GENE3I	2,389	2,096	1,549	1,811	2,211									
Solyc07g048100	BRCT domain-containing protein (AHRD V3.3 *** A0A103Y1F5_CYNCS)		P:GO:0000077; C:G(	P:DNA damage checkpoint; C:nucleus; F:histone binding; P:pos			IPR001357 (SMART): IPR001357 (PF.	1,776	1,326	1,323	1,444	1,057									
Solyc07g048110	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT3G21620.1)		C:GO:0016020	C:membrane			IPR003864 (PFAM): IPR027815 (PFAI	1,891	1,329	0,286	0,170	0,330									
Solyc07g048120	Ubiquitin fusion degradation 1 (AHRD V3.3 *** A0A0B0MFM6_GOSAR)		F:GO:0005515; P:G(	F:protein binding; P:ubiquitin-dependent protein catabolic proces			G3DSA:2.40.40.50 (GENE3D): IPR00	18,993	17,205	30,552	32,005	28,171									
Solyc07g049120	PLATZ transcription factor family protein (AHRD V3.3 *** A0A061EE86_THECC)		F:GO:0008270	F:zinc ion binding			IPR000315 (PFAM): IPR006734 (PFAI	0,000	0,097	0,000	0,000	0,000									
Solyc07g049130	LOW QUALITY:PLATZ transcription factor family protein (AHRD V3.3 *** A0A061EE86_THECC)		F:GO:0008270	F:zinc ion binding			IPR006734 (PFAM): IPR000315 (PFAI	0,000	0,116	0,000	0,000	0,000									
Solyc07g049140	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** O24639_SOLTU)		F:GO:0004180; P:G(	F:carboxypeptidase activity; P:proteolysis			IPR004231 (PFAM): IPR009632 (PRC	5919,395	4787,783	15306,401	15246,038	14011,774									
Solyc07g049160	Ribonuclease 3 family protein (AHRD V3.3 *** B9GTV4_POPTR)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR000999 (SMART): IPR014720 (SM	14,508	15,403	16,856	18,430	12,753									
Solyc07g049165	Ribonuclease 3 family protein (AHRD V3.3 *** B9GTV4_POPTR)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR000999 (SMART): G3DSA:3.30.16	12,822	13,271	12,903	11,618	12,245									
Solyc07g049180	LysM receptor-like kinase (AHRD V3.3 *** E2FYC4_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR018392 (SM	27,587	79,278	21,256	22,419	22,686	1,546	0,000					up		
Solyc07g049190	LysM receptor-like kinase variant SlBti9-1a (AHRD V3.3 *-* G1EN31_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR036779 (G3DSA:3.10.350.GENE3I	2,952	3,670	2,043	2,394	2,259									
Solyc07g049200	Coiled-coil domain-containing protein 21, putative isoform 2 (AHRD V3.3 *** A0A061DLJ7_THECC)						mobidb-lite (MOBIDB_LITE): PTHR367	10,545	9,444	43,081	47,906	37,011									
Solyc07g049210	BAH-PHD domain-containing protein (AHRD V3.3 *** A0A0K9P0E3_ZOSMR)		F:GO:0003682	F:chromatin binding			IPR001965 (SMART): IPR001025 (SM	16,644	13,003	24,231	24,014	22,410									
Solyc07g049220	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9GTV0_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR002554 (PFAM): IPR002554 (PIRS	27,479	22,062	53,122	46,658	42,872									
Solyc07g049230	RmlC-like cupins superfamily protein (AHRD V3.3 *** AT2G32650.2)						IPR008579 (PFAM): IPR014710 (G3D	10,891	16,220	19,387	21,309	23,306									
Solyc07g049240	Peroxidase (AHRD V3.3 *** K4CF27_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,019	0,019	0,000	0,000	0,000									
Solyc07g049250	LOW QUALITY:Paired amphipathic helix protein Sin3 (AHRD V3.3 *-* A0A151TFV5_CAJCA)		F:GO:0003714; P:G(	F:transcription corepressor activity; P:regulation of transcriptior			G3DSA:1.20.1160.11 (GENE3D): IPR(	0,000	0,000	0,025	0,149	0,024									
Solyc07g049260	UBA/UBX domain protein (AHRD V3.3 *** AT4G22150.1)		F:GO:0005515	F:protein binding			IPR001012 (SMART): IPR012989 (SM	25,601	30,685	52,362	47,108	43,370									
Solyc07g049270	RNA binding protein (AHRD V3.3 *** A0A0K9NY52_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	1,857	1,878	2,111	2,650	2,031									
Solyc07g049280	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (AHRD V3.3 *** K4CF31_SOLLC)		F:GO:0003872; F:G(	F:6-phosphofructok	EC:2.7.1.9; EC:2.7.1	Diphosphate--fructos	IPR022953 (PRINTS): G3DSA:3.40.5(	10,761	13,318	8,395	8,537	9,164									
Solyc07g049290	Major facilitator superfamily protein (AHRD V3.3 *** AT3G21670.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	50,625	56,409	12,129	20,049	27,201			1,159	0,000				up	
Solyc07g049300	Endoglucanase (AHRD V3.3 *** M0ZJ27_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012341 (G3DSA:1.50.10.GENE3D	26,881	15,976	0,109	0,075	0,165									
Solyc07g049310	Major facilitator superfamily protein (AHRD V3.3 *** AT1G05030.1)	pGlcT4	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI(	10,301	9,737	7,850	6,212	7,558									
Solyc07g049320	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7J799_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM): PTHR11119 (PAN	2,226	1,413	0,485	1,113	0,870									
Solyc07g049350	G1/S-specific cyclin-E protein (AHRD V3.3 *** AT2G32970.4)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	25,150	17,720	25,487	31,139	25,693									
Solyc07g049360	Small ubiquitin-related modifier (AHRD V3.3 *** A0A0V0H2J3_SOLCH)		F:GO:0005515; P:G(	F:protein binding; P:protein sumoylation			IPR000626 (SMART): IPR022617 (PF.	59,319	55,250	62,064	51,661	59,172									
Solyc07g049370	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SH66_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): IPR000490 (PF.	18,196	21,049	1,547	0,602	0,632									
Solyc07g049385	SHK1 binding protein 1 (AHRD V3.3 --* AT4G31120.2)							1,270	0,584	0,406	0,249	0,282									
Solyc07g049390	Armadillo repeat-containing protein (AHRD V3.3 *** G0Y6R0_GOSHI)		F:GO:0005515	F:protein binding			IPR000225 (SMART): IPR006911 (PF.	30,697	17,743	8,399	9,077	9,208	-0,762	0,005					down		
Solyc07g049410	Dual specificity protein phosphatase, putative (AHRD V3.3 *** B9SSI3_RICCO)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR020422 (SMART): IPR000340 (PF.	10,572	11,489	11,870	12,600	12,671									
Solyc07g049420	60S acidic ribosomal protein family (AHRD V3.3 *** AT5G24510.1),Pfam:PF00428		P:GO:0002181; F:G(	P:cytoplasmic translation; F:structural constituent of ribosome; I			IPR038716 (G3DSA:1.10.10.GENE3D	0,000	0,000	0,022	0,000	0,000									
Solyc07g049430	GDSL esterase/lipase (AHRD V3.3 *** W9STE9_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	1,097	1,415	0,000	0,025	0,000									
Solyc07g049440	GDSL esterase/lipase (AHRD V3.3 *** W9S4N1_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	111,014	79,330	66,202	56,859	50,400									
Solyc07g049450	Protein disulfide isomerase family (AHRD V3.3 *** A9CPA7_SOYBN)		F:GO:0016853; P:G(	F:isomerase activity; P:cell redox homeostasis			PR00421 (PRINTS): IPR005788 (TIGF	84,859	82,201	97,259	87,509	82,570									
Solyc07g049460	laccase		F:GO:0005507; P:G(	F:copper ion bindin	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR011707 (PFAM): IPR001117 (PFAI	0,019	0,064	0,093	0,201	0,118									
Solyc07g049470	Triacylglycerol lipase 2, putative (AHRD V3.3 *-* B9SSJ8_RICCO)		C:GO:0016021	C:integral component of membrane			PTHR36703 (PANTHER)	3,643	3,720	6,815	7,665	5,631									
Solyc07g049480	Cleavage and polyadenylation specificity factor family protein (AHRD V3.3 *** B9IJR9_POPTR)		F:GO:0003723; F:G(	F:RNA binding; F:endoribonuclease activity; C:mRNA cleavage			IPR001279 (SMART): IPR021718 (SM	33,159	26,978	33,052	31,598	32,919									
Solyc07g049490	Ethylene Response Factor F.3	ERF.F3	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	29,904	33,340	38,905	33,834	32,912									
Solyc07g049495	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT5G36670.5)							0,398	0,527	0,613	0,418	0,520									
Solyc07g049500	Argonaute6	AGO.6	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR014811 (SMART): IPR003165 (SM	19,954	15,974	12,243	12,322	12,951									
Solyc07g049530	1-aminocyclopropane-1-carboxylate oxidase 1	ACO1	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	151,329	659,109	3196,939	3521,249	3061,248	2,143	0,004					up		
Solyc07g049540	Beta-expansin-like protein (AHRD V3.3 *** Q9AXE4_TOBAC)	EXPB5	C:GO:0005576; P:G(	C:extracellular region; P:sexual reproduction			IPR007118 (PRINTS): IPR005795 (PF	0,212	1,549	0,000	0,000	0,000									
Solyc07g049550	1-aminocyclopropane-1-carboxylate oxidase 1 (AHRD V3.3 *** ACCO1_SOLLC)	ACO3	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFAI	0,978	4,843	39,081	67,404	41,905	2,329	0,007			0,790	0,025	up		up

Solyc07g049560	Tyrosine specific protein phosphatase family protein (AHRD V3.3 *** Q32W70_CAPAN)		F:GO:0016791	F:phosphatase activity			IPR020428 (PRINTS): IPR029021 (G3	9,257	13,773	9,764	10,418	9,075									
Solyc07g049570	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** K4CF58_SOLLC)		P:GO:0006633; F:GC	P:fatty acid biosynthetic process; F:transferase activity, transfe			IPR020841 (SMART): IPR017568 (TIG	14,251	13,439	24,787	21,465	21,245									
Solyc07g049580	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT3G07890.5)		F:GO:0005096; C:GC	F:GTPase activator activity; C:cell; P:intracellular protein transr			IPR000195 (SMART): G3DSA:1.10.8.2	19,935	18,140	8,610	8,465	10,608									
Solyc07g049590	Ankyrin repeat and BTB/POZ domain protein (AHRD V3.3 *** A0A072UZJ2_MEDTR)		F:GO:0005515	F:protein binding			IPR000210 (SMART): G3DSA:3.30.71	5,066	5,202	8,955	8,074	7,891									
Solyc07g049600	Fimbrin, putative (AHRD V3.3 *** B9T216_RICCO)		F:GO:0051015; P:GC	F:actin filament binding; P:actin filament bundle assembly			IPR001715 (SMART): IPR036872 (G3	0,496	2,739	0,025	0,000	0,023	2,472	0,000					up		
Solyc07g049610	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyco			IPR004263 (PFAM): mobidb-lite (MOB	56,846	45,476	8,890	11,877	13,946									
Solyc07g049630	LOW QUALITY:Pectinesterase (AHRD V3.3 --* V4LDC7_EUTSA)							32,340	27,750	13,431	12,669	13,422									
Solyc07g049640	LOW QUALITY:Myb-like transcription factor family protein (AHRD V3.3 *-* G7KXD8_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6C G2-like	0,102	0,179	0,000	0,000	0,023									
Solyc07g049650	LOW QUALITY:josephin-like protein (AHRD V3.3 --* AT5G01225.1)							0,154	0,121	0,047	0,121	0,119									
Solyc07g049660	Benzyl alcohol O-benzoyltransferase (AHRD V3.3 *-* BEBT_TOBAC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	4,369	9,811	0,890	0,439	1,207	1,190	0,013					up		
Solyc07g049670	Benzyl alcohol O-benzoyltransferase (AHRD V3.3 *** BEBT_TOBAC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	11,606	26,824	1,507	1,500	3,074	1,231	0,001					up		
Solyc07g049680	Condensin complex subunit 2 (AHRD V3.3 *** A0A022R1C5_ERYGU)		C:GO:0000796; P:GC	C:condensin complex; P:mitotic chromosome condensation			IPR022816 (PIRSF): IPR022816 (PFA	7,485	5,532	1,107	0,483	1,359									
Solyc07g049690	hydroperoxide lyase	hpl	F:GO:0004497; F:GC	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR002403 (PRINTS): IPR036396 (G3	61,254	95,520	218,704	217,881	222,726	0,668	0,043					up		
Solyc07g049700	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,063	0,098	0,125	0,270	0,118									
Solyc07g049710	Vacuolar ATPase subunit e-like (AHRD V3.3 *** Q8GUB2_MESCR)		F:GO:0015078; P:GC	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR008389 (PFAM): PTHR12263:SF3	22,255	22,019	30,345	30,607	29,998									
Solyc07g049720	10kDa polypeptide precursor of photosystem 2		F:GO:0003677; F:GC	F:DNA binding; F:DI	EC:5.99.1.2	DNA topoisomerase	IPR001631 (PRINTS): IPR013499 (SM	171,794	154,240	173,484	182,019	175,192									
Solyc07g049730	transmembrane protein, putative (DUF1068) (AHRD V3.3 *** AT1G05070.1)		C:GO:0016021	C:integral component of membrane			IPR010471 (PFAM): mobidb-lite (MOB	85,197	110,946	52,384	55,082	51,578									
Solyc07g049740	Lipid-A-disaccharide synthase (AHRD V3.3 *** W9SCL5_9ROSA)		F:GO:0008915; P:GC	F:lipid-A-disaccharic	EC:2.4.1.182	Lipid-A-disaccharide	IPR003835 (PFAM): IPR003835 (PAN	5,093	5,603	3,394	3,677	4,133									
Solyc07g049750	Dentin sialophosphoprotein (AHRD V3.3 *** B9GTV9_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	24,850	25,717	27,741	25,897	24,583									
Solyc07g049760	LOW QUALITY:Cell differentiation protein rcd1 (AHRD V3.3 --* A0A199VDW4_ANACO)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex				0,000	0,000	0,000	0,000	0,023									
Solyc07g049765	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 --* AT5G24280.3)							0,021	0,000	0,000	0,000	0,000									
Solyc07g049770	Cell differentiation protein RCD1-like protein (AHRD V3.3 *-* A0A087SMK7_AUXPR)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex			PF04078 (PFAM): IPR011989 (G3DS/	0,019	0,021	0,000	0,000	0,000									
Solyc07g049780	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex			PF04078 (PFAM): IPR011989 (G3DS/	0,631	0,444	0,025	0,075	0,047									
Solyc07g049790	Cell differentiation protein rcd1, putative, expressed (AHRD V3.3 *** Q10CF3_ORYSJ)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex			IPR011989 (G3DSA:1.25.10.GENE3D	0,061	0,039	0,000	0,000	0,000									
Solyc07g049800	Cell differentiation protein RCD1 like (AHRD V3.3 *** A0A0B2PWJ4_GLYSO)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex			PF04078 (PFAM): IPR011989 (G3DS/	0,019	0,000	0,000	0,000	0,000									
Solyc07g051810	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)		P:GO:0006402; C:GC	P:mRNA catabolic process; C:CCR4-NOT complex			PF04078 (PFAM): PTHR12262 (PANT	0,303	0,425	0,000	0,000	0,000									
Solyc07g051820	Cellulose synthase family protein (AHRD V3.3 *** B9GTW0_POPTR)		C:GO:0016020; F:GC	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR005150 (PFAM): IPR029044 (G3D	19,421	16,743	1,185	0,560	1,893									
Solyc07g051840	WRKY transcription factor 17	WRKY17	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			mobidb-lite (MOBIL WRKY	5,912	10,032	13,576	21,233	20,434			0,588	0,004	0,648	0,001		up	up
Solyc07g051845	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT1G63860.5)							0,000	0,000	0,025	0,000	0,024									
Solyc07g051850	Aspartic proteinase, putative (AHRD V3.3 *** B9SVA7_RICCO)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR008139 (SM	531,907	536,443	551,746	518,967	576,703									
Solyc07g051860	MAP kinase kinase kinase 50	MAPKKK50	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,241	0,309	2,269	2,294	1,371									
Solyc07g051870	MAP kinase kinase kinase 51	MAPKKK51	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	0,019	0,085	1,777	2,635	0,896									
Solyc07g051880	MAP kinase kinase kinase 52		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	0,343	0,794	35,966	32,589	22,017			-0,709	0,014				down	
Solyc07g051890	MAP kinase kinase kinase 53	MAPKKK53	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,057	0,000	2,135	1,301	1,487									
Solyc07g051920	MAP kinase kinase kinase 54	MAPKKK54	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,158	0,179	0,050	0,072	0,023									
Solyc07g051930	MAP kinase kinase kinase 55	MAPKKK55	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	0,175	0,113	0,340	0,345	0,189									
Solyc07g051940	Sesquiterpene synthase (AHRD V3.3 *** G8H5N2_SOLHA)		F:GO:0000287; F:GC	F:magnesium ion binding; F:zinc ion binding; F:terpene synthase			IPR006564 (SMART): IPR036965 (G3	0,235	0,240	0,000	0,022	0,000									
Solyc07g051950	S-type anion channel SLAH1 (AHRD V3.3 *** W9QIC7_9ROSA)		C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport			IPR038665 (G3DSA:1.50.10.GENE3D	0,613	0,261	9,986	38,512	14,908					1,950	0,000			up
Solyc07g051960	SNF2 domain-containing protein (AHRD V3.3 *** D7KEB6_ARALL)		F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR001841 (SM	0,000	0,043	0,000	0,000	0,023									
Solyc07g051980	SNF2 domain-containing protein (AHRD V3.3 *** D7KEB6_ARALL)		F:GO:0005524	F:ATP binding			IPR001841 (SMART): IPR014001 (SM	0,352	0,021	0,443	0,342	0,117									
Solyc07g052010	SNF2 domain-containing protein (AHRD V3.3 *** D7KEB6_ARALL)		F:GO:0005524	F:ATP binding			IPR000330 (PFAM): PTHR10799 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc07g052020	SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 *-* AT3G12810.2)		F:GO:0005524	F:ATP binding			IPR014001 (SMART): IPR038718 (G3	0,019	0,000	0,000	0,000	0,000									
Solyc07g052025	Cytochrome P450 (AHRD V3.3 *-* A0A103Y9Y5_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR036396 (G3	0,444	0,019	0,596	0,338	0,164									
Solyc07g052040	Tubulin beta chain (AHRD V3.3 *-* TBB_HORVU)		F:GO:0005200; F:GC	F:structural constituent of cytoskeleton; F:GTP binding; C:micro			IPR002453 (PRINTS): IPR000217 (PF	1,952	1,336	0,499	0,193	0,472									
Solyc07g052060	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,021	0,000	0,000	0,000	0,000									
Solyc07g052070	Cytochrome P450 (AHRD V3.3 *** A0A118JYC4_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,021	0,166	0,000	0,000	0,024									
Solyc07g052073	Cytochrome P450 (AHRD V3.3 *-* A0A103Y9Y5_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PFAM): IPR036396 (G3D	0,000	0,021	0,600	0,092	0,501									
Solyc07g052077	Cytochrome P450 (AHRD V3.3 *** A0A103JVN2_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,000	0,021	0,798	0,120	0,404									
Solyc07g052100	SNF2 domain-containing protein (AHRD V3.3 *** D7KEB6_ARALL)		F:GO:0005524; F:GC	F:ATP binding; F:metal ion binding			IPR001841 (SMART): IPR001650 (SM	0,115	0,079	0,075	0,000	0,094									
Solyc07g052110	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT4G26600.1)		F:GO:0008168	F:methyltransferase activity			IPR023267 (PRINTS): IPR001678 (PF	66,055	65,547	56,804	48,262	52,226									
Solyc07g052170	LOW QUALITY:Dirigent protein (AHRD V3.3 *** K4CFB6_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAN	0,084	0,043	0,022	0,025	0,023									
Solyc07g052175	LOW QUALITY:splicing factor Prp18 family protein (AHRD V3.3 *** AT1G03140.1)		C:GO:0005681; P:GC	C:spliceosomal complex; P:RNA splicing			IPR014906 (SMART): IPR036285 (G3	0,142	0,144	0,072	0,075	0,047									
Solyc07g052200	LOW QUALITY:Pre-mRNA-splicing factor syf2 (AHRD V3.3 *-* A0A0B0PRU4_GOSAR)		C:GO:0000974; C:GC	C:Prp19 complex; C:catalytic step 2 spliceosome; C:post-mRNA			IPR013260 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc07g052203	Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE): PTHR409	0,266	0,520	0,000	0,000	0,000									
Solyc07g052207	Glycine-rich cell wall structural protein 1 (AHRD V3.3 --* GRP1_PETHY)						PTHR40903 (PANTHER)	0,259	0,880	0,000	0,022	0,024									
Solyc07g052230	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2S927_GLYSO)		F:GO:0005507; F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR001117 (PFAM): IPR008972 (G3D	54,363	59,131	2,819	2,673	3,253									
Solyc07g052240	L-ascorbate oxidase-like protein (AHRD V3.3 *** A2Q4H7_MEDTR)		F:GO:0005507; F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR011706 (PFAM): IPR008972 (G3D	10,275	11,496	0,022	0,049	0,283									
Solyc07g052250	Unknown protein (AHRD V3.3)							0,639	0,826	0,591	0,593	0,729									
Solyc07g052255	low-molecular-weight cysteine-rich 40 (AHRD V3.3 -** AT2G14935.1)							0,000	0,037	0,000	0,000	0,000									
Solyc07g052260	low-molecular-weight cysteine-rich 59 (AHRD V3.3 --* AT4G30070.1)							0,631	1,837	3,125	2,043	1,880	1,544	0,025					up		
Solyc07g052270	hydroxysteroid dehydrogenase 1 (AHRD V3.3 *** AT5G50700.1)		C:GO:0016021; F:GC	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS): IPR002347 (PF	3,045	3,783	0,422	0,921	0,469									
Solyc07g052290	Membrane metalloprotease ARASP, chloroplastic (AHRD V3.3 *** ARASP_ARATH)		F:GO:0004222; F:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR001478 (SMART): IPR001478 (PF	12,576	13,850	17,698	19,661	22,600									
Solyc07g052300	R2R3MYB transcription factor 101	R2R3MYB7	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,288	0,144	0,000	0,000	0,000									
Solyc07g052310	LOW QUALITY:CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (AHRD V3.3 --* AT3G48180.1)						PTHR33386 (PANTHER): PTHR33386	0,733	0,960	0,215	0,373	0,257									
Solyc07g052320	Hexosyltransferase (AHRD V3.3 *** K4CFD1_SOLLC)		P:GO:0006486; F:GC	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR025298 (PFAM): G3DSA:3.90.550	6,228	5,682	10,750	11,217	9,303									
Solyc07g052340	3'-5' exonuclease domain protein (AHRD V3.3 *** G7JDJ9_MEDTR)		F:GO:0000166; F:GC	F:nucleotide binding; F:nucleic acid binding; C:intracellular; P:nu			IPR002562 (SMART): G3DSA:3.30.42	9,060	7,849	4,435	5,928	4,984									
Solyc07g052350	Aconitate hydratase (AHRD V3.3 *** K4CFD4_SOLLC)		F:GO:0003994; F:GC	F:aconitate hydrata	EC:4.2.1.3	Aconitate hydratase	IPR001030 (PRINTS): IPR006249 (TIC	218,393	235,764	239,239	239,521	237,583									
Solyc07g052370	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,000	0,080	0,121	0,282	0,378									
Solyc07g052380	Protein DETOXIFICATION (AHRD V3.3 *** K4CFD7_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	3,628	6,477	1,329	1,166	1,061									
Solyc07g052390	glutamate receptor-like 3.1	GLR3_1	F:GO:0004970; C:GC	F:ionotropic glutamate receptor activity; C:membrane			PR01176 (PRINTS): IPR001320 (SMA	15,890	16,771	6,637	7,088	6,827									
Solyc07g052400	glutamate receptor-like 3.2	GLR3_2	F:GO:0004930; F:GC	F:G protein-coupled receptor activity; F:ionotropic glutamate rec			IPR000337 (PRINTS): IPR001320 (SM	25,821	31,678	3,210	2,987	5,227									
Solyc07g052410	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G54840.2)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): PTHR	0,059	0,021	0,000	0,000	0,000									
Solyc07g052420	protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform (AHRD V3.3 --* AT1G51690.5)						mobidb-lite (MOBIDB_LITE): PTHR367	20,929	22,799	59,184	64,213	54,098									
Solyc07g052430	Transmembrane protein 97 (AHRD V3.3 *** A0A0B2QIV9_GLYSO),Pfam:PF10914		C:GO:0016021	C:integral component of membrane			IPR016964 (PIRSF): PF10914 (PFAM	6,220	8,892	9,213	12,825	12,094									
Solyc07g052440	Transmembrane protein 97 (AHRD V3.3 *** A0A0B2QIV9_GLYSO),Pfam:PF10914		C:GO:0016021	C:integral component of membrane			PF10914 (PFAM): IPR016964 (PIRSF	0,237	0,406	0,093	0,075	0,023									
Solyc07g052453	Syntaxin, putative (AHRD V3.3 *** B9SUS4_RICCO)		C:GO:0016020; P:GC	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART): IPR006011 (SM	0,000	0,000	0,000	0,022	0,000									
Solyc07g052460	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G31050.7)		P:GO:0010089	P:xylem development			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,524	0,786	0,071	0,025	0,046									
Solyc07g052470	Syntaxin, putative (AHRD V3.3 *** B9SUS4_RICCO)		C:GO:0016020; P:GC	C:membrane; P:vesicle-mediated transport			IPR006011 (SMART): IPR000727 (SM	0,434	0,172	0,813	0,722	0,637									
Solyc07g052480	isocitrate lyase LEU18678		F:GO:0004451; P:GC	F:isocitrate lyase a	EC:4.1.3.1	Isocitrate lyase	G3DSA:1.10.10.850 (GENE3D): IPR0(	0,325	0,578	1,509	2,310	2,163									
Solyc07g052490	Myb transcription factor (AHRD V3.3 *-* A0A072UKM9_MEDTR)	MYB_ATV	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB_related	0,291	0,101	0,442	0,559	0,561									
Solyc07g052510	peroxidase (TPX1)	px1	F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,565	1,602	0,245	0,249	0,281									
Solyc07g052530	Peroxidase (AHRD V1 **** Q07445_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,056	0,099	0,000	0,000	0,000									
Solyc07g052540	Peroxidase (AHRD V1 **** Q07445_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,043	0,000	0,025	0,000									
Solyc07g052550	Peroxidase (AHRD V1 **** Q07445_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	1,350	0,763	0,318	0,618	0,882									
Solyc07g052560	TraB family protein (AHRD V3.3 *-* AT1G05270.1)		C:GO:0031307	C:integral component of mitochondrial outer membrane			PTHR21530 (PANTHER): PTHR21530	2,637	3,026	2,988	2,603	2,755									
Solyc07g052565	TraB family protein (AHRD V3.3 *-* AT1G05270.1)		C:GO:0031307	C:integral component of mitochondrial outer membrane			IPR002816 (PFAM): PTHR21530 (PAN	0,021	0,000	0,025	0,000	0,024									
Solyc07g052570	histone-lysine N-methyltransferase ATXR2 (AHRD V3.3 *** AT3G21820.1)		F:GO:0005515	F:protein binding			IPR001214 (SMART): G3DSA:2.170.2	18,163	17,490	14,755	18,300	16,247									
Solyc07g052580	LOW QUALITY:F-box protein, putative (AHRD V3.3 *** Q6L3P8_SOLDE)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,277	0,254	0,316	0,170	0,356									
Solyc07g052590	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IQB5_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,973	2,980	2,458	2,154	2,821									
Solyc07g052600	Peroxisome biogenesis protein 22 (AHRD V3.3 *** A0A0B2RXJ0_GLYSO)		P:GO:0007031	P:peroxisome organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	33,697	33,446	36,267	37,557	35,377									
Solyc07g052610	cyclinU1_1	CycU1_1	P:GO:0000079; F:GC	P:regulation of cyclin-dependent protein serine/threonine kinase			G3DSA:1.10.472.10 (GENE3D): IPR0(	3,221	6,216	0,793	0,835	2,746	0,976	0,037	1,749	0,000			up	up	
Solyc07g052620	LOW QUALITY:Zinc finger, B-box (AHRD V3.3 *** A0A118JXT6_CYNCS)	BBX17	F:GO:0008270	F:zinc ion binding			IPR000315 (SMART): IPR000315 (PF	0,726	1,224	0,816	0,216	0,473									
Solyc07g052640	Transferring glycosyl group transferase (AHRD V3.3 *** A0A072UKL4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR006740 (PFAM): G3DSA:3.90.550	13,190	20,063	12,780	14,038	13,945									
Solyc07g052650	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:integral component			IPR006740 (PFAM): G3DSA:3.90.550	0,452	0,195	0,000	0,050	0,000									
Solyc07g052660	Blue copper protein (AHRD V3.3 *** W9S2S3_9ROSA)		F:GO:0009055	F:electron transfer activity			PR01217 (PRINTS): IPR003245 (PFA	0,000	0,060	0,000	0,000	0,000									
Solyc07g052670	bHLH transcription factor 053	bHLH053	F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	6,531	9,714	2,130	1,864	2,311									
Solyc07g052680	ATP binding microtubule motor family protein (AHRD V3.3 --* AT3G51150.4)		C:GO:0016021; F:GC	C:integral component of membrane; F:kinase activity; P:phosph			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,472	0,997	0,240	0,171	0,186									
Solyc07g052690	Beta-amylase (AHRD V3.3 *-* K4CFG8_SOLLC)		P:GO:0000272; F:GC	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS): IPR001554 (PF	5,985	7,269	18,649	16,732	19,041									
Solyc07g052695	Beta-amylase (AHRD V3.3 *** K4CFG8_SOLLC)		P:GO:0000272; F:GC	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS): IPR001371 (PF	13,545	17,119	48,071	40,951	43,791									
Solyc07g052700	AGAMOUS-like MADS-box transcription factor (AHRD V3.3 *** B2ZX81_CRYJA)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR002100 (PRINT M-type_MADS	62,499	55,978	134,492	119,144	123,842									
Solyc07g052703	F-box family protein (AHRD V3.3 --* AT1G25211.1)							0,038	0,096	0,075	0,048	0,095									
Solyc07g052707	Formin-like protein (AHRD V3.3 *-* G8IRK0_SOLLC)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR002100 (PRINTS): IPR002100 (SM	0,000	0,000	0,000	0,025	0,000									
Solyc07g052720	MADS-box transcription factor (AHRD V3.3 *** A0A072UYG7_MEDTR)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR002100 (PRINTS): IPR002100 (SM	1,646	1,782	1,403	1,582	1,532									
Solyc07g052730	formin I2I isoform		C:GO:0016021	C:integral component of membrane			IPR015425 (SMART): G3DSA:1.20.58	0,340	0,132	0,124	0,216	0,235									
Solyc07g052740	DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 --* AT4G00390.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): PTHR316	34,801	25,623	22,892	17,941	20,754									
Solyc07g052750	STOREKEEPER protein (AHRD V3.3 *-* STK_SOLTU)		P:GO:0006355	P:regulation of transcription, DNA-templated			PTHR31662:SF1 (PANTHER): IPR007	1,378	1,260	1,363	0,827	1,107									
Solyc07g052760	DNA-binding storekeeper protein-related transcriptional regulator, putative (AHRD V3.3 *** A0A061E9M7_TH		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAN GeBP	17,724	17,424	10,486	8,782	8,380									
Solyc07g052770	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	2,812	3,331	0,025	0,025	0,213									
Solyc07g052780	TIR-NBS-LRR class disease resistance protein (AHRD V3.3 *-* A2I7Q5_9ROSI)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction			IPR000157 (SMART): IPR035897 (G3	0,300	2,541	0,161	0,173	0,282	3,066	0,000					up		
Solyc07g052790	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.2)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR003591 (SMA	0,443	16,006	0,146	1,057	1,647	5,176	0,000	3,404	0,000			up	up	
Solyc07g052800	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT5G17680.1)		F:GO:0005515; P:GC	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	0,040	0,546	0,000	0,073	0,047									
Solyc07g052820	LOW QUALITY:STOREKEEPER protein (AHRD V3.3 *-* STK_SOLTU)		P:GO:0006355	P:regulation of transcription, DNA-templated			PTHR31662:SF1 (PANTHER): IPR007	0,000	0,000	0,000	0,000	0,023									
Solyc07g052830	DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 *-* AT4G00390.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAN GeBP	22,177	18,435	26,510	26,146	25,421									
Solyc07g052840	pumilio 1 (AHRD V3.3 --* AT2G29200.2)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	1,261	0,991	1,084	1,272	0,892									
Solyc07g052850	plant glycogenin-like starch initiation protein 3 (AHRD V3.3 --* AT4G33330.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	1,935	1,179	1,641	1,487	1,439									
Solyc07g052855	Formin-like protein (AHRD V3.3 *-* K4CFH2_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.58.2220 (GENE3D): PTH	2,858	1,475	1,943	1,809	2,144									
Solyc07g052860	LOW QUALITY:STOREKEEPER protein (AHRD V3.3 *-* STK_SOLTU)		P:GO:0006355	P:regulation of transcription, DNA-templated			PTHR31662:SF1 (PANTHER): IPR007	0,490	0,257	0,436	0,529	0,283									
Solyc07g052870	STOREKEEPER protein (AHRD V3.3 *-* STK_SOLTU)		P:GO:0006355	P:regulation of transcription, DNA-templated			PTHR31662:SF1 (PANTHER): IPR007	1,386	0,483	1,048	0,816	0,991	-1,489	0,036					down		
Solyc07g052880	Formin-like protein (AHRD V3.3 *-* K4CFH2_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (PFAM): G3DSA:1.20.58.2	2,963	1,659	1,912	2,147	1,694									
Solyc07g052910	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769:SF4	0,201	0,081	0,051	0,126	0,072									
Solyc07g052920	Krueppel-like factor 17 (AHRD V3.3 *** A0A0B0PNN6_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	14,797	12,621	27,474	26,224	24,627									
Solyc07g052930	bHLH transcription factor141		P:GO:0006355; F:GC	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	0,910	0,876	0,619	0,488	0,567									
Solyc07g052940	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9NPD0_ZOSMR)		F:GO:0005515	F:protein binding			IPR001214 (SMART): IPR032675 (G3	136,602	100,990	135,967	142,615	140,016									
Solyc07g052950	Zinc finger A20 and AN1 domain-containing stress-associated protein 10 (AHRD V3.3 --* SAP10_ORYSJ)						PTHR35318 (PANTHER): PTHR35318	0,159	0,061	0,203	0,097	0,166									
Solyc07g052960	GRAS family TF - fruit shelf-life regulator	FSR	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAN GRAS	3,479	3,717	449,951	475,247	368,423									
Solyc07g052970	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** A0A072UUN1_MEDTR)		F:GO:0005515	F:protein binding			IPR027356 (PFAM): G3DSA:3.30.710	1,633	1,083	1,899	1,878	1,559									
Solyc07g052980	xyloglucan endotransglycosylase/hydrolase 16	xth16	F:GO:0004553; C:GC	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucc	IPR008264 (PRINTS): IPR000757 (PF	11,205	11,330	1,610	1,985	1,392									
Solyc07g052990	LOW QUALITY:Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 --* AT2G43490.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR345	16,295	13,155	10,863	20,580	12,928					0,922	0,000			up
Solyc07g053000	Fasciclin-arabinogalactan-like protein (AHRD V3.3 *** G7IRK3_MEDTR)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			IPR000782 (SMART): PTHR33985:SF	0,138	0,019	0,049	0,050	0,023									
Solyc07g053010	NBS-LRR type disease resistance protein (AHRD V3.3 *** Q19PJ0_POPTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR003593 (SMA	13,448	10,399	13,837	15,893	16,702									
Solyc07g053020	NBS-LRR type disease resistance protein (AHRD V3.3 *** Q19PJ0_POPTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR003593 (SMA	21,485	17,655	8,953	8,629	10,246									
Solyc07g053030	GH3 family protein (AHRD V3.3 *** A0A0K9NRD8_ZOSMR)						IPR004993 (PFAM): PTHR31901:SF2	1,050	0,758	0,799	3,647	3,170			1,950	0,000	2,158	0,000		up	up
Solyc07g053050	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (SMART): IPR002048 (PF	19,194	6,945	5,419	16,975	8,792	-1,438	0,000			1,641	0,000	down		up
Solyc07g053055	aldehyde oxidase 1 (AHRD V3.3 --* AT5G20960.2)							1,618	1,729	1,489	2,088	2,093									
Solyc07g053060	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SFK0_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	19,908	16,463	17,568	18,609	18,293									
Solyc07g053070	Purple acid phosphatase (AHRD V3.3 *** K4CFK5_SOLLC)		F:GO:0003993; F:GC	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR008963 (G3DSA:2.60.40.GENE3D	0,021	0,000	0,000	0,050	0,000									
Solyc07g053080	Serine/threonine-protein kinase (AHRD V3.3 *-* K4CFK6_SOLLC)		F:GO:0004672; P:GC	F:protein kinase activity; P:protein phosphorylation			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,195	0,073	0,288	0,171	0,213									
Solyc07g053100	Serine/threonine-protein kinase (AHRD V3.3 *** U5FEZ9_POPTR)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR003609 (SM	22,326	16,378	22,487	21,818	20,495									
Solyc07g053110	Serine/threonine-protein kinase (AHRD V3.3 *-* M1CGZ4_SOLTU)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): PTHF	0,021	0,039	0,025	0,000	0,000									
Solyc07g053120	Serine/threonine-protein kinase (AHRD V3.3 *-* K4CFL1_SOLLC)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): G3DSA:3.30.20	0,951	5,563	0,215	0,173	0,142	2,566	0,000					up		
Solyc07g053130	Serine/threonine-protein kinase (AHRD V3.3 *** K4CFL1_SOLLC)		F:GO:0004674; F:GC	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	2,957	12,747	2,126	2,762	4,527	2,131	0,000	1,086	0,008			up	up	

Solyc07g053140	Zinc finger, B-box (AHRD V3.3 *** A0A103Y7X2_CYNCS)	BBX31	F:GO:0008270	F:zinc ion binding			IPR000315 (SMART): IPR000315 (PF	41,048	30,704	32,509	46,693	21,356			-0,607	0,006	0,527	0,005		down	up
Solyc07g053150	Frataxin (AHRD V3.3 *** A0A103XS88_CYNCS)		F:GO:0004322; C:G(	F:ferroxidase activi	EC:1.16.3.1; EC:1.1(	Ferroxidase; Oxidizin	IPR002908 (PRINTS): IPR002908 (SM	5,953	5,899	13,331	11,753	11,021									
Solyc07g053160	DUF1644 family protein (AHRD V3.3 *** G7J3N5_MEDTR)						IPR012866 (PFAM): PTHR31197 (PAN	34,772	31,590	44,488	40,348	40,261									
Solyc07g053165	Protein kinase (AHRD V3.3 *-* J7M953_NICBE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	59,612	78,772	35,894	29,602	44,365									
Solyc07g053170	MAP kinase kinase kinase 56	MAPKKK56	F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	mobidb-lite (MOBIDB_LITE): mobidb-lit	111,851	134,199	65,595	56,213	80,148									
Solyc07g053180	Leucine-rich repeat family protein (AHRD V3.3 *** D7M2Q7_ARALL)		F:GO:0005515	F:protein binding			IPR003591 (SMART): SM00365 (SMA	88,145	110,752	56,822	54,737	59,600									
Solyc07g053190	Enhancer of polycomb-like protein (AHRD V3.3 *** K4CFL7_SOLLC)		P:GO:0006357; C:G(	P:regulation of transcription by RNA polymerase II; C:Piccolo N			IPR019542 (PFAM): mobidb-lite (MOB	16,610	13,534	15,102	14,428	13,679									
Solyc07g053200	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)						IPR006015 (PRINTS): IPR014729 (G3	3,070	2,330	1,345	1,680	1,909									
Solyc07g053210	DNA repair metallo-beta-lactamase family protein (AHRD V3.3 *** AT1G27410.1)		C:GO:0000784; F:G(	C:nuclear chromosc	EC:3.1.11; EC:3.1.1!	Acting on ester bonds	IPR011084 (PFAM): PTHR23240 (PAN	1,206	0,975	0,600	0,614	0,569									
Solyc07g053220	Serine/threonine-protein kinase (AHRD V3.3 *** M1DRI9_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR003609 (SM	37,030	29,841	24,339	30,592	31,205									
Solyc07g053225	Transmembrane amino acid transporter family protein (AHRD V3.3 --* AT1G08230.6)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,043	0,046	0,000	0,024									
Solyc07g053230	R2R3MYB transcription factor 83	R2R3MYB83	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	25,203	29,252	1,961	1,840	3,185									
Solyc07g053240	R2R3MYB transcription factor 81	R2R3MYB81	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,922	0,690	0,044	0,221	0,116									
Solyc07g053250	F-box protein family (AHRD V3.3 --* A0A151SU61_CAJCA)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	9,730	7,583	5,806	6,429	7,084									
Solyc07g053255	F-box protein (AHRD V3.3 *-* G7KUJ4_MEDTR)						PTHR44355 (PANTHER): PTHR44355	0,158	0,134	0,122	0,263	0,095									
Solyc07g053260	tft9	tft9	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR023410 (SM	386,495	336,785	346,925	289,572	329,371									
Solyc07g053270	Riboflavin kinase/fmn hydrolase (AHRD V3.3 *** A0A072VB74_MEDTR)		F:GO:0008531; P:G(	F:riboflavin kinase ;	EC:2.7.1.26	Riboflavin kinase	IPR006439 (PRINTS): IPR023198 (G3	1,213	1,976	2,702	2,687	2,512									
Solyc07g053280	Ketol-acid reductoisomerase (AHRD V3.3 *** K4CFM5_SOLLC)		F:GO:0004455; P:G(	F:ketol-acid reductc	EC:1.1.1.86	Ketol-acid reductoisc	IPR016206 (PIRSF): IPR013116 (PFA	1236,121	1143,549	1401,204	1313,271	1316,980									
Solyc07g053290	bHLH transcription factor 054		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (SMAF bHLH	7,065	6,195	4,762	4,339	6,601									
Solyc07g053300	ABC transporter family protein (AHRD V3.3 *** B9I1V7_POPTR)	ABCG18	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF	0,019	0,037	0,000	0,000	0,000									
Solyc07g053310	Adaptin ear-binding coat-associated protein 1 (AHRD V3.3 *** A0A151SEN7_CAJCA)		P:GO:0006897; C:G(	P:endocytosis; C:membrane			IPR012466 (PFAM): IPR011993 (G3D	24,635	21,729	28,838	26,948	25,578									
Solyc07g053320	Microtubule-associated protein 70-3 (AHRD V3.3 --* MP703_ARATH)						PTHR34659 (PANTHER): PTHR34659	18,784	17,615	28,242	30,953	29,146									
Solyc07g053330	Protein trichome birefringence (AHRD V3.3 *** A0A199W0G2_ANACO)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	0,076	0,584	0,000	0,000	0,000									
Solyc07g053350	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; F:G(	C:Golgi apparatus; F:O-acetyltransferase activity			IPR025846 (PFAM): IPR026057 (PFA	0,904	1,490	0,620	0,836	0,537									
Solyc07g053360	Late embryogenesis abundant domain-containing family protein (AHRD V3.3 *** B9IQP9_POPTR)						IPR004238 (PFAM): mobidb-lite (MOB	4,337	5,973	4,746	11,471	3,659									
Solyc07g053375	methionine synthase 2 (AHRD V3.3 --* AT3G03780.3)							0,164	0,140	0,318	0,239	0,212									
Solyc07g053380	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XH40_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	1,247	1,193	1,491	1,399	0,729									
Solyc07g053390	LOW QUALITY:AUXIN RESPONSE FACTOR 13 (AHRD V3.3 --* AT1G34170.3)							0,098	0,018	0,000	0,022	0,000									
Solyc07g053410	TCP transcription factor 10	TCP10	P:GO:0009965; P:G(	P:leaf morphogenesis; P:cell differentiation; P:positive regulatio			IPR017887 (PFAM TCP	0,059	0,083	0,000	0,000	0,000									
Solyc07g053420	RING/U-box superfamily protein (AHRD V3.3 *** AT2G42360.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (SMART): IPR001841 (PF	0,223	0,178	0,000	0,022	0,000									
Solyc07g053430	Glucan endo-1,3-beta-glucosidase-like protein 1 (AHRD V3.3 *-* A0A151TPB7_CAJCA)		C:GO:0016020	C:membrane			IPR012946 (SMART): IPR012946 (PF	31,967	33,647	12,963	11,671	11,862									
Solyc07g053440	Tubby-like F-box protein 3 (AHRD V3.3 --* TLP3_ARATH)							21,456	24,097	23,636	22,868	22,096									
Solyc07g053450	BZIP family transcription factor (AHRD V3.3 *** A0A072VB17_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	1,395	0,530	1,000	0,937	0,447									
Solyc07g053470	elongation factor family protein (AHRD V3.3 *** AT2G31060.2)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR005225 (TI(	61,905	58,455	73,938	63,377	62,241									
Solyc07g053480	Rab family GTPase (AHRD V3.3 *** D8RE14_SELML)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00174 (SMAR	26,555	33,050	5,760	5,074	5,264									
Solyc07g053490	Optic atrophy 3 protein (OPA3) (AHRD V3.3 *** A0A061GM20_THECC)		C:GO:0005739; P:G(	C:mitochondrion; P:regulation of lipid metabolic process			IPR010754 (PFAM): IPR010754 (PAN	7,009	6,869	9,424	9,747	9,131									
Solyc07g053495	Cytochrome P450 (AHRD V3.3 *-* A0A061FSW2_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR036396 (G3	0,336	0,323	0,360	0,258	0,164									
Solyc07g053520	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061E036_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,945	2,896	4,376	4,411	3,913									
Solyc07g053525	Glyceraldehyde-3-phosphate dehydrogenase-like family protein (AHRD V3.3 --* AT1G34200.1)							23,449	22,054	18,550	18,826	16,264									
Solyc07g053530	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** A0A072VC68_MEDTR)		C:GO:0005886; P:G(	C:plasma membrane; P:plant-type secondary cell wall biogenesi			IPR000782 (SMART): IPR000782 (PF	0,261	0,402	0,025	0,000	0,000									
Solyc07g053540	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** A0A072VC68_MEDTR)		C:GO:0005886; P:G(	C:plasma membrane; P:response to salt stress; P:response to a			IPR000782 (SMART): IPR000782 (PF	30,098	22,875	0,140	0,239	0,280									
Solyc07g053550	Glutaredoxin, putative (AHRD V3.3 *** A0A061E5A7_THECC)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR011905 (TIGRFAM): IPR002109 (F	9,489	21,866	87,654	127,753	91,213	1,228	0,010					up		
Solyc07g053560	phosphorelay protein (AHRD V3.3 *** AT5G44150.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,494	3,621	5,776	5,036	5,510									
Solyc07g053565	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 --* NU2C_BRANA)							0,000	0,039	0,000	0,022	0,000									
Solyc07g053570	Zinc finger family protein (AHRD V3.3 *** U5FMI7_POPTR)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	1,345	1,533	0,934	0,969	1,278									
Solyc07g053580	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G44170.1)		F:GO:0008168; F:G(	F:methyltransferase activity; F:transferase activity; P:methylatio			PTHR14614:SF7 (PANTHER): PTHR1	30,107	23,987	25,638	18,029	21,121					-0,508	0,005			down
Solyc07g053585	Peptidyl-tRNA hydrolase II (PTH2) family protein (AHRD V3.3 --* AT5G16870.1)							1,691	1,426	1,754	1,125	1,180									
Solyc07g053590	NAC domain-containing protein (AHRD V3.3 *** A0A060A134_BOENI)	NAC066	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,973	0,562	0,000	0,000	0,024									
Solyc07g053600	Receptor-like protein kinase HSL1 (AHRD V3.3 *** HSL1_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (SMART): IPR003591 (SM	10,680	14,596	3,366	3,585	4,855									
Solyc07g053610	Homeodomain-like transcriptional regulator (AHRD V3.3 *** AT5G44180.3)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR018501 (SMAF HB-other	129,912	97,098	94,233	96,282	96,567									
Solyc07g053620	DnaJ like protein (t19-8 gene)	t19d8	C:GO:0005829; F:G(	C:cytosol; F:unfolded protein binding; P:chaperone cofactor-dep			IPR001623 (PRINTS): IPR001623 (SM	30,553	22,931	55,546	51,157	49,641									
Solyc07g053630	Two-component response regulator-like APRR2 (AHRD V3.3 *** A0A151SET7_CAJ	GLK1	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 G2-like	0,889	0,951	0,134	0,121	0,496									
Solyc07g053640	LOW QUALITY:Arabinogalactan-protein (AHRD V3.3 *-* Q41256_NICAL)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,866	5,294	24,957	29,480	16,340									
Solyc07g053650	26S proteasome regulatory subunit (AHRD V3.3 *** I0YWJ7_COCSC)		C:GO:0000502; F:G(	C:proteasome complex; F:enzyme regulator activity; P:regulatio			IPR016643 (PIRSF): PF18051 (PFAM	208,838	200,401	292,326	309,486	283,575									
Solyc07g053660	WD40 repeat-like protein (AHRD V3.3 *** I0Z366_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	38,021	37,175	40,891	40,405	39,288									
Solyc07g053670	nuclear fusion defective 6 (AHRD V3.3 *** AT2G20585.7)						PTHR33156:SF2 (PANTHER): PTHR3	11,619	14,394	16,858	16,171	15,060									
Solyc07g053680	LOW QUALITY:NAC transcription factor (AHRD V3.3 *** B3VK71_TOBAC)	NAC067	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,082	0,036	0,000	0,000	0,000									
Solyc07g053690	Nucleic acid-binding, OB-fold-like protein (AHRD V3.3 *** I3SMP7_MEDTR)						G3DSA:2.40.50.140 (GENE3D): mobic	34,002	32,350	27,232	25,696	26,729									
Solyc07g053700	Reticulon-like protein (AHRD V3.3 *** K4CFR5_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): mobidb-lite (MOB	0,255	0,345	0,000	0,050	0,000									
Solyc07g053710	Tyrosine aminotransferase-like protein (AHRD V3.3 *** A0A0B0P9X3_GOSAR)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR004839 (PFAM): IPR015422 (G3D	34,184	31,471	23,394	20,503	24,533									
Solyc07g053720	S-alkyl-thiohydroximate lyase-like	TAT2	P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR015422 (G3DSA:3.90.1150.GENE	24,936	17,754	4,443	3,764	5,758									
Solyc07g053730	Nucleolar GTP-binding protein 1 (AHRD V3.3 *** K4CFR8_SOLLC)		F:GO:0005525; C:G(	F:GTP binding; C:nucleolus			IPR006073 (PRINTS): IPR012973 (PF	37,226	44,814	27,801	22,465	28,577									
Solyc07g053740	Ethylene Response Factor F.4	ERF.F4	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRINT ERF	254,088	150,372	85,923	219,998	126,271					1,359	0,000			up
Solyc07g053750	Zinc finger transcription factor 50	C3H50	F:GO:0046872	F:metal ion binding			IPR000571 (SMAF C3H	4,589	3,770	0,643	1,558	0,235									
Solyc07g053760	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G28400.1)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	13,715	29,560	5,173	5,028	5,436	1,131	0,017					up		
Solyc07g053790	targeting protein for XKLP2 (AHRD V3.3 *** AT1G03780.2)		C:GO:0005819; C:G(	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027330 (PFAM): IPR027329 (PFA	0,000	0,041	0,025	0,000	0,024									
Solyc07g053800	RING 1A (AHRD V3.3 *** AT5G44280.1)		F:GO:0016874	F:ligase activity			IPR001841 (SMART): IPR013083 (G3	6,192	7,585	6,068	5,930	5,984									
Solyc07g053810	Squamosa promoter binding protein 4		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR036893 (G3DS SBP	0,000	0,000	0,075	0,000	0,023									
Solyc07g053820	Mad3/BUB1 homology region 1 (AHRD V3.3 *** A0A103XTQ9_CYNCS)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR013212 (SM	1,297	1,101	0,236	0,189	0,234									
Solyc07g053830	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 *** ADT1_SOLTU)		C:GO:0005743; F:G(	C:mitochondrial inner membrane; F:transmembrane transporter			IPR002113 (PRINTS): IPR002067 (PF	95,797	84,233	228,745	170,176	186,221					-0,423	0,006			down
Solyc07g053840	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PTR8_ZOSMR)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR001611 (PFA	0,019	0,018	0,050	0,025	0,047									
Solyc07g053850	RING/U-box superfamily protein (AHRD V3.3 *** AT4G28370.4)		F:GO:0008270	F:zinc ion binding			IPR001841 (SMART): IPR011016 (SM	7,540	6,033	8,596	10,756	9,086									
Solyc07g053860	RNA polymerase II subunit 5-mediating-like protein (AHRD V3.3 *** W9QYL8_9ROSA)		P:GO:0000122; F:G(	P:negative regulation of transcription by RNA polymerase II; F:c			IPR009053 (G3DSA:1.10.287.GENE3	6,835	7,453	9,144	8,719	7,968									
Solyc07g053870	Helicase family protein (AHRD V3.3 *** U5FHT2_POPTR)		F:GO:0005524	F:ATP binding			IPR001650 (SMART): IPR014001 (SM	10,901	8,912	12,246	13,716	13,368									
Solyc07g053880	Early nodulin-like protein (AHRD V3.3 *** A0A072VAV5_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	0,155	0,195	0,000	0,000	0,023									
Solyc07g053890	O-acyltransferase WSD1 (AHRD V3.3 *** A0A151TQI5_CAJCA)		F:GO:0004144; P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR004255 (PFAM): IPR009721 (PFA	0,075	0,124	0,198	0,409	0,281									
Solyc07g053900	DUF506 family protein (AHRD V3.3 *** G7JTT3_MEDTR)						IPR006502 (PFAM): IPR006502 (TIGF	0,040	0,136	0,000	0,000	0,000									
Solyc07g053910	Protein kinase superfamily protein (AHRD V3.3 *** AT1G53050.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	68,309	88,802	72,362	78,344	86,470									
Solyc07g053920	Mannan endo-1,4-beta-mannosidase 2 (AHRD V3.3 *** MAN2_ARATH)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	13,061	9,476	4,160	3,928	4,392									
Solyc07g053930	LOW QUALITY:pyrroline-5-carboxylate reductase (AHRD V3.3 *** AT4G03600.1)		C:GO:0016021	C:integral component of membrane			PTHR34656 (PANTHER): PTHR34656	0,577	0,357	0,832	0,466	0,377									
Solyc07g053940	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7IPT2_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR34274 (PANTHER): PTHR34274	0,314	0,310	0,169	0,122	0,047									
Solyc07g053950	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 --* A0A0K1ZCQ4_9ASTE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,911	9,710	7,624	5,492	6,830									
Solyc07g053960	Ubiquitin conjugating enzyme, putative (AHRD V3.3 *** B9RVZ2_RICCO)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin conjugating enzyme activity			SM00212 (SMART): IPR016135 (G3D	23,927	20,954	31,128	31,175	30,009									
Solyc07g053970	Two pore calcium channel protein 1 (AHRD V3.3 *** TPC1_ARATH)		F:GO:0005245; F:G(	F:voltage-gated calcium channel activity; F:calcium ion binding;			IPR002048 (SMART): IPR005821 (PF	27,564	26,260	2,811	3,758	3,786									
Solyc07g053980	Callose synthase-like protein (AHRD V3.3 *** G7JSU8_MEDTR)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan synth	IPR026899 (SMART): IPR003440 (PF	62,357	109,332	14,248	14,076	16,694	0,835	0,005					up		
Solyc07g053990	Structural constituent of cell wall, putative (AHRD V3.3 *** B9RVZ9_RICCO)						IPR010820 (PFAM): mobidb-lite (MOB	50,699	55,129	54,244	50,745	54,259									
Solyc07g054000	cyclin delta-3 (AHRD V3.3 --* AT2G23370.1)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,385	0,220	2,952	2,606	2,648									
Solyc07g054010	LOW QUALITY:Elongation factor 1-alpha (AHRD V3.3 --* M8C3H7_AEGTA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc07g054020	LOW QUALITY:B-block-binding subunit of TFIIIC protein (AHRD V3.3 --* AT1G59453.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,147	0,000	0,141									
Solyc07g054030	LOW QUALITY:oxidoreductase/transition metal ion-binding protein (AHRD V3.3 --* AT3G51940.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,096	0,124	0,117									
Solyc07g054040	protein kinase family protein (AHRD V3.3 --* AT4G12020.4)							0,000	0,039	0,119	0,189	0,143									
Solyc07g054050	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G22690.4)							0,256	0,196	1,585	2,352	1,915									
Solyc07g054060	Phospho-N-acetylmuramoyl-pentapeptide-transferase, putative (AHRD V3.3 *-* A0A061EAV9_THECC)						PTHR34683 (PANTHER): PTHR34683	10,456	8,859	165,853	223,300	145,136									
Solyc07g054070	DTW domain-containing family protein (AHRD V3.3 *** U5FYC3_POPTR)						IPR005636 (SMART): IPR005636 (PF	2,227	1,847	15,934	7,439	10,937					-1,091	0,000			down
Solyc07g054080	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G19310.1)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR018957 (PF	31,653	43,189	24,521	15,105	21,181					-0,695	0,000			down
Solyc07g054090	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RW07_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	14,106	13,965	13,859	15,053	13,871									
Solyc07g054100	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RW07_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	5,121	5,689	3,984	2,948	3,418									
Solyc07g054110	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9RW07_RICCO)						PTHR24015:SF644 (PANTHER): PTHF	0,697	0,827	0,716	0,577	0,753									
Solyc07g054115	Malate dehydrogenase [NADP], chloroplastic (AHRD V3.3 --* MDHP_MAIZE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,041	0,000	0,000	0,000									
Solyc07g054120	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS): SM00365 (SMAR	0,139	0,399	0,000	0,000	0,023									
Solyc07g054130	mitochondrial ribosomal protein S7 (AHRD V3.3 --* ATMG01270.1)							0,122	0,418	0,050	0,000	0,117									
Solyc07g054140	Syntaxin, putative (AHRD V3.3 *** B9SLK9_RICCO)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART): G3DSA:1.20.58	0,240	0,186	0,000	0,025	0,046									
Solyc07g054145	CAAX amino terminal protease family protein (AHRD V3.3 *** AT2G20725.1)		C:GO:0016020	C:membrane			IPR003675 (PFAM): PTHR43592 (PAN	24,117	5,816	7,377	16,896	10,723	-2,026	0,000			1,192	0,000	down		up
Solyc07g054160	Tetraspanin family protein (AHRD V3.3 *** AT2G20740.1)		C:GO:0016021	C:integral component of membrane			IPR018499 (PFAM): PTHR19282:SF1	27,012	21,296	34,879	36,538	34,145									
Solyc07g054170	expansin B3 (AHRD V3.3 *** AT4G28250.1)	EXPB1	C:GO:0005576; P:G(	C:extracellular region; P:sexual reproduction			IPR005795 (PRINTS): IPR007118 (PF	1,390	1,565	0,047	0,000	0,023									
Solyc07g054180	Clathrin light chain protein (AHRD V3.3 *** AT2G20760.1)		F:GO:0005198; P:G(	F:structural molecule activity; P:intracellular protein transport; P			IPR000996 (PFAM): mobidb-lite (MOB	0,399	0,610	0,025	0,000	0,000									
Solyc07g054190	Riboflavin synthase alpha chain (AHRD V3.3 *** A0A0B0N493_GOSAR)		F:GO:0004746; P:G(	F:riboflavin synthas	EC:2.5.1.9	Riboflavin synthase	IPR001783 (TIGRFAM): IPR026017 (F	23,544	21,945	46,308	39,838	42,180									
Solyc07g054200	pre-mRNA splicing factor-like protein (AHRD V3.3 *** AT4G03430.3)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:protein binding; C:nucleus			IPR003107 (SMART): IPR019734 (SM	44,453	58,033	57,633	52,281	54,024									
Solyc07g054210	light dependent NADH:protochlorophyllide oxidoreductase 2	POR2	F:GO:0016630; P:G(	F:protochlorophyllid	EC:1.3.1.33	Protochlorophyllide r	IPR002347 (PRINTS): G3DSA:3.40.50	98,410	134,159	181,561	171,692	246,295			0,437	0,012				up	
Solyc07g054220	Ethylene-responsive transcription factor ERF053 (AHRD V3.3 *** A0A0B2RF70_GLYSO)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRINT ERF	12,712	9,961	5,850	7,796	5,699									
Solyc07g054230	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061E4V2_THECC)		P:GO:0015031	P:protein transport			G3DSA:1.20.1260.60 (GENE3D): IPR(	0,000	0,039	0,000	0,000	0,024									
Solyc07g054237	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT1G65690.1)		C:GO:0016020	C:membrane			PTHR31852:SF35 (PANTHER): PTHR	0,000	0,124	0,000	0,022	0,000									
Solyc07g054250	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT1G54540.1)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	0,037	0,000	0,000	0,000	0,000									
Solyc07g054260	Sulfate transport ATP-binding protein (AHRD V3.3 --* A0A0S3QP22_TAKLE)							0,454	0,732	0,000	0,145	0,095									
Solyc07g054270	Plant/F9H3-4 protein (AHRD V3.3 *** A0A072VLR0_MEDTR)						IPR008507 (PFAM): PTHR31343:SF3	43,063	31,676	20,718	20,819	23,274									
Solyc07g054280	Tyrosine decarboxylase (AHRD V3.3 *** Q000T5_ARICO)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:carboxy-lyase activit			IPR010977 (PRINTS): IPR015422 (G3	0,184	0,147	0,025	0,022	0,023									
Solyc07g054290	photosystem II family protein (AHRD V3.3 *** AT1G03600.1)		P:GO:0010207	P:photosystem II assembly			IPR025585 (PFAM): IPR038450 (G3D	22,949	51,815	30,412	38,227	55,998	1,202	0,000	0,879	0,000			up	up	
Solyc07g054300	Phosphatase 2C family protein (AHRD V3.3 *** U5FGH9_POPTR)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	11,032	10,214	12,652	12,008	12,602									
Solyc07g054310	Cell wall protein (AHRD V3.3 *** I6QN83_HELAN)		C:GO:0016021	C:integral component of membrane			IPR034565 (PANTHER)	71,260	73,901	0,072	0,097	0,141									
Solyc07g054315	Tuliposide A-converting enzyme 1, chloroplastic (AHRD V3.3 --* TCEA1_TULGE)							1,241	1,444	1,324	1,175	1,057									
Solyc07g054320	Organic solute transporter ostalpha protein (AHRD V3.3 *** G7J9A4_MEDTR)		P:GO:0009626	P:plant-type hypersensitive response			IPR005178 (PFAM): mobidb-lite (MOB	39,747	30,321	67,299	60,431	58,516									
Solyc07g054330	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR006566 (SMART): IPR001810 (PF	4,107	4,632	4,358	4,472	5,644									
Solyc07g054340	LOW QUALITY:RNI-like superfamily protein (AHRD V3.3 --* AT3G18150.1)							2,953	2,675	2,569	2,808	2,775									
Solyc07g054350	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 --* NU4C_PSINU)							0,075	0,000	0,025	0,025	0,023									
Solyc07g054370	F-box family protein (AHRD V3.3 *** T1RU12_SILVU)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR006566 (PFA	5,908	4,798	4,863	5,193	5,255									
Solyc07g054390	LOW QUALITY:QWRF motif protein (DUF566) (AHRD V3.3 *** AT2G20815.1)		C:GO:0044424	C:intracellular part			IPR007573 (PFAM): mobidb-lite (MOB	0,080	0,060	0,025	0,051	0,023									
Solyc07g054400	Centromere protein S (AHRD V3.3 *-* W9S2H7_9ROSA)		F:GO:0046982; C:G(	F:protein heterodimerization activity; C:FANCM-MHF complex			IPR009072 (G3DSA:1.10.20.GENE3D	2,555	2,415	1,373	0,918	1,132									
Solyc07g054410	LOW QUALITY:Micronuclear linker histone polyprotein-like protein (AHRD V3.3 *** A0A061E2Z9_THECC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,138	0,116	0,025	0,072	0,072									
Solyc07g054420	Formiminotransferase-cyclodeaminase, putative (AHRD V3.3 *** B9RW60_RICCO)		F:GO:0005542; F:G(	F:folic acid binding; F:transferase activity			IPR012886 (SMART): IPR013802 (SM	1,937	2,184	2,408	2,193	2,376									
Solyc07g054430	Glutamate formiminotransferase 1 (AHRD V3.3 *** B4F7V5_MAIZE)		F:GO:0005542; F:G(	F:folic acid binding; F:transferase activity			IPR012886 (SMART): IPR037064 (G3	1,440	2,360	0,352	0,630	0,731									
Solyc07g054440	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase-like protein (AHRD V3.3 *** Q9LR71_ARATH)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297 (PAN	20,401	17,818	46,298	45,733	36,946									
Solyc07g054450	Ultrapetala (AHRD V3.3 *** A0A0D4D604_CROSA)		F:GO:0003677	F:DNA binding			IPR000770 (PFAM): IPR020533 (PAN	36,250	26,727	173,217	148,671	142,092									
Solyc07g054460	H/ACA ribonucleoprotein complex non-core subunit NAF1 (AHRD V3.3 *-* W9R7R8_9ROSA)		P:GO:0000493; P:G(	P:box H/ACA snoRNP assembly; P:pseudouridine synthesis; F:I			IPR007504 (PFAM): IPR038664 (G3D	22,065	23,835	16,997	13,634	14,061									
Solyc07g054470	methionyl-tRNA synthetase (AHRD V3.3 -** AT5G10695.1)						PTHR33320:SF5 (PANTHER): PTHR3	0,922	0,802	1,363	1,284	1,035									
Solyc07g054480	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JXH0_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	11,498	10,877	10,223	9,730	10,331									
Solyc07g054490	Secretory carrier membrane family protein (AHRD V3.3 *** B9N299_POPTR)		P:GO:0015031; C:G(	P:protein transport; C:integral component of membrane			IPR007273 (PFAM): mobidb-lite (MOB	36,167	34,943	14,991	13,252	14,784									
Solyc07g054500	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGQ2_ARATH)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	11,830	17,301	2,721	2,684	3,909									
Solyc07g054540	Lipoyl synthase (AHRD V3.3 *** W9RNC4_9ROSA)		C:GO:0005739; P:G(	C:mitochondrion; P:	EC:2.8.1.8	Lipoyl synthase	IPR006638 (SMART): IPR003698 (PIF	37,459	35,325	74,552	76,313	69,613									
Solyc07g054550	LOW QUALITY:3-ketoacyl-CoA synthase 10 (AHRD V3.3 --* AT2G26250.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc07g054560	LOW QUALITY:CK25 (AHRD V3.3 *** Q1W1G0_TOBAC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,551	5,754	0,065	0,000	0,047									
Solyc07g054580	Indole-3-acetic acid-amido synthetase GH3.5, putative (AHRD V3.3 *** B9RW45_RICCO)						IPR004993 (PFAM): PTHR31901:SF1(	0,080	0,018	0,000	0,000	0,000									

Solyc07g054600	F-box family protein (AHRD V3.3 *-* T1RU12_SILVU)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR032675 (G3	2,717	3,058	1,899	3,092	2,005									
Solyc07g054610	F-box/RNI-like superfamily protein (AHRD V3.3 *-* AT3G58860.1)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	2,511	1,944	1,857	2,057	1,813									
Solyc07g054620	F-box/RNI-like superfamily protein (AHRD V3.3 *** A0A061E967_THECC)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR032675 (G3	4,651	4,760	5,448	6,356	5,459									
Solyc07g054630	B3 domain-containing transcription factor VRN1 (AHRD V3.3 *** A0A0B0PU79_GOSAR)		F:GO:0003677	F:DNA binding	IPR003340 (SMAF B3	7,058	7,060	9,626	11,020	10,561									
Solyc07g054660	LOW QUALITY:homeodomain GLABROUS 2 (AHRD V3.3 --* AT1G05230.9)					0,000	0,021	0,000	0,000	0,000									
Solyc07g054670	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial (AHRD V3.3 *** NDB2_ARATH)		F:GO:0005509: F:G(	F:calcium ion binding; F:oxidoreductase activity; P:oxidation-re(	IPR023753 (PFAM): G3DSA:3.50.50.1	5,789	8,519	3,861	5,879	5,616									
Solyc07g054680	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T4W4_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	0,744	0,733	0,760	0,980	0,894									
Solyc07g054690	LOW QUALITY:BnaA01g17000D protein (AHRD V3.3 *** A0A078DPQ5_BRANA)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,178	0,350	0,000	0,000	0,024									
Solyc07g054710	LOW QUALITY:Peptidoglycan-binding lysin domain-containing protein (AHRD V3.3 *** A0A103XTI0_CYNCS		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	IPR036779 (G3DSA:3.10.350.GENE3I	0,042	0,018	0,047	0,000	0,000									
Solyc07g054730	LOW QUALITY:Wound-responsive family protein, putative (AHRD V3.3 *** A0A061E4N2_THECC)				IPR022251 (PFAM): IPR022251 (PAN	60,140	71,731	64,598	54,232	59,306									
Solyc07g054740	Vesicle-associated 4-2-like protein (AHRD V3.3 *** A0A0B0MUH3_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane	IPR000535 (PFAM): IPR013783 (G3D	7,916	5,319	1,511	1,204	1,483									
Solyc07g054745	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)				IPR022251 (PFAM): mobidb-lite (MOB	0,463	0,073	0,000	0,000	0,023									
Solyc07g054750	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)				IPR022251 (PFAM): IPR022251 (PAN	0,019	0,019	0,301	0,000	0,190									
Solyc07g054760	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G10265.1)				IPR022251 (PFAM): IPR022251 (PAN	39,914	25,637	82,809	53,986	39,257			-1,079	0,000	-0,613	0,000		down	down
Solyc07g054770	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)				IPR022251 (PFAM): IPR022251 (PAN	20,850	14,538	38,499	33,365	26,236			-0,555	0,042				down	
Solyc07g054780	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G10265.1)				IPR022251 (PFAM): IPR022251 (PAN	75,902	62,484	109,620	91,285	73,463			-0,580	0,015				down	
Solyc07g054790	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)				IPR022251 (PFAM): PTHR33090:SF8	6,584	7,011	10,189	7,354	10,899									
Solyc07g054800	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G10265.1)				IPR022251 (PFAM): PTHR33090:SF8	0,585	0,297	0,319	0,191	0,425									
Solyc07g054810	LOW QUALITY:glutamate-1-semialdehyde 2,1-aminomutase 2 (AHRD V3.3 --* AT3(GSA-AM				mobidb-lite (MOBIDB_LITE): mobidb-lit	2,176	1,423	0,881	0,591	0,990									
Solyc07g054820	Protein THYLAKOID FORMATION1, chloroplastic (AHRD V3.3 *** THF1_SOLTU)		P:GO:0010207	P:photosystem II assembly	IPR017499 (PFAM): IPR017499 (PAN	30,134	39,176	39,029	44,201	63,491			0,699	0,000				up	
Solyc07g054830	diacylglycerol kinase	dgk1	F:GO:0003951: F:G(	F:NAD+ kinase acti EC:2.7.1.23: EC:2.7. NAD(+) kinase: Diac	IPR001206 (SMART): IPR000756 (SM	27,422	63,918	25,501	26,681	31,750	1,243	0,037					up		
Solyc07g054840	R2R3MYB transcription factor 41	R2R3MYB41	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,000	0,039	0,000	0,000	0,000									
Solyc07g054850	transmembrane protein (AHRD V3.3 *** AT4G28100.1)		C:GO:0016021: C:G(	C:integral component of membrane; C:anchored component of r	IPR040376 (PANTHER): PTHR34056:	14,165	11,512	9,852	6,868	8,832									
Solyc07g054860	Tyrosine decarboxylase (AHRD V3.3 *** Q000T5_ARICO)		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:carboxy-lyase activit	IPR010977 (PRINTS): IPR002129 (PF	54,073	46,561	4,449	0,938	1,722			-1,371	0,022	-2,234	0,004		down	down
Solyc07g054870	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G36690.2)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3I	0,000	0,036	0,022	0,000	0,000									
Solyc07g054880	methylketone synthase Ie		P:GO:0009694: P:G(	P:jasmonic acid me EC:3.1.1.1 Carboxylesterase	IPR029058 (G3DSA:3.40.50.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc07g054920	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G44800.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR027443 (G3D	10,874	6,703	0,000	0,025	0,023									
Solyc07g054930	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G44800.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR026992 (PFAM): IPR005123 (PFA	1,566	0,772	0,000	0,050	0,000									
Solyc07g054940	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G44800.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3I	6,637	4,552	0,000	0,000	0,000									
Solyc07g054950	cyclinD6_1	CycD6_1	C:GO:0005634: P:G(	C:nucleus; P:regulation of cell cycle	IPR004367 (SMART): IPR013763 (SM	0,019	0,000	0,000	0,000	0,000									
Solyc07g055000	R2R3MYB transcription factor 72	R2R3MYB72	F:GO:0003677	F:DNA binding	IPR001005 (SMAF MYB	0,000	0,210	0,000	0,000	0,023									
Solyc07g055010	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061GX23_THECC)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding	IPR006121 (PFAM): G3DSA:3.30.70.1	0,690	1,559	0,050	0,000	0,047									
Solyc07g055020	F-box protein family (AHRD V3.3 *** A0A151SU61_CAJCA)		F:GO:0005515	F:protein binding	IPR001810 (SMART): IPR006527 (PF.	20,433	14,572	14,856	14,235	14,451									
Solyc07g055025	Mitochondrial 37S ribosomal protein S27 (AHRD V3.3 -** A0A0B2P5W5_GLYSO)		C:GO:0005840	C:ribosome		0,624	0,415	0,330	0,361	0,304									
Solyc07g055030	Mitochondrial 37S ribosomal protein S27 (AHRD V3.3 *** A0A0B2P5W5_GLYSO)		C:GO:0005840	C:ribosome	IPR013219 (PFAM): mobidb-lite (MOB	0,059	0,121	0,044	0,025	0,024									
Solyc07g055040	LOW QUALITY:Agenet-like domain-containing protein (AHRD V3.3 *** A0A103YGJ9_CYNCS)				IPR014002 (SMART): IPR008395 (PF.	1,042	0,920	1,787	1,720	1,321									
Solyc07g055050	ATP synthase protein I-like protein (AHRD V3.3 *** AT2G31040.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	39,375	52,777	22,778	19,445	36,996			0,695	0,019				up	
Solyc07g055060	Phosphoenolpyruvate carboxylase (AHRD V3.3 *** CAPP_PICAB)		P:GO:0006099: F:G(	P:tricarboxylic acid EC:4.1.1.31: EC:4.1. Phosphoenolpyruvate	IPR021135 (PRINTS): IPR021135 (PF	184,768	173,829	400,442	390,071	365,069									
Solyc07g055065	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *-* AT2G42610.2)		C:GO:0005634: P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus	IPR006936 (PFAM): mobidb-lite (MOB	44,965	26,480	10,323	7,477	7,960	-0,734	0,031					down		
Solyc07g055080	Proteasome subunit alpha type (AHRD V3.3 *** K4CG47_SOLLC)		F:GO:0004298: P:G(	F:threonine-type en EC:3.4.25 Acting on peptide bor	IPR000426 (SMART): IPR001353 (PF.	10,743	13,064	30,795	36,284	26,294									
Solyc07g055090	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** V5PZR5_9CARY)		F:GO:0003677: F:G(	F:DNA binding; F:zinc ion binding	IPR000058 (SMART): IPR002653 (SM	0,061	0,000	0,000	0,000	0,000									
Solyc07g055100	Transcription factor, putative (AHRD V3.3 *-* B9S9B5_RICCO)		F:GO:0003677	F:DNA binding	PF13837 (PFAM): Trihelix	6,842	5,824	0,432	0,315	0,723									
Solyc07g055110	Protein PATRONUS 1 (AHRD V3.3 *** PANS1_ARATH)		P:GO:0007346	P:regulation of mitotic cell cycle	mobidb-lite (MOBIDB_LITE): IPR0393:	0,098	0,019	0,000	0,025	0,023									
Solyc07g055120	F-box protein (AHRD V3.3 *** T1RVG4_STRHE)		F:GO:0005515	F:protein binding	IPR006553 (SMART): IPR032675 (G3	0,061	0,169	0,150	0,100	0,165									
Solyc07g055130	MAP kinase kinase kinase 57	MAPKKK57	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	20,145	17,403	11,306	9,584	12,830									
Solyc07g055140	DUF688 family protein (AHRD V3.3 *** G7JCM3_MEDTR)				IPR007789 (PFAM): mobidb-lite (MOB	10,466	8,628	17,221	16,960	16,978									
Solyc07g055145	folic acid binding / transferase (AHRD V3.3 --* AT2G20830.6)				mobidb-lite (MOBIDB_LITE)	0,101	0,105	0,221	0,355	0,306									
Solyc07g055150	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A151RTN6_CAJCA)		F:GO:0016702: P:G(	F:oxidoreductase a EC:1.13.11 Acting on single donc	IPR012864 (PFAM): PTHR22966:SF3(	0,141	0,041	0,258	0,476	0,188									
Solyc07g055160	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G42690.1)		P:GO:0006629: F:G(	P:lipid metabolic prc EC:1.13.11; EC:3.1. Acting on single donc	IPR012864 (PFAM): G3DSA:3.40.50.1	21,493	22,786	2,539	2,799	3,156									
Solyc07g055170	DNA repair Rad51-like protein (AHRD V3.3 *** A0A072V7S1_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:A EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	PR01874 (PRINTS): IPR016467 (PIRS	1,233	1,504	1,118	0,903	1,038									
Solyc07g055180	Protein kinase family protein (AHRD V3.3 *** F4J5Y7_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	4,942	5,992	0,676	0,627	0,986									
Solyc07g055190	Peroxidase (AHRD V3.3 *** K4CG58_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	5,170	2,183	2,022	3,161	1,882	-1,213	0,015					down		
Solyc07g055200	SISK	SK	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	68,867	52,832	45,196	37,627	43,895									
Solyc07g055210	Aspartate aminotransferase (AHRD V3.3 *** K4CG60_SOLLC)		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:transaminase activit	IPR000796 (PRINTS): IPR015422 (G3	138,775	154,233	227,908	204,021	202,475									
Solyc07g055215	RING/FYVE/PHD zinc finger superfamily protein, putative (AHRD V3.3 *-* A0A061GDI8_THECC)		F:GO:0008270	F:zinc ion binding	IPR011016 (SMART): IPR013083 (G3	0,850	0,923	0,744	1,058	0,827									
Solyc07g055217	Transcription factor ILI2 (AHRD V3.3 --* ILI2_ORYSI)					0,000	0,018	0,025	0,025	0,000									
Solyc07g055220	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T3G5_RICCO)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	2,915	1,968	2,075	2,325	2,214									
Solyc07g055230	homeodomain GLABROUS 7 (AHRD V3.3 --* AT5G52170.3)				mobidb-lite (MOBIDB_LITE)	42,041	42,664	35,541	31,926	35,013									
Solyc07g055235	Ovate transcriptional repressor (AHRD V3.3 --* G7JKF5_MEDTR)		P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR038933 (PANTHER): PTHR33057:	0,059	0,043	0,025	0,000	0,047									
Solyc07g055250	peptidoglycan-binding LysM domain-containing protein (AHRD V3.3 --* AT5G08200.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	IPR018392 (SMART): IPR018392 (PF.	41,151	45,393	19,597	20,293	19,596									
Solyc07g055260	DnaJ (AHRD V3.3 *** A0A126DIH0_ARAHY)		F:GO:0005506: F:G(	F:iron ion binding; F:electron transfer activity; P:electron transp	IPR001623 (PRINTS): IPR001623 (SM	19,720	18,413	21,972	22,575	30,949			0,490	0,003				up	
Solyc07g055270	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** G7IM74_MEDTR)				IPR012881 (PFAM): PTHR31865:SF7	1,510	2,900	0,793	0,835	0,473									
Solyc07g055280	WRKY transcription factor 78	WRKY78	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (SMAF WRKY	1,678	2,087	1,792	1,634	1,761									
Solyc07g055290	LES245570 Rab11 GTPase	rab11a	F:GO:0003924: F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00176 (SMAR	18,325	18,446	21,249	24,494	21,353									
Solyc07g055300	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S8D6_RICCO)		F:GO:0003824: P:G(	F:catalytic activity; P:trehalose biosynthetic process	IPR003337 (TIGRFAM): G3DSA:3.40.!	31,612	27,093	40,187	41,360	36,304									
Solyc07g055310	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061E4M2_THECC)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	5,158	5,918	7,941	7,352	7,045									
Solyc07g055320	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** A0A072UQU8_MEDTR)		F:GO:0004222: F:G(	F:metalloendopeptic EC:3.4.24 Acting on peptide bor	IPR003593 (SMART): G3DSA:1.20.58	216,724	319,882	439,326	431,449	577,478	0,588	0,023	0,392	0,013			up	up	
Solyc07g055330	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061ECA4_THECC)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm; P:ubiquitin-dependent protein catabolic	IPR001841 (SMART): IPR001841 (PF.	8,234	5,327	3,025	2,691	2,498									
Solyc07g055340	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT2G42770.1)		C:GO:0016021	C:integral component of membrane	IPR007248 (PFAM): mobidb-lite (MOB	14,784	16,611	41,686	43,721	41,696									
Solyc07g055400	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BT35_SOLPN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): PIRSF000654 (	0,000	0,021	0,000	0,000	0,000									
Solyc07g055410	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BT35_SOLPN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): G3DSA:3.30.200	0,000	0,000	0,000	0,000	0,023									
Solyc07g055420	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BTD1_SOLPN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:1.10.51	0,037	0,000	0,000	0,000	0,000									
Solyc07g055440	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	0,270	0,780	0,533	0,022	0,400									
Solyc07g055460	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	0,674	3,921	0,469	0,000	1,434	2,537	0,000					up		
Solyc07g055470	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	5,936	11,023	3,045	7,179	7,161	0,919	0,049			1,241	0,001	up		up
Solyc07g055480	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,248	0,750	0,000	0,000	0,046									
Solyc07g055490	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	4,154	2,437	1,504	1,259	2,065									
Solyc07g055495	Cytochrome P450 family protein (AHRD V3.3 *-* U5FW61_POPTR)		F:GO:0004497: F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase	IPR002403 (PRINTS): IPR036396 (G3	0,098	0,620	0,047	0,075	0,072									
Solyc07g055530	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	9,314	11,132	7,654	6,636	7,531									
Solyc07g055540	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	16,305	22,114	13,342	13,890	16,809									
Solyc07g055550	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc07g055560	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0004672: F:G(	F:protein kinase activity; F:iron ion binding; F:ATP binding; P:pr(	IPR001128 (PRINTS): IPR002401 (PF	0,058	0,258	0,734	1,790	2,043			1,448	0,029	1,269	0,031		up	up
Solyc07g055570	Serine/threonine-protein kinase (AHRD V3.3 *-* M1BGA7_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:1.10.510.	0,038	0,152	0,025	0,025	0,023									
Solyc07g055610	Disease resistance protein (TIR-NBS-LRR class), putative (AHRD V3.3 *** G7IQ97_MEDTR)		F:GO:0005515: P:G(	F:protein binding; P:signal transduction; F:ADP binding	PR00364 (PRINTS): IPR000157 (SMA	0,000	0,000	0,000	0,022	0,000									
Solyc07g055625	Disease resistance protein N-like protein (AHRD V3.3 --* A0A0H4BN04_NICAL)		P:GO:0007165: F:G(	P:signal transduction; F:ADP binding		0,021	0,000	0,000	0,000	0,000									
Solyc07g055630	Serine/threonine-protein kinase (AHRD V3.3 *-* M1BGA2_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): G3DSA:3.30.20	0,349	0,644	0,094	0,359	0,306									
Solyc07g055640	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BTD1_SOLPN)		F:GO:0004674: F:G(	F:protein serine/thr EC:2.7.11 Transferring phosphc	IPR001480 (SMART): IPR000719 (SM	9,991	14,695	11,216	15,842	16,836									
Solyc07g055650	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BTD1_SOLPN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): PIRSF000615 (	3,112	3,601	4,872	5,959	5,247									
Solyc07g055660	Glycine-rich protein, putative (AHRD V3.3 *** A0A061EWE7_THECC)		F:GO:0004386	F:helicase activity EC:3.6.1.15 Nucleoside-triphosph	PTHR36751 (PANTHER)	18,939	12,931	47,612	41,453	37,856									
Solyc07g055670	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BTY2_SOLPN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (SMART): PIRSF000654 (	6,740	16,303	0,617	0,685	1,157	1,296	0,033					up		
Solyc07g055690	Serine/threonine-protein kinase (AHRD V3.3 *** G4XXY5_NICAT)		P:GO:0048544	P:recognition of pollen	IPR001480 (SMART): IPR036426 (G3	0,830	1,747	0,194	0,258	0,630									
Solyc07g055695	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT1G06470.4)		C:GO:0005793: C:G(	C:endoplasmic reticulum-Golgi intermediate compartment; C:cis	IPR004853 (PFAM): PTHR44827 (PAN	19,085	15,921	11,652	13,512	12,337									
Solyc07g055710	SolycHsfA4b	HSF-21	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	2,378	6,990	1,119	1,219	1,146									
Solyc07g055720	Heat shock protein, putative (AHRD V3.3 *** Q8LD91_ARATH)	Hsp26.5			IPR008978 (G3DSA:2.60.40.GENE3D	2,616	4,838	0,476	0,382	1,357									
Solyc07g055730	Trichome birefringence-like protein (AHRD V3.3 *** G7JPR2_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR026057 (PFAM): IPR025846 (PFA	0,037	0,095	0,000	0,000	0,000									
Solyc07g055750	Strictosidine synthase-like protein (AHRD V3.3 *** A7WPL3_TOBAC)		P:GO:0009058: F:G(	P:biosynthetic proc EC:4.3.3.2 Strictosidine synthas	IPR011042 (G3DSA:2.120.10.GENE3I	0,000	0,000	0,000	0,000	0,023									
Solyc07g055760	Zinc finger CCCH domain-containing protein 36 (AHRD V3.3 --* C3H36_ORYSJ)					1,240	1,401	1,953	1,530	1,724									
Solyc07g055770	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	2,587	2,667	2,925	3,043	2,872									
Solyc07g055780	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794: F:G(	C:Golgi apparatus; F:O-acetyltransferase activity	IPR026057 (PFAM): IPR025846 (PFA	0,079	0,041	0,000	0,000	0,000									
Solyc07g055790	Trichome birefringence-like protein (AHRD V3.3 *** G7JPR2_MEDTR)		C:GO:0005794: F:G(	C:Golgi apparatus; F:O-acetyltransferase activity	IPR025846 (PFAM): IPR026057 (PFA	0,529	0,636	0,025	0,050	0,000									
Solyc07g055800	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR026057 (PFAM): IPR025846 (PFA	0,000	0,000	0,051	0,117	0,024									
Solyc07g055810	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (SMART): G3DSA:3.30.20	3,418	16,615	0,433	0,385	0,468	2,312	0,000					up		
Solyc07g055820	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.2		F:GO:0005515	F:protein binding	IPR001611 (PFAM): IPR032675 (G3D	0,098	0,082	0,071	0,468	0,047									
Solyc07g055830	Elongin-A (AHRD V3.3 *** A0A0B0MEQ4_GOSAR)		P:GO:0006357: C:G(	P:regulation of transcription by RNA polymerase II; C:elongin co	IPR010684 (PFAM): mobidb-lite (MOB	39,417	45,804	42,887	35,903	40,626									
Solyc07g055840	Citrate synthase (AHRD V3.3 *** K4CGB7_SOLLC)		F:GO:0046912	F:transferase activity, transferring acyl groups, acyl groups con	IPR002020 (PRINTS): IPR016142 (G3	6,550	7,992	15,237	14,647	16,282									
Solyc07g055850	Ubiquinone biosynthesis O-methyltransferase, mitochondrial (AHRD V3.3 *** K4CGB8_SOLLC)		P:GO:0006744: F:G(	P:ubiquinone biosynthetic process; F:2-polyprenyl-6-methoxy-1.	IPR010233 (TIGRFAM): PF13489 (PF	11,685	11,548	8,435	8,244	9,616									
Solyc07g055860	type 5 protein serine/threonine phosphatase 62 kDa isoform	pp5	F:GO:0004721: F:G(	F:phosphoprotein pl EC:3.1.3.16 Protein-serine/threor	IPR006186 (PRINTS): IPR019734 (SM	92,215	82,489	131,427	131,448	130,533									
Solyc07g055870	MAP kinase kinase kinase 58	MAPKKK58	F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR002110 (SMART): IPR020683 (PF.	5,522	5,450	3,658	4,784	4,419									
Solyc07g055890	LOW QUALITY:tRNA (met) cytidine acetyltransferase, putative (DUF616) (AHRD V3.3 --* AT1G53040.6)					0,000	0,018	0,000	0,000	0,000									
Solyc07g055900	LOW QUALITY:ATP-dependent DNA helicase (AHRD V3.3 *** K4CGC3_SOLLC)		P:GO:0000723: F:G(	P:telomere mainten EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	2,346	2,173	1,558	1,498	2,029									
Solyc07g055910	Embryonic flower 1 (AHRD V3.3 *-* A0A087GD72_ARAAL)				mobidb-lite (MOBIDB_LITE): mobidb-lit	17,277	21,423	8,007	9,929	12,623			0,656	0,009				up	
Solyc07g055920	Tomato AGAMOUS-like 1	TAGL1	F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRIN MIKC_MADS	171,858	143,648	333,459	325,284	290,201									
Solyc07g055930	Hexosyltransferase (AHRD V3.3 *** K4CGC6_SOLLC)	GAUT15	F:GO:0047262	F:polygalacturonate EC:2.4.1.43 Polygalacturonate 4-	IPR029044 (G3DSA:3.90.550.GENE3I	67,862	64,578	116,976	160,842	154,161					0,462	0,003			up
Solyc07g055940	secretion-regulating guanine nucleotide exchange factor (AHRD V3.3 *-* AT3G58800.1)		C:GO:0016021	C:integral component of membrane	PTHR35128 (PANTHER)	3,201	3,027	5,740	6,349	5,677									
Solyc07g055950	Protodermal factor 1.1 (AHRD V3.3 *** F2YRC9_GOSHI)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,677	0,975	0,022	0,143	0,093									
Solyc07g055960	Unknown protein (AHRD V3.3)					0,019	0,021	0,000	0,048	0,000									
Solyc07g055970	LOW QUALITY:Cytochrome P450 family protein (AHRD V3.3 *** B9GT44_POPTR)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,000	0,039	0,000	0,022	0,000									
Solyc07g055980	Haloacid dehalogenase superfamily protein (AHRD V3.3 *** I7AYD7_PHAVU)		P:GO:0016311: F:G(	P:dephosphorylation; F:phosphatase activity	IPR027706 (PFAM): IPR010021 (TIGF	11,852	14,916	24,745	20,661	20,205									
Solyc07g055990	Xyloglucan endotransglucosylase/hydrolase 7 (AHRD V1 **** C0IRG6_ACTDE)		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR008264 (PRINTS): G3DSA:2.60.12	16,423	15,540	3,719	7,477	5,145					1,001	0,028			up
Solyc07g056000	xyloglycan endo-transglycosylase		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR008264 (PRINTS): IPR000757 (PF	265,833	53,290	23,717	76,578	54,649	-2,295	0,000	1,199	0,002	1,690	0,000	down	up	up
Solyc07g056010	conserved oligomeric Golgi complex subunit 4 (AHRD V3.3 *** AT4G01395.1)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:Golgi vesicle transport	IPR013167 (SMART): G3DSA:1.20.58	95,203	96,893	108,742	96,387	93,616									
Solyc07g056020	Translation initiation factor IF-2 (AHRD V3.3 *** W9QCR7_9ROSA)		F:GO:0003743: F:G(	F:translation initiatic EC:3.6.1.15 Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:2.40.3(	112,727	142,321	180,638	182,042	235,171			0,378	0,021				up	
Solyc07g056030	Nuclear-interacting partner of ALK (AHRD V3.3 *** W9QKR2_9ROSA)		C:GO:0005634: F:G(	C:nucleus; F:zinc ion binding	IPR012935 (PFAM): mobidb-lite (MOB	152,775	153,682	171,904	170,706	174,887									
Solyc07g056040	CASP-like protein (AHRD V3.3 *** K4CGD7_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir	IPR006459 (TIGRFAM): IPR006702 (F	6,789	5,832	8,680	11,299	6,541									
Solyc07g056050	Transmembrane 9 superfamily member (AHRD V3.3 *** M1D2K2_SOLTU)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM): PTHR10766:SF4	101,727	131,365	82,776	89,556	82,896									
Solyc07g056060	pesticidal crystal cry8Ba protein (AHRD V3.3 *** AT4G24610.1)		P:GO:0009737	P:response to abscisic acid	PTHR31110:SF3 (PANTHER): PTHR3	1,753	2,408	2,329	2,770	2,636									
Solyc07g056070	Mitochondrial 37S ribosomal protein S27 (AHRD V3.3 *** A0A0B2P5W5_GLYSO)		C:GO:0005840	C:ribosome	IPR013219 (PFAM): mobidb-lite (MOB	4,199	5,051	6,097	6,957	6,781									
Solyc07g056080	LOW QUALITY:Acidic endochitinase SE2 (AHRD V3.3 --* CHIE_BETVU)		C:GO:0016021	C:integral component of membrane	PTHR35420 (PANTHER)	0,245	0,590	0,212	0,562	0,352									
Solyc07g056100	LOW QUALITY:ArgH (DUF639) (AHRD V3.3 --* AT2G21720.2)		C:GO:0016021	C:integral component of membrane	PTHR35420 (PANTHER)	0,000	0,018	0,050	0,050	0,093									
Solyc07g056110	Vacuolar cation/proton exchanger, putative (AHRD V3.3 *** B9SEZ0_RICCO)		P:GO:0006816: F:G(	P:calcium ion transport; F:calcium:proton antiporter activity; C:ir	IPR004713 (TIGRFAM): G3DSA:1.20.!	19,882	13,315	23,682	25,651	23,488									
Solyc07g056120	PhD-finger protein, putative (AHRD V3.3 *-* Q8LA17_ARATH)		F:GO:0003677	F:DNA binding	IPR001965 (SMART): IPR001005 (SM	9,034	6,625	10,410	9,843	9,045									
Solyc07g056140	ADP-glucose pyrophosphorylase small subunit	AGPase S1	P:GO:0005978: F:G(	P:glycogen biosynth EC:2.7.7.27 Glucose-1-phosphate	G3DSA:2.160.10.10 (GENE3D): IPR0	319,747	350,641	72,997	47,995	90,739									
Solyc07g056150	Ras-related protein (AHRD V3.3 *** W9R1W6_9ROSA)		F:GO:0003924: F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): SM00173 (SMAR	77,027	78,900	53,492	53,245	49,931									
Solyc07g056160	CYP724B2 mRNA for cytochrome P450	CYP724B2	F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS): IPR001128 (PF	0,434	0,515	0,000	0,076	0,024									
Solyc07g056170	Subtilisin-like protease family protein (AHRD V3.3 *** B9IAW9_POPTR)		F:GO:0004252: P:G(	F:serine-type endor EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	3,329	5,859	1,220	2,941	1,849	0,843	0,046			1,259	0,004	up		up
Solyc07g056190	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061DNE7_THECC)				G3DSA:3.30.70.100 (GENE3D): PTHF	0,236	0,204	0,025	0,173	0,094									
Solyc07g056200	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061DNE7_THECC)				G3DSA:3.30.70.100 (GENE3D): PTHF	0,264	1,445	0,269	0,661	0,781									
Solyc07g056210	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *-* A0A061GZF7_THECC)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D): PTHF	0,000	0,000	0,000	0,050	0,000									
Solyc07g056220	Vacuolar protein sorting-associated protein 16-like protein (AHRD V3.3 *** W9QLH6_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C:cytoplasm; P:intracellular protein transport;	IPR006925 (PFAM): IPR038132 (G3D	62,011	58,558	71,454	67,817	66,860									
Solyc07g056230	Cytochrome B561-related protein, putative (AHRD V3.3 *** A0A061GEA2_THECC)		C:GO:0016021: P:G(	C:integral component of membrane; P:oxidation-reduction proce	IPR006593 (SMART): IPR006593 (PF.	0,019	0,000	0,000	0,000	0,000									
Solyc07g056240	TRNA-methyltransferase (AHRD V3.3 *** A0A061DM84_THECC)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:integral component of men	PTHR36742 (PANTHER)	3,239	3,491	1,600	1,341	2,583									

Solyc07g056250	Protein glycosylationmyb-like TTH transcriptional regulator (AHRD V3.3 *** A0A077SLH0_9MAGN)		P:GO:0006629; F:G(	P:lipid metabolic process; F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	7,954	6,567	2,711	2,515	2,498									
Solyc07g056260	Callose synthase-like protein (AHRD V3.3 *** G7IXI4_MEDTR)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan synth	IPR026899 (SMART): IPR003440 (PF.	62,960	55,151	45,695	51,391	45,935									
Solyc07g056270	Kinase family protein (AHRD V3.3 *** B9GT27_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	24,591	17,651	7,993	5,698	8,150									
Solyc07g056280	WRKY transcription factor 30	WRKY30	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	0,326	0,419	1,144	1,706	1,267									
Solyc07g056290	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G78400.1)	PG37-1	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR006626 (SMART): IPR000743 (PF.	0,229	0,170	0,000	0,025	0,000									
Solyc07g056310	Glucan endo-1,3-beta-glucosidase 1 (AHRD V3.3 *** A0A0B2RVC0_GLYSO)		C:GO:0016021; C:G(	C:integral component of membrane; C:anchored component of r			IPR012946 (SMART): IPR012946 (PF.	0,991	0,545	0,884	1,063	0,873									
Solyc07g056320	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7K3C7_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (SMART): IPR002123 (PF.	21,278	13,610	0,868	1,514	1,638									
Solyc07g056330	Ribose-phosphate pyrophosphokinase, putative (AHRD V3.3 *** B9T1G2_RICCO)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	SM01400 (SMART): G3DSA:3.40.50.2	0,409	0,417	0,050	0,000	0,142									
Solyc07g056340	RNA-binding protein, putative (AHRD V3.3 *** B9T754_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF.	29,011	22,596	12,459	11,260	15,914									
Solyc07g056350	mitogen-activated protein kinase 12	mapk12	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF.	113,710	84,335	48,754	40,331	42,535									
Solyc07g056360	LOW QUALITY:BHLH transcription factor (AHRD V3.3 *-* I1M6X1_SOYBN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,140	0,616	0,000	0,000	0,000									
Solyc07g056370	Myosin heavy chain-related family protein (AHRD V3.3 *** B9H808_POPTR)		C:GO:0016021	C:integral component of membrane			SSF57997 (SUPERFAMILY)	50,362	53,527	64,129	57,278	54,464									
Solyc07g056390	Endoplasmic oxidoreductin-1, putative (AHRD V3.3 *** B9T812_RICCO)		F:GO:0003756; C:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	IPR007266 (PFAM): IPR007266 (PIRS	14,643	19,611	24,913	33,011	26,296					0,411	0,028			up
Solyc07g056400	Protein kinase superfamily protein (AHRD V3.3 *** AT3G14370.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	4,821	5,653	0,441	0,149	0,214									
Solyc07g056410	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CGH4_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR003591 (SM	1,363	1,830	39,293	45,057	49,680									
Solyc07g056420	glutathione S-transferase AY082341	GSTU18	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	99,033	129,092	895,451	1007,362	727,957									
Solyc07g056430	Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC)	GSTU19	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	4,217	4,912	74,269	70,525	43,512			-0,773	0,004				down	
Solyc07g056440	Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC)	GSTU20	F:GO:0005515	F:protein binding			IPR004045 (PFAM): PF13410 (PFAM)	4,963	4,378	6,320	5,529	4,640									
Solyc07g056450	Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC)	GSTU21	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	0,040	0,145	0,000	0,000	0,071									
Solyc07g056460	Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC)	GSTU22	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	0,644	0,696	0,122	0,117	0,188									
Solyc07g056470	Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC)	GSTU23	F:GO:0005515	F:protein binding			PF13410 (PFAM): G3DSA:3.40.30.10	2,378	5,717	2,030	2,098	3,405	1,285	0,001					up		
Solyc07g056480	glutathione S-transferase/peroxidase	GSTU24	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): PF1	5,258	10,292	6,270	4,780	8,102	0,993	0,009					up		
Solyc07g056490	Glutathione s-transferase	GSTU25	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:1.20.105(	106,228	99,228	61,995	68,330	71,910									
Solyc07g056500	glutathione S-transferase T5	GSTU26	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	39,031	46,682	79,572	74,296	77,991									
Solyc07g056510	Glutathione S-transferase (AHRD V1 **** D3Y4H6_9ROSI)	GSTU27	F:GO:0005515	F:protein binding			PF13410 (PFAM): G3DSA:3.40.30.10	2,020	1,234	84,618	157,752	109,000					0,901	0,000			up
Solyc07g056520	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** A0A072V9D1_MEDTR)		P:GO:0016579; F:G(	P:protein deubiquitii	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	27,671	26,021	25,195	27,842	26,333									
Solyc07g056525	Transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 --* AT3G07610.3)							0,077	0,097	0,576	0,988	0,683									
Solyc07g056530	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT3G14410.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM): mobidb-lite (MOB	3,470	3,953	1,301	1,108	1,361									
Solyc07g056540	glycolate oxidase X92888		F:GO:0010181; F:G(	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR012133 (PIRSF): IPR013785 (G3D	76,712	305,509	35,760	48,799	153,277	2,019	0,000	2,095	0,000			up	up	
Solyc07g056550	bystin-like protein (AHRD V3.3 *** AT1G31660.1)		P:GO:0006364; P:G(	P:rRNA processing; P:embryo sac development; P:pollen devel(			IPR007955 (PFAM): mobidb-lite (MOB	68,272	70,267	76,560	72,257	69,690									
Solyc07g056560	cytokinin response factor 2 (AHRD V3.3 --* AT4G23750.2)							2,337	2,443	2,982	2,393	2,685									
Solyc07g056570	notabilis	not	F:GO:0016702; P:G(	F:oxidoreductase a(	EC:1.13.11	Acting on single donc	IPR004294 (PFAM): mobidb-lite (MOB	320,402	526,362	343,699	279,512	421,746									
Solyc07g056580	ethylene receptor 2	ETR2	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR003018 (SM	22,824	15,862	50,697	53,844	54,242									
Solyc07g056590	RNA-binding protein, putative (AHRD V3.3 *** B9SVC9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	25,602	28,027	47,872	45,730	41,051									
Solyc07g056600	VQ motif-containing protein (AHRD V3.3 *** AT1G78410.2)		F:GO:0005515; P:G(	F:protein binding; P:response to oxidative stress			IPR008889 (PFAM): IPR039608 (PAN	0,061	0,114	0,000	0,000	0,047									
Solyc07g056610	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)						IPR004314 (PFAM): IPR025521 (PFA	0,938	2,273	0,000	0,000	0,000									
Solyc07g056615	Mei2-like protein (AHRD V3.3 *-* Q8S3W5_HORVD)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA binding; C:nucleus; C:nuclear spe			IPR007201 (PFAM): PTHR44127 (PAN	0,082	0,039	0,000	0,025	0,000									
Solyc07g056630	RING-type E3 ubiquitin ligase (AHRD V3.3 *** A0A076JXY8_VITVI)		P:GO:0016567; P:G(	P:protein ubiquitination; P:regulation of organ growth; F:ubiquitir			mobidb-lite (MOBIDB_LITE): mobidb-lit	19,999	22,383	26,067	24,600	28,317									
Solyc07g056640	cycling DOF factor 2 (AHRD V3.3 --* AT5G39660.3)							3,360	6,124	1,169	0,821	1,738									
Solyc07g056650	Interactor of constitutive active ROPs protein, putative (AHRD V3.3 *** A0A072V8T5_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,176	1,671	0,143	0,147	0,143									
Solyc07g056660	Vacuolar sorting protein 39 (AHRD V3.3 *** AT4G36630.1)		P:GO:0016192	P:vesicle-mediated transport			IPR019453 (PFAM): IPR019452 (PFA	52,865	44,372	52,622	56,979	54,887									
Solyc07g056670	gibberellin 2-oxidase 2	ga2ox-2	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	2,980	43,836	182,024	308,803	170,880	3,896	0,000			0,765	0,000	up		up
Solyc07g056690	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)						IPR004314 (PFAM): PTHR31589:SF2	0,076	0,251	0,898	1,265	0,519									
Solyc07g056700	LOW QUALITY:Armadillo/beta-catenin-like repeat family protein (AHRD V3.3 --* AT1G68940.3)							4,109	4,885	26,532	23,771	16,358			-0,700	0,009				down	
Solyc07g056703	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *-* AT2G44210.1)						IPR004314 (PFAM): PTHR31589:SF2	0,038	0,230	0,025	0,092	0,047									
Solyc07g056707	NEP-interacting protein, putative (DUF239) (AHRD V3.3 *-* AT4G10220.1)						IPR004314 (PFAM): PTHR31589 (PAN	0,019	0,308	0,000	0,000	0,000									
Solyc07g061710	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.2)						IPR025521 (PFAM): IPR004314 (PFA	0,021	0,037	0,000	0,047	0,024									
Solyc07g061720	gibberellin 2-oxidase 4	ga2ox-4	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR026992 (PFA	0,771	1,872	0,118	0,145	0,119									
Solyc07g061730	gibberellin 2-oxidase 5	ga2ox-5	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR026992 (PFA	0,725	2,788	0,284	0,536	0,567	1,948	0,002					up		
Solyc07g061740	Ankyrin repeat-containing-like protein (AHRD V3.3 *** A0A061FUD1_THECC)		F:GO:0005515; C:G(	F:protein binding; C:integral component of membrane; P:regulati			IPR002110 (SMART): IPR020683 (PF.	1,800	2,843	0,312	0,850	1,011									
Solyc07g061750	Ankyrin repeat-containing-like protein (AHRD V3.3 *** A0A061FUD1_THECC)		F:GO:0005515; C:G(	F:protein binding; C:integral component of membrane; P:regulati			IPR002110 (SMART): IPR020683 (PF.	0,063	0,039	0,000	0,000	0,000									
Solyc07g061760	Ankyrin repeat-containing-like protein (AHRD V3.3 *** A0A061FUD1_THECC)		F:GO:0005515	F:protein binding			IPR002110 (SMART): IPR036770 (G3	0,000	0,018	0,000	0,000	0,000									
Solyc07g061780	Ubiquitin carboxyl-terminal hydrolase 15-like protein (AHRD V3.3 *** A0A0B0MG64_GOSAR)		P:GO:0016579; F:G(	P:protein deubiquitii	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR002893 (PFAM): G3DSA:3.90.70.1	60,671	49,468	45,209	41,041	43,059									
Solyc07g061790	SOUL heme-binding family protein (AHRD V3.3 *** AT1G17100.1)		F:GO:0020037	F:heme binding			IPR011256 (G3DSA:3.20.80.GENE3D	51,304	91,239	55,846	62,597	131,535	0,858	0,004	1,233	0,000			up	up	
Solyc07g061800	SOUL heme-binding family protein (AHRD V3.3 *** AT1G17100.1)		F:GO:0020037	F:heme binding			IPR006917 (PFAM): IPR011256 (G3D	48,511	22,635	13,450	7,354	16,979					-0,868	0,001			down
Solyc07g061860	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT1G08125.2)							0,000	0,000	0,000	0,000	0,023									
Solyc07g061870	LOW QUALITY:UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT5G04480.2)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	0,000	0,018	0,000	0,000	0,000									
Solyc07g061890	LOW QUALITY:Heat stress transcription factor B-4b, putative (AHRD V3.3 *** A0A061FAG8_THECC)						PTHR37611 (PANTHER)	0,117	0,123	0,190	0,174	0,141									
Solyc07g061900	50S ribosomal protein L4, putative (AHRD V3.3 *** B9SHY1_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR023574 (G3DSA:3.40.1370.GENE	17,117	31,009	32,682	39,280	49,838	0,886	0,004	0,606	0,000			up	up	
Solyc07g061905	autoinhibited Ca2+-ATPase 1 (AHRD V3.3 --* AT1G27770.3)							0,117	0,126	0,047	0,097	0,118									
Solyc07g061910	Peptide transporter (AHRD V3.3 *-* G7JZV7_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,155	0,179	0,240	0,124	0,307									
Solyc07g061920	glucan synthase-like 4 (AHRD V3.3 *** AT3G14570.1)		C:GO:0000148; F:G(	C:1,3-beta-D-glucar	EC:2.4.1.34	1,3-beta-glucan synth	IPR026899 (SMART): IPR039431 (PF.	8,989	5,815	5,445	9,334	6,824					0,783	0,004			up
Solyc07g061930	response regulator 14 (AHRD V3.3 --* AT2G01760.2)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding; C:integral component of membra			mobidb-lite (MOBIDB_LITE): mobidb-lit	19,142	20,181	15,915	15,302	15,377									
Solyc07g061940	Acetolactate synthase (AHRD V3.3 *** A0A0V0IYE7_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.2.1.6	Acetolactate synthas	G3DSA:3.40.50.1220 (GENE3D): IPR(	545,647	528,527	340,382	345,111	371,713									
Solyc07g061950	Calcium-dependent lipid-binding domain protein (AHRD V3.3 *** A0A072VA30_MEDTR)		F:GO:0008289	F:lipid binding			IPR000008 (PRINTS): IPR000008 (SM	61,545	110,353	40,880	34,576	43,464	0,867	0,018					up		
Solyc07g061960	Hydroxyacylglutathione hydrolase 3 (AHRD V3.3 *** F4HRK0_ARATH)		F:GO:0051213; P:G(	F:dioxygenase activity; P:oxidation-reduction process			IPR001279 (SMART): IPR001279 (PF.	36,019	39,185	62,744	59,636	60,058									
Solyc07g061970	60S ribosomal protein L18a-like protein (AHRD V3.3 *** A0A199VD98_ANACO)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	21,721	22,949	8,641	8,419	9,694									
Solyc07g061980	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	0,183	0,167	0,025	0,022	0,023									
Solyc07g061990	solanesyl diphosphate synthase	SPS	P:GO:0008299; P:G(	P:isoprenoid biosynthetic process; P:photosynthesis; F:transfer			IPR000092 (PFAM): IPR014120 (TIGF	47,113	65,712	79,709	95,667	134,852			0,755	0,000				up	
Solyc07g062010	LOW QUALITY:Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0NBZ5_GOSAR)						IPR012946 (SMART): IPR012946 (PF.	0,021	0,018	0,000	0,000	0,000									
Solyc07g062020	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0NBZ5_GOSAR)						IPR012946 (SMART): IPR012946 (PF.	0,757	0,365	0,000	0,000	0,000									
Solyc07g062030	Chalcone-flavonone isomerase family protein (AHRD V3.3 *** K4CGN6_SOLLC)	CHI	F:GO:0016872	F:intramolecular lyase activity			IPR016087 (PFAM): IPR016089 (G3D	1,280	1,471	1,111	1,101	0,942									
Solyc07g062040	Protein kinase family protein (AHRD V3.3 *** C6ZRS4_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	1,795	4,336	0,165	0,370	0,467	1,294	0,033					up		
Solyc07g062050	SH2 domain protein A (AHRD V3.3 *** AT1G17040.1)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			G3DSA:2.60.120.2 STAT	20,647	17,337	24,835	23,945	24,616									
Solyc07g062060	Methionine sulfoxide reductase (AHRD V3.3 *** A0A0D5BY62_MAIZE)		P:GO:0006979; P:G(	P:response to oxida	EC:1.8.4.12	Peptide-methionine (I	IPR002579 (PFAM): IPR002579 (TIGF	34,340	42,989	224,661	210,511	249,846									
Solyc07g062070	Ribokinase (AHRD V3.3 *** M1AA65_SOLTU)		F:GO:0004747; P:G(	F:ribokinase activity	EC:2.7.1.15	Ribokinase	IPR002139 (PRINTS): IPR011611 (PF	4,639	4,567	11,496	16,115	13,820									
Solyc07g062080	mitogen-activated protein kinase 11	mapk11	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	60,332	77,730	67,194	78,846	69,692									
Solyc07g062090	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)						PTHR33916 (PANTHER): PTHR33916	0,000	0,078	0,000	0,000	0,000									
Solyc07g062100	PHD-zinc-finger-like domain protein (AHRD V3.3 *** G7ZV42_MEDTR)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation; F:metal ion binding			IPR001965 (SMART): PF13832 (PFAM	1,016	1,315	0,097	0,045	0,139									
Solyc07g062105	Fatty acyl-CoA reductase (AHRD V3.3 --* V7AFN1_PHAVU)							1,895	1,966	2,733	3,119	2,379									
Solyc07g062110	Protein FLX-like 1 (AHRD V3.3 *** FLXL1_ARATH)						mobidb-lite (MOBIDB_LITE): IPR0403	17,762	18,038	26,552	23,701	25,411									
Solyc07g062120	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4CGP5_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D): G3	0,703	0,875	0,646	0,510	1,053									
Solyc07g062130	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rha		F:GO:0008460; P:G(	F:dTDP-glucose 4,6	EC:4.2.1.46	dTDP-glucose 4,6-de	IPR005888 (TIGRFAM): IPR016040 (F	0,485	0,837	0,366	0,145	0,187									
Solyc07g062140	trehalose-phosphate synthase 1	tps1	F:GO:0003825; P:G(	F:alpha,alpha-treha	EC:2.4.1.15	Alpha,alpha-trehalose	IPR001830 (PFAM): G3DSA:3.40.50.2	119,213	130,644	35,639	22,323	38,238					-0,673	0,004			down
Solyc07g062150	NAD kinase (AHRD V3.3 *** F2Z9R6_NICBE)		F:GO:0003951; P:G(	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR017438 (G3DSA:3.40.50.GENE3D	6,285	5,197	10,153	10,814	9,645									
Solyc07g062160	Zinc finger, B-box (AHRD V3.3 *** A0A103Y421_CYNCS)	BBX22	F:GO:0008270	F:zinc ion binding			IPR000315 (SMAF DBB	66,519	69,819	82,855	83,315	84,052									
Solyc07g062170	Kinase family protein (AHRD V3.3 *** D7LY50_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	3,142	2,009	2,181	1,533	1,582									
Solyc07g062180	Integral membrane family protein (AHRD V3.3 *** A0A072V9R4_MEDTR)	VTE6	C:GO:0016021	C:integral component of membrane			IPR002794 (PFAM): IPR002794 (PAN	10,259	11,266	32,046	38,062	31,515									
Solyc07g062190	Ribosomal protein L13 family protein (AHRD V3.3 *** AT1G78630.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005823 (TIGRFAM): IPR005822 (F	76,705	123,674	68,226	73,982	93,976	0,716	0,003	0,459	0,002			up	up	
Solyc07g062200	bHLH transcription factor 088		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase			IPR036638 (G3DS bHLH	0,000	0,019	0,000	0,000	0,000									
Solyc07g062210	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	0,061	0,094	0,159	0,320	0,326									
Solyc07g062220	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; F:G(	C:Golgi apparatus; F:O-acetyltransferase activity			IPR025846 (PFAM): IPR026057 (PFA	4,230	3,980	3,642	4,706	3,599									
Solyc07g062230	Seipin (AHRD V3.3 *** A0A1D1ZHH9_9ARAE)		P:GO:0019915	P:lipid storage			IPR009617 (PFAM): PTHR21212:SF3	0,122	0,142	0,000	0,216	0,093									
Solyc07g062250	epstein-barr nuclear antigen (AHRD V3.3 *** AT3G14830.4)						PTHR34541:SF2 (PANTHER): PTHR3	61,585	60,799	53,217	49,755	53,128									
Solyc07g062260	Brassinazole-resistant 1 protein (AHRD V3.3 *** G7IR04_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:transcription, DNA			IPR008540 (PFAM BES1	20,624	23,669	4,805	6,798	9,404			0,963	0,026				up	
Solyc07g062270	Gamma-glutamyl hydrolase, putative (AHRD V3.3 *** B9SEV4_RICCO)		F:GO:0008242	F:omega peptidase	EC:3.4.19	Acting on peptide bor	IPR029062 (G3DSA:3.40.50.GENE3D	20,218	16,292	24,904	24,381	20,943									
Solyc07g062280	Gamma-glutamyl hydrolase (AHRD V3.3 *** X5HY53_IPONI)		F:GO:0008242	F:omega peptidase	EC:3.4.19	Acting on peptide bor	IPR029062 (G3DSA:3.40.50.GENE3D	0,777	0,938	0,288	0,123	0,258									
Solyc07g062290	Ubiquitin domain-containing protein (AHRD V3.3 *** AT1G53400.1)						IPR038169 (G3DSA:1.20.225.GENE3	0,139	0,118	0,025	0,072	0,141									
Solyc07g062300	NHL repeat-containing protein (AHRD V3.3 *** A0A118K6E2_CYNCS)						IPR011042 (G3DSA:2.120.10.GENE3	36,954	39,727	15,510	13,411	19,451									
Solyc07g062310	UNE1-like protein (AHRD V3.3 *** G7ITF5_MEDTR)		P:GO:0009639; P:G(	P:response to red or far red light; P:negative gravitropism			IPR006943 (PFAM): IPR040225 (PAN	35,057	37,348	10,391	9,822	16,140									
Solyc07g062360	Duplicated homeodomain-like superfamily protein (AHRD V3.3 --* AT1G14350.4)		P:GO:0006970; P:G(	P:response to osmotic stress; P:cellular response to nitrogen st			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,831	2,149	0,000	0,000	0,000									
Solyc07g062380	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM): PTHR22952:SF1	0,459	0,369	0,049	0,100	0,000									
Solyc07g062390	Tubby-like F-box protein (AHRD V3.3 *** K4CGS2_SOLLC)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS): IPR000007 (PF	16,004	12,875	18,170	16,901	15,462									
Solyc07g062395	phytochrome interacting factor 3-like 5 (AHRD V3.3 --* AT2G20180.8)						mobidb-lite (MOBIDB_LITE)	0,202	0,134	0,197	0,150	0,047									
Solyc07g062410	Suppressor of gene silencing 3, putative (AHRD V3.3 --* A0A061FQZ7_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	14,889	14,683	5,908	4,257	4,898									
Solyc07g062420	LOW QUALITY:centrosomal protein of 135 kDa-like protein (AHRD V3.3 --* AT2G37370.3)						PTHR34778 (PANTHER): PTHR34778	0,019	0,000	0,000	0,000	0,000									
Solyc07g062430	Bifunctional polynucleotide phosphatase/kinase (AHRD V3.3 *** A0A0B0PGG4_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR001510 (SMART): IPR006551 (TIG	13,756	13,731	11,709	11,202	13,084									
Solyc07g062440	LOW QUALITY:BnaA05g24630D protein (AHRD V3.3 *** A0A078E8V1_BRANA)		C:GO:0009507; P:G(	C:chloroplast; P:embryo development ending in seed dormancy			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,102	0,144	0,146	0,075	0,165									
Solyc07g062450	Rab3 GTPase-activating protein non-catalytic subunit (AHRD V3.3 *** AT3G14910.1)		P:GO:0043087	P:regulation of GTPase activity			IPR032839 (PFAM): mobidb-lite (MOB	6,056	5,793	8,512	9,660	8,631									
Solyc07g062460	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (AHRD V3.3 *** PNAA_PRUDU)						IPR021102 (PFAM): PTHR31104:SF1	5,043	4,528	0,285	0,289	0,333									
Solyc07g062470	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM): mobidb-lite (MOB	29,208	32,457	5,747	5,072	5,204									
Solyc07g062480	Serine/threonine-protein kinase (AHRD V3.3 *-* M1CRP0_SOLTU)		F:GO:0030246	F:carbohydrate binding			IPR001480 (SMART): IPR001480 (PF.	1,220	5,979	1,442	0,757	2,074	2,313	0,013					up		
Solyc07g062490	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A067JEE7_JATCU)		F:GO:0030246	F:carbohydrate binding			IPR001480 (SMART): IPR001480 (PF.	4,681	84,668	0,681	1,685	5,530	4,202	0,000	3,006	0,000			up	up	
Solyc07g062500	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	39,290	48,855	20,411	21,919	32,721			0,676	0,033				up	
Solyc07g062510	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	0,459	0,787	1,425	1,198	1,345									
Solyc07g062520	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	28,672	26,044	19,776	19,442	20,209									
Solyc07g062530	phosphoenolpyruvate carboxylase 2		P:GO:0006099; F:G(	P:tricarboxylic acid	EC:4.1.1.31; EC:4.1.	Phosphoenolpyruvate	IPR021135 (PRINTS): G3DSA:1.20.14	2412,715	1610,178	1034,544	580,566	880,732	-0,555	0,042			-0,831	0,000	down		down
Solyc07g062540	Mannosyltransferase (AHRD V3.3 *** K4CGT7_SOLLC)		F:GO:0000030	F:mannosyltransferase activity			IPR005599 (PFAM): mobidb-lite (MOB	9,494	11,260	13,579	15,015	12,847									
Solyc07g062545	Alpha-1,2-mannosyltransferase ALG9 (AHRD V3.3 --* A0A0A9MP14_ARUDO)							0,019	0,000	0,000	0,000	0,000									
Solyc07g062550	3-phosphoshikimate 1-carboxyvinyltransferase (AHRD V3.3 *** A0A0A6Z9T0_HEVBR)		F:GO:0008760; P:G(	F:UDP-N-acetylgluc	EC:2.5.1.7	UDP-N-acetylglucosa	IPR036968 (G3DSA:3.65.10.GENE3D	20,204	19,576	0,159	0,805	0,678									
Solyc07g062560	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *** A0A103XBC9_CYNCS)		C:GO:0005615	C:extracellular space			PF01190 (PFAM): IPR006041 (PTHR3	0,058	0,000	0,000	0,000	0,000									
Solyc07g062570	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** A9PA76_POPTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; C:cytosol; C:plasma membrane; P:po			SM00212 (SMART): IPR016135 (G3D	111,931	113,935	164,338	168,705	155,699									
Solyc07g062580	TPR repeat thioredoxin TTL1-like protein (AHRD V3.3 *** A0A072V9X4_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:cell redox homeostasis			IPR019734 (SMART): PF13432 (PFAM	43,815	39,344	18,088	19,322	19,863									
Solyc07g062590	Hexosyltransferase (AHRD V3.3 *** K4CGU2_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR002659 (PFAM): PTHR11214:SF1	8,945	8,515	9,874	11,987	8,925									
Solyc07g062600	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 *-* AT3G14980.6)		P:GO:0035556; F:G(	P:intracellular signal transduction; F:metal ion binding			mobidb-lite (MOBIDB_LITE): IPR03108	14,355	16,749	11,543	9,226	12,144									
Solyc07g062605	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 *-* AT3G14980.6)		P:GO:0035556; F:G(	P:intracellular signal transduction; F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	37,257	37,283	29,234	26,092	30,838									
Solyc07g062610	Class I glutamine amidotransferase-like superfamily protein isoform 1 (AHRD V3.3 *** A0A061FFJ1_THECC)						IPR002818 (PFAM): IPR006287 (TIGF	61,304	61,897	89,818	70,696	83,824					-0,342	0,042			down
Solyc07g062620	Kinase family protein (AHRD V3.3 *** B9NAB5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	19,402	22,062	22,772	25,147	21,825									
Solyc07g062630	ABC transporter family protein (AHRD V3.3 *** B9I1V7_POPTR)	ABCG19	F:GO:0005524; C:G(	F:ATP binding; C:m(	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR003439 (PF.	0,082	0,021	0,236	0,292	0,094									
Solyc07g062640	tetraacyldisaccharide 4'-kinase family protein (AHRD V3.3 --* AT3G20480.5)		C:GO:0005776; C:G(	C:autophagosome; C:phagophore			mobidb-lite (MOBIDB_LITE): mobidb-lit	26,280	21,679	33,192	36,173	32,286									
Solyc07g062650	Malate dehydrogenase (AHRD V3.3 *** K4CGU8_SOLLC)		P:GO:0005975; P:G(	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR015955 (G3DSA:3.90.110.GENE3	310,380	325,249	403,781	336,721	368,855									
Solyc07g062660	Transcription factor GTE4 (AHRD V3.3 *** A0A0B2R809_GLYSO)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR001487 (SM	40,643	41,430	47,447	46,798	45,308									
Solyc07g062670	LOW QUALITY:Clavata3/ESR (CLE) gene family member (AHRD V3.3 --* A0A072TRR8_MEDTR)						IPR039617 (PANTHER): PTHR36016:	0,805	3,274	17,803	68,875	17,470	2,031	0,041			1,958	0,000	up		up
Solyc07g062680	lanceolate	TCP2	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	5,505	7,003	1,981	2,096	2,287									
Solyc07g062685	Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B (AHRD V3.3 *** A0A0B0PLB6_GOSAR)		F:GO:0003700	F:DNA-binding transcription factor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,099	0,096	0,022	0,000	0,047									
Solyc07g062700	sodium/calcium exchanger family protein / calcium-binding EF hand family protein (AHRD V3.3 *** AT1G5321		F:GO:0005509; C:G(	F:calcium ion binding; C:integral component of membrane; P:tra			IPR002048 (SMART): G3DSA:1.10.23	261,407	504,680	134,567	176,032	189,388	0,972	0,030					up		
Solyc07g062710	BZIP family transcription factor (AHRD V3.3 *** G8A005_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	0,161	0,043	0,022	0,000	0,024									
Solyc07g062720	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G53190.2)		F:GO:0008270; F:G(	F:zinc ion binding; F:ligase activity; F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	6,303	4,568	0,882	0,615	1,033									
Solyc07g062730	LOW QUALITY:Serine/Threonine-kinase pakA-like protein (AHRD V3.3 *-* AT3G15095.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	11,463	9,786	2,685	3,127	3,265									
Solyc07g062740	Serine/arginine repetitive matrix protein 2, putative (AHRD V3.3 *** A0A061F6Z0_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,029	2,640	8,148	9,770	9,571									
Solyc07g062750	Polynucleotidyl transferase ribonuclease H-like superfamily protein (AHRD V3.3 *-* A0A0G4APF7_9ROSI)		F:GO:0003676	F:nucleic acid binding			IPR036397 (G3DSA:3.30.420.GENE3	2,406	2,468	1,227	1,635	1,909									

Solyc07g062760	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061F		F:GO:0005524	F:ATP binding			IPR003593 (SMART): PF17862 (PFAM	38,771	38,195	36,019	36,384	39,147									
Solyc07g062780	E3 SUMO-protein ligase MMS21-like protein (AHRD V3.3 *** A0A0B0PRY8_GOSAR)		P:GO:0000724; F:GO	P:double-strand break repair via homologous recombination; F:z			IPR013083 (G3DSA:3.30.40.GENE3D	5,397	6,036	3,338	2,667	3,411									
Solyc07g062790	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)		F:GO:0003677	F:DNA binding			IPR001356 (SMAF HD-ZIP	0,138	0,259	0,025	0,000	0,000									
Solyc07g062810	Branched-chain-amino-acid aminotransferase-like protein (AHRD V3.3 *** I3SQ86_MEDTR)		F:GO:0008696; F:GO	F:4-amino-4-deoxyc	EC:4.1.3.38	Aminodeoxychorisma	IPR001544 (PFAM): G3DSA:3.20.10.1	0,836	1,552	1,004	1,389	1,523									
Solyc07g062820	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT4G18520.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,922	3,344	5,968	5,083	4,694									
Solyc07g062840	goblet	GOB	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,198	0,196	0,236	0,242	0,189									
Solyc07g062860	ARM repeat superfamily protein (AHRD V3.3 *** A0A061F7T1_THECC)		P:GO:0043248	P:proteasome assembly			IPR011989 (G3DSA:1.25.10.GENE3D	30,149	28,642	90,636	107,125	80,550									
Solyc07g062870	30S ribosomal protein S20 (AHRD V3.3 *** A0A060IGE4_PANGI)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR002583 (PFAM): IPR036510 (G3D	12,780	23,387	23,183	25,795	34,203	0,898	0,000	0,558	0,000			up	up	
Solyc07g062880	Protein yippee-like (AHRD V3.3 *** K4CGX1_SOLLC)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	29,102	26,952	39,544	34,374	35,025									
Solyc07g062890	Protein yippee-like (AHRD V3.3 *** K4CGX2_SOLLC)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	23,031	28,336	15,934	13,758	15,309									
Solyc07g062900	Protein yippee-like (AHRD V3.3 *-* A0A0V0H2B2_SOLCH)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			mobidb-lite (MOBIDB_LITE): IPR0390	2,780	2,457	1,881	2,564	2,333									
Solyc07g062903	Protein yippee-like (AHRD V3.3 --* A0A0V0H400_SOLCH)						mobidb-lite (MOBIDB_LITE)	2,972	2,327	1,691	2,050	2,805									
Solyc07g062905	Protein yippee-like (AHRD V3.3 *-* A0A0V0H2B2_SOLCH)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			PTHR13848:SF13 (PANTHER): IPR03	0,383	0,247	0,286	0,283	0,212									
Solyc07g062907	Protein yippee-like (AHRD V3.3 *-* A0A0V0H2B2_SOLCH)		F:GO:0046872	F:metal ion binding			IPR039058 (PANTHER): PTHR13848:	2,729	2,033	1,974	1,917	2,306									
Solyc07g062910	Protein yippee-like (AHRD V3.3 *** A0A0V0H2B2_SOLCH)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	0,137	0,019	0,072	0,147	0,117									
Solyc07g062920	Protein yippee-like (AHRD V3.3 *-* A0A0V0H2B2_SOLCH)		C:GO:0000151; F:GO	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): mobidb-lite (MOB	36,598	35,836	34,135	37,009	35,052									
Solyc07g062930	protein methyltransferase PrmA-like		P:GO:0006479; F:GO	P:protein methylation; F:protein methyltransferase activity			PF06325 (PFAM): G3DSA:3.40.50.15(	0,401	0,750	0,834	0,771	0,921									
Solyc07g062940	Kinase family protein (AHRD V3.3 *** B9N1E7_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:3.30.20	43,311	47,614	52,818	54,791	50,007									
Solyc07g062950	Serine/Threonine-kinase WNK (WNK)-like protein (AHRD V3.3 *** A0A072VKL1_MEDTR)						IPR025610 (PFAM): mobidb-lite (MOB	10,383	13,707	4,354	4,135	5,441									
Solyc07g062960	LOW QUALITY:polypyrimidine tract-binding protein 2 (AHRD V3.3 --* AT5G53180.6)		F:GO:0016301; P:GO	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,232	0,293	0,046	0,173	0,048									
Solyc07g062970	protein phosphatase 2C	dig3	F:GO:0004722; P:GO	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR036457 (G3	100,052	92,465	473,073	481,381	404,649									
Solyc07g062980	Squamosa promoter-binding protein, putative (AHRD V3.3 *** B9T4B7_RICCO)		F:GO:0003677; C:GO	F:DNA binding; C:nucleus			IPR036893 (G3DS SBP	0,084	0,194	0,000	0,000	0,000									
Solyc07g062990	Cold-responsive protein WCOR15 (AHRD V3.3 --* A0A193H6V8_AEGBI)							0,021	0,000	0,000	0,000	0,000									
Solyc07g063000	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGV8_ARATH)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR003591 (SMART): SM00365 (SMA	7,994	6,896	10,491	14,658	11,158									
Solyc07g063010	3-hydroxyacyl-CoA dehydrogenase family protein (AHRD V3.3 *** AT3G15290.1)		F:GO:0003857; P:GO	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	IPR022694 (PIRSF): IPR006176 (PFA	63,398	40,772	76,281	58,048	66,262	-0,610	0,017			-0,390	0,013	down		down
Solyc07g063020	Early nodulin-like protein (AHRD V3.3 *-* A0A072VCH6_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,555	0,536	2,010	3,413	2,265									
Solyc07g063040	Methylthioribulose 1-phosphate dehydratase / enolase-phosphatase E1 (AHRD V3.3 *** A0A061R779_9CHL		F:GO:0000287; C:GO	F:magnesium ion bi	EC:3.1.3.77	Acireductone synthas	IPR001303 (SMART): IPR001303 (PF	75,361	65,269	127,505	121,807	117,187									
Solyc07g063050	transmembrane protein (AHRD V3.3 *** AT4G13530.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	78,814	62,652	67,282	58,355	63,103									
Solyc07g063060	haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *-* AT5G53850.6)		F:GO:0000287; C:GO	F:magnesium ion bi	EC:4.2.1.19; EC:3.1.	Methylthioribulose 1-	G3DSA:1.10.720.60 (GENE3D)	0,160	0,080	0,071	0,073	0,095									
Solyc07g063070	VQ motif-containing protein (AHRD V3.3 *** A0A061F8J1_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	11,883	11,573	12,692	14,727	12,377									
Solyc07g063080	Dynamin family protein (AHRD V3.3 *** D7KKE2_ARALL)		F:GO:0003924; F:GO	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR001401 (SM	1,122	1,005	0,071	0,050	0,072									
Solyc07g063100	Proton pump interactor 1 (AHRD V3.3 *** D5L6G0_SOLTU)		C:GO:0005783; C:GO	C:endoplasmic reticulum; C:plasma membrane; P:regulation of p			mobidb-lite (MOBIDB_LITE): mobidb-lit	436,838	453,257	520,076	476,017	503,857									
Solyc07g063110	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** F4JIW2_ARATH		F:GO:0008375; C:GO	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297 (PAN	7,730	6,916	134,581	178,400	138,659									
Solyc07g063120	Ubiquitin ligase protein cop1, putative (AHRD V3.3 *** B9T5N2_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR020472 (PRINTS): IPR000719 (SM	47,613	52,551	51,758	53,663	55,315									
Solyc07g063130	Kinase superfamily protein (AHRD V3.3 *** A0A061F6L1_THECC)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	56,485	48,315	39,701	36,491	41,006									
Solyc07g063140	Glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial (AHRD V3.3 *** K4CGZ7_SOLL		P:GO:0006450	P:regulation of translational fidelity			IPR003837 (TIGRFAM): G3DSA:1.10.	6,035	6,377	6,462	8,035	8,442									
Solyc07g063145	piezo-type mechanosensitive ion channel component (AHRD V3.3 --* AT2G48060.3)							0,199	0,145	0,122	0,148	0,212									
Solyc07g063150	DUF616 family protein (AHRD V3.3 *** G7IRA5_MEDTR)		P:GO:0006672; C:GO	P:ceramide metabolic process; C:integral component of membra			IPR006852 (PFAM): mobidb-lite (MOB	16,824	13,328	16,954	18,283	16,261									
Solyc07g063160	Cytochrome c oxidase copper chaperone (AHRD V3.3 *** A0A0B0PK07_GOSAR)		C:GO:0005758; P:GO	C:mitochondrial intermembrane space; P:copper ion transport; F			IPR007745 (PFAM): G3DSA:1.10.287	7,791	9,063	16,372	15,758	16,161									
Solyc07g063165	3-deoxy-manno-octulosonate cytidylyltransferase (AHRD V3.3 *-* A0A0B2RRY9_GLYSO)		F:GO:0016740	F:transferase activity			IPR029044 (G3DSA:3.90.550.GENE3	0,398	0,813	0,274	0,335	0,163									
Solyc07g063170	Sodium/calcium exchanger family protein (AHRD V3.3 --* AT5G17850.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,753	2,001	1,646	1,738	1,315									
Solyc07g063190	Thioredoxin (AHRD V3.3 *** A0A103YK44_CYNCS)		P:GO:0006662; F:GO	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR013766 (PFA	68,756	111,095	74,707	78,519	109,030	0,719	0,004	0,543	0,001			up	up	
Solyc07g063200	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G42030.1)		F:GO:0046872	F:metal ion binding			IPR001841 (SMART): IPR013083 (G3	25,123	25,011	20,873	33,721	26,721					0,692	0,012			up
Solyc07g063210	Expansin (AHRD V3.3 *** G4XZZ0_9GENT)	EXPA25	C:GO:0005576; P:GO	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	0,042	0,103	0,025	0,000	0,000									
Solyc07g063220	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SNN7_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	7,093	8,099	7,512	6,513	6,850									
Solyc07g063230	Choline transporter-related family protein (AHRD V3.3 *** B9HZW2_POPTR)		C:GO:0005886; C:GO	C:plasma membrane; C:phragmoplast; C:secondary plasmodesr			IPR007603 (PFAM): PTHR12385:SF1	6,281	4,447	2,223	0,998	1,227					-1,128	0,022			down
Solyc07g063240	Protein silencing defective protein (AHRD V3.3 *** G7IPR8_MEDTR)						IPR013899 (SMART): IPR013899 (PF	162,643	313,908	26,544	18,542	34,164	0,971	0,034					up		
Solyc07g063260	MLO-like protein (AHRD V3.3 *** K4CH09_SOLLC)		P:GO:0006952; C:GO	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	14,879	17,965	18,851	19,537	20,732									
Solyc07g063270	GTP-binding family protein (AHRD V3.3 *** AT1G52980.1)		F:GO:0005525; C:GO	F:GTP binding; C:nucleolus			IPR006073 (PRINTS): G3DSA:3.40.50	174,942	152,784	121,314	118,679	127,375									
Solyc07g063280	Nucleolar GTP-binding protein 2 (AHRD V3.3 *-* A0A151RE97_CAJCA)		C:GO:0005730	C:nucleolus			IPR012971 (PFAM): mobidb-lite (MOB	0,057	0,079	0,115	0,177	0,188									
Solyc07g063290	Transcription factor tfiiic, tau55-like protein, putative (AHRD V3.3 *** A0A072VBF0_MEDTR)						IPR019481 (PFAM): mobidb-lite (MOB	2,574	2,145	3,001	2,789	2,972									
Solyc07g063300	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT3G15430.6)		F:GO:0016874	F:ligase activity			IPR000408 (PRINTS): IPR009091 (G3	15,119	14,301	21,783	22,599	18,562									
Solyc07g063310	LanC-like protein 2 (AHRD V3.3 *** A0A0B0NT52_GOSAR)		F:GO:0003824	F:catalytic activity			IPR020464 (PRINTS): IPR007822 (PF	33,749	22,095	45,999	43,890	41,473	-0,583	0,037					down		
Solyc07g063320	LanC-like protein 2 (AHRD V3.3 *** A0A0B0NT52_GOSAR)		F:GO:0003824	F:catalytic activity			IPR020464 (PRINTS): IPR007822 (PF	2,735	2,949	3,345	5,709	2,085									
Solyc07g063330	WD-repeat protein, putative (AHRD V3.3 *** B9T7M5_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (SM	41,286	34,735	52,274	53,450	53,429									
Solyc07g063340	Fiber protein Fb34 (AHRD V3.3 *** A0A0A0L071_CUCSA)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769:SF3	94,083	64,888	70,866	67,397	61,384									
Solyc07g063350	COP1-interacting protein, putative (AHRD V3.3 *** A0A072VAF6_MEDTR)		C:GO:0005634; C:GO	C:nucleus; C:plasma membrane; P:response to light stimulus; P:			mobidb-lite (MOBIDB_LITE): mobidb-lit	76,510	35,930	2,322	0,384	1,657	-1,060	0,010					down		
Solyc07g063390	Beta-glucosidase (AHRD V3.3 *** B4FQQ6_MAIZE)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS): G3DSA:3.20.2	18,403	20,677	45,580	60,774	58,245					0,418	0,004			up
Solyc07g063400	ABC transporter G family member (AHRD V3.3 *** A0A0K9Q0M2_ZOSMR)	ABCG20	F:GO:0005524; C:GO	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): G3DSA:3.40.50	0,131	0,165	0,000	0,122	0,000									
Solyc07g063410	JA2-like	SNAC070	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	12,698	17,702	24,503	23,781	18,811									
Solyc07g063420	NAC domain transcription factor	NAC3	F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	57,494	39,319	79,188	81,648	61,188									
Solyc07g063430	Peroxisomal membrane (Mpv17/PMP22) family protein (AHRD V3.3 *** F4JI90_ARATH)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM): PTHR11266:SF7	490,759	370,443	438,122	352,978	390,630									
Solyc07g063440	Trafficking particle complex subunit 10 (AHRD V3.3 *** A0A0B0PCG8_GOSAR)		F:GO:0005515	F:protein binding			IPR022233 (PFAM): IPR021773 (PFA	102,765	85,386	92,356	88,400	90,193									
Solyc07g063450	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *** A0A0B0MWK3_GOSAR)		F:GO:0003677; F:GO	F:DNA binding; F:protein binding; F:oxidoreductase activity; P:o			IPR036188 (G3DSA:3.50.50.GENE3D	12,206	10,113	11,252	11,492	12,962									
Solyc07g063460	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G54400.1)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0	60,328	76,495	23,049	24,576	31,441			0,445	0,034				up	
Solyc07g063470	LOW QUALITY:methionyl-tRNA synthetase (AHRD V3.3 -** AT5G10695.1)						PTHR33320:SF5 (PANTHER): PTHR3	0,000	0,000	0,000	0,025	0,024									
Solyc07g063475	protein kinase family protein (AHRD V3.3 *** AT5G54380.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR024788 (PF	52,183	22,523	57,891	82,806	86,851	-1,185	0,000	0,581	0,009	0,519	0,026	down	up	up
Solyc07g063480	protein kinase family protein (AHRD V3.3 *-* AT5G54380.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	0,475	0,543	0,561	0,628	0,636									
Solyc07g063490	Root cap/late embryogenesis-like protein (AHRD V3.3 *** A0A072VAI7_MEDTR)						PTHR31656 (PANTHER): PTHR31656	1,722	0,875	0,569	0,571	0,658									
Solyc07g063500	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *** A0A0B0MWK3_GOSAR)		F:GO:0003677; F:GO	F:DNA binding; F:protein binding; F:oxidoreductase activity; P:o			G3DSA:3.90.660.10 (GENE3D): IPR0	0,819	0,760	0,545	0,460	0,681									
Solyc07g063510	Cystathionine beta-lyase family protein (AHRD V3.3 *** G7LD70_MEDTR)		F:GO:0003824; F:GO	F:catalytic activity; F:pyridoxal phosphate binding			IPR015421 (G3DSA:3.40.640.GENE3	4,361	4,261	5,676	4,347	6,706									
Solyc07g063520	Organic solute transporter ostalpha protein (AHRD V3.3 *** G7ILE3_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR005178 (PFAM): PTHR23423:SF3	82,790	163,702	104,600	106,395	118,635	1,009	0,007					up		
Solyc07g063530	U3 small nucleolar RNA-associated protein 14 B isoform 3 (AHRD V3.3 *** A0A061FEA7_THECC)		C:GO:0016021	C:integral component of membrane			PTHR36785 (PANTHER)	43,589	51,613	90,340	95,275	108,376									
Solyc07g063540	1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase (AHRD V3.3 *** A0A0B0PDZ2_GOSAR)						PTHR35292 (PANTHER): PTHR35292	13,871	14,290	15,891	10,879	13,870					-0,544	0,010			down
Solyc07g063550	Arf GTPase activating protein (AHRD V3.3 *** A0A103YJY6_CYNCS)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (SM	103,010	130,412	86,793	86,120	97,449									
Solyc07g063560	Cotton fiber expressed protein (AHRD V3.3 *** A0A109Y892_GOSBA)		C:GO:0016020	C:membrane			IPR025520 (PFAM): IPR008480 (PFA	0,946	1,179	0,289	0,763	0,467									
Solyc07g063570	Cytochrome c-type biogenesis ccda-like chloroplastic protein (AHRD V3.3 *** CCDA_ARATH)		C:GO:0016020; P:GO	C:membrane; P:cytochrome complex assembly; P:oxidation-red			IPR003834 (PFAM): PTHR31272:SF6	16,256	17,578	33,597	28,452	33,217									
Solyc07g063580	Vacuolar sorting protein 9 (VPS9) domain-containing protein (AHRD V3.3 --* AT3G19770.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,424	3,433	3,020	2,552	2,750									
Solyc07g063590	Myosin VIII-B (AHRD V3.3 *** B0CN64_NICBE)		F:GO:0003774; F:GO	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR001609 (SM	15,961	10,934	6,549	5,432	5,755									
Solyc07g063600	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1BNX7_SOLTU)		P:GO:0009765; C:GO	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	50,392	330,215	30,094	59,687	108,012	2,740	0,000	1,839	0,000	0,990	0,000	up	up	up
Solyc07g063610	Dynein light chain family protein (AHRD V3.3 *** B9N570_POPTR)		P:GO:0007017; C:GO	P:microtubule-based process; C:dynein complex			IPR001372 (SMART): IPR001372 (PF	3,356	14,717	3,795	6,155	6,456	2,150	0,000					up		
Solyc07g063620	membrane lipoprotein lipid attachment site-like protein, putative (DUF1223) (AHRD V3.3 *** AT4G27350.1)						IPR010634 (PFAM): mobidb-lite (MOB	85,034	87,898	108,532	149,699	84,651					0,468	0,027			up
Solyc07g063630	Vesicle-associated 4-2-like protein (AHRD V3.3 *** A0A0B0MUH3_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR000535 (PFAM): IPR013783 (G3D	56,177	54,949	44,988	48,328	41,318									
Solyc07g063650	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9SIG8_RICCO)		F:GO:0004843; F:GO	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001607 (SMART): IPR015940 (SM	81,192	80,161	157,173	147,538	125,869									
Solyc07g063670	LOW QUALITY:mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT4G28840.2)		F:GO:0003700	F:DNA-binding transcription factor activity			IPR014855 (PFAM NZZ/SPL	0,040	0,043	0,000	0,000	0,000									
Solyc07g063680	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)						IPR006015 (PRINTS): IPR014729 (G3	55,574	59,444	91,842	81,442	79,090									
Solyc07g063690	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0	3,606	4,981	0,047	0,169	0,000									
Solyc07g063700	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR003609 (SM	0,000	0,098	0,641	0,472	0,426									
Solyc07g063710	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	0,021	0,039	0,147	0,388	0,521									
Solyc07g063720	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR003609 (SM	0,080	0,186	0,312	0,095	0,142									
Solyc07g063730	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR003609 (SM	0,395	1,482	0,975	0,393	0,521									
Solyc07g063735	Serine/threonine-protein kinase (AHRD V3.3 *-* M1BNV7_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,000	0,000	0,044	0,051	0,024									
Solyc07g063737	RNA polymerase II transcription mediator (AHRD V3.3 --* AT4G00450.3)							0,000	0,000	0,000	0,025	0,000									
Solyc07g063740	Ferredoxin-like protein (AHRD V3.3 *** G7J8F5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR035940 (G3DSA:3.40.33.GENE3D	0,021	0,021	0,000	0,025	0,096									
Solyc07g063750	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR000719 (SM	0,142	0,061	0,709	1,040	0,614									
Solyc07g063770	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IT75_SOLCH)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR001480 (SM	0,927	10,645	2,110	4,456	6,418	3,529	0,000	1,589	0,000			up	up	
Solyc07g063780	Serine/threonine-protein kinase (AHRD V3.3 *** M1BP20_SOLTU)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (SMART): IPR003609 (SM	0,000	0,244	0,025	0,025	0,118									
Solyc07g063820	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IT75_SOLCH)		F:GO:0004674; F:GO	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (SMART): IPR003609 (SM	3,436	4,613	1,013	1,017	1,598									
Solyc07g063830	bHLH transcription factor142		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	2,056	2,301	0,717	0,653	0,757									
Solyc07g063850	IAA-amido synthetase 3-9	GH3_9					IPR004993 (PFAM): PTHR31901:SF2	0,927	1,296	1,256	2,514	1,109					0,980	0,041			up
Solyc07g063860	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT3G07460.1)		C:GO:0016021	C:integral component of membrane			IPR036758 (G3DSA:2.30.240.GENE3	21,166	22,476	2,165	1,832	2,766									
Solyc07g063870	HEAT repeat-containing 8 (AHRD V3.3 *** A0A0B0NMT2_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	108,062	114,879	129,489	131,567	132,799									
Solyc07g063880	Beta-glucosidase, putative (AHRD V3.3 *** B9SY45_RICCO)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS): G3DSA:3.20.2	0,119	0,120	0,046	0,375	0,518									
Solyc07g063900	RNA binding protein, putative (AHRD V3.3 *-* B9SY46_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	83,064	88,506	197,673	205,304	194,169									
Solyc07g063905	RING/U-box superfamily protein (AHRD V3.3 --* AT3G13430.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,121	0,064	0,022	0,000	0,000									
Solyc07g063910	Ribosomal protein L2 family (AHRD V3.3 *** AT4G36130.1)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022669 (SMART): IPR002171 (SM	104,577	103,762	86,980	73,945	79,525									
Solyc07g063930	Organic cation transporter, putative (AHRD V3.3 *** B9SY49_RICCO)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			IPR005828 (PFAM): G3DSA:1.20.125	4,511	5,706	101,824	99,330	83,461									
Solyc07g063940	SCARECROW	GRAS2	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	50,441	174,235	37,930	24,770	40,197	1,809	0,002					up		
Solyc07g063950	calcium/calmodulin-regulated receptor-like kinase		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	2,851	4,199	0,905	1,008	1,343									
Solyc07g063960	50S ribosomal protein L24, chloroplastic (AHRD V3.3 *** RK24_TOBAC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005824 (SMART): IPR005824 (PF	29,176	57,666	96,908	100,101	130,170	1,010	0,000	0,423	0,047			up	up	
Solyc07g063970	C2H2-like zinc finger protein (AHRD V3.3 *** G7JF39_MEDTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.90.228.1 C2H2	0,552	0,632	0,000	0,000	0,000									
Solyc07g063990	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --*		P:GO:0006355	P:regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,309	0,163	0,220	0,271	0,353									
Solyc07g064010	Formin-like protein (AHRD V3.3 *** K4CH84_SOLLC)		F:GO:0005199; C:GO	F:structural constituent of cell wall; C:integral component of mer			PR01217 (PRINTS): IPR015425 (SMA	4,409	4,093	3,595	4,799	4,795									
Solyc07g064020	Heat shock protein (AHRD V3.3 *** A7UNS9_9ROSI)	Hsp21.6B					IPR002068 (PFAM): IPR008978 (G3D	6,291	5,909	5,334	5,592	5,002									
Solyc07g064030	Kinesin-like protein (AHRD V3.3 *** K4CH86_SOLLC)		F:GO:0003777; F:GO	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	12,136	11,124	3,693	2,646	4,229									
Solyc07g064040	bHLH transcription factor143	bHLH143	F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	107,581	104,538	105,872	98,873	99,660									
Solyc07g064050	Hexosyltransferase (AHRD V3.3 *** K4CH88_SOLLC)	GAUT12	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	0,139	0,180	0,025	0,025	0,000									
Solyc07g064060	Breast carcinoma-amplified sequence 3 (AHRD V3.3 *** A0A0B0NHS9_GOSAR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	54,943	49,468	119,359	115,681	110,191									
Solyc07g064070	U4/U6 small nuclear ribonucleoprotein Prp31 (AHRD V3.3 *** A0A0B0PVX3_GOSAR)		P:GO:0000244; C:GO	P:spliceosomal tri-snRNP complex assembly; C:U4/U6 x U5 tri-s			G3DSA:1.10.246.90 (GENE3D): IPR0	0,079	0,121	0,144	0,241	0,260									
Solyc07g064080	amino-terminal region of chorein (AHRD V3.3 *** AT3G20720.2)						IPR026854 (PFAM): mobidb-lite (MOB	60,149	53,964	76,866	78,878	75,189									
Solyc07g064110	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SA19_RICCO)		F:GO:0005515	F:protein binding			IPR033443 (PFAM): IPR002885 (PFA	27,253	21,769	29,654	34,142	30,904									
Solyc07g064120	ABC transporter B family protein (AHRD V3.3 *** G7JF16_MEDTR)	ABCB12	F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR011527 (PF	0,726	0,556	0,072	0,117	0,143									
Solyc07g064130	Polyubiquitin (AHRD V3.3 *** UBI1P_NICSY)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): IPR000626 (SM	2580,554	2705,717	4574,244	4113,786	3954,238									
Solyc07g064140	Ammonium transporter 1 member 1 (AHRD V3.3 --* AMT11_ARATH)							0,716	0,573	1,784	1,193	1,649									
Solyc07g064150	Protein translation factor SUI1 homolog (AHRD V3.3 *** SUI1_ORYSJ)		F:GO:0003743; P:GO	F:translation initiation factor activity; P:translational initiation			IPR001950 (PFAM): G3DSA:3.30.780	1221,236	1088,006	675,649	682,377	674,821									
Solyc07g064160	Thiamine thiazole synthase, chloroplastic (AHRD V3.3 *** K4CH99_SOLLC)		P:GO:0009228	P:thiamine biosynthetic process			PR00419 (PRINTS): PF01946 (PFAM)	5206,451	4241,462	1720,283	935,144	1679,175					-0,878	0,009			down
Solyc07g064170	pectin esterase	pme1.9	F:GO:0004857; F:GO	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR006501 (TIG	9214,849	4530,840	7335,233	5307,891	6442,178	-0,997	0,000			-0,464	0,014	down		down
Solyc07g064180	pectin methylesterase 2	pme2.1	F:GO:0004857; F:GO	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR000070 (PF	413,941	217,029	573,909	408,312	470,228	-0,904	0,000			-0,488	0,009	down		down
Solyc07g064190	pectin methylesterase LePME3		F:GO:0004857; F:GO	F:enzyme inhibitor a	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR006501 (SMART): IPR035513 (G3	0,078	0,019	0,869	1,477	1,106									
Solyc07g064200	COBRA-like protein (AHRD V3.3 *** L0ASI2_POPTO)		P:GO:0010215; P:GO	P:cellulose microfibril organization; P:cell growth; C:anchored co			IPR006918 (PFAM): PTHR31052:SF2	0,288	0,200	0,945	4,387	1,493					2,221	0,000			up
Solyc07g064210	LOW QUALITY:Grain softness protein (AHRD V3.3 -** G8CLR7_PSAJU)						IPR016140 (SMART): IPR016140 (PF	117,125	108,469	0,266	0,327	0,024									
Solyc07g064220	LOW QUALITY:Grain softness protein (AHRD V3.3 -** G8CLR7_PSAJU)		F:GO:0045735	F:nutrient reservoir activity			IPR000617 (PRINTS): IPR016140 (SM	2,284	2,241	0,125	0,127	0,070									
Solyc07g064230	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G27100.2)						IPR000195 (SMART): G3DSA:1.10.8.2	7,082	9,129	2,252	2,720	2,419									
Solyc07g064240	Early nodulin-like protein (AHRD V3.3 *** A0A072VAV5_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	2,881	3,874	0,560	0,900	0,777									
Solyc07g064250	Protein disulfide-isomerase 5-4 (AHRD V3.3 *** A0A0B2SSL7_GLYSO)		P:GO:0045454	P:cell redox homeostasis			IPR039542 (PFAM): G3DSA:3.40.30.1	108,999	93,415	129,173	116,930	113,348									
Solyc07g064260	F-box/RNI superfamily protein (AHRD V3.3 *-* A0A061F6J1_THECC)		F:GO:0005515	F:protein binding			IPR013101 (PFAM): IPR001810 (PFA	0,756	0,620	2,036	2,261	2,026									
Solyc07g064270	Glucose-6-phosphate/phosphate-translocator family protein (AHRD V3.3 *** B9I0B8_POPTR)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport			IPR004853 (PFAM): IPR004696 (TIGF	42,999	41,476	106,849	101,000	88,585									
Solyc07g064280	Tryptophan synthase (AHRD V3.3 *** K4CHA9_SOLLC)		P:GO:0000162; F:GO	P:tryptophan biosyn	EC:4.2.1.2	Tryptophan synthase	IPR023026 (PIRSF): IPR001926 (PFA	31,982	27,318	18,854	14,015	19,277									
Solyc07g064290	Ras-related small GTP-binding family protein (AHRD V3.3 *** G7K3G2_MEDTR)		F:GO:0003924; F:GO	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): SM00175 (SMAR	7,060	17,189	7,127	8,357	7,808	1,306	0,025					up		
Solyc07g064300	Dystrobrevin alpha (AHRD V3.3 *** A0A0B0PJT5_GOSAR)		C:GO:0016020	C:membrane			IPR027951 (PFAM): mobidb-lite (MOB	13,439	11,978	14,794	14,535	14,663									
Solyc07g064320	Eukaryotic translation initiation factor 2B (eIF-2B) family protein (AHRD V3.3 --* AT1G53900.3)						mobidb-lite (MOBIDB_LITE): PTHR364	4,096	3,713	1,724	1,903	2,047									

Solyc07g064330	DNA polymerase (AHRD V3.3 *** Q3LHT0_TOBAC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA pc	IPR002298 (PRINTS): IPR001098 (SM	21,855	19,146	23,524	22,911	24,946									
Solyc07g064340	Kinase family protein (AHRD V3.3 *** U5GUL9_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	6,150	5,892	6,966	6,315	6,779									
Solyc07g064350	Protein KRI1 like (AHRD V3.3 *** A0A0B2Q3E3_GLYSO)		P:GO:0000447; C:G(	P:endonucleolytic cleavage in ITS1 to separate SSU-rRNA from			IPR018034 (PFAM): IPR024626 (PFA	36,699	53,678	36,797	31,563	33,612	0,576	0,022					up		
Solyc07g064360	LOW QUALITY:serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)						IPR019557 (PFAM): mobidb-lite (MOB	0,416	1,072	0,044	0,094	0,187									
Solyc07g064370	Aminotransferase-like, plant mobile domain family protein (AHRD V3.3 *-* AT5G18510.1)						IPR019557 (PFAM): mobidb-lite (MOB	1,717	1,540	1,438	2,406	1,698									
Solyc07g064373	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)						IPR019557 (PFAM): PTHR16007:SF4	1,644	1,557	0,755	1,461	0,893									
Solyc07g064380	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)						IPR019557 (PFAM): IPR025558 (PFA	3,738	3,822	2,248	2,730	2,483									
Solyc07g064390	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G16580.1)		F:GO:0003824	F:catalytic activity			IPR001932 (SMART): IPR001932 (SM	1,499	1,226	0,461	0,162	0,564									
Solyc07g064400	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151T1F8_CAJCA)						IPR019557 (PFAM): PTHR16007:SF4	2,560	2,141	0,554	0,362	0,798									
Solyc07g064410	Kua-ubiquitin conjugating enzyme hybrid, localization (AHRD V3.3 *** A0A103XYI2_CYNCS)						IPR019547 (PFAM): PTHR44910 (PAN	0,337	0,538	25,529	18,423	28,509									
Solyc07g064420	inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** AT4G27020.1)						PTHR31354:SF0 (PANTHER): PTHR3	6,619	6,836	27,319	29,990	33,697									
Solyc07g064440	inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** AT4G27020.1)						PTHR31354:SF0 (PANTHER): PTHR3	27,495	19,725	70,169	75,509	67,370									
Solyc07g064450	Cytochrome P450 (AHRD V3.3 *** A0A061FD55_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,276	0,277	0,398	0,145	0,238									
Solyc07g064470	Cytochrome P450 (AHRD V3.3 *-* A0A061FD55_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3	0,279	0,367	0,262	0,192	0,212									
Solyc07g064475	Transmembrane proteins 14C (AHRD V3.3 *** A0A061F6B6_THECC)		C:GO:0016020	C:membrane			IPR005349 (PFAM): G3DSA:1.20.58.1	7,766	10,050	9,072	8,590	8,943									
Solyc07g064480	LOW QUALITY:DTW domain protein (AHRD V3.3 *-* G7K8G0_MEDTR)						IPR005636 (SMART): IPR005636 (PF	1,550	1,670	0,857	0,726	0,963									
Solyc07g064490	CRS2-associated factor 1 (AHRD V3.3 *** A0A072THI3_MEDTR)		F:GO:0003723	F:RNA binding			IPR001890 (SMART): IPR001890 (PF	0,365	1,215	0,289	0,394	0,281									
Solyc07g064500	Purple acid phosphatase (AHRD V3.3 *** K4CHD0_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR008963 (G3DSA:2.60.40.GENE3D	0,061	0,240	0,267	0,240	0,141									
Solyc07g064510	RNA-binding family protein (AHRD V3.3 *** A0A061FD24_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	241,796	243,216	284,054	271,837	282,316									
Solyc07g064520	RNA helicase DEAD24	DEAD24	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR014001 (SMART): IPR001650 (SM	22,447	22,331	17,705	17,301	16,815									
Solyc07g064540	E3 ubiquitin-protein ligase SHPRH (AHRD V3.3 *-* W9RI37_9ROSA)		F:GO:0005524; F:G(	F:ATP binding; F:ligase activity; F:metal ion binding				0,310	0,169	0,193	0,293	0,376									
Solyc07g064550	Ataxin-2 (AHRD V3.3 *** A0A0B0NEZ9_GOSAR)		C:GO:0010494; P:G(	C:cytoplasmic stress granule; P:regulation of cytoplasmic mRNA			IPR025852 (PFAM): mobidb-lite (MOB	10,289	11,713	11,951	11,898	10,735									
Solyc07g064560	AT hook, DNA-binding motif-containing protein (AHRD V3.3 *** A0A103YJM2_CYNCS)		F:GO:0043565	F:sequence-specific DNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	26,085	35,969	43,763	38,192	45,525									
Solyc07g064570	Rho GTPase-activating 32 (AHRD V3.3 *** A0A0B0PG63_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	16,159	16,415	12,403	12,124	12,587									
Solyc07g064580	actin cytoskeleton-regulatory complex pan-like protein (AHRD V3.3 *** AT1G50660.1)						mobidb-lite (MOBIDB_LITE): PTHR310	36,468	48,946	16,631	13,691	14,855									
Solyc07g064590	inducible plastid-lipid associated protein	chrdi	F:GO:0004843; P:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR003323 (PFAM): G3DSA:3.90.70.8	19,050	18,835	32,454	33,021	30,579									
Solyc07g064600	inducible plastid-lipid associated protein		C:GO:0005829; C:G(	C:cytosol; C:membrane; F:deaminase activity; P:organonitroge			IPR006175 (PFAM): IPR006056 (TIGF	1,393	2,548	1,027	1,029	1,347									
Solyc07g064610	alcium-dependent protein kinase 1	cdpk1	F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (SMART): IPR002048 (SM	71,137	109,252	29,700	32,746	39,023									
Solyc07g064615	Thioredoxin superfamily protein (AHRD V3.3 --* AT1G21350.5)							0,159	0,085	0,072	0,095	0,093									
Solyc07g064620	Translation factor SUI1 (AHRD V3.3 *** S5VDU4_9FABA)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			G3DSA:3.30.780.10 (GENE3D): IPR0(	153,709	216,786	356,687	495,322	363,721					0,477	0,009			up
Solyc07g064625	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7MDP3_ARALL)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	10,968	9,433	9,700	12,010	11,259									
Solyc07g064630	RNI-like superfamily protein (AHRD V3.3 *** AT4G26980.1)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:SCF ubiquitin ligase co			IPR006553 (SMART): IPR032675 (G3	12,583	11,598	14,396	15,758	13,960									
Solyc07g064640	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 (AHRD V3.3 *** M1C0L3_SOLTU)		F:GO:0008137; F:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR007763 (PFAM): mobidb-lite (MOB	3,940	4,776	5,585	5,764	4,733									
Solyc07g064650	senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *-* AT4G21970.1)		C:GO:0009506	C:plasmodesma			IPR007608 (PFAM): mobidb-lite (MOB	2,439	2,384	4,899	4,312	3,387									
Solyc07g064660	LOW QUALITY:Geranylgeranyl diphosphate synthase (AHRD V3.3 *** A0A1B0RS86_9ROSI)		P:GO:0008299	P:isoprenoid biosynthetic process			IPR000092 (PFAM): IPR008949 (G3D	0,000	0,082	3,752	3,683	1,598			-1,227	0,041				down	
Solyc07g064670	Hexosyltransferase (AHRD V3.3 *** K4CHE6_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR025298 (PFAM): G3DSA:3.90.550	96,896	78,750	53,822	52,175	43,787									
Solyc07g064680	Autophagy-related protein (AHRD V3.3 *** A0A0V0GZ47_SOLCH)		C:GO:0005737; P:G(	C:cytoplasm; P:autophagy; P:cellular response to nitrogen starv			IPR004241 (PFAM): G3DSA:3.10.20.9	87,353	68,640	223,306	185,593	172,358									
Solyc07g064690	LOW QUALITY:50S ribosomal protein L34 (AHRD V3.3 *** AT1G29040.1)		C:GO:0005773; C:G(	C:vacuole; C:chloroplast			IPR037103 (G3DSA:3.30.1330.GENE	35,729	24,035	110,876	114,408	100,903	-0,545	0,048					down		
Solyc07g064700	Bromodomain-containing protein, putative (AHRD V3.3 *** A0A061F5J3_THECC)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR001487 (SM	48,260	50,290	45,506	44,769	49,287									
Solyc07g064710	Tetraacyldisaccharide 4'-kinase family protein (AHRD V3.3 *** U5GWH8_POPTR)		F:GO:0005524; F:G(	F:ATP binding; F:tet	EC:2.7.1.13	Tetraacyldisaccharid	IPR003758 (PFAM): IPR003758 (PAN	4,064	4,663	5,081	4,935	4,735									
Solyc07g064720	GDSL esterase/lipase (AHRD V3.3 *** W9RB61_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	2,113	10,025	1,657	1,563	1,909	2,266	0,002					up		
Solyc07g064730	GDSL esterase/lipase (AHRD V3.3 *** W9RB61_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	0,042	0,192	0,246	0,736	0,212									
Solyc07g064740	Rab3 GTPase-activating protein catalytic subunit (AHRD V3.3 *** AT5G55060.1)		F:GO:0005096	F:GTPase activator activity			IPR026147 (PFAM): mobidb-lite (MOB	14,178	30,334	13,320	13,117	16,168	1,122	0,004					up		
Solyc07g064760	Eukaryotic release factor 1 (eRF1) family protein (AHRD V3.3 --* AT4G27650.3)		C:GO:0016021	C:integral component of membrane			PTHR37196 (PANTHER)	0,282	0,433	0,118	0,075	0,187									
Solyc07g064770	Outer envelope protein 80, chloroplastic (AHRD V3.3 --* OEP80_ORYSI)						PR01228 (PRINTS): mobidb-lite (MOB	0,808	0,720	0,025	0,000	0,000									
Solyc07g064790	calcium ATPase 2 (AHRD V3.3 --* AT4G37640.1)						PR01228 (PRINTS): mobidb-lite (MOB	21,994	24,749	1,558	2,436	0,371									
Solyc07g064800	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** A0A0D	F:GO:0004149; P:G(	F:dihydrolipoyllysine	EC:2.3.1.61	Dihydrolipoyllysine-re			IPR001078 (PFAM): IPR000089 (PFA	74,639	74,053	100,208	101,370	102,055									
Solyc07g064810	Imidazole glycerol phosphate synthase hisHF family protein (AHRD V3.3 *** B9GFE9_POPTR)		P:GO:0000105; F:G(	P:histidine biosynthetic process; F:imidazoleglycerol-phosphate			IPR010139 (TIGRFAM): IPR004651 (T	43,653	39,176	54,101	43,277	51,946									
Solyc07g064820	LOW QUALITY:MAP kinase kinase kinase 59	MAPKKK59	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): G3DSA:1.10.51	12,069	11,759	1,728	3,264	2,440									
Solyc07g064830	Starch branching enzyme III (AHRD V3.3 *** I0B8P4_WHEAT)		F:GO:0003844; F:G(	F:1,4-alpha-glucan l	EC:2.4.1.18	1,4-alpha-glucan bra	IPR006047 (SMART): IPR013783 (G3	13,977	16,072	12,378	15,620	18,421			0,569	0,006				up	
Solyc07g064840	Oral cancer-overexpressed protein 1 (AHRD V3.3 *** A0A0B2RBT1_GLYSO)						IPR019191 (PFAM): mobidb-lite (MOB	8,595	7,751	11,331	10,257	9,420									
Solyc07g064850	Adenylyltransferase and sulfurtransferase MOCS3 (AHRD V3.3 *** K4CHG4_SOLLC)		P:GO:0002143; F:G(	P:tRNA wobble posi	EC:2.8.1.1	Thiosulfate sulfurtran	IPR001763 (SMART): IPR036873 (G3	12,742	10,776	10,555	9,946	9,998									
Solyc07g064860	pumilio 13 (AHRD V3.3 --* AT5G43090.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,021	0,000	0,075	0,000									
Solyc07g064870	Endoglucanase (AHRD V3.3 *** M1C0J8_SOLTU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbo			IPR001701 (PFAM): IPR012341 (G3D	18,889	21,067	1,908	1,805	2,367									
Solyc07g064880	Small ubiquitin-related modifier (AHRD V3.3 *** A0A0V0GSM0_SOLCH)		F:GO:0005515; P:G(	F:protein binding; P:protein sumoylation			IPR000626 (SMART): IPR022617 (PF	28,782	27,890	41,863	36,839	35,252									
Solyc07g064890	Ethylene Response Factor F.2	ERF.F2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN' ERF	136,151	107,163	163,938	152,638	144,764									
Solyc07g064900	extracellular ligand-gated ion channel protein (DUF3537) (AHRD V3.3 *** AT3G20300.1)		C:GO:0016021	C:integral component of membrane			IPR021924 (PFAM): PTHR31963:SF4	41,608	32,206	65,486	76,433	69,113									
Solyc07g064910	EH domain-containing protein 1 (AHRD V3.3 *** A0A1D1YR31_9ARAE)		F:GO:0005509; F:G(	F:calcium ion binding; F:protein binding; F:GTP binding			IPR000261 (SMART): IPR002048 (SM	27,286	25,687	20,308	17,602	21,286									
Solyc07g064920	Upstream activation factor subunit spp27 (AHRD V3.3 *** A0A0B2NVJ3_GLYSO)		F:GO:0005515	F:protein binding			IPR019835 (SMART): IPR003121 (PF	10,068	10,504	13,706	14,846	13,889									
Solyc07g064930	GrpE protein homolog (AHRD V3.3 *** K4CHH2_SOLLC)		F:GO:0000774; P:G(	F:adenyl-nucleotide exchange factor activity; P:protein folding; I			IPR000740 (PRINTS): IPR013805 (G3	19,748	23,663	35,111	35,367	31,709									
Solyc07g064940	Thioredoxin-like protein (AHRD V3.3 *** W9RN22_9ROSA)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			IPR013766 (PFAM): G3DSA:3.40.30.1	5,229	6,544	8,466	8,998	8,954									
Solyc07g064950	trigger factor type chaperone family protein (AHRD V3.3 *** AT5G55220.1)		P:GO:0006457; P:G(	P:protein folding; P:protein transport			IPR036611 (G3DSA:3.30.70.GENE3D	5,993	7,533	15,821	16,412	19,613									
Solyc07g064960	Phosphatidate cytidylyltransferase (AHRD V3.3 *** K4CHH5_SOLLC),Pfam:PF01148		C:GO:0016020; F:G(	C:membrane; F:transferase activity, transferring phosphorus-co			PF01148 (PFAM): PTHR13773:SF13 (	0,873	1,178	0,274	0,169	0,304									
Solyc07g064970	Microtubule associated family protein (AHRD V3.3 *** B9GJD5_POPTR)		P:GO:0000226; F:G(	P:microtubule cytoskeleton organization; F:microtubule binding			PF03999 (PFAM): G3DSA:1.20.58.152	117,132	108,997	86,626	92,365	87,747									
Solyc07g064980	lyst-Interacting Protein5-like protein		C:GO:0005634; C:G(	C:nucleus; C:multivesicular body; P:defense response, incompa			IPR023175 (G3DSA:1.25.40.GENE3D	64,446	81,633	73,723	81,786	75,390									
Solyc07g064990	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (AHRD V3.3 *** B9GJG7_POPTR)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM): G3DSA:1.10.120	0,311	0,197	0,000	0,000	0,046									
Solyc07g065000	PHD-finger protein (AHRD V3.3 *** G7K8Q7_MEDTR)		F:GO:0003682	F:chromatin binding			IPR001025 (SMART): IPR001965 (SM	21,927	24,588	25,778	26,592	24,596									
Solyc07g065010	lipid-binding serum glycoprotein family protein (AHRD V3.3 *** AT1G04970.1)		C:GO:0005615; F:G(	C:extracellular space; F:lipid binding			IPR001124 (SMART): G3DSA:3.15.10	30,582	21,448	36,861	41,641	38,558									
Solyc07g065020	Serine/threonine-protein phosphatase (AHRD V3.3 *** K4CHI1_SOLLC)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR006186 (SM	30,513	27,999	37,424	33,767	33,290									
Solyc07g065030	Syntaxin-51 (AHRD V3.3 *** A0A0B2QVT0_GLYSO)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			IPR000727 (SMART): G3DSA:1.20.5.1	60,955	54,577	75,885	72,661	73,777									
Solyc07g065040	Transcription initiation factor TFIID subunit-like protein (AHRD V3.3 *** G7KXV7_MEDTR)		C:GO:0000124; C:G(	C:SAGA complex; C:transcription factor TFIID complex; P:regula			IPR004823 (SMART): IPR011442 (PF	0,119	0,057	0,051	0,123	0,000									
Solyc07g065050	Cell division protein FtsZ-1-like protein (AHRD V3.3 *** W9RBJ2_9ROSA)	FTsZ1	F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR003008 (PRINTS): IPR018316 (SM	2,717	2,393	2,762	3,536	2,735									
Solyc07g065060	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** G7K4B1_MEDTR)		F:GO:0008374	F:O-acyltransferase activity			IPR017088 (PIRSF): IPR032805 (PFA	1,744	1,639	0,196	0,632	0,634									
Solyc07g065070	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55360.1)		F:GO:0008374; C:G(	F:O-acyltransferase activity; C:integral component of membrane			IPR032805 (PFAM): PTHR31595 (PAN	0,438	0,203	0,047	0,000	0,072									
Solyc07g065080	Fimbrin-like potential actin filament bundling protein (AHRD V1 *--* Q5AC06_CANAL)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly			IPR001715 (SMART): IPR001715 (PF	91,048	119,918	93,275	84,890	95,900									
Solyc07g065090	polygalacturonase inhibitor protein		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR001611 (PFA	67,774	77,402	37,192	24,289	31,281					-0,611	0,020			down
Solyc07g065110	Lipid transfer protein (AHRD V3.3 *** G7J041_MEDTR)		F:GO:0005504; P:G(	F:fatty acid binding; P:systemic acquired resistance			IPR016140 (SMART): G3DSA:1.10.11	7,305	22,022	2,226	0,269	0,619			-1,831	0,027				down	
Solyc07g065120	Glycerophosphoryl diester phosphodiesterase, putative (AHRD V3.3 *** B9SSQ8_RICCO)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR030395 (PFAM): IPR017946 (G3D	200,917	171,118	200,005	252,313	249,323									
Solyc07g065125	bric-a-brac protein (AHRD V3.3 --* AT3G11591.1)		C:GO:0016021	C:integral component of membrane				1,307	1,033	0,711	0,636	1,134									
Solyc07g065130	Calcium-binding protein, putative (AHRD V3.3 *** B9T038_RICCO)		F:GO:0004674; P:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR011989 (G3DSA:1.25.10.GENE3D	0,839	0,713	0,022	0,073	0,024									
Solyc07g065140	Beta-1,2-xylosyltransferase (AHRD V3.3 *** Q2UVB5_SOLTU)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM): IPR007657 (PAN	33,446	41,487	17,049	17,146	16,500									
Solyc07g065160	Calcium-binding EF hand family protein (AHRD V3.3 --* AT1G21630.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,122	0,279	0,025	0,000	0,094									
Solyc07g065165	Pirin-like protein (AHRD V3.3 *** A0A0B2SAS7_GLYSO)						IPR014710 (G3DSA:2.60.120.GENE3	2,637	4,172	0,605	0,707	0,776									
Solyc07g065170	40S ribosomal protein S8 (AHRD V3.3 *** K4CHJ6_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.168.20 (GENE3D): G3DS	93,901	110,782	114,029	103,685	101,192									
Solyc07g065180	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG (AHRD V3.3 *** Q01BB2_OSTTA)		F:GO:0016787	F:hydrolase activity			G3DSA:3.40.50.450 (GENE3D): IPR0	5,602	7,335	11,103	10,373	11,044									
Solyc07g065185	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT3G06130.1)						G3DSA:3.30.70.100 (GENE3D): PTHR	0,000	0,000	0,025	0,000	0,024									
Solyc07g065200	Mitochondrial import inner membrane translocase subunit tim22 (AHRD V3.3 *** A0A0B0NT47_GOSAR)		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion comple			PF02466 (PFAM): mobidb-lite (MOBID	33,536	38,484	68,406	68,489	66,291									
Solyc07g065210	Kinesin related protein (AHRD V3.3 *** Q8GZU1_SOLLC)	tkr	F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	0,397	0,885	0,022	0,000	0,000									
Solyc07g065220	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** G5DXN7_SILLA)						IPR000008 (PFAM): IPR035892 (G3D	35,257	40,015	67,346	79,542	70,022									
Solyc07g065240	Leucine-rich repeat protein kinase family protein, putative (AHRD V3.3 *** A0A061FCG5_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	0,287	0,199	0,349	0,417	0,400									
Solyc07g065250	MAP kinase kinase kinase 60	MAPKKK60	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:3.30.2	6,678	14,128	7,711	7,014	5,971	1,103	0,008					up		
Solyc07g065260	WRKY transcription factor 18	WRKY18	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR003657 (SMAF WRKY	33,543	25,835	31,397	27,714	30,824									
Solyc07g065270	GRAS7	GRAS7	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	52,402	53,936	120,945	109,477	109,555									
Solyc07g065280	NADH-ubiquinone oxidoreductase subunit (AHRD V3.3 *** A0A1D1ZJA2_9ARAE)		C:GO:0005747; C:G(	C:mitochondrial respiratory chain complex I; C:integral compone			IPR019721 (PFAM): PTHR34062 (PAN	56,514	54,793	102,180	90,463	94,744									
Solyc07g065290	Zinc finger transcription factor 51	C3H51	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (SMART): IPR000571 (SM	5,917	4,109	25,446	32,561	33,162									
Solyc07g065310	DUF21 domain-containing protein (AHRD V3.3 *** W9R460_9ROSA)		F:GO:0050660	F:flavin adenine dinucleotide binding			IPR005170 (SMART): IPR000644 (SM	28,060	30,634	58,967	61,175	54,457									
Solyc07g065320	ABC subfamily C transporter (AHRD V3.3 *** A0A0D3RBU8_WHEAT)	ABCC5	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003593 (SMART): IPR036640 (G3	6,273	7,221	2,882	4,619	5,502			0,920	0,003				up	
Solyc07g065330	Germin-like protein (AHRD V3.3 *** Q8GSQ5_9BRYO)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (SM	0,195	0,256	0,391	0,421	0,425									
Solyc07g065340	Serine acetyltransferase (AHRD V3.3 *** Q6STL5_NICPL)		C:GO:0005737; P:G(	C:cytoplasm; P:cys	EC:2.3.1.3	Serine O-acetyltrans	IPR010493 (SMART): IPR001451 (PF	9,483	15,346	85,435	109,205	51,482	0,721	0,011	-0,732	0,004			up	down	
Solyc07g065370	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative (AHRD V3.3 *** A0A	F:GO:0003682	F:chromatin binding				IPR001025 (SMART): IPR014002 (SM	103,089	121,955	117,871	110,432	104,968									
Solyc07g065380	putative zinc transporter		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR003689 (PFAM): mobidb-lite (MOB	59,476	93,468	70,228	73,344	77,369	0,678	0,045					up		
Solyc07g065390	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 --* AT1G52240.1)							1,525	1,095	2,105	2,101	2,106									
Solyc07g065400	Mitochondrial import inner membrane translocase subunit TIM50-C (AHRD V1 *-*- D3TQJ3_GLOMM)		F:GO:0004721; C:G(	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threonine phosphatase		6,079	5,222	6,763	6,524	6,876									
Solyc07g065410	LOW QUALITY:Melanin-concentrating hormone receptor 1 (AHRD V3.3 *** A0A1D1ZFH6_9ARAE)		P:GO:0071281; P:G(	P:cellular response to iron ion; P:cellular response to ethylene s			PTHR33513:SF2 (PANTHER): PTHR3	9,670	10,089	47,929	38,935	36,524									
Solyc07g065420	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G06990.1)						IPR006460 (TIGRFAM): IPR006460 (F	0,315	0,487	19,251	15,237	13,784			-0,484	0,047				down	
Solyc07g065440	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT3G06130.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			PTHR22814 (PANTHER): PTHR22814	0,637	0,555	0,483	0,290	0,212									
Solyc07g065450	Outward rectifying potassium channel protein (AHRD V3.3 *** AT5G55630.2)		F:GO:0005267; C:G(	F:potassium channel activity; C:membrane; P:potassium ion tra			IPR003280 (PRINTS): IPR013099 (PF	1,767	1,689	0,889	0,876	1,055									
Solyc07g065460	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT4G16400.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR341	1,066	1,015	0,304	0,346	0,658									
Solyc07g065470	Cysteine synthase (AHRD V3.3 *** A0A0A0K304_CUCSA)		F:GO:0004124; C:G(	F:cysteine synthase	EC:2.5.1.47; EC:4.4.	Cysteine synthase; (	IPR001926 (PFAM): mobidb-lite (MOB	7,549	5,458	6,882	6,130	5,603									
Solyc07g065480	Na-translocating NADH-quinone reductase subunit A (AHRD V3.3 *** AT5G55640.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	6,661	5,894	12,381	9,916	10,112									
Solyc07g065490	Protein DEK (AHRD V3.3 *** A0A0B2PUB3_GLYSO)		F:GO:0016874	F:ligase activity			IPR014876 (PFAM): G3DSA:1.10.10.6	256,925	223,256	304,174	291,957	272,852									
Solyc07g065500	CCAAT-binding transcription factor		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	3,036	8,417	1,981	1,310	1,802	1,497	0,000					up		
Solyc07g065510	RNA-binding protein, putative (AHRD V3.3 *** B9S9T2_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR012677 (G3	26,901	29,470	39,512	36,885	32,665									
Solyc07g065520	RNA-binding protein, putative (AHRD V3.3 *** B9S9T2_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (SMART): IPR000504 (PF	24,374	25,288	34,331	32,254	29,375									
Solyc07g065530	LOW QUALITY:Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT1G15750.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,120	3,015	1,533	1,885	1,130									
Solyc07g065540	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** A0A072UY96_MEDTR)		C:GO:0016021; C:G(	C:integral component of membrane; C:anchored component of r			IPR000782 (SMART): IPR036378 (G3	50,155	34,190	3,826	5,323	4,265									
Solyc07g065550	NAD-dependent protein deacetylase SRT1 (AHRD V3.3 *** SIR1_ARATH)		F:GO:0070403	F:NAD+ binding			IPR003000 (PFAM): G3DSA:3.40.50.1	6,737	5,357	3,523	3,430	3,482									
Solyc07g065560	Histone H2B (AHRD V3.3 *** H2B_CAPAN)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000558 (PRINTS): IPR000558 (SM	0,000	0,039	0,000	0,000	0,000									
Solyc07g065570	Nuclear transcription factor Y subunit B (AHRD V3.3 *-* B7FGV1_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YB	6,166	3,977	0,000	0,000	0,000									
Solyc07g065580	Nuclear transcription factor Y subunit B (AHRD V3.3 *-* B7FGV1_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YB	0,399	0,136	0,000	0,000	0,000									
Solyc07g065590	Nicotinamide-nucleotide adenylyltransferase (AHRD V3.3 *** K4CHN7_SOLLC)		P:GO:0009435; F:G(	P:NAD biosynthetic process; F:nucleotidyltransferase activity			IPR014729 (G3DSA:3.40.50.GENE3D	8,836	8,042	15,048	17,115	16,385									
Solyc07g065600	inner centromere protein, ARK-binding region protein (AHRD V3.3 *-* AT5G55820.8)						IPR005635 (PFAM): mobidb-lite (MOB	3,915	3,668	0,632	0,482	0,849									
Solyc07g065610	Clade XIV lectin receptor kinase (AHRD V3.3 *** K4CHN9_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	0,376	0,351	0,071	0,092	0,069									
Solyc07g065620	Poly (A)-specific ribonuclease PARN-like protein (AHRD V3.3 *** A0A0B0MAX3_GOSAR)		F:GO:0003676	F:nucleic acid binding			IPR036397 (G3DSA:3.30.420.GENE3	23,095	23,497	31,473	33,116	33,703									
Solyc07g065630	E3 ubiquitin-protein ligase UPL1 (AHRD V3.3 *** W9QFS0_9ROSA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			IPR015940 (SMART): IPR000569 (SM	353,623	299,170	464,686	508,415	499,491									
Solyc07g065640	RPM1-interacting 4-like protein (AHRD V3.3 *** A0A0B0MIJ4_GOSAR)		C:GO:0005886; P:G(	C:plasma membrane; P:defense response signaling pathway, re			IPR008700 (PFAM): mobidb-lite (MOB	77,851	76,475	44,696	36,986	45,760									
Solyc07g065650	Transmembrane emp24 domain-containing protein (AHRD V3.3 *** A0A151S058_CAJCA)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.4.1.12	Cellulose synthase (l	IPR009038 (SMART): IPR009038 (PF	38,969	40,872	70,299	72,985	63,801									
Solyc07g065660	Cellulose synthase family protein (AHRD V3.3 *** B9GFY5_POPTR)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (l	IPR029044 (G3DSA:3.90.550.GENE3	1,646	4,736	1,505	1,822	1,889	1,546	0,004					up		
Solyc07g065670	RING/U-box superfamily protein (AHRD V3.3 --* AT5G03180.4)							2,369	6,292	6,117	3,366	4,676	1,427	0,007			-0,854	0,001	up		down
Solyc07g065680	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT5G55860.1)		C:GO:0005829; C:G(	C:cytosol; C:plasma membrane; P:chloroplast avoidance mover			IPR008545 (PFAM): mobidb-lite (MOB	62,260	78,590	73,412	64,035	65,940									
Solyc07g065690	Sucrase/ferredoxin-like family protein (AHRD V3.3 *** AT4G26620.1)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.30.10 (GENE3D): G3DSA	11,319	10,379	14,064	11,459	12,595									
Solyc07g065700	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G55840.1)						IPR011074 (SMART): IPR001251 (SM	93,157	91,418	65,961	46,462	58,674									
Solyc07g065710	Protein kinase (AHRD V3.3 *** Q02494_MAIZE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): IPR000719 (PF	66,163	73,500	52,163	50,158	49,263									
Solyc07g065720	complex 1 protein, LYR family protein (AHRD V3.3 *** AT5G51960.2),Pfam:PF13233						IPR039443 (PFAM): PTHR35763 (PAN	1,607	2,026	2,703	3,325	2,567									
Solyc07g065730	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199ULL4_ANACO)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (TIGRFAM): IPR032867 (F	5,395	4,795	6,885	5,572	6,127									
Solyc07g065735	GBF-interacting protein 1, putative isoform 1 (AHRD V3.3 *** A0A061F5J5_THECC)		F:GO:0005515	F:protein binding			IPR009719 (PFAM): mobidb-lite (MOB	6,380	4,071	7,135	5,923	6,536									
Solyc07g065740	UPF0414 transmembrane protein C20orf30 (AHRD V3.3 *** A0A1D1Y0B4_9ARAE)		C:GO:0016021	C:integral component of membrane			IPR008590 (PFAM): PTHR15664 (PAN	10,681	12,235	15,272	15,493	15,615									
Solyc07g065760	Coiled-coil domain-containing 22 (AHRD V3.3 *** A0A0B0P8X3_GOSAR),Pfam:PF05667		F:GO:0097602; P:G(	F:cullin family protein binding; P:positive regulation of ubiquitin-c			IPR008530 (PFAM): mobidb-lite (MOB	9,293	10,576	15,408	14,543	14,793									
Solyc07g065765	Coiled-coil domain-containing protein 22 (AHRD V3.3 *-* A0A1D1Z6I0_9ARAE),Pfam:PF05667		F:GO:0097602; P:G(	F:cullin family protein binding; P:positive regulation of ubiquitin-c			IPR008530 (PFAM): IPR008530 (PAN	2,104	2,127	3,614	3,895	3,124									
Solyc07g065790	LOW QUALITY:transmembrane protein C9orf5 protein (AHRD V3.3 *** AT5G55960.1)		C:GO:0016021	C:integral component of membrane			IPR002549 (PFAM): mobidb-lite (MOB	24,579	22,476	24,803	23,280	22,879									
Solyc07g065800	Protein CWC15 like (AHRD V3.3 *** A0A0B2SG97_GLYSO)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:spliceosomal complex			IPR006973 (PFAM): mobidb-lite (MOB	60,520	58,176	88,117	87,012	81,361									

Solyc07g065810	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** AT5G55970.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (SMART): IPR001841 (PF	0,080	0,061	3,623	4,804	3,714									
Solyc07g065820	Calcineurin B (AHRD V3.3 *** Q8L7F6_PEA)		F:GO:0005509	F:calcium ion binding			PR00450 (PRINTS): IPR002048 (SMA	21,844	21,184	31,563	36,224	27,631									
Solyc07g065840	molecular chaperone Hsp90-2	Hsp90-2	F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS): IPR003594 (SM	5447,138	5204,285	3285,948	3068,842	3182,694									
Solyc07g065850	Got1/Sft2-like family protein		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			IPR007305 (PFAM): mobidb-lite (MOB	16,483	18,089	29,341	28,949	26,324									
Solyc07g065860	Receptor protein kinase, putative (AHRD V3.3 *** B9T1Q4_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR003591 (SM	19,144	15,248	86,780	90,538	78,585									
Solyc07g065870	Regulatory protein recX (AHRD V3.3 *** W9RVE2_9ROSA)		P:GO:0006282	P:regulation of DNA repair			IPR036388 (G3DSA:1.10.10.GENE3D	4,723	5,028	5,575	4,875	5,358									
Solyc07g065880	Kinesin motor family protein (AHRD V3.3 *** B9N5N8_POPTR)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (SM	1,357	1,352	0,046	0,000	0,070									
Solyc07g065890	Uridine kinase (AHRD V3.3 *** K4CHR5_SOLLC)		F:GO:0005524; P:G(	F:ATP binding; P:nucleoside metabolic process; F:kinase activit			PR00988 (PRINTS): G3DSA:3.40.50.3	31,197	40,450	26,400	26,195	21,166									
Solyc07g065900	fructose-bisphosphate aldolase, cytoplasmic isozyme 1		F:GO:0004332; P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR000741 (PFAM): IPR013785 (G3D	7,598	40,642	1,293	2,625	7,547	2,441	0,000	2,516	0,000	0,996	0,035	up	up	up
Solyc07g065910	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): PTHR31852 (PAN	0,434	0,279	0,097	0,070	0,047									
Solyc07g065920	DUF2431 domain protein (AHRD V3.3 *-* G7IY67_MEDTR)						IPR019446 (PFAM): PTHR11538:SF5	33,823	25,332	7,025	5,536	3,884									
Solyc07g065930	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A097PQ10_SOLLC)		F:GO:0005515	F:protein binding			IPR000210 (SMART): G3DSA:3.30.71	11,526	10,818	12,474	15,319	14,271									
Solyc07g065940	Transmembrane protein, putative (AHRD V3.3 *** G7K4U4_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR36753 (PANTHER)	0,506	0,302	0,532	0,720	0,609									
Solyc07g065950	Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *** W9QQU0_9ROSA)		F:GO:0005515	F:protein binding			IPR001680 (SMART): G3DSA:1.10.22	160,624	134,658	125,380	122,646	125,910									
Solyc07g065960	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SXA3_RICCO)						IPR001623 (PRINTS): IPR001623 (SM	2,332	3,459	3,660	3,203	3,171									
Solyc07g065970	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SXA3_RICCO)						IPR001623 (PRINTS): IPR001623 (SM	5,992	8,282	11,780	12,621	15,713									
Solyc07g065980	alkaline alpha-galactosidase seed imbibition protein	sip	F:GO:0003824	F:catalytic activity			IPR008811 (PFAM): IPR013785 (G3D	65,099	71,373	477,620	524,771	412,440									
Solyc07g065985	Oleosin (AHRD V3.3 *-* A0A103Y4G9_CYNCS)		C:GO:0012511; C:G(	C:monolayer-surrounded lipid storage body; C:integral compone			IPR000136 (PFAM): mobidb-lite (MOB	1,613	1,667	0,704	1,071	0,308									
Solyc07g066000	Amino acid permease (AHRD V3.3 *-* S8CYC9_9LAMI)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM): PTHR22950:SF2	0,019	0,041	0,049	0,050	0,070									
Solyc07g066010	Amino acid transporter, putative (AHRD V3.3 *** B9T659_RICCO)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): PTHR22950 (PAN	19,047	18,448	40,699	44,985	32,170									
Solyc07g066020	Amino acid transporter, putative (AHRD V3.3 *** B9T658_RICCO)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): mobidb-lite (MOB	3,294	2,474	3,068	2,948	2,679									
Solyc07g066030	Proteasome activator subunit 4 (AHRD V3.3 *** A0A142CD27_9LAMI)		F:GO:0016504; F:G(	F:peptidase activator activity; F:lysine-acetylated histone bindir			IPR032430 (PFAM): PTHR32170:SF3	74,560	72,859	105,624	140,494	116,567					0,413	0,025			up
Solyc07g066060	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G56130.1)		C:GO:0000346; F:G(	C:transcription export complex; F:protein binding; P:mRNA expo			IPR020472 (PRINTS): IPR001680 (SM	11,529	13,147	24,949	24,983	22,431									
Solyc07g066070	KH domain-containing protein (AHRD V3.3 *** A0A199VDB7_ANACO)		F:GO:0003723	F:RNA binding			IPR004087 (SMART): IPR032377 (PF	80,160	66,844	55,296	55,842	56,120									
Solyc07g066080	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A1D1XIE8_9ARAE)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			SM00212 (SMART): IPR016135 (G3D	10,653	12,407	33,716	33,112	32,136									
Solyc07g066090	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G55690.3)						IPR001251 (SMART): IPR011074 (SM	25,552	23,809	35,463	33,470	33,871									
Solyc07g066100	GPI-anchored protein LORELEI (AHRD V3.3 *** A0A1D1ZCL0_9ARAE)		C:GO:0016021	C:integral component of membrane			PTHR31533:SF2 (PANTHER): IPR039	2,445	2,475	1,881	2,462	2,425									
Solyc07g066120	Actin-related family protein (AHRD V3.3 *** B9GHK1_POPTR)		F:GO:0005515	F:protein binding			IPR004000 (SMART): IPR001810 (SM	54,350	43,542	83,252	80,176	88,038									
Solyc07g066130	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G13340.3)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	0,000	0,019	0,025	0,000	0,000									
Solyc07g066150	Photosystem I reaction center subunit V family protein (AHRD V3.3 *** A9PEV3_POPTR)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis			IPR016370 (PIRSF): IPR000549 (PFA	135,344	381,172	74,415	106,136	203,113	1,521	0,000	1,445	0,000			up	up	
Solyc07g066160	LOW QUALITY:Tapetum-specific zinc finger protein 1 (AHRD V3.3 *** P93716_PETHY)		F:GO:0003676	F:nucleic acid binding			IPR013087 (SMAF C2H2	0,390	0,272	1,382	4,602	1,442					1,746	0,000			up
Solyc07g066170	WPP domain-interacting protein		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	17,741	17,660	20,138	20,930	19,977									
Solyc07g066180	Tir-nbs resistance protein (AHRD V3.3 *** A0A061F4L1_THECC)		P:GO:0000725; F:G(	P:recombinational repair; F:ADP binding			IPR003593 (SMART): G3DSA:3.40.50	0,949	0,634	1,692	2,303	1,546									
Solyc07g066190	PRA1 family protein (AHRD V3.3 *** K4CHU5_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): IPR004895 (PAN	1,186	1,119	1,536	1,967	1,887									
Solyc07g066200	Elongation factor G (AHRD V3.3 *** A0A0B0MLE6_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	59,940	57,227	67,052	74,561	68,454									
Solyc07g066210	Chloride channel protein (AHRD V3.3 *** Q9ARC6_SOLLC)		F:GO:0005247; P:G(	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR001807 (PRINTS): IPR000644 (SM	23,022	18,814	33,668	33,939	29,877									
Solyc07g066220	WRKY transcription factor 2	WRKY2	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (SMAF WRKY	44,775	39,105	21,888	22,353	24,717									
Solyc07g066230	Receptor kinase (AHRD V3.3 *** A0A0K9P920_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR003591 (SMART): IPR000719 (SM	25,716	34,466	13,820	15,927	18,074									
Solyc07g066240	F-box family protein (AHRD V3.3 *** D7KMZ7_ARALL)		F:GO:0005515	F:protein binding			IPR006553 (SMART): IPR001810 (PF	7,152	8,483	20,541	21,649	20,073									
Solyc07g066260	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G16220.1)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (SMART): IPR001932 (PF	65,741	103,515	39,568	35,026	46,486									
Solyc07g066270	6-phosphogluconolactonase, putative (AHRD V3.3 *** B9RWU5_RICCO)		P:GO:0005975; P:G(	P:carbohydrate met	EC:3.1.1.31; EC:3.1.	6-phosphogluconolac	IPR006148 (PFAM): IPR005900 (TIGF	21,309	23,322	13,617	13,182	13,620									
Solyc07g066280	RNA methyltransferase family protein (AHRD V3.3 *** AT5G64150.1)		P:GO:0006479; F:G(	P:protein methylation; F:protein methyltransferase activity			IPR004556 (TIGRFAM): G3DSA:3.40.!	17,067	15,485	23,715	21,903	21,485									
Solyc07g066290	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *** AT1G79030.1)		C:GO:0016021	C:integral component of membrane			IPR001623 (PRINTS): IPR001623 (SM	24,428	16,247	9,720	8,713	10,274									
Solyc07g066300	DNA gyrase subunit B (AHRD V3.3 *-* A0A1D1Z0E0_9ARAE)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	14,653	12,405	14,918	20,722	18,363					0,475	0,020			up
Solyc07g066310	Photosystem II 10 kDa polypeptide family protein (AHRD V3.3 *** A9PH94_POPTR)		C:GO:0009654; P:G(	C:photosystem II oxygen evolving complex; P:photosynthesis			IPR006814 (PFAM): PTHR34369:SF2	541,423	893,001	510,159	648,179	888,026	0,749	0,009	0,797	0,000			up	up	
Solyc07g066320	DNA repair protein recA (AHRD V3.3 *** U5GXJ6_POPTR)		F:GO:0003697; F:G(	F:single-stranded D	EC:3.6.1.3; EC:3.6.1.	Adenosinetriphospha	IPR013765 (PRINTS): IPR003593 (SM	15,933	18,490	48,628	46,878	47,335									
Solyc07g066330	NAC domain-containing protein (AHRD V3.3 *** W0C8Y8_9FABA)	NAC072	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,306	0,222	0,425	0,957	0,470									
Solyc07g066340	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G16650.1)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			IPR025714 (PFAM): PTHR12496:SF0	6,544	4,469	3,682	3,368	4,046									
Solyc07g066350	serine/arginine repetitive matrix-like protein (AHRD V3.3 *** AT1G56020.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,187	3,586	0,894	0,641	0,514									
Solyc07g066360	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 -** G7JV71_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,192	0,156	0,489	0,705	0,678									
Solyc07g066370	SNARE-associated protein-like protein (AHRD V3.3 *** AT1G79070.2)		P:GO:0006886; C:G(	P:intracellular protein transport; C:BLOC-1 complex			IPR028119 (PFAM): mobidb-lite (MOB	18,194	16,315	13,291	13,607	11,973									
Solyc07g066385	alpha-vacuolar processing enzyme (AHRD V3.3 --* AT2G25940.1)							10,524	11,791	17,858	16,950	15,183									
Solyc07g066390	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y4I4_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	2,445	2,568	3,505	3,469	4,988									
Solyc07g066410	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7JUE1_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR001680 (PF	33,798	31,200	34,427	32,744	31,542									
Solyc07g066420	Peptidyl-prolyl cis-trans isomerase-like protein (AHRD V3.3 *** A0A072U025_MEDTR)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR001878 (SM	30,392	27,698	25,432	23,071	23,391									
Solyc07g066430	Obg-like ATPase 1 (AHRD V3.3 *** K4CHW8_SOLLC)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR023192 (G3	16,973	21,741	19,126	19,665	22,262									
Solyc07g066440	Trypsin family protein (AHRD V3.3 *** A0A061FA64_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	32,201	35,074	46,503	44,563	46,052									
Solyc07g066450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G12940.2)						IPR027443 (G3DSA:2.60.120.GENE3	14,721	11,133	14,075	13,497	13,701									
Solyc07g066460	Protein lojap (AHRD V3.3 *** A0A151S2U3_CAJCA)		C:GO:0009507; P:G(	C:chloroplast; P:negative regulation of translation; F:ribosomal l			G3DSA:3.30.460.10 (GENE3D): IPR0	15,032	25,072	61,230	75,426	72,936	0,765	0,001					up		
Solyc07g066470	Porphobilinogen deaminase, putative (AHRD V3.3 *** B9S2Z0_RICCO)	HEMC/PBGD	F:GO:0004418; P:G(	F:hydroxymethylbila	EC:2.5.1.61	Hydroxymethylbilane	IPR000860 (PRINTS): IPR022417 (PF	63,300	112,975	198,966	216,062	230,924	0,863	0,000					up		
Solyc07g066480	flacca	flc	F:GO:0006777; F:G(	F:Mo-molybdopterin	EC:2.8.1.9	Molybdenum cofacto	IPR015422 (G3DSA:3.90.1150.GENE	13,680	12,845	32,332	31,584	30,750									
Solyc07g066485	cysteine-rich RLK (RECEPTOR-like protein kinase) 41 (AHRD V3.3 --* AT4G00970.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc07g066510	Zinc finger protein CONSTANS (AHRD V3.3 *** W9R0E5_9ROSA)		F:GO:0005515	F:protein binding			IPR010402 (PFAM): PTHR31717 (PAN	0,038	0,039	0,000	0,050	0,024									
Solyc07g066520	Interactor of constitutive active ROPs 2 (AHRD V3.3 *** A0A061FHC7_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	25,509	19,506	26,109	24,248	26,300									
Solyc07g066530	Tetratricopeptide repeat-containing family protein (AHRD V3.3 *** B9H631_POPTR)		F:GO:0005515	F:protein binding			IPR019734 (SMART): IPR011990 (G3	5,636	6,088	4,720	4,394	4,634									
Solyc07g066540	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G12870.1)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane			PTHR33287:SF7 (PANTHER): PTHR3:	0,286	0,326	0,122	0,075	0,093									
Solyc07g066550	LRR receptor-like kinase, putative (AHRD V3.3 *** A0A072U125_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR000719 (SMART): IPR001245 (PF	2,591	3,758	2,333	2,652	3,833									
Solyc07g066560	Small auxin up-regulated RNA65	SAUR65	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF3	1,797	2,346	1,477	1,880	1,348									
Solyc07g066570	filamentous hemagglutinin transporter (AHRD V3.3 *** AT1G79160.1)						mobidb-lite (MOBIDB_LITE): PTHR331	5,276	6,735	2,590	3,312	3,127									
Solyc07g066580	Sulfurtransferase (AHRD V3.3 *** C0LIR4_SOLLC)		F:GO:0004792	F:thiosulfate sulfurtr	EC:2.8.1.1	Thiosulfate sulfurtran	IPR001763 (SMART): IPR001763 (PF	66,278	73,147	104,354	92,935	107,914									
Solyc07g066600	phosphoglycerate kinase (AHRD V3.3 *** AT1G79550.2)		F:GO:0004618; P:G(	F:phosphoglycerate	EC:2.7.2.3	Phosphoglycerate kir	IPR001576 (PRINTS): IPR001576 (PF	853,810	832,313	901,028	698,724	855,875					-0,363	0,042			down
Solyc07g066610	phosphoglycerate kinase		F:GO:0004618; P:G(	F:phosphoglycerate	EC:2.7.2.3	Phosphoglycerate kir	IPR001576 (PRINTS): IPR001576 (PI	252,502	458,125	207,820	200,426	350,061	0,887	0,005	0,749	0,000			up	up	
Solyc07g066620	metalloprotease VIRESCENT3-like		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	G3DSA:1.20.58.760 (GENE3D): PTHF	12,977	15,778	15,328	16,942	17,212									
Solyc07g066630	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT2G07640.1),Pfam:PF13561						IPR002347 (PRINTS): IPR002347 (PF	60,039	75,291	93,002	93,729	100,963									
Solyc07g066640	transglycosylase (AHRD V3.3 *** AT1G16290.2)						G3DSA:1.10.530.10 (GENE3D): IPR0(	0,117	0,288	0,215	0,361	0,163									
Solyc07g066650	Defective in cullin neddylation protein (AHRD V3.3 *** K4CHY8_SOLLC)		F:GO:0005515	F:protein binding			G3DSA:1.10.238.200 (GENE3D): IPR(	118,278	115,662	150,175	136,915	137,863									
Solyc07g066660	cyclinB3_1	CycB3_1	C:GO:0005634	C:nucleus			IPR004367 (SMART): IPR013763 (SM	19,625	17,501	9,181	9,926	10,533									
Solyc07g066670	Ent-kaurene synthase (AHRD V3.3 *-* G5CV50_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR005630 (PFAM): PTHR31739:SF3	19,138	18,077	51,534	55,363	48,651									
Solyc07g066675	Ent-kaurene synthase (AHRD V3.3 *** G5CV50_SOLLC)		F:GO:0010333	F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	15,973	15,738	44,356	46,988	41,879									
Solyc08g005000	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9T103_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (SMART): G3DSA:3.20.20	6,165	5,534	1,851	1,924	2,306									
Solyc08g005010	CAAX protease self-immunity protein (AHRD V3.3 *** AT4G17840.1)		C:GO:0016020	C:membrane			IPR003675 (PFAM): PTHR36736 (PAN	42,968	46,733	19,964	19,884	32,748			0,708	0,004				up	
Solyc08g005015	microspore-specific promoter 2 (AHRD V3.3 --* AT5G46795.1)		C:GO:0009507; P:G(	C:chloroplast; P:pollen development			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,782	0,886	1,040	0,924	1,201									
Solyc08g005020	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT3G13700.1)		C:GO:0005829	C:cytosol			mobidb-lite (MOBIDB_LITE): mobidb-lit	39,982	36,264	41,345	36,553	36,435									
Solyc08g005030	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT4G35040.4)						mobidb-lite (MOBIDB_LITE)	7,738	7,398	8,054	8,188	6,991									
Solyc08g005040	LOW QUALITY:Pollen-specific small CDPK-interacting protein 1 (AHRD V3.3 *** M4T2L5_PETIN)						mobidb-lite (MOBIDB_LITE): PTHR360	0,021	0,039	0,000	0,000	0,000									
Solyc08g005050	transcription factor MYC1		F:GO:0046983	F:protein dimerization activity			IPR011598 (SMAF bHLH	202,397	97,318	50,572	109,102	60,629	-1,031	0,000			1,111	0,000	down		up
Solyc08g005060	cobalt ion binding protein (AHRD V3.3 *** AT1G71310.2)		P:GO:0000724; F:G(	P:double-strand break repair via homologous recombination; F:(			G3DSA:3.30.390.80 (GENE3D): PTHF	3,047	5,641	1,893	2,102	2,492									
Solyc08g005070	Arf gtpase-activating protein, putative (AHRD V3.3 *** B9SNV8_RICCO)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (SM	134,671	124,416	86,573	84,129	75,517									
Solyc08g005090	LOW QUALITY:DUF740 family protein (AHRD V3.3 *-* G7KDT4_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,323	11,121	3,598	2,558	3,201									
Solyc08g005100	PLATZ transcription factor family protein (AHRD V3.3 *** G7KDS6_MEDTR)						IPR006734 (PFAM): mobidb-lite (MOB	1,812	1,002	1,119	0,723	0,615									
Solyc08g005120	Cinnamoyl-CoA reductase-like protein (AHRD V3.3 *** G7KDR3_MEDTR)	CCR	F:GO:0016491	F:oxidoreductase activity			G3DSA:3.40.50.720 (GENE3D): G3DS	0,061	0,160	0,596	1,181	0,847									
Solyc08g005130	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4CI05_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.134; EC:2.:	Inositol-tetrakisphos	G3DSA:3.40.50.11370 (GENE3D): IPI	2,272	3,123	1,096	1,029	0,751									
Solyc08g005140	Protein kinase family protein (AHRD V3.3 *** Q94K14_ARATH)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (SMART): G3DSA:1.10.51	11,570	9,782	16,308	16,208	15,174									
Solyc08g005150	E3 ubiquitin-protein ligase RNF14 (AHRD V3.3 *** A0A0B0NK20_GOSAR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR002867 (SMART): IPR006575 (SM	29,436	25,725	37,119	36,555	37,049									
Solyc08g005160	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G10200.2)						mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,024									
Solyc08g005170	SolycHsfA1a	HSF-02	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	24,619	24,112	35,643	35,325	30,950									
Solyc08g005190	Pre-mRNA-splicing factor CWC22 (AHRD V3.3 *** A0A0B0NK35_GOSAR)		F:GO:0003723; F:G(	F:RNA binding; F:protein binding			IPR003890 (SMART): IPR003891 (SM	38,546	25,987	32,209	31,316	29,404									
Solyc08g005200	Syntaxin-like protein (AHRD V3.3 *** Q3HRZ4_SOLTU)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			IPR006011 (SMART): IPR000727 (SM	14,309	14,525	13,429	11,515	11,518									
Solyc08g005210	dolichol phosphate-mannose biosynthesis regulatory protein-like protein (AHRD V3.3 *** AT1G74340.2)		P:GO:0019348; C:G(	P:dolichol metabolic process; C:integral component of endoplas			IPR009914 (PFAM): PTHR15039:SF1	4,646	5,378	10,807	9,233	9,184									
Solyc08g005220	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT2G35490.1)						IPR006843 (PFAM): mobidb-lite (MOB	2,839	4,479	1,656	1,692	2,849									
Solyc08g005230	GRIP/coiled-coil protein, putative (DUF1664) (AHRD V3.3 *** AT1G27000.1)		C:GO:0016021	C:integral component of membrane			IPR012458 (PFAM): PTHR31903:SF3	147,113	148,854	198,003	192,796	192,992									
Solyc08g005240	Lysine-specific demethylase (AHRD V3.3 *** A0A199VZ18_ANACO)		P:GO:0006338; F:G(	P:chromatin remodeling; F:methyltransferase activity; P:methyla			IPR003347 (SMART): IPR003349 (SM	0,647	0,717	0,149	0,371	0,376									
Solyc08g005250	Lysine-specific demethylase REF6 (AHRD V3.3 *-* W9R3C0_9ROSA)		C:GO:0005634; F:G(	C:nucleus; F:methyltransferase activity; P:methylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,322	0,270	0,118	0,173	0,046									
Solyc08g005260	Myb family transcription factor family protein (AHRD V3.3 *** U5GMY7_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	1,420	1,541	0,996	0,943	0,823									
Solyc08g005270	Poly [ADP-ribose] polymerase (AHRD V3.3 *** A0A0V0ISK3_SOLCH)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylt	IPR022003 (PFAM): G3DSA:3.90.228	167,570	166,889	193,748	199,841	195,773									
Solyc08g005280	Cellulose synthase (AHRD V3.3 *** A0A118JX74_CYNCS)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (l	IPR029044 (G3DSA:3.90.550.GENE3	0,114	0,316	0,191	0,353	0,305									
Solyc08g005290	BZIP transcription factor family protein (AHRD V3.3 *** G7KB04_MEDTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	29,471	26,404	39,601	40,352	39,440									
Solyc08g005300	DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061G7X0_THECC)						IPR024593 (PFAM): mobidb-lite (MOB	9,227	8,460	11,600	10,209	10,482									
Solyc08g005305	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G56080.2)							2,157	1,907	2,218	2,360	1,813									
Solyc08g005310	Guanine nucleotide-binding protein alpha-2 subunit (AHRD V3.3 *** W9S534_9ROSA)		F:GO:0003924; P:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001019 (PRINTS): IPR001019 (SM	21,671	17,213	19,436	19,523	17,881									
Solyc08g005312	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT5G02920.1)		F:GO:0005515	F:protein binding			IPR001810 (SMART): IPR001810 (PF	0,019	0,000	0,025	0,000	0,000									
Solyc08g005318	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT3G28410.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,118	0,141	0,218	0,361	0,282									
Solyc08g005320	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR006566 (SMART): IPR001810 (PF	0,668	0,662	0,777	0,721	0,702									
Solyc08g005330	F-box/RNI-like superfamily protein, putative (AHRD V3.3 *** A0A061GGX0_THECC)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,040	0,118	0,122	0,025	0,023									
Solyc08g005350	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			PTHR44765 (PANTHER): IPR036047 (	13,157	13,790	19,494	16,867	19,382									
Solyc08g005360	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): PTHR44765 (PAN	0,163	0,206	0,714	0,584	0,660									
Solyc08g005380	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 --* AT5G24280.3)						IPR010264 (PFAM)	0,000	0,078	0,025	0,022	0,000									
Solyc08g005390	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XWV8_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,856	3,354	3,377	2,461	2,784									
Solyc08g005400	Cytosine-specific methyltransferase (AHRD V3.3 *-* A0A061G618_THECC)		F:GO:0003682	F:chromatin binding			IPR001025 (SMART): IPR001025 (PF	14,082	13,363	4,737	5,059	4,975									
Solyc08g005405	Cytosine-specific methyltransferase (AHRD V3.3 *-* A0A061G618_THECC)		F:GO:0008168	F:methyltransferase activity			IPR001525 (PRINTS): G3DSA:3.90.12	15,058	16,134	5,484	5,006	5,650									
Solyc08g005420	WD40 repeat-containing protein (AHRD V3.3 *** A0A103YEC3_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:anaphase-promoting complex binding; F:ub			IPR001680 (SMART): IPR015943 (G3	41,214	30,456	36,775	35,828	35,578									
Solyc08g005430	Growth-regulating factor (AHRD V3.3 *** A0A072TW62_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-tem			IPR014978 (SMAF GRF	4,080	4,788	1,426	1,183	1,152									
Solyc08g005440	NBS-LRR disease resistance protein (AHRD V3.3 *** G7IVT3_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	1,617	1,893	0,935	0,960	0,803									
Solyc08g005450	CAX interacting protein 4 (AHRD V3.3 *** U5GND6_POPTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			PF13917 (PFAM): mobidb-lite (MOBID	258,866	234,407	140,792	130,246	136,592									
Solyc08g005460	Protein BREVIS RADIX (AHRD V3.3 *** BRX_ARATH)						IPR013591 (PFAM): IPR027988 (PFA	0,905	1,184	0,312	0,364	0,377									
Solyc08g005470	MAP kinase (AHRD V3.3 *** I7ENF6_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (SMART): PIRSF000654 (	70,134	79,917	119,489	128,039	116,345									
Solyc08g005480	DHHC-type zinc finger family protein (AHRD V3.3 --* AT4G00840.2)							15,209	15,463	20,130	24,752	22,488									
Solyc08g005490	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G31850.4)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	356,051	281,768	76,233	54,889	82,711									
Solyc08g005493	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT3G26490.4)							0,135	0,176	0,218	0,195	0,094									
Solyc08g005500	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT5G35450.2)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,637	0,433	0,851	0,578	0,868									
Solyc08g005510	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (SMA	3,911	2,608	4,018	5,097	4,900									
Solyc08g005520	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A103XFQ8_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	17,912	16,198	18,460	15,860	17,130									
Solyc08g005525	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 --* AT4G00080.1)							2,075	1,468	2,279	2,154	1,787									
Solyc08g005530	threonine aldolase 1 (AHRD V3.3 --* AT1G08630.7)							0,059	0,060	0,047	0,025	0,071									
Solyc08g005540	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmer			G3DSA:1.20.1740.10 (GENE3D): IPR(	4,697	4,367	4,477	4,641	5,643									
Solyc08g005560	transglutaminase-like and tetratricopeptide repeat-containing protein						IPR032698 (PFAM): PTHR31350:SF4	179,059	121,420	28,983	23,160	39,889									
Solyc08g005570	UPF0420 protein C16orf58 like (AHRD V3.3 *** A0A0B2S9E9_GLYSO)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast envelope; P:response to UV-B; I			IPR006968 (PFAM): IPR006968 (PAN	8,274	9,871	6,762	7,339	8,783									
Solyc08g005575	Protein root UVB sensitive 1, chloroplastic (AHRD V3.3 *-* RUS1_ARATH)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast envelope; P:response to UV-B; I			IPR006968 (PANTHER): PTHR12770:	2,539	3,360	1,808	3,009	2,245									
Solyc08g005580	ABC transporter family protein (AHRD V3.3 *** U5GKR9_POPTR)	ABCG21	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1.	Adenosinetriphospha	IPR003593 (SMART): IPR013525 (PF	0,739	0,349	0,654	1,167	1,036									
Solyc08g005590	SWIb domain-containing protein (AHRD V3.3 *** Q6V9I4_SOLCH)		F:GO:0005515	F:protein binding			IPR019835 (SMART): IPR003121 (PF	7,229	7,680	10,529	9,092	9,338									
Solyc08g005600	Glycine-rich protein A3 (AHRD V3.3 *** A0A1D1Y762_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,140	0,210	0,000	0,000	0,000									

Solyc08g005610	xyloglucan endotransglucosylase-hydrolase 5		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	36,202	13,266	15,008	64,227	43,208	-1,426	0,005	1,520	0,000	2,096	0,000	down	up	up
Solyc08g005630	Long-chain-alcohol oxidase (AHRD V3.3 *** K4CI54_SOLLC)		F:GO:0046577; F:GC	F:long-chain-alcoho	EC:1.1.3.2	Long-chain-alcohol o	IPR036188 (G3DSA:3.50.50.GENE3D	31,691	23,292	590,333	695,265	398,793									
Solyc08g005640	Terpene synthase (AHRD V3.3 *** G5CV51_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,213	0,315	0,025	0,000	0,000									
Solyc08g005650	Cytochrome P450-1 (AHRD V3.3 *** K4CI56_SOLLC)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	13,680	16,204	5,158	6,390	4,923									
Solyc08g005690	LOW QUALITY:syntaxin of plants 32 (AHRD V3.3 --* AT3G24350.2)							1,639	1,816	0,719	0,705	0,981									
Solyc08g005700	trigalactosyldiacylglycerol 1 (AHRD V3.3 --* AT1G19800.6)							0,750	0,798	0,384	0,545	0,423									
Solyc08g005720	Terpene synthase 18 (AHRD V3.3 *-* R9R6F3_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,099	0,058	2,340	6,027	0,759			-1,617	0,001				down	
Solyc08g005725	Cytochrome P450-2 (AHRD V3.3 *** R9R6P9_SOLPI)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS): IPR001128 (PF	0,260	0,738	11,608	16,046	10,049									
Solyc08g005750	Benzyl alcohol O-benzoyltransferase (AHRD V3.3 *-* A0A0B0MGB1_GOSAR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,000	0,000	0,025	0,047	0,023									
Solyc08g005760	Alcohol acyl transferase (AHRD V3.3 *** Q6QLX4_SOLLC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,000	0,000	0,946	1,449	0,353									
Solyc08g005770	alcohol acyl transferase		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	0,499	0,275	165,247	139,498	92,436									
Solyc08g005780	Beta-amylase (AHRD V3.3 *** K4CI67_SOLLC)		P:GO:0000272; F:GC	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001554 (PRIN' BES1	28,036	23,888	24,836	23,996	24,574									
Solyc08g005790	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): IPR004963 (PAN	0,040	0,019	0,215	0,095	0,187									
Solyc08g005800	Pectinacetylesterase family protein (AHRD V3.3 *** G7L754_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): IPR004963 (PAN	497,602	395,548	87,785	27,074	41,521			-1,084	0,003	-1,695	0,000		down	down
Solyc08g005850	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G64830.1)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	0,194	0,956	0,000	0,000	0,000									
Solyc08g005860	putrescine-binding periplasmic protein-like protein (AHRD V3.3 *** AT1G31410.1)		P:GO:0015846; F:GC	P:polyamine transport; F:polyamine binding; C:periplasmic spac			IPR001188 (PRINTS): G3DSA:3.40.19	9,889	10,887	35,968	39,525	37,575									
Solyc08g005870	R2R3MYB transcription factor 8	R2R3MYB8	F:GO:0003677	F:DNA binding			IPR001005 (SMAF MYB	0,000	0,000	0,022	0,000	0,000									
Solyc08g005880	Protein DETOXIFICATION (AHRD V3.3 *** K4CI77_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	0,077	0,082	0,025	0,000	0,023									
Solyc08g005890	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	4,166	2,262	0,144	0,140	0,280									
Solyc08g005900	Trihelix transcription factor GT-3a-like protein (AHRD V3.3 *** G7K6R0_MEDTR)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR001005 (SMAF Trihelix	17,383	17,673	21,050	21,555	17,421									
Solyc08g005910	Ankyrin repeat family protein (AHRD V3.3 *** A0A061G768_THECC)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): IPR002110 (SM	125,737	118,969	133,333	118,661	118,209									
Solyc08g005920	Mediator of RNA polymerase II transcription subunit 28 (AHRD V3.3 *** A0A199VWH7_ANACO)		P:GO:0006355; C:GC	P:regulation of transcription, DNA-templated; C:mediator comple			mobidb-lite (MOBIDB_LITE): IPR0344!	9,165	8,099	7,196	5,833	7,838									
Solyc08g005930	F-box/kelch-repeat protein SKIP25, putative (AHRD V3.3 *** G7K6R4_MEDTR)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3I	2,172	1,410	0,000	0,025	0,000									
Solyc08g005940	Proteinase inhibitor II (AHRD V3.3 *** B3F0C1_TOBAC)		P:GO:0000226; F:GC	P:microtubule cytoskeleton organization; F:calmodulin binding; C			mobidb-lite (MOBIDB_LITE): PTHR147	5,950	5,710	0,099	0,047	0,023									
Solyc08g005960	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT2G45180.1)						IPR016140 (SMART): IPR027923 (PF.	7,697	7,834	0,424	0,887	1,344									
Solyc08g005970	Protein arginine N-methyltransferase (AHRD V3.3 *** K4CI86_SOLLC)		F:GO:0008168; P:GC	F:methyltransferase activity; P:peptidyl-arginine N-methylation			G3DSA:3.40.50.150 (GENE3D): G3DS	92,488	76,913	54,392	50,963	52,583									
Solyc08g005980	high-affinity nickel-transport family protein (AHRD V3.3 *** AT2G16800.1)		C:GO:0016021	C:integral component of membrane			IPR039447 (PFAM): PTHR33876 (PAN	17,059	21,426	9,342	9,893	10,477									
Solyc08g005990	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (AHRD V3.3 *-* M1B6Y1_SOLTU)		F:GO:0016740	F:transferase activity			IPR014387 (PIRSF): PTHR15362 (PA	10,702	9,158	25,805	26,892	21,365									
Solyc08g006000	keratin-associated protein (DUF1218) (AHRD V3.3 *** AT4G31130.1)		C:GO:0005886; C:GC	C:plasma membrane; C:integral component of membrane			IPR009606 (PFAM): PTHR31769:SF9	33,399	35,978	79,799	82,945	72,176									
Solyc08g006010	WD repeat domain phosphoinositide-interacting 3 (AHRD V3.3 *** A0A0B0P0U0_GOSAR)		F:GO:0005515	F:protein binding			IPR001680 (SMART): IPR015943 (G3	2,964	4,645	7,586	6,695	8,336									
Solyc08g006025	NAC domain-containing protein (AHRD V3.3 *-* I6YR01_9CARY)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DSA:3.30.310.GENE3I	0,000	0,018	0,047	0,072	0,000									
Solyc08g006030	Myosin heavy chain-related (AHRD V3.3 *-* A0A061GI21_THECC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.5.340 (GENE3D): PTHR3	14,728	15,719	13,648	12,925	13,308									
Solyc08g006040	40S ribosomal protein S6 (AHRD V3.3 *** K4CI93_SOLLC)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001377 (SMART): IPR001377 (PF.	118,056	130,545	94,811	83,235	87,098									
Solyc08g006050	embryo defective 1303 (AHRD V3.3 *** AT1G56200.2)		C:GO:0009507; P:GC	C:chloroplast; P:chloroplast organization; P:thylakoid membrane			mobidb-lite (MOBIDB_LITE): IPR0402!	0,458	0,662	0,887	0,773	1,155									
Solyc08g006060	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G31860.1)		F:GO:0004722; P:GC	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threon	IPR001932 (SMART): IPR001932 (SM	42,359	37,110	43,637	42,481	44,977									
Solyc08g006070	Protein AIG2, putative (AHRD V3.3 *** B9SPS5_RICCO)						G3DSA:3.10.490.10 (GENE3D): IPR0(	12,162	11,968	9,714	9,890	9,963									
Solyc08g006080	Exostosin-like 3 (AHRD V3.3 *** W9S9Z8_9ROSA)		P:GO:0006486; C:GC	P:protein glycosylation; C:integral component of membrane; F:tr			IPR015338 (PFAM): IPR029044 (G3D	14,453	18,886	9,192	6,928	7,592									
Solyc08g006090	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4CI98_SOLLC)		P:GO:0000413; F:GC	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR024936 (PII	14,430	13,613	24,987	24,402	23,877									
Solyc08g006100	plant/protein (Protein of unknown function, DUF599) (AHRD V3.3 *** AT5G10580.3)		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31881:SF6	0,021	0,000	0,000	0,000	0,000									
Solyc08g006110	BZIP transcription factor (AHRD V3.3 *** G7I545_MEDTR)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (SMAF bZIP	78,255	73,339	24,331	20,215	25,515									
Solyc08g006120	mitochondrial import inner membrane translocase subunit tim16-like		C:GO:0005744; P:GC	C:TIM23 mitochondrial import inner membrane translocase com			IPR036869 (G3DSA:1.10.287.GENE3I	10,039	10,116	15,780	17,608	15,153									
Solyc08g006150	Gamma-glutamylcyclotransferase (AHRD V3.3 *** K4CIA4_SOLLC)		F:GO:0003839; P:GC	F:gamma-glutamylc	EC:4.3.2.9	Gamma-glutamylcycl	G3DSA:3.10.490.10 (GENE3D): IPR0(	74,904	56,566	37,233	28,900	33,078									
Solyc08g006155	7-dehydrocholesterol reductase, putative (AHRD V3.3 *-* B9RHV1_RICCO)		C:GO:0005730	C:nucleolus			IPR013865 (PFAM): mobidb-lite (MOB	0,699	0,571	1,216	1,348	0,830									
Solyc08g006160	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT5G19940.1)		C:GO:0009534; C:GC	C:chloroplast thylakoid; C:chloroplast envelope			IPR006843 (PFAM): mobidb-lite (MOB	44,694	70,689	115,150	111,559	135,540	0,688	0,007					up		
Solyc08g006170	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K1X6_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	11,659	11,426	13,168	13,214	13,253									
Solyc08g006180	F-box family protein (AHRD V3.3 *-* D7MV05_ARALL)						PTHR44259 (PANTHER): SSF101898	1,784	2,508	2,070	1,189	1,908									
Solyc08g006190	transcriptional factor B3 family protein (AHRD V3.3 *** AT1G26680.4)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,000	0,019	0,000	0,000	0,000									
Solyc08g006200	Transcriptional factor B3 family protein (AHRD V3.3 *** AT2G24700.1)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	0,000	0,018	0,000	0,022	0,000									
Solyc08g006210	Transcriptional factor B3 family protein (AHRD V3.3 *** AT2G24700.1)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,729	0,103	0,316	0,119	0,071									
Solyc08g006220	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT2G24700.1)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	10,831	8,697	8,794	9,109	7,588									
Solyc08g006230	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G00260.1)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	8,951	7,286	7,630	6,608	5,687									
Solyc08g006240	Transcriptional factor B3 family protein (AHRD V3.3 *** AT2G24700.1)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	0,182	0,114	0,050	0,025	0,000									
Solyc08g006250	Copper transporter, putative (AHRD V3.3 *** A0A061GWU0_THECC)		F:GO:0005375; C:GC	F:copper ion transmembrane transporter activity; C:integral com			IPR007274 (PFAM): PTHR12483:SF4	12,318	11,354	8,456	8,500	10,676									
Solyc08g006251	no pollen germination related 2 (AHRD V3.3 --* AT4G28600.3)							0,021	0,000	0,000	0,000	0,000									
Solyc08g006252	BR enhanced expression 1 (AHRD V3.3 --* AT1G18400.1)							0,000	0,019	0,000	0,022	0,000									
Solyc08g006254	serine/threonine-protein kinase AFC1 (AHRD V3.3 --* AT3G53570.5)							0,019	0,000	0,000	0,000	0,000									
Solyc08g006258	serine/threonine-protein kinase AFC1 (AHRD V3.3 --* AT3G53570.5)							0,000	0,041	0,025	0,000	0,000									
Solyc08g006260	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G00260.1)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	11,378	8,721	4,133	4,396	4,451									
Solyc08g006280	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G00260.1)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	0,037	0,097	0,000	0,050	0,024									
Solyc08g006310	Cellulose synthase-like protein (AHRD V3.3 *** L0ASU5_POPTO)		C:GO:0016021; F:GC	C:integral component of membrane; F:transferase activity			IPR001173 (PFAM): IPR029044 (G3D	7,752	5,522	0,477	0,287	0,559									
Solyc08g006320	WRKY transcription factor 11	WRKY11	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR018872 (PFAM WRKY	187,281	203,403	56,588	100,119	75,531					0,826	0,000			up
Solyc08g006330	UDP-xylose phenolic glycosyltransferase	gtsatom	F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	7,615	12,689	28,512	49,131	38,685			0,437	0,041	0,788	0,000		up	up
Solyc08g006350	Glycosyltransferase (AHRD V3.3 *** K4CIC3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	11,816	16,597	9,122	14,869	17,195			0,910	0,000	0,706	0,003		up	up
Solyc08g006360	Glycosyltransferase (AHRD V3.3 *** K4CIC9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,000	0,000	0,000	0,072	0,046									
Solyc08g006380	Glycosyltransferase (AHRD V3.3 *** K4CIC2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,042	0,000	0,025	0,000	0,000									
Solyc08g006410	Glycosyltransferase (AHRD V3.3 *** K4CIC9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	1,870	0,631	0,022	0,072	0,116	-1,518	0,046					down		
Solyc08g006420	nucleoporin (AHRD V3.3 *** AT4G31570.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	88,134	61,757	68,413	78,062	77,296									
Solyc08g006430	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *-* B9RNP5_RICCO)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding; F:oxidoreductase acti			IPR012677 (G3DSA:3.30.70.GENE3D	118,489	143,904	102,107	95,563	100,833									
Solyc08g006450	LOW QUALITY:WW domain-containing protein (AHRD V3.3 --* AT3G13225.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc08g006460	RING/U-box superfamily protein (AHRD V3.3 *** AT5G10650.2)		P:GO:0016567; F:GC	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein ligas			IPR013083 (G3DSA:3.30.40.GENE3D	27,881	20,634	39,140	45,567	42,876									
Solyc08g006470	Zinc finger protein (AHRD V3.3 *** A0A0B2RI16_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR041661 (PFAM): G3DSA:3.30.160	2,311	5,265	1,149	1,042	1,457									
Solyc08g006480	nuclear pore complex protein (AHRD V3.3 *-* AT3G10650.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,851	10,144	7,730	7,794	7,539									
Solyc08g006490	transcriptional factor B3 family protein (AHRD V3.3 *** AT4G31690.1)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	0,021	0,039	0,000	0,000	0,023									
Solyc08g006500	glutamate receptor-like 2.6	GLR2_6	F:GO:0004970; C:GC	F:ionotropic glutamate receptor activity; C:membrane			IPR001320 (PFAM): G3DSA:3.40.190	4,572	4,726	2,244	2,039	1,761									
Solyc08g006510	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G10730.1)		F:GO:0003954; P:GC	F:NADH dehydrogei	EC:1.6.99.3	NADH dehydrogenas	G3DSA:3.40.50.720 (GENE3D): IPR0'	30,518	30,551	81,331	73,131	76,443									
Solyc08g006520	Glutamine dumper 4, putative (AHRD V3.3 *** A0A061GHE4_THECC)		P:GO:0080143	P:regulation of amino acid export			PTHR33228:SF5 (PANTHER): IPR040	0,649	0,182	0,240	0,273	0,284									
Solyc08g006530	CONSTANS-like protein (AHRD V3.3 *** Q0MQL9_SOLTU)	BBX4	F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR000315 (PFAM CO-like	26,644	37,224	6,496	9,850	11,124			0,768	0,012				up	
Solyc08g006540	FKBP-type peptidyl-prolyl cis-trans isomerase		P:GO:0000413; F:GC	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	G3DSA:3.10.50.40 (GENE3D): IPR00'	6,586	14,538	2,909	2,342	5,181	1,171	0,000					up		
Solyc08g006550	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9SE39_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.2010 (GENE3D): IPR(	0,217	0,375	0,047	0,025	0,000									
Solyc08g006560	3-ketoacyl-acyl carrier protein synthase III (AHRD V3.3 *** AT1G62640.2)		F:GO:0004315; P:GC	F:3-oxoacyl-[acyl-ca	EC:2.3.1.41; EC:2.3.	Beta-ketoacyl-[acyl-c	IPR004655 (TIGRFAM): IPR016039 ((	0,061	0,254	0,000	0,025	0,000									
Solyc08g006570	Bonsai protein (AHRD V3.3 *** Q2HV02_MEDTR)		P:GO:0010152; P:GC	P:pollen maturation; P:inflorescence development; P:phyllome d			mobidb-lite (MOBIDB_LITE): PTHR286	36,583	34,223	39,088	33,278	34,441									
Solyc08g006580	Transmembrane protein, putative (AHRD V3.3 *** A0A072V1M8_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35755 (PANTHER)	4,698	3,406	3,700	3,377	3,433									
Solyc08g006600	Dynamin-related 3A-like protein (AHRD V3.3 *-* A0A0B0P0I4_GOSAR)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.120.1240 (GENE3D): IPF	11,834	13,633	9,854	9,021	9,910									
Solyc08g006605	dynamin related protein (AHRD V3.3 *** AT2G14120.4)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR000375 (PF	16,053	15,491	10,976	13,027	13,057									
Solyc08g006610	polyphosphatidylinositol phosphatase (AHRD V3.3 *** AT2G45320.1)		C:GO:0016021	C:integral component of membrane			PTHR35723 (PANTHER): IPR029044 (	11,314	9,260	9,772	10,997	9,603									
Solyc08g006620	DnaJ/Hsp40 cysteine-rich domain superfamily protein (AHRD V3.3 *** AT2G24860.1)						PTHR15852 (PANTHER): PTHR15852	3,516	3,250	4,552	5,639	5,697									
Solyc08g006630	Spindle and kinetochore-associated 2 (AHRD V3.3 *** A0A0B0NFW8_GOSAR)		C:GO:0000940; C:GC	C:condensed chromosome outer kinetochore; C:spindle microtu			IPR026762 (PFAM): IPR026762 (PAN	0,995	1,101	0,967	0,333	0,564									
Solyc08g006640	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** D8RQT3_SELML)		P:GO:0009247; F:GC	P:glycolipid biosynthetic process; F:transferase activity, transfe			IPR009695 (PFAM): IPR007235 (PFA	21,622	43,359	17,091	16,065	18,088	1,031	0,000					up		
Solyc08g006645	monodehydroascorbate reductase 1 (AHRD V3.3 --* AT3G52880.2)							0,082	1,601	0,071	0,000	0,093									
Solyc08g006650	ER membrane protein complex subunit-like protein (AHRD V3.3 *** G7I7L8_MEDTR)		P:GO:0034975; C:GC	P:protein folding in endoplasmic reticulum; C:ER membrane prot			IPR009445 (PFAM): IPR009445 (PIRS	39,983	44,587	70,919	68,647	66,449									
Solyc08g006660	LOW QUALITY:Conserved oligomeric Golgi complex subunit 2 (AHRD V3.3 *** A0A0B0MZ88_GOSAR)		P:GO:0007030; P:GC	P:Golgi organization; P:protein transport; C:membrane			IPR024602 (PFAM): IPR024603 (PFA	28,071	37,247	21,125	21,830	20,109									
Solyc08g006670	Mediator of RNA polymerase II transcription subunit 30 (AHRD V3.3 *** MED30_ARATH)		C:GO:0016592	C:mediator complex			mobidb-lite (MOBIDB_LITE): mobidb-lit	15,914	13,814	15,853	15,708	15,969									
Solyc08g006680	Major facilitator superfamily protein (AHRD V3.3 *** AT5G25050.1)		C:GO:0016021	C:integral component of membrane			IPR004324 (TIGRFAM): G3DSA:1.20.'	7,117	12,194	6,494	8,215	6,095	0,803	0,028					up		
Solyc08g006690	Plant invertase/pectin methylesterase inhibitor superfamily protein, putative (AHRD V3.3 *** A0A061DYJ0_T		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM): IPR006501 (TIGF	0,000	0,021	0,000	0,000	0,000									
Solyc08g006700	Enhancer of rudimentary homolog (AHRD V3.3 *** M1CHJ6_SOLTU)		P:GO:0006221; P:GC	P:pyrimidine nucleotide biosynthetic process; P:positive regulat			IPR000781 (PIRSF): IPR000781 (PFA	11,460	10,802	18,798	20,219	17,686									
Solyc08g006705	RNI-like superfamily protein (AHRD V3.3 --* AT4G02760.9)							0,159	0,060	0,150	0,242	0,189									
Solyc08g006710	Light-independent protochlorophyllide reductase subunit N (AHRD V3.3 --* CHLN_M	POR-N	F:GO:0004601; F:GC	F:peroxidase activity; F:glutathione peroxidase activity; P:response to oxidative stress; P:oxidation-red				0,061	0,142	0,000	0,000	0,024									
Solyc08g006720	Glutathione peroxidase (AHRD V3.3 *** K4CIG0_SOLLC)	GPX	F:GO:0004602; P:GC	F:glutathione peroxi	EC:1.11.1.9; EC:1.1'	Glutathione peroxida:	IPR000889 (PRINTS): IPR000889 (PII	48,395	74,766	109,292	92,578	134,036	0,655	0,005					up		
Solyc08g006730	Tyramine N-feruloyltransferase 4/11 (AHRD V3.3 *** THT11_TOBAC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): IPR039534 (PTH	0,021	0,021	0,097	0,073	0,142									
Solyc08g006740	aromatic amino acid decarboxylase 2	aadc2	F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015421 (G3DSA:3.40.640.GENE3I	0,236	0,261	0,253	0,802	0,257									
Solyc08g006750	Aromatic amino acid decarboxylase 2 (AHRD V3.3 *** Q1KSC4_SOLLC)		F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR002129 (PFAM): IPR015422 (G3D	0,040	0,041	0,121	0,318	0,235									
Solyc08g006760	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	7,335	9,250	4,506	3,266	4,837									
Solyc08g006770	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	6,028	5,564	17,405	22,888	14,244									
Solyc08g006780	Nucleoid-associated protein (AHRD V3.3 *** A0A199V9B5_ANACO)		F:GO:0003677	F:DNA binding			IPR004401 (PFAM): IPR036894 (G3D	21,606	32,783	125,450	157,725	122,169	0,628	0,010					up		
Solyc08g006790	Early nodulin-like protein (AHRD V3.3 *** G7J9U0_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,617	0,764	0,000	0,000	0,000									
Solyc08g006800	transmembrane protein (AHRD V3.3 *** AT4G31830.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,634	1,407	0,296	0,827	0,000									
Solyc08g006820	Transmembrane 9 superfamily member (AHRD V3.3 *** M1CHH8_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): IPR004240 (PAN	53,618	51,234	53,215	52,783	49,915									
Solyc08g006830	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** A0A072V8S2_MEDTR)		F:GO:0008171	F:O-methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	4,568	5,128	1,625	2,274	2,607									
Solyc08g006840	30S ribosomal protein S15 (AHRD V3.3 *** W9RE90_9ROSA)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005290 (TIGRFAM): IPR000589 (F	21,316	20,682	26,048	25,304	25,461									
Solyc08g006870	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** G7I878_MEDTR)		F:GO:0005515; P:GC	F:protein binding; P:auxin transport; P:plant organ development			IPR027356 (PFAM): G3DSA:3.30.710	13,144	8,414	0,896	1,504	1,252									
Solyc08g006875	Subtilisin-like protease SBT3.13 (AHRD V3.3 --* SBT3D_ARATH)							0,042	0,037	0,000	0,000	0,000									
Solyc08g006880	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *** G7IP56	ABCC6	F:GO:0005524; C:GC	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR011527 (PFAM): G3DSA:3.40.50.3	66,217	74,366	38,873	43,468	51,101									
Solyc08g006890	Tubulin alpha chain (AHRD V3.3 *** TBA_PRUDU)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002452 (PRINTS): IPR000217 (PF	2834,097	2784,652	498,072	422,795	513,445									
Solyc08g006900	60S ribosomal protein L32, putative (AHRD V3.3 *** B9T5H6_RICCO)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001515 (PFAM): IPR001515 (PAN	51,327	58,051	33,669	30,153	31,050									
Solyc08g006910	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT5G23430.3)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	10,368	9,143	9,931	9,227	9,308									
Solyc08g006913	Kunitz-type trypsin inhibitor beta chain (AHRD V3.3 --* ID5B_PROJU)							0,140	0,037	0,267	0,050	0,165									
Solyc08g006917	ATP-dependent RNA helicase DEAH12, chloroplastic (AHRD V3.3 --* DEAHC_ARATH)							0,496	0,215	0,358	0,291	0,304									
Solyc08g006930	Photosystem I reaction center subunit psaK (AHRD V3.3 *** W9SCM1_9ROSA)		C:GO:0009522; P:GC	C:photosystem I; P:photosynthesis			IPR016370 (PIRSF): IPR023618 (G3D	117,659	246,217	42,812	64,636	128,568	1,094	0,010	1,582	0,000	0,598	0,019	up	up	up
Solyc08g006940	F-box family protein (AHRD V3.3 *** D7M2J7_ARALL)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	19,244	18,385	30,932	26,633	28,159									
Solyc08g006950	AT hook motif DNA-binding family protein (AHRD V3.3 *-* AT5G46640.1)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): mobidb-lite (MOB	5,642	5,155	3,471	3,345	3,731									
Solyc08g006960	AP-2 complex subunit mu (AHRD V3.3 *** AP2M_ARATH)	CAC	P:GO:0006886; P:GC	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR001392 (PRINTS): IPR028565 (PF	43,652	47,882	57,595	54,360	52,723									
Solyc08g006970	Leucine-rich repeat-containing protein (AHRD V3.3 *** A0A118JUZ5_CYNCS)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	9,069	7,652	13,875	14,074	13,472									
Solyc08g006980	RING/U-box superfamily protein (AHRD V3.3 *** AT2G35330.2)						PF13920 (PFAM): IPR013083 (G3DS/	192,503	188,268	222,648	212,832	218,926									
Solyc08g006990	aluminum activated malate transporter family protein (AHRD V3.3 *** AT5G46610.1)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): PTHR31086 (PAN	0,000	0,036	0,000	0,000	0,000									
Solyc08g007000	Protein phosphatase 2C (AHRD V3.3 *** A0A124SBW4_CYNCS)		F:GO:0004722; P:GC	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threon	IPR001932 (PFAM): mobidb-lite (MOB	13,825	11,400	3,375	2,942	3,322									
Solyc08g007005	Di-glucose binding protein with Kinesin motor domain-containing protein (AHRD V3.3 --* AT2G22610.3)		F:GO:0000166; F:GC	F:nucleotide binding; F:motor activity; F:microtubule motor activ			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,120	0,174	0,169	0,122	0,281									
Solyc08g007010	ABC transporter family protein (AHRD V3.3 *** A0A097P9T4_HEVBR)		P:GO:0016226	P:iron-sulfur cluster assembly			IPR000825 (PFAM): IPR011542 (TIGF	17,446	23,708	77,045	71,680	69,332									
Solyc08g007030	Ubiquitin (AHRD V3.3 *** A0A103XFF1_CYNCS)		F:GO:0005515	F:protein binding			IPR019387 (PFAM): G3DSA:3.10.20.9	9,718	9,060	11,885	13,412	11,875									
Solyc08g007040	Glycine cleavage system h protein (AHRD V3.3 *** A0A0A0LI67_CUCSA)		C:GO:0005960; P:GC	C:glycine cleavage complex; P:glycine decarboxylation via glyci			G3DSA:2.40.50.100 (GENE3D): IPR0:	5,210	23,959	1,075	1,198	6,118	2,226	0,000	2,488	0,000			up	up	
Solyc08g007060	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmer			IPR000109 (PFAM): G3DSA:1.20.125	1,525	1,344	0,319	0,458	0,588									
Solyc08g007070	Disease resistance protein RPM1 (AHRD V3.3 --* A0A0B2PXN4_GLYSO)							0,141	0,076	0,025	0,000	0,000									
Solyc08g007080	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** G7JZV2_MEDTR)		F:GO:0004439; F:GC	F:phosphatidylinosit	EC:3.1.3.36	Phosphoinositide 5-p	IPR036691 (G3DSA:3.60.10.GENE3D	35,737	58,444	38,443	48,692	45,119									
Solyc08g007100	Haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** B9MTX7_POPTR)		F:GO:0016787	F:hydrolase activity			IPR006439 (PRINTS): IPR023214 (G3	5,390	5,829	7,702	6,896	7,075									
Solyc08g007110	Regulator of nonsense transcripts 1 homolog (AHRD V3.3 *** RENT1_ARATH)		P:GO:0000184; F:GC	P:nuclear-transcribe	EC:3.6.1.15	Nucleoside-triphosph	IPR006935 (PFAM): IPR041677 (PFA	156,630	126,931	182,062	183,722	175,838									
Solyc08g007120	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT1G32740.1)		F:GO:0004842; P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR017066 (PIRSF): PF13920 (PFAM	3,512	7,639	0,197	0,270	0,211									
Solyc08g007130	Beta-amylase (AHRD V3.3 *** K4CIK0_SOLLC)		P:GO:0000272; F:GC	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS): G3DSA:3.20.20	3,972	5,723	1,062	1,377	1,458									
Solyc08g007140	60S ribosomal protein L37a (AHRD V3.3 *** RL37A_GOSHI)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR011331 (G3DSA:2.20.25.GENE3D	126,749	142,007	111,461	95,119	99,887									
Solyc08g007150	Peroxidase (AHRD V3.3 *** K4CIK2_SOLLC)		F:GO:0004601; P:GC	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,184	0,326	0,441	0,196	0,351									
Solyc08g007160	Calcineurin B-like protein (AHRD V3.3 *** A1XCM9_POPEU)		F:GO:0005509; F:GC	F:calcium ion binding; F:protein binding			PR00450 (PRINTS): IPR002048 (PFA	7,401	7,027	4,363	3,561	4,262									
Solyc08g007170	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *-* A0A061DWU0_THECC)		C:GO:0005634; F:GC	C:nucleus; F:sequence-specific DNA binding; F:transcription rec			PF13837 (PFAM): Trihelix	29,457	35,773	25,401	23,489	23,112									
Solyc08g007180	Light harvesting-like protein (AHRD V3.3 *** I3SI55_MEDTR)		C:GO:0009535	C:chloroplast thylakoid membrane			mobidb-lite (MOBIDB_LITE): PTHR141	14,196	16,768	16,876	15,675	17,189									

Solyc08g007190	GATA transcription factor, putative (AHRD V3.3 *** B9SYZ6_RICCO)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR013088 (G3DS GATA	46,534	63,885	27,253	30,359	29,229									
Solyc08g007200	Vesicle-associated protein 2-1 (AHRD V3.3 *** W9S0E2_9ROSA)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR000535 (PFAM); IPR016763 (PIRS	1,501	2,158	0,755	1,061	1,034									
Solyc08g007210	Transferase, putative (AHRD V3.3 *** B9T0L5_RICCO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM); IPR023213 (G3D	3,243	4,788	8,982	10,819	7,052									
Solyc08g007220	Nuclear RNA binding protein-like (AHRD V3.3 *** Q38M48_SOLTU)		F:GO:0003723	F:RNA binding			IPR006861 (PFAM); mobidb-lite (MOB	122,377	145,438	148,209	134,119	131,575									
Solyc08g007230	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A024CAT9_BRAJU)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	2,406	1,846	0,900	1,019	0,681									
Solyc08g007240	Nudix hydrolase (AHRD V3.3 *** A0A061G4C5_THECC)		F:GO:0016787	F:hydrolase activity			IPR003293 (PRINTS); G3DSA:3.40.63	87,019	41,465	13,812	10,933	11,670	-1,039	0,001					down		
Solyc08g007250	Disease resistance protein (AHRD V3.3 *** W9RZV6_9ROSA)		F:GO:0005515; F:GC	F:protein binding; F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	4,613	7,502	3,234	5,129	5,294			0,708	0,025				up	
Solyc08g007260	LOW QUALITY:Exostosin family protein (AHRD V3.3 *-* AT4G16745.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM); PTHR11062:SF5	0,000	0,000	0,072	0,000	0,046									
Solyc08g007270	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GYL8_POPTR)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000047 (PRIN HD-ZIP	1,631	1,615	0,374	0,070	0,164									
Solyc08g007295	Disease resistance protein (AHRD V3.3 *-* W9RZV6_9ROSA)		F:GO:0043531	F:ADP binding			PTHR43909 (PANTHER); PTHR43909	0,042	0,018	0,025	0,000	0,000									
Solyc08g007300	myb family transcription factor (AHRD V3.3 *-* AT5G41020.1)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D); PF139	7,657	6,468	7,426	6,848	8,063									
Solyc08g007310	Exostosin family protein (AHRD V3.3 *** AT4G16745.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM); IPR004263 (PAN	17,398	19,309	6,253	7,273	9,122									
Solyc08g007320	Tryptophan RNA-binding attenuator protein-like (AHRD V3.3 *** A0A061G527_THECC)		C:GO:0016021	C:integral component of membrane			IPR036983 (G3DSA:3.60.160.GENE3	14,380	14,155	25,215	27,610	22,952									
Solyc08g007330	DNA mismatch repair protein mutS (AHRD V3.3 *** A0A0K9NP06_ZOSMR)		F:GO:0005524; P:GC	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			IPR017261 (PIRSF); IPR007696 (PFA	5,244	4,425	3,074	2,551	2,919									
Solyc08g007340	Protein transport protein Sec16B (AHRD V3.3 *** W9SEE7_9ROSA)		P:GO:0048208	P:COPII vesicle coating			IPR024340 (PFAM); IPR024298 (PFA	97,907	91,291	88,118	87,887	86,691									
Solyc08g007350	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHU8_9ROSA)		F:GO:0003676; P:GC	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR036397 (G3DSA:3.30.420.GENE3	0,684	0,427	0,231	0,264	0,282									
Solyc08g007360	Protein transport protein Sec16B (AHRD V3.3 *** W9SEE7_9ROSA)		P:GO:0048208	P:COPII vesicle coating			IPR024340 (PFAM); IPR024298 (PFA	115,331	110,774	125,705	126,674	116,761									
Solyc08g007370	RNA binding protein, putative (AHRD V3.3 *-* B9RNB1_RICCO)		F:GO:0003676; F:GC	F:nucleic acid binding; F:protein binding			IPR012677 (G3DSA:3.30.70.GENE3D	19,754	17,026	30,077	30,363	25,029									
Solyc08g007380	Histidine triad nucleotide-binding 3 (AHRD V3.3 *** A0A0B0MT42_GOSAR)		F:GO:0003824	F:catalytic activity			IPR001310 (PRINTS); PF11969 (PFAI	3,776	4,455	10,744	9,707	8,206									
Solyc08g007400	Autophagy-related protein (AHRD V3.3 *-* K4CIM7_SOLLC)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR004241 (PFAM); G3DSA:3.10.20.9	8,583	7,809	15,323	15,911	14,032									
Solyc08g007410	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein (AHRD V3.3 *** AT4G16510.1)		F:GO:0002161	F:aminoacyl-tRNA ε	EC:3.1.1.1	Carboxylesterase	IPR036754 (G3DSA:3.90.960.GENE3	3,947	3,806	7,749	7,179	7,087									
Solyc08g007420	LELDH2 L-lactate dehydrogenase	ldh2	F:GO:0004459; C:GC	F:L-lactate dehydro	EC:1.1.1.27	L-lactate dehydrogen	IPR001557 (PRINTS); G3DSA:3.40.50	10,047	13,002	3,411	2,773	2,963									
Solyc08g007430	NIT2	nit2	C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM); G3DSA:1.20.125	0,000	0,075	0,025	0,022	0,000									
Solyc08g007435	Auxin responsive SAUR protein (AHRD V3.3 *** A0A103XGA7_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM); PTHR31374 (PAN	0,136	0,225	0,000	0,000	0,024									
Solyc08g007440	Phytoene synthase (AHRD V3.3 *** B6TWB6_MAIZE)		C:GO:0005739; P:GC	C:mitochondrion; P:mitochondrial respiratory chain complex I as			PF00494 (PFAM); IPR008949 (G3DSA	7,826	6,790	21,299	20,085	21,108									
Solyc08g007460	Lipid transfer protein (AHRD V3.3 *** I3SGW1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR016140 (PFAM); G3DSA:1.10.110	0,530	3,362	2,755	15,137	9,769	2,663	0,015	1,816	0,000	2,454	0,000	up	up	up
Solyc08g007470	HAT transposon superfamily (AHRD V3.3 *** A0A061G5I4_THECC)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM); IPR007021 (PFA	8,981	8,666	10,153	12,372	10,693									
Solyc08g007475	Viscotoxin-A2 (AHRD V3.3 --* THN2_VISAL)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc08g007480	DUF1442 family protein (AHRD V3.3 *** G7KG69_MEDTR)						IPR009902 (PFAM); G3DSA:3.40.50.1	0,369	0,394	0,342	0,243	0,376									
Solyc08g007490	Class I peptide chain release factor (AHRD V3.3 *** AT1G62850.3)		P:GO:0006415; F:GC	P:translational termination; F:translation release factor activity,			G3DSA:3.30.160.20 (GENE3D); mobic	14,290	14,378	15,633	15,325	14,456									
Solyc08g007500	PPR containing protein (AHRD V3.3 *** AT4G22758.1)						IPR040358 (PANTHER); PTHR33270:	0,063	0,110	0,261	0,120	0,118									
Solyc08g007510	Cornichon family protein (AHRD V3.3 *** AT1G12390.1)		P:GO:0016192	P:vesicle-mediated transport			IPR003377 (PFAM); PTHR12290:SF1	2,447	1,868	2,843	2,862	1,955									
Solyc08g007520	Exosome complex component (AHRD V3.3 *** W9RYG2_9ROSA)		F:GO:0004527; P:GC	F:exonuclease activity; P:nucleic acid phosphodiester bond hyd			IPR001247 (PFAM); IPR027408 (G3D	0,021	0,000	0,000	0,022	0,023									
Solyc08g007530	AT hook, DNA-binding motif-containing protein (AHRD V3.3 *** A0A103XG23_CYNCS)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D); IPR	24,805	18,785	22,635	15,983	19,271					-0,499	0,006			down
Solyc08g007540	ACT domain-containing family protein (AHRD V3.3 *** B9N3K8_POPTR)						G3DSA:3.30.70.260 (GENE3D); IPR0	2,963	2,125	2,927	3,866	3,301									
Solyc08g007545	Actin-related protein 6 (AHRD V3.3 --* ARP6_ORYSI)							0,486	0,520	0,262	0,218	0,234									
Solyc08g007550	no pollen germination related 2 (AHRD V3.3 --* AT4G28600.3)							0,101	0,099	0,072	0,075	0,117									
Solyc08g007560	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TPA5_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D); IPR	0,100	0,188	0,047	0,048	0,023									
Solyc08g007570	Homeobox-leucine zipper protein HOX9, putative (AHRD V3.3 *** A0A061DUZ5_THECC)						IPR039312 (PANTHER); PTHR33601:	0,059	0,078	0,049	0,000	0,000									
Solyc08g007580	Ycf49-like protein (AHRD V3.3 *** A0A0B0NIP1_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR019634 (PFAM); PTHR33833:SF3	0,742	0,622	2,519	3,444	2,445									
Solyc08g007590	Sodium Bile acid symporter family (AHRD V3.3 *** AT4G22840.1)		C:GO:0016020	C:membrane			IPR038770 (G3DSA:1.20.1530.GENE	19,146	18,443	23,555	20,072	21,067									
Solyc08g007610	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); G3DSA:2.60.40	0,356	1,917	0,022	0,022	0,023									
Solyc08g007620	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); IPR010259 (PF	35,048	112,305	0,932	0,425	1,934									
Solyc08g007630	Disease resistance protein (AHRD V3.3 *** A0A068EX87_SOLHA)		F:GO:0005515; F:GC	F:protein binding; F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	6,229	4,314	1,583	2,540	2,731									
Solyc08g007640	resistance complex protein I2C-4	i2c4	F:GO:0005515	F:protein binding			IPR001611 (PFAM); IPR032675 (G3D	3,151	2,417	1,657	1,020	1,267									
Solyc08g007650	Subtilisin-like protease (AHRD V3.3 *-* Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); IPR000209 (PF	0,119	0,117	0,100	0,176	0,047									
Solyc08g007660	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR000209 (PFAM); G3DSA:2.60.40.2	0,192	0,156	0,118	0,094	0,165									
Solyc08g007670	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); IPR010259 (PF	2,348	2,203	1,891	1,708	2,025									
Solyc08g007680	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252; P:GC	F:serine-type endoι	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS); IPR036852 (G3	0,057	0,099	0,000	0,025	0,095									
Solyc08g007710	ATP synthase subunit b (AHRD V3.3 *** A0A1D1Y2F8_9ARAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	4,880	4,862	4,840	4,666	4,459									
Solyc08g007711	SWIB complex BAF60b domain-containing family protein (AHRD V3.3 --* B9HS93_POPTR)							0,021	0,000	0,000	0,000	0,000									
Solyc08g007712	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G74630.2)							0,019	0,000	0,000	0,022	0,023									
Solyc08g007716	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G08610.1)							0,000	0,000	0,025	0,025	0,000									
Solyc08g007718	no pollen germination related 2 (AHRD V3.3 --* AT4G28600.3)							0,000	0,000	0,050	0,047	0,024									
Solyc08g007740	YTH domain-containing protein (AHRD V3.3 *** A0A103XRB5_CYNCS)		F:GO:0003723	F:RNA binding			IPR007275 (PFAM); G3DSA:3.10.590	5,784	4,439	3,268	2,914	2,645									
Solyc08g007750	YTH domain-containing protein (AHRD V3.3 *** A0A103XRB5_CYNCS)		F:GO:0003723	F:RNA binding			IPR007275 (PFAM); G3DSA:3.10.590	13,492	12,172	15,466	17,664	14,740									
Solyc08g007755	Adenosine monophosphate-protein transferase and cysteine protease ibpA (AHRD V3.3 --* A0A0B0PY85_GOSAR)							0,960	0,619	1,024	1,143	1,009									
Solyc08g007760	YTH domain-containing protein (AHRD V3.3 *** A0A103XRB5_CYNCS)		F:GO:0003723	F:RNA binding			G3DSA:3.10.590.10 (GENE3D); IPR0	16,444	12,649	16,336	16,068	17,077									
Solyc08g007770	Expansin-like protein (AHRD V3.3 *-* Q0WT83_ARATH)		C:GO:0005576; C:GC	C:extracellular region; C:chloroplast thylakoid membrane; P:plar			IPR007118 (PRINTS); IPR002963 (PF	86,570	103,823	44,924	44,894	81,133			0,850	0,000				up	
Solyc08g007790	3-hydroxy-3-methylglutaryl coenzyme A synthase	hmgs	F:GO:0004421; P:GC	F:hydroxymethylglut	EC:2.3.3.1	Hydroxymethylglutary	IPR010122 (TIGRFAM); IPR016039 (C	13,471	10,644	25,207	19,391	22,218					-0,374	0,046			down
Solyc08g007800	SPX domain-containing family protein (AHRD V3.3 *** B9GW54_POPTR)		C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM); IPR004331 (PFA	6,365	5,089	32,009	38,118	25,054									
Solyc08g007805	NADH dehydrogenase 1 alpha subcomplex subunit 8 (AHRD V3.3 *-* A0A0K9PKB1_ZOSMR)		C:GO:0005747; P:GC	C:mitochondrial respiratory chain complex I; P:mitochondrial ele			IPR010625 (PFAM); IPR016680 (PAN	1,348	2,799	1,491	2,026	2,163									
Solyc08g007820	C-repeat binding factor (AHRD V3.3 *** A0A0B5KMN4_ACTCH)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	5,243	15,251	8,235	12,840	10,708	1,569	0,000					up		
Solyc08g007830	C-repeat binding factor (AHRD V3.3 *** E7D090_PRUPE)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,942	4,916	1,783	2,014	2,594	2,411	0,000					up		
Solyc08g007840	Dehydration-responsive element binding factor (AHRD V3.3 *** X2JR99_POPNI)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR036955 (G3DSA:3.30.730.GENE3	0,124	0,266	0,075	0,000	0,048									
Solyc08g007845	Protein DETOXIFICATION (AHRD V3.3 *** A0A068UMQ2_COFCA)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM); IPR002528 (F	0,279	0,700	136,807	136,812	66,293			-1,049	0,002				down	
Solyc08g007860	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT1G12640.1)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	34,622	35,503	100,634	118,537	100,741									
Solyc08g007865	Cytochrome P450 family protein (AHRD V3.3 *** B9GKM6_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR036396 (G3DSA:1.10.630.GENE3	0,000	0,000	0,025	0,147	0,071									
Solyc08g007890	Aldehyde dehydrogenase (AHRD V3.3 *-* Q43274_MAIZE)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR016162 (G3DSA:3.40.605.GENE3	0,059	0,039	11,656	15,066	7,866									
Solyc08g007910	MAP kinase kinase kinase 61	MAPKKK61	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:regulation of transcri			IPR001245 (PRINTS); IPR013767 (PF	16,942	23,152	20,287	22,113	18,463									
Solyc08g007920	SUN-like protein 19	SUN19	F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 (GENE3D); IPR00	0,019	0,064	0,258	0,684	0,329									
Solyc08g007930	SUN-like protein 20	SUN20	F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 (GENE3D); IPR00	0,000	0,000	0,025	0,000	0,000									
Solyc08g007940	Pollen-specific protein SF3 (AHRD V3.3 *** A0A0B2QVK4_GLYSO)		F:GO:0046872	F:metal ion binding			IPR001781 (PFAM); G3DSA:2.10.110	0,000	0,202	0,000	0,000	0,000									
Solyc08g007950	30S ribosomal S1 (AHRD V3.3 *** A0A0B0MP62_GOSAR)		F:GO:0003676	F:nucleic acid binding			IPR003029 (PFAM); G3DSA:2.40.50.1	21,438	27,596	31,386	33,664	39,079									
Solyc08g007970	Myosin heavy chain-related protein, putative (AHRD V3.3 *** A0A061GCE0_THECC)		P:GO:0016539	P:intein-mediated protein splicing			IPR019448 (PFAM); mobidb-lite (MOB	34,119	34,551	25,834	28,909	27,543									
Solyc08g007980	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)						IPR038595 (G3DSA:3.20.90.GENE3D	0,492	0,477	0,478	0,411	0,332									
Solyc08g007990	RNA-binding NOB1-like protein (AHRD V3.3 *** AT5G41190.1)		F:GO:0004521; P:GC	F:endoribonuclease activity; P:maturation of SSU-rRNA; C:preri			G3DSA:3.40.50.1010 (GENE3D); IPR	175,137	131,573	104,198	101,827	95,674									
Solyc08g008000	Serine/threonine dehydratase (AHRD V3.3 *** A0A0K9PIX5_ZOSMR)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:5.1.1.18; EC:4.3.	Serine racemase; L-s	G3DSA:3.40.50.1100 (GENE3D); G3D	2,415	1,955	3,386	2,950	2,404									
Solyc08g008010	Serine/threonine dehydratase (AHRD V3.3 *** A0A0K9PIX5_ZOSMR)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:5.1.1.18; EC:4.3.	Serine racemase; L-s	G3DSA:3.40.50.1100 (GENE3D); IPR	11,055	8,846	14,991	14,016	12,867									
Solyc08g008020	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT4G11610.2)		C:GO:0016021	C:integral component of membrane			IPR000008 (PFAM); IPR013583 (PFA	6,739	6,080	3,668	3,591	3,236									
Solyc08g008030	AT hook motif DNA-binding family protein, putative (AHRD V3.3 *** A0A061G6C0_THECC)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM); G3DSA:3.30.133	10,342	10,187	19,608	19,686	18,567									
Solyc08g008040	rRNA-processing protein UTP23 like (AHRD V3.3 *** A0A0B2NPV2_GLYSO)		C:GO:0032040	C:small-subunit processome			IPR006984 (PFAM); G3DSA:3.40.50.1	21,285	23,840	26,993	27,619	24,519									
Solyc08g008050	plasma membrane intrinsic protein 1.1	PIP1.1	F:GO:0015267; C:GC	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR000425 (PF	1,999	1,259	0,391	0,168	0,519									
Solyc08g008070	BTB/POZ domain-containing protein (AHRD V3.3 *** W9R367_9ROSA)		P:GO:0051260	P:protein homooligomerization			G3DSA:3.30.710.10 (GENE3D); IPR0	14,205	10,872	6,285	9,598	6,500					0,610	0,025			up
Solyc08g008080	RING/U-box superfamily protein (AHRD V3.3 *** AT1G63840.1)		F:GO:0008270; C:GC	F:zinc ion binding; C:integral component of membrane; F:ligase			IPR013083 (G3DSA:3.30.40.GENE3D	18,110	17,762	2,014	1,360	2,275									
Solyc08g008087	1-aminocyclopropane-1-carboxylate synthase (AHRD V3.3 *** P93235_SOLLC)		F:GO:0003824; P:GC	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			PR00753 (PRINTS); IPR015421 (G3D	25,209	19,690	3,436	7,868	3,664					1,189	0,007			up
Solyc08g008120	DET1 complexing ubiquitin ligase (AHRD V3.3 *** AT5G41560.1)		P:GO:0032434	P:regulation of proteasomal ubiquitin-dependent protein cataboli			IPR018276 (PFAM); mobidb-lite (MOB	2,635	2,461	1,137	0,890	1,268									
Solyc08g008130	E3 SUMO-protein ligase pli1 (AHRD V3.3 *** A0A0B0PPF6_GOSAR)		F:GO:0008270; F:GC	F:zinc ion binding; F:SUMO transferase activity			IPR013083 (G3DSA:3.30.40.GENE3D	42,717	34,402	38,315	36,071	38,483									
Solyc08g008140	Sumo ligase, putative (AHRD V3.3 --* B9RCI3_RICCO)		F:GO:0003824	F:catalytic activity				2,998	2,168	3,695	2,975	3,220									
Solyc08g008150	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *-* O82354_AR		C:GO:0016021	C:integral component of membrane			PTHR31852:SF52 (PANTHER); PTHR	0,290	0,933	0,050	0,215	0,351									
Solyc08g008160	WD-repeat protein (AHRD V3.3 *** E5GBV4_CUCME)		F:GO:0005515; C:GC	F:protein binding; C:nucleolus; P:ribosomal large subunit biogen			IPR015943 (G3DSA:2.130.10.GENE3	17,666	16,944	22,242	19,130	19,194									
Solyc08g008170	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9RCK2_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (PFAM); IPR000719 (PFA	29,403	37,694	37,199	34,259	37,148									
Solyc08g008180	Loricrin-like (AHRD V3.3 *** A0A0K9PKU0_ZOSMR)						mobidb-lite (MOBIDB_LITE); PTHR318	32,310	24,106	39,882	32,303	31,806									
Solyc08g008200	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:GC	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	0,000	0,021	0,000	0,000	0,000									
Solyc08g008210	vacuolar proton ATPase subunit E	vpae	P:GO:0015991; C:GC	P:ATP hydrolysis cc	EC:3.6.1.3; EC:3.6.1.	Adenosinetriphospha	IPR038495 (G3DSA:3.30.2320.GENE	161,158	165,520	127,224	123,996	118,198									
Solyc08g008220	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** Q84YH5_GOSAR)		F:GO:0005524; P:GC	F:ATP binding; P:protein ubiquitination; F:ubiquitin conjugating e			IPR016135 (G3DSA:3.10.110.GENE3	654,627	662,565	589,525	548,939	565,567									
Solyc08g008230	Protein kinase family protein (AHRD V3.3 --* AT5G38210.3)							33,061	25,651	18,208	14,498	16,608									
Solyc08g008240	Protein kinase family protein (AHRD V3.3 *** AT1G64300.2)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM); IPR010632 (PFA	0,241	0,206	0,121	0,117	0,165									
Solyc08g008250	Protein KTI12 like (AHRD V3.3 *** A0A0B2QZ37_GLYSO)		P:GO:0002098; P:GC	P:tRNA wobble uridine modification; P:regulation of transcriptior			IPR013641 (PFAM); G3DSA:3.40.50.3	17,153	18,958	19,533	18,186	17,204									
Solyc08g008270	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** AT1G64355.1)		C:GO:0016021	C:integral component of membrane			IPR021995 (PFAM); mobidb-lite (MOB	3,631	4,214	3,522	4,537	5,691									
Solyc08g008273	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_PEA)						mobidb-lite (MOBIDB_LITE)	0,256	0,319	0,259	0,263	0,236									
Solyc08g008277	WRKY transcription factor-30 (AHRD V3.3 *-* B6VB04_CAPAN)		F:GO:0003677	F:DNA binding			PTHR32096 (PANTHER); PTHR32096	0,470	1,722	0,212	0,122	0,236	1,887	0,045					up		
Solyc08g008280	WRKY transcription factor 53	WRKY53	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036576 (G3DS WRKY	14,501	27,524	3,053	4,945	6,822									
Solyc08g008285	LOW QUALITY:WRKY family transcription factor (AHRD V3.3 *-* AT4G11070.2)		F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036576 (G3DSA:2.20.25.GENE3D	0,666	0,754	1,319	1,459	1,344									
Solyc08g008290	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT5G65685.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	266,065	186,707	284,685	222,334	219,880									
Solyc08g008305	Ethylene-responsive transcription factor ERF061 (AHRD V3.3 *** A0A0B2R037_GLYSO)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINTS); IPR036955 (G3	0,103	0,142	0,071	0,048	0,000									
Solyc08g008310	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0G2SJB5_SALMI)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D); G3	1,426	1,248	0,961	1,062	1,174									
Solyc08g008320	Inner membrane protein OXA1 (AHRD V3.3 *** B9GL61_POPTR)		C:GO:0016021; F:GC	C:integral component of membrane; F:membrane insertase acti			IPR028055 (TIGRFAM); IPR001708 (F	6,898	6,053	5,262	5,596	4,911									
Solyc08g008330	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* A0A1C6ZUU3_9ASPA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,614	1,577	9,628	11,678	6,820									
Solyc08g008340	Nucleoside diphosphate kinase (AHRD V3.3 *** K4CIW8_SOLLC)		F:GO:0004550; P:GC	F:nucleoside diphos	EC:2.7.4.6	Nucleoside-diphosph	IPR001564 (PRINTS); IPR034907 (PF	2,844	3,309	5,665	5,528	4,886									
Solyc08g008350	ribosome maturation factor (AHRD V3.3 *** AT4G10970.7),Pfam:PF07078						mobidb-lite (MOBIDB_LITE); mobidb-lit	31,866	32,624	42,971	40,150	38,825									
Solyc08g008360	DUF4228 domain protein (AHRD V3.3 *** A0A072TUQ1_MEDTR)						IPR025322 (PFAM); PTHR33148 (PAN	0,037	0,097	0,175	0,048	0,071									
Solyc08g008370	DCD (Development and cell death) domain protein (AHRD V3.3 *** A0A072TUZ0_MEDTR)						IPR013989 (PFAM); mobidb-lite (MOB	591,742	502,084	136,872	301,271	237,464			0,793	0,009	1,140	0,000		up	up
Solyc08g008380	Auxin Response Factor 9B	ARF9B	F:GO:0003677; F:GC	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR015300 (G3DS ARF	26,789	25,657	15,511	12,890	16,320									
Solyc08g008410	Plant regulator RWP-RK family protein (AHRD V3.3 *** G7IAL8_MEDTR)		F:GO:0005515	F:protein binding			IPR000270 (PFAM Nin-like	22,030	27,404	9,965	8,967	10,590									
Solyc08g008420	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4CIX6_SOLLC)		C:GO:0005743; P:GC	C:mitochondrial inner membrane; P:mitochondrial pyruvate trans			IPR005336 (PFAM); PTHR14154:SF1	0,060	0,039	0,000	0,022	0,071									
Solyc08g008440	Oxysterol-binding protein-related protein 3C (AHRD V3.3 --* ORP3C_ARATH)						mobidb-lite (MOBIDB_LITE)	0,000	0,080	0,147	0,073	0,094									
Solyc08g008450	Glycosyltransferase (AHRD V3.3 *** A0A0E0QZN3_ORYRU)		P:GO:0008643; C:GC	P:carbohydrate transport; C:integral component of membrane; C			G3DSA:3.40.50.2000 (GENE3D); G3D	0,040	0,059	0,093	0,070	0,047									
Solyc08g008455	Protein KINESIN LIGHT CHAIN-RELATED 3 (AHRD V3.3 *** KLCR3_ARATH)		F:GO:0005515	F:protein binding			PF13374 (PFAM); IPR011990 (G3DS/	39,481	42,448	27,012	24,452	24,696									
Solyc08g008470	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT4G10840.2)		C:GO:0005737; C:GC	C:cytoplasm; C:microtubule; C:plasma membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	15,560	13,761	11,966	10,062	9,970									
Solyc08g008490	WD-repeat protein, putative (AHRD V3.3 *** B9RYR0_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR015943 (G3	32,857	31,429	79,878	85,527	77,716									
Solyc08g008500	Dof zinc finger protein (AHRD V3.3 *** A0A0B6VI93_TOBAC)		F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,137	0,115	0,047	0,022	0,000									
Solyc08g008510	FAS-associated factor 2-B (AHRD V3.3 *** W9S3Z8_9ROSA)		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D); G3DS/	35,072	40,996	50,207	49,285	48,117									
Solyc08g008520	Protein yippee-like (AHRD V3.3 *** K4CIY6_SOLLC)		F:GO:0046872	F:metal ion binding			IPR004910 (PFAM); IPR039058 (PAN	12,692	9,186	23,141	23,934	18,973									
Solyc08g008530	2-keto-3-deoxy-L-rhamnonate aldolase (AHRD V3.3 *** W9QTL7_9ROSA)		F:GO:0003824	F:catalytic activity			IPR040442 (G3DSA:3.20.20.GENE3D	26,211	31,092	36,656	31,778	34,622									
Solyc08g008550	Kinase (AHRD V3.3 *** D7LYS2_ARALL)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); PIRS	30,599	40,232	74,974	75,096	75,718									
Solyc08g008580	Cystathionine beta-lyase/cystathionine gamma-synthase (AHRD V3.3 *** A0A072VNE2_MEDTR)		F:GO:0003824; F:GC	F:catalytic activity; F:pyridoxal phosphate binding			IPR000277 (PFAM); IPR015422 (G3D	0,310	0,181	0,340	0,100	0,304									
Solyc08g008590	ubiquitin-ribosomal fusion protein		F:GO:0003735; F:GC	F:structural constituent of ribosome; F:protein binding; C:ribosoı			IPR019956 (PRINTS); IPR038587 (G3	43,004	52,924	53,205	48,392	48,342									
Solyc08g008600	bHLH transcription factor 055		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM bHLH	0,040	0,018	0,123	0,076	0,069									
Solyc08g008610	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061G3V4_THECC)		C:GO:0016021; F:GC	C:integral component of membrane; F:hydrolase activity			IPR000073 (PRINTS); IPR000073 (PF	3,543	2,321	0,313	0,317	0,562									
Solyc08g008630	beta-carotene isomerase D27 (AHRD V3.3 *** AT1G64680.2)		F:GO:0016853	F:isomerase activity			PTHR33591:SF1 (PANTHER); IPR038	19,172	49,508	6,850	9,306	21,863	1,395	0,000	1,670	0,000			up	up	
Solyc08g008660	NAC domain-containing protein, putative (AHRD V3.3 *** A0A061G3T7_THECC)	NAC075	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,180	0,456	0,000	0,000	0,000									
Solyc08g008670	Phosphomannomutase (AHRD V3.3 *** PMM_SOLLC)		F:GO:0004615; C:GC	F:phosphomannomu	EC:5.4.2.8	Phosphomannomutas	IPR006379 (TIGRFAM); IPR023214 (C	14,413	16,003	8,515	8,513	8,674									
Solyc08g013670	photosystem I reaction center subunit		C:GO:0009522; P:GC	C:photosystem I; P:photosynthesis			G3DSA:4.10.1190.10 (GENE3D); IPR	62,684	147,946	19,577	33,959	65,079	1,266	0,005	1,727	0,000	0,796	0,008	up	up	up
Solyc08g013680	Soluble inorganic pyrophosphatase (AHRD V3.3 *** A0T3E7_SOLTU)		F:GO:0000287; F:GC	F:magnesium ion bi	EC:3.6.1.1	Inorganic diphosphat	IPR008162 (PFAM); IPR036649 (G3D	0,000	0,059	1,460	2,035	1,295									
Solyc08g013690	B3 domain-containing protein (AHRD V3.3 *** A0A1D1Z5C9_9ARAE)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,352	0,371	0,386	0,460	0,257									
Solyc08g013700	B3 domain-containing protein (AHRD V3.3 *** A0A1D1Z5C9_9ARAE)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,276	0,365	0,378	0,414	0,282									
Solyc08g013710	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *-* AT2G37950.1)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	11,447	12,597	11,182	10,887	11,452									
Solyc08g013720	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein (AHRD V3.3 *** F4KAB4_ARATH)						G3DSA:3.40.50.150 (GENE3D); PTHF	5,889	7,643	2,592	3,224	3,921									
Solyc08g013730	NOD26-like intrinsic protein5.1	NIP5.1	F:GO:0015267; C:GC	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR023271 (G3	63,321	50,856	22,486	21,634	21,863									
Solyc08g013740	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G10440.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM); G3DSA:3.40.50.1	1,424	0,627	0,187	0,076	0,189									

Solyc08g013750	F-box family protein (AHRD V3.3 *-* D7M2J7_ARALL)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): IPR(	3,607	2,891	3,269	2,583	3,481									
Solyc08g013754	Protein DETOXIFICATION (AHRD V3.3 --* F6H230_VITVI)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transporter activity; F:antiporter activity; C:me			0,000	0,043	0,000	0,100	0,024									
Solyc08g013756	F-box/LRR protein (AHRD V3.3 *-* G7IP48_MEDTR)		P:GO:0016567; C:G(	P:protein ubiquitination; C:SCF ubiquitin ligase complex; P:SCF-		IPR032675 (G3DSA:3.80.10.GENE3D	0,880	1,150	1,005	0,892	0,710									
Solyc08g013770	F-box/RNI-like superfamily protein, putative (AHRD V3.3 *-* A0A061GGX0_THECC)					PTHR44765 (PANTHER)	0,063	0,021	0,025	0,025	0,023									
Solyc08g013780	F-box family protein (AHRD V3.3 *-* D7M2J7_ARALL)					IPR032675 (G3DSA:3.80.10.GENE3D	0,059	0,018	0,072	0,120	0,023									
Solyc08g013790	F-box/LRR protein (AHRD V3.3 *-* G7I6M1_MEDTR)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): PTH	0,259	0,076	0,121	0,316	0,239									
Solyc08g013800	F-box/LRR protein (AHRD V3.3 *** A0A072V906_MEDTR)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): IPR(	1,332	1,101	0,209	0,050	0,140									
Solyc08g013805	F-box/LRR protein (AHRD V3.3 *** A0A072V906_MEDTR)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,036	0,025	0,000	0,142									
Solyc08g013820	putative F-box/LRR-repeat protein		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	7,049	7,036	5,744	5,435	5,314									
Solyc08g013830	LOW QUALITY:Transferase family protein (AHRD V3.3 *** U5G7I4_POPTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR023213 (G3DSA:3.30.559.GENE3I	0,000	0,000	0,000	0,025	0,000									
Solyc08g013840	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JYQ1_MEDTR)		F:GO:0016787	F:hydrolase activity		IPR041492 (PFAM): IPR023198 (G3D	0,928	1,208	1,357	1,738	2,099									
Solyc08g013845	Glycosyltransferase (AHRD V3.3 *** M1BVJ8_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D): IPR(	3,400	3,946	1,177	1,470	1,768									
Solyc08g013850	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JW03_CYNCS)		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	3,875	3,259	1,762	2,324	3,481			0,965	0,009				up	
Solyc08g013860	Malic enzyme (AHRD V3.3 *** K4CJ21_SOLLC)		F:GO:0004471; F:G(	F:malate dehydroge EC:1.1.1.38; EC:1.1	Malate dehydrogenas	IPR001891 (PRINTS): IPR012302 (PF	140,739	139,271	114,416	106,176	114,088									
Solyc08g013880	GPI-anchored protein (AHRD V3.3 *** AT2G30700.1)					IPR040336 (PANTHER): PTHR33831::	17,392	18,286	18,800	18,683	16,271									
Solyc08g013890	GPI-anchored protein (AHRD V3.3 *-* AT2G30700.2)					PTHR33831:SF3 (PANTHER): IPR040	2,010	2,173	1,726	1,780	1,360									
Solyc08g013900	Plant regulator RWP-RK family protein (AHRD V3.3 *** AT2G43500.9)		F:GO:0005515	F:protein binding		IPR003035 (PFAM Nin-like	5,925	8,230	3,825	5,806	6,068									
Solyc08g013910	Plant cadmium resistance 2, putative (AHRD V3.3 *** A0A061E1P7_THECC)		C:GO:0016021	C:integral component of membrane		IPR006461 (TIGRFAM): IPR006461 (F	0,120	0,308	0,000	0,025	0,023									
Solyc08g013930	Peroxidase (AHRD V3.3 *** K4CJ27_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	0,038	0,000	0,000	0,022	0,000									
Solyc08g013940	Serine/Threonine kinase family protein (AHRD V3.3 *** G7ISK8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:1.10.510.10 (GENE3D): IPR(	2,655	2,499	0,399	0,386	0,798									
Solyc08g013960	Disease resistance protein (AHRD V3.3 *-* W9RZV6_9ROSA)		F:GO:0043531	F:ADP binding		PTHR43906 (PANTHER): PTHR43906	0,040	0,021	0,000	0,025	0,024									
Solyc08g013970	Disease resistance protein (AHRD V3.3 *** W9RZV6_9ROSA)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:1.10.8.43	0,080	0,119	0,172	0,286	0,140									
Solyc08g013980	histone H2A deubiquitinase (DUF3755) (AHRD V3.3 *** AT3G07565.1)		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.60 (GENE3D): IPR02:	2,946	2,406	1,359	1,560	1,305									
Solyc08g013990	AUGMIN subunit 2 (AHRD V3.3 *** AUG2_ARATH)		P:GO:0031023; P:G(	P:microtubule organizing center organization; P:spindle assembl		IPR028346 (PFAM): mobidb-lite (MOB	19,382	14,204	16,090	19,470	16,180									
Solyc08g014000	lipoxygenase A	LOX1	F:GO:0005515; F:G(	F:protein binding; F: EC:1.13.11	Acting on single donc	IPR013819 (PRINTS): IPR001246 (PF	5523,061	2929,504	10050,720	6172,020	7660,343	-0,888	0,000			-0,701	0,000	down		down
Solyc08g014010	Transmembrane protein, putative (AHRD V3.3 *** A0A072VMY8_MEDTR)		C:GO:0016021	C:integral component of membrane		IPR040283 (PANTHER): IPR040283 (I	0,422	1,286	4,923	4,175	4,883									
Solyc08g014020	ER protein carbohydrate-binding protein (AHRD V3.3 --* AT1G24485.1)						2,268	1,902	1,280	1,171	0,988									
Solyc08g014030	GRAS family transcription factor (AHRD V3.3 *** A0A061EK79_THECC)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR005202 (PFAM GRAS	4,265	2,711	0,051	0,000	0,142									
Solyc08g014040	Methyltransferase family protein (AHRD V3.3 *** G7KPC6_MEDTR)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation		G3DSA:3.40.50.150 (GENE3D): IPR0'	7,895	7,421	9,768	10,564	9,824									
Solyc08g014050	Glycosyltransferase (AHRD V3.3 *** K4CJ38_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups		G3DSA:3.40.50.2000 (GENE3D): IPR(	0,356	0,275	0,320	0,217	0,332									
Solyc08g014060	Eukaryotic translation initiation factor eIF2A family protein (AHRD V3.3 *** A0A0G4AP04_9ROSI)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; P:transla		IPR013979 (PFAM): IPR015943 (G3D	38,853	38,938	37,278	35,565	34,760									
Solyc08g014080	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EJY7_THECC)		F:GO:0008270	F:zinc ion binding		IPR022143 (PFAM): IPR013083 (G3D	9,579	5,982	3,485	3,615	3,245									
Solyc08g014090	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G09040.3)					PTHR34130 (PANTHER): PTHR34130	0,000	0,000	0,047	0,000	0,023									
Solyc08g014100	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061EU55_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding		IPR011990 (G3DSA:1.25.40.GENE3D	7,378	7,629	9,521	8,988	8,477									
Solyc08g014120	ethylene responssive protein 33	er33	F:GO:0046983	F:protein dimerization activity		PTHR16223 (PANTHER): PTHR16223	112,135	118,492	68,738	70,223	98,394			0,514	0,023				up	
Solyc08g014130	Isopropylmalate synthase (AHRD V3.3 *** K4CJ46_SOLLC)		F:GO:0003852; P:G(	F:2-isopropylmalate EC:2.3.3.13	2-isopropylmalate sy	G3DSA:3.30.160.270 (GENE3D): IPR(	40,129	38,555	326,652	567,786	435,191			0,411	0,006	0,800	0,000		up	up
Solyc08g014140	LOW QUALITY:Integrin-linked protein kinase family (AHRD V3.3 --* AT3G58760.6)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; C:extracellular region; F:manganese ior			0,000	0,021	0,000	0,000	0,000									
Solyc08g014150	C2 domain-containing protein / GRAM domain-containing protein (AHRD V3.3 *** AT3G59660.1)					IPR000008 (PRINTS): IPR000008 (PF	4,313	6,651	4,083	6,754	5,645					0,721	0,013			up
Solyc08g014240	Isopropylmalate synthase (AHRD V3.3 *** A0A0G2T9V8_SOLPN)		F:GO:0003824	F:catalytic activity		IPR013785 (G3DSA:3.20.20.GENE3D	0,000	0,000	0,000	0,022	0,000									
Solyc08g014260	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151RU32_CAJCA)					IPR019557 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,000	0,047									
Solyc08g014280	SUN-like protein 21	SUN21	F:GO:0005515	F:protein binding		G3DSA:1.20.5.190 (GENE3D): IPR02!	2,671	3,071	0,137	0,239	0,567									
Solyc08g014290	Serine-threonine protein phosphatase, putative, expressed (AHRD V3.3 *** Q8L676_ORYSJ)		F:GO:0016787	F:hydrolase activity		IPR004843 (PFAM): PTHR11668 (PAI	11,682	23,051	24,367	21,657	21,770	1,007	0,001					up		
Solyc08g014300	FAM136A-like protein (DUF842) (AHRD V3.3 *** AT1G05730.1)					IPR008560 (PFAM): IPR008560 (PAN	2,791	2,724	3,898	3,519	2,950									
Solyc08g014330	Amine oxidase (AHRD V3.3 *** K4CJ66_SOLLC)		F:GO:0005507; F:G(	F:copper ion bindinc EC:1.4.3.21	Primary-amine oxida:	IPR015802 (PFAM): IPR015798 (PFA	0,452	0,266	0,000	0,047	0,000									
Solyc08g014340	Cysteine synthase (AHRD V3.3 *** K4CJ67_SOLLC)		F:GO:0004124; P:G(	F:cysteine synthase EC:2.5.1.47	Cysteine synthase	G3DSA:3.40.50.1100 (GENE3D): IPR(	117,858	143,649	67,805	70,799	79,966									
Solyc08g014350	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT5G16250.1)		C:GO:0016021	C:integral component of membrane		PTHR34124:SF5 (PANTHER): PTHR3	0,000	0,083	0,000	0,000	0,000									
Solyc08g014380	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity		IPR004963 (PFAM): PTHR21562:SF3!	0,000	0,036	0,147	0,255	0,118									
Solyc08g014390	LOW QUALITY:DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0K1ZD49_9LAMI)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6	DNA-directed RNA polymerase		0,000	0,064	0,000	0,075	0,023									
Solyc08g014420	mitogen-activated protein kinase 2	mpk2	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:3.30.200.20 (GENE3D): G3DS	16,162	13,473	15,602	19,161	15,976									
Solyc08g014425	Mitogen-activated protein kinase (AHRD V3.3 *-* Q84MI5_SOLLC)		P:GO:0000165; F:G(	P:MAPK cascade; F EC:2.7.11; EC:2.7.1	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): G3DS	4,819	4,766	6,234	6,191	4,475									
Solyc08g014430	Formin-like protein (AHRD V3.3 *** K4CJ74_SOLLC)		C:GO:0016021	C:integral component of membrane		G3DSA:1.20.58.2220 (GENE3D): IPR(	2,222	3,481	0,222	0,047	3,039									
Solyc08g014440	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7K3T4_MEDTR)		F:GO:0003712; F:G(	F:transcription core EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	G3DSA:3.30.710.10 (GENE3D): IPR(	9,656	8,153	5,460	5,535	6,845									
Solyc08g014450	Integrin-linked protein kinase family (AHRD V3.3 *** AT2G43850.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		IPR020683 (PFAM): G3DSA:3.30.200	13,938	11,214	14,680	17,787	14,854									
Solyc08g014470	Amidohydrolase family (AHRD V3.3 *** AT3G55850.6)		F:GO:0016810	F:hydrolase activity, acting on carbon-nitrogen (but not peptide)		G3DSA:3.20.20.140 (GENE3D): G3DS	94,308	94,620	73,940	63,607	73,650									
Solyc08g014480	glycoside hydrolase family 2 protein (AHRD V3.3 *** AT3G54440.3)		F:GO:0004565; P:G(	F:beta-galactosidas EC:3.2.1.23	Beta-galactosidase	IPR006101 (PRINTS): IPR006103 (PF	67,475	68,666	66,273	60,110	69,873									
Solyc08g014485	glycoside hydrolase family 2 protein (AHRD V3.3 *-* AT3G54440.2)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR006104 (PFAM): PTHR10066:SF7:	9,919	9,928	9,460	9,536	11,342									
Solyc08g014490	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc		IPR003480 (PFAM): IPR023213 (G3D	0,040	0,155	0,000	0,000	0,000									
Solyc08g014510	Zinc finger protein (AHRD V3.3 *** W9RXF5_9ROSA)		F:GO:0046872	F:metal ion binding		G3DSA:4.10.1060.10 (GENE3D): IPR(	9,123	9,219	9,832	8,360	8,627									
Solyc08g014550	60S ribosomal L9 (AHRD V3.3 *** A0A0B0N9P7_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;		IPR020040 (PFAM): IPR000702 (PIRS	24,907	29,073	23,236	22,487	21,380									
Solyc08g014570	Ankyrin repeat family protein (AHRD V3.3 *** AT2G31820.1)		F:GO:0005515	F:protein binding		IPR026961 (PFAM): IPR036770 (G3D	35,717	26,505	4,754	3,190	7,837									
Solyc08g014580	Type II inositol 5-phosphatase, putative (AHRD V3.3 *** B9RM01_RICCO)		F:GO:0005515	F:protein binding		IPR015943 (G3DSA:2.130.10.GENE3I	3,192	1,733	0,065	0,075	0,046									
Solyc08g014590	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast		G3DSA:3.40.50.300 (GENE3D): IPR0(	0,060	0,000	0,000	0,000	0,000									
Solyc08g014600	S-adenosyl-L-methionine-dependent methyltransferase (AHRD V3.3 *** I0YZQ6_COCSC)		F:GO:0008757	F:S-adenosylmethionine-dependent methyltransferase activity		IPR008854 (PFAM): G3DSA:3.40.50.1	3,259	4,067	1,812	2,093	2,541									
Solyc08g014610	Aminotransferase (AHRD V3.3 *** D2KZ08_WHEAT)		F:GO:0008483; F:G(	F:transaminase activity; F:pyridoxal phosphate binding		IPR015422 (G3DSA:3.90.1150.GENE	0,388	0,377	0,000	0,000	0,000									
Solyc08g015620	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes (AHRD V3.3 *** B6U7J5_MAIZE)					mobidb-lite (MOBIDB_LITE): mobidb-lit	5,385	8,541	15,916	17,337	16,146									
Solyc08g015630	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** M1CD44_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion bi EC:2.7.1.134; EC:2.'	Inositol-tetrakisphosr	G3DSA:3.30.470.100 (GENE3D): PIR!	19,259	15,282	23,838	22,526	19,857									
Solyc08g015640	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT2G31010.2)						0,580	0,322	0,065	0,269	0,259									
Solyc08g015650	La-related protein 7 (AHRD V3.3 *** W9RF44_9ROSA)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprote		IPR002344 (PRINTS): IPR036388 (G3	30,600	30,750	44,520	42,464	40,153									
Solyc08g015660	6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** K4CJ96_SOLLC)		F:GO:0000906; P:G(	F:6,7-dimethyl-8-rib EC:2.5.1.78	6,7-dimethyl-8-ribitylli	IPR034964 (TIGRFAM): IPR036467 ((	6,608	8,573	2,957	2,655	3,335									
Solyc08g015670	Glucose-1-phosphate adenylyltransferase, putative (AHRD V3.3 *** B9T528_RICCO)		P:GO:0009058; F:G(	P:biosynthetic process; F:nucleotidyltransferase activity		IPR005835 (PFAM): IPR029044 (G3D	0,059	0,059	0,000	0,000	0,000									
Solyc08g015680	Potassium transporter (AHRD V3.3 *** M1BTK3_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai		IPR003855 (TIGRFAM): IPR003855 (F	0,021	0,000	0,000	0,000	0,000									
Solyc08g015690	Late embryogenesis abundant protein Lea14 (AHRD V3.3 *** A0A0K9PIU3_ZOSMR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:cytosol; C:plasma membrane; P:response		G3DSA:2.60.40.1820 (GENE3D): IPR(	294,256	299,989	349,031	315,213	342,444									
Solyc08g015694	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT5G02920.1)		F:GO:0005515	F:protein binding		IPR013103 (PFAM): IPR032675 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc08g015696	F-box/RNI-like superfamily protein (AHRD V3.3 *-* AT5G02930.1)		F:GO:0005515	F:protein binding		IPR001810 (PFAM): IPR032675 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc08g015710	LOW QUALITY:F-box/RNI-like superfamily protein, putative (AHRD V3.3 *** A0A061GGX0_THECC)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,062	0,000	0,025	0,000									
Solyc08g015730	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): IPR(	0,058	0,154	0,022	0,095	0,047									
Solyc08g015750	F-box/RNI-like superfamily protein, putative (AHRD V3.3 *** A0A061GGX0_THECC)		F:GO:0005515	F:protein binding		IPR006566 (PFAM): IPR001810 (PFA	0,058	0,058	0,000	0,025	0,000									
Solyc08g015770	RING/U-box superfamily protein (AHRD V3.3 *** AT1G53490.1)		F:GO:0016874	F:ligase activity		IPR013083 (G3DSA:3.30.40.GENE3D	0,784	0,928	0,121	0,195	0,258									
Solyc08g015780	Ankyrin repeat family protein (AHRD V3.3 *** AT3G59910.2)					IPR036770 (G3DSA:1.25.40.GENE3D	76,829	69,413	61,648	53,206	57,216									
Solyc08g015800	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT5G02920.1)		F:GO:0005515	F:protein binding		PTHR44765 (PANTHER): IPR036047 (	0,021	0,100	0,096	0,048	0,093									
Solyc08g015820	LOW QUALITY:EXS (ERD1/XPR1/SYG1) family protein (AHRD V3.3 --* AT1G68740.2)						0,449	0,276	0,339	0,390	0,423									
Solyc08g015845	Weak chloroplast movement under blue light 1-like protein (AHRD V3.3 *-* A0A0B0P410_GOSAR)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac		IPR008545 (PFAM): PTHR32054:SF2	0,000	0,018	0,000	0,000	0,000									
Solyc08g015860	Rab GDP dissociation inhibitor (AHRD V3.3 *** C0LSK7_NICBE)		F:GO:0005093; P:G(	F:Rab GDP-dissociation inhibitor activity; P:small GTPase medi		IPR018203 (PRINTS): IPR000806 (PF	113,059	118,741	142,313	132,672	134,798									
Solyc08g015870	MLO-like protein (AHRD V3.3 *** K4CJB5_SOLLC)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane		IPR004326 (PFAM): mobidb-lite (MOB	111,973	118,109	75,581	92,443	84,726									
Solyc08g015890	F-box/RNI-like superfamily protein, putative (AHRD V3.3 *-* A0A061GGX0_THECC)					PTHR44765 (PANTHER)	0,019	0,000	0,000	0,050	0,000									
Solyc08g015940	Epidermal patterning factor-like protein, putative (AHRD V3.3 *** G7JGZ2_MEDTR),Pfam:PF17181		P:GO:0010374	P:stomatal complex development		PF17181 (PFAM): PTHR33109:SF16 (	3,045	1,585	0,087	0,125	0,117									
Solyc08g015960	Methionyl-tRNA synthetase, putative (AHRD V3.3 *** B9STA0_RICCO)		F:GO:0000049	F:tRNA binding		IPR002547 (PFAM): G3DSA:2.40.50.1	18,766	28,687	19,787	19,395	25,250	0,640	0,008					up		
Solyc08g015990	Golgi to ER traffic 4 (AHRD V3.3 *** A0A0B0NU26_GOSAR)		F:GO:0005515	F:protein binding		IPR007317 (PFAM): IPR011990 (G3D	38,520	37,721	97,062	100,981	92,042									
Solyc08g016000	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)		C:GO:0016021	C:integral component of membrane		IPR008896 (PFAM): PTHR33163:SF1:	0,019	0,021	0,025	0,025	0,000									
Solyc08g016010	Apyrase-like protein (AHRD V3.3 *** A0MWC2_TOBAC)		F:GO:0016787	F:hydrolase activity		G3DSA:3.30.420.150 (GENE3D): IPR(	53,404	50,729	33,785	33,031	34,972									
Solyc08g016050	Guanine nucleotide exchange factor SPIKE 1 (AHRD V3.3 *** SPK1_ARATH)		F:GO:0005085; P:G(	F:guanyl-nucleotide exchange factor activity; P:small GTPase n		G3DSA:1.20.58.740 (GENE3D): IPR0'	44,672	39,224	33,423	32,528	33,336									
Solyc08g016060	Dedicator of cytokinesis (AHRD V3.3 *-* A0A0K9P947_ZOSMR)		F:GO:0005085; P:G(	F:guanyl-nucleotide exchange factor activity; P:small GTPase n		PTHR23317:SF76 (PANTHER): IPR02	6,541	5,330	4,190	4,152	4,749									
Solyc08g016070	Dedicator of cytokinesis (AHRD V3.3 *-* A0A0K9P947_ZOSMR)		F:GO:0005085; P:G(	F:guanyl-nucleotide exchange factor activity; P:small GTPase n		IPR027007 (PFAM): IPR026791 (PAN	24,708	19,028	18,952	20,943	18,702									
Solyc08g016080	high chlorophyll fluorescence phenotype 173 (AHRD V3.3 *** AT1G16720.1)					IPR013857 (PFAM): G3DSA:3.40.50.7	58,244	58,590	85,105	75,729	101,788									
Solyc08g016090	Transcription factor 25 (AHRD V3.3 *** A0A103XS75_CYNCS)		C:GO:0005829	C:cytosol		IPR006994 (PFAM): mobidb-lite (MOB	21,419	20,383	26,813	31,006	28,270									
Solyc08g016150	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 180 (AHRD V3.3 *** Q9FQZ1_TOBAC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		mobidb-lite (MOBIDB_LITE): PTHR337	4,384	2,953	0,466	1,525	0,816									
Solyc08g016160	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NPK0_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral		IPR038770 (G3DSA:1.20.1530.GENE	0,234	0,443	0,025	0,025	0,024									
Solyc08g016170	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** A0A0V0IG10_SOLCH)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:transferase activity, transfe		IPR017568 (TIGRFAM): IPR014031 (F	43,779	69,566	88,303	89,782	95,724	0,694	0,005					up		
Solyc08g016180	60S ribosomal protein L18a (AHRD V3.3 *** K4CJE2_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation		G3DSA:3.10.20.10 (GENE3D): G3DS/	152,694	169,007	126,317	116,941	116,297									
Solyc08g016190	60S ribosomal protein L18a, putative (AHRD V3.3 *-* B9S129_RICCO)		C:GO:0005840; C:G(	C:ribosome; C:integral component of membrane		PTHR10052:SF30 (PANTHER): IPR02	9,154	7,774	15,704	15,399	14,983									
Solyc08g016210	Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *** G7JP58_MEDTR)		F:GO:0005515	F:protein binding		PR00019 (PRINTS): IPR032675 (G3D	2,376	16,886	1,708	1,967	5,398	2,848	0,001	1,649	0,000			up	up	
Solyc08g016270	Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *** A0A072UHL0_MEDTR)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,099	0,172	0,044	0,074	0,000									
Solyc08g016310	Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *** A0A072UGV6_MEDTR)		F:GO:0005515	F:protein binding		IPR001611 (PFAM): IPR032675 (G3D	38,850	106,101	3,320	2,732	7,078	1,472	0,002					up		
Solyc08g016320	LOW QUALITY:MYB transcription factor (AHRD V3.3 --* B4FQD3_MAIZE)					mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,000	0,000	0,000									
Solyc08g016340	LOW QUALITY:Protein kinase (AHRD V3.3 *-* C6ZRX8_SOYBN)		F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11	Transferring phospho	PTHR27001 (PANTHER): PTHR27001	0,038	0,064	0,000	0,000	0,000									
Solyc08g016380	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT5G04370.3)						0,159	0,037	0,243	0,120	0,140									
Solyc08g016400	cytochrome P450, family 96, subfamily A, polypeptide 11 (AHRD V3.3 --* AT4G39500.2)						0,021	0,000	0,100	0,170	0,071									
Solyc08g016410	carotenoid cleavage dioxygenase 8 (AHRD V3.3 --* AT4G32810.2)						39,084	32,189	20,643	20,492	19,327									
Solyc08g016415	kinesin-like calmodulin-binding protein (ZWICHEL) (AHRD V3.3 --* AT5G65930.2)		C:GO:0005886	C:plasma membrane			0,000	0,021	0,050	0,050	0,000									
Solyc08g016420	Prefoldin subunit 6 (AHRD V3.3 *** A0A0B2Q9N0_GLYSO)		P:GO:0006457; C:G(	P:protein folding; C:prefoldin complex; F:unfolded protein bindinc		IPR009053 (G3DSA:1.10.287.GENE3I	16,561	19,476	22,795	22,830	19,413									
Solyc08g016430	LOW QUALITY:Glutamate receptor 2.6 (AHRD V3.3 --* GLR26_ARATH)						0,416	0,290	0,658	0,805	1,062									
Solyc08g016440	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT2G13980.1)					mobidb-lite (MOBIDB_LITE)	7,750	9,929	10,183	15,520	12,922									
Solyc08g016500	Potassium channel (AHRD V3.3 *-* Q9LEG6_SOLLC)		F:GO:0005249; P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra		IPR003938 (PRINTS): IPR005821 (PF	4,446	5,070	4,052	6,928	5,450									
Solyc08g016510	Proteasome subunit alpha type (AHRD V3.3 *** M1AKV3_SOLTU)		F:GO:0004298; C:G(	F:threonine-type en EC:3.4.25	Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	69,382	65,802	93,277	85,723	83,319									
Solyc08g016550	Unknown protein (AHRD V3.3)						1,986	2,335	1,173	0,969	1,532									
Solyc08g016560	R3H domain protein (AHRD V3.3 --* AT1G03250.3)						0,000	0,019	0,000	0,025	0,023									
Solyc08g016565	ABC-2 type transporter family protein isoform 2 (AHRD V3.3 --* A0A061GX61_THECC)						0,284	0,265	0,068	0,097	0,119									
Solyc08g016581	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain-contain		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity		IPR003653 (PFAM): mobidb-lite (MOB	0,138	0,162	0,290	0,116	0,259									
Solyc08g016582	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity		G3DSA:3.30.310.130 (GENE3D): IPR(	0,061	0,242	0,146	0,263	0,213									
Solyc08g016584	UDP-glucose 4-epimerase 5 (AHRD V3.3 --* UGE5_ARATH)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,059	0,074	0,172	0,075	0,024									
Solyc08g016586	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)					IPR015410 (PFAM): mobidb-lite (MOB	0,242	0,627	0,294	0,488	0,681									
Solyc08g016588	Zinc finger CCCH domain-containing protein 54 (AHRD V3.3 --* C3H54_ORYSJ)						5,449	5,250	2,094	4,086	2,907					0,962	0,005			up
Solyc08g016620	transmembrane protein (DUF616) (AHRD V3.3 *** AT5G46220.1)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra		IPR006852 (PFAM): IPR008901 (PAN	0,715	0,666	0,000	0,000	0,023									
Solyc08g016630	LOW QUALITY:NmrA-like negative transcriptional regulator family protein (AHRD V3.3 --* AT1G19540.2)		P:GO:0016032; C:G(	P:viral process; C:host cell junction; C:host cell plasmodesma; F		IPR028919 (PFAM): PTHR33054 (PAI	0,042	0,037	0,025	0,051	0,047									
Solyc08g016660	Gibberellin 2 oxidase (AHRD V3.3 *** Q53C60_NEROL)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process		PR00682 (PRINTS): IPR026992 (PFA	0,098	0,136	0,000	0,022	0,024									
Solyc08g016670	Calcyclin-binding protein, putative (AHRD V3.3 *** B9S113_RICCO)		F:GO:0015631; F:G(	F:tubulin binding; F:ubiquitin protein ligase binding; F:S100 prote		IPR007052 (PFAM): IPR008978 (G3D	111,643	88,899	207,594	192,631	215,580									
Solyc08g016720	9-cis-epoxycarotenoid dioxygenase2		F:GO:0016702; P:G(	F:oxidoreductase a EC:1.13.11	Acting on single donc	IPR004294 (PFAM): PTHR10543:SF4:	13,654	16,752	5,052	3,603	3,951									
Solyc08g016750	Pyruvate dehydrogenase E1 component subunit beta (AHRD V3.3 *** A0A0B0NLW1_GOSAR)		F:GO:0003824	F:catalytic activity		IPR005475 (PFAM): IPR033248 (PFA	53,445	72,709	83,209	84,266	90,714									
Solyc08g016760	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_SILLA)						0,248	0,306	0,187	0,097	0,141									
Solyc08g016770	Histidine decarboxylase (AHRD V3.3 *** W0KR26_TOBAC)		F:GO:0016831; P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR002129 (PFAM): IPR015421 (G3D	0,974	0,313	0,834	0,466	1,927									
Solyc08g021820	auxin-regulated IAA29	IAA29	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t		IPR033389 (PFAM): G3DSA:3.10.20.9	12,825	24,716	11,117	15,463	10,771	0,973	0,003					up		
Solyc08g021870	Ankyrin repeat-containing protein (AHRD V3.3 *-* A0A124SAK7_CYNCS)		F:GO:0005515	F:protein binding		IPR036770 (G3DSA:1.25.40.GENE3D	3,485	4,189	5,924	5,836	5,399									
Solyc08g021880	Ankyrin repeat family protein (AHRD V3.3 *-* F8WLB2_CITUN)		C:GO:0016021	C:integral component of membrane		IPR026961 (PFAM): PTHR24177:SF1	0,264	0,229	0,215	0,487	0,307									
Solyc08g021890	DnaJ homolog subfamily C member 13 (AHRD V3.3 *-* W9QGW5_9ROSA)		P:GO:0000578; C:G(	P:embryonic axis specification; C:vacuolar membrane; C:endop		mobidb-lite (MOBIDB_LITE): PTHR369	0,038	0,000	0,022	0,050	0,024									
Solyc08g021920	DnaJ homolog subfamily C member 13 (AHRD V3.3 *** W9QGW5_9ROSA)		P:GO:0000578; C:G(	P:embryonic axis specification; C:vacuolar membrane; C:endop		IPR036869 (G3DSA:1.10.287.GENE3I	168,249	152,163	204,093	224,205	216,401									
Solyc08g021940	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *-* AT5G11100.1)		F:GO:0008289	F:lipid binding		IPR039010 (PFAM): PTHR10774 (PAI	0,735	1,239	0,050	0,196	0,094									
Solyc08g021960	EamA-like transporter family (AHRD V3.3 *** AT4G32140.1)		C:GO:0016021	C:integral component of membrane		IPR000620 (PFAM): PTHR23051:SF7	11,229	15,095	6,461	6,816	6,327									
Solyc08g021990	26S protease regulatory subunit-like protein (AHRD V3.3 *** D3G8A3_LOLPR)		F:GO:0005524; F:G(	F:ATP binding; F:pr(EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:2.40.50.140 (GENE3D): IPR0(	0,021	0,000	0,000	0,025	0,000									
Solyc08g022020	LOW QUALITY:V-type proton ATPase subunit C (AHRD V3.3 --* VATC_HORVU)						0,142	0,121	0,140	0,198	0,163									
Solyc08g022030	Myosin heavy chain-related protein (AHRD V3.3 *** AT4G32190.1)		P:GO:0007131; C:G(	P:reciprocal meiotic recombination; C:chloroplast; P:regulation (		PTHR23160 (PANTHER): PTHR23160	14,159	18,539	11,295	11,710	14,095									
Solyc08g022060	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G17750.1)						2,275	2,338	2,776	2,322	2,672									

Solyc08g022070	Prolyl oligopeptidase family protein (AHRD V3.3 *** AT1G76140.1)		F:GO:0004252; P:GO	F:serine-type endop	EC:3.4.21	Acting on peptide bor	IPR002470 (PRINTS); G3DSA:2.130.1	60,367	55,070	79,514	84,452	82,137									
Solyc08g022080	BZIP transcription factor (AHRD V3.3 *-* Q93YM7_TOBAC)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR020983 (PFAM) bZIP	73,633	66,279	92,436	83,028	83,895									
Solyc08g022100	LOW QUALITY:Plasma-membrane choline transporter family protein (AHRD V3.3 --* AT3G04440.2)							0,380	0,403	0,658	0,507	0,638									
Solyc08g022110	BZIP transcription factor (AHRD V3.3 *-* Q93YM7_TOBAC)		F:GO:0003700; F:GO	F:DNA-binding transcription factor activity; F:protein binding; P:r			mobidb-lite (MOBIDB_LITE); mobidb-lit	38,941	31,818	48,189	47,529	46,735									
Solyc08g022120	UPF0747 protein Exig_1968 (AHRD V3.3 *** A0A1D1XFP0_9ARAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	22,495	18,889	32,406	29,307	27,382									
Solyc08g022130	F-box-like/WD repeat-containing protein TBL1XR1 (AHRD V3.3 --* A0A1D1XH95_9ARAE)							12,411	11,104	6,090	7,877	5,584									
Solyc08g022150	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_SOLTU)		C:GO:0009535; C:GO	C:chloroplast thylakoid membrane; C:chloroplast stroma; F:oxid			PTHR11993:SF27 (PANTHER); PTHR	0,000	0,021	0,000	0,000	0,000									
Solyc08g022170	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_ATRBE)		C:GO:0005886; C:GO	C:plasma membran	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR038290 (G3DSA:1.10.645.GENE3	0,058	0,062	0,074	0,275	0,210									
Solyc08g022210	Methylthioribose-1-phosphate isomerase (AHRD V3.3 *** K4CJP1_SOLLC)		P:GO:0044249	P:cellular biosynthetic process			IPR011559 (TIGRFAM); IPR005251 (T	127,394	107,882	102,512	86,443	95,607									
Solyc08g022215	Cytochrome c biogenesis protein CcsA (AHRD V3.3 *-* CCSA_SOLBU)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation;			G3DSA:1.10.287.10 (GENE3D); IPR0	0,000	0,000	0,047	0,000	0,023									
Solyc08g022240	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GDS7_THECC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.50.12520 (GENE3D); IPF	1,124	0,544	0,187	0,047	0,093									
Solyc08g023270	Myosin heavy chain-related family protein (AHRD V3.3 *** B9I192_POPTR)						PTHR38378 (PANTHER)	2,541	2,521	7,792	9,583	9,057									
Solyc08g023280	RING/U-box superfamily protein (AHRD V3.3 --* AT3G07200.3)		P:GO:0006281	P:DNA repair			PF13923 (PFAM); IPR036420 (G3DSA	7,875	6,771	0,769	0,456	0,964									
Solyc08g023320	LOW QUALITY:hAT transposon superfamily protein (AHRD V3.3 *-* AT1G43260.1)		F:GO:0003677; C:GO	F:DNA binding; C:integral component of membrane; F:protein di			PTHR32166 (PANTHER)	0,000	0,036	0,000	0,000	0,187									
Solyc08g023340	Lectin (AHRD V3.3 --* LEC_LENCU)							0,081	0,057	0,274	0,191	0,398									
Solyc08g023420	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GDS7_THECC)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM); G3DSA:3.40.50.1	0,061	0,075	0,000	0,047	0,023									
Solyc08g023440	Early-responsive to dehydration stress family protein (AHRD V3.3 *** B9GJG0_POPTR)		C:GO:0016020	C:membrane			IPR027815 (PFAM); IPR003864 (PFA	39,651	36,004	37,089	53,489	41,499					0.529	0.007			up
Solyc08g023460	LEM3 (Ligand-effect modulator 3) family protein (AHRD V3.3 *** A0A072V9A6_MEDTR)		C:GO:0016020	C:membrane			IPR005045 (PIRSF); IPR005045 (PFA	13,798	12,479	20,015	22,083	17,438									
Solyc08g023465	exocyst subunit exo70 family protein B1 (AHRD V3.3 --* AT5G58430.1)							0,396	0,221	0,591	0,528	0,496									
Solyc08g023470	geranyl pyrophosphate synthase	GPPS	P:GO:0008299	P:isoprenoid biosynthetic process			IPR000092 (PFAM); IPR008949 (G3D	27,745	27,499	50,141	51,549	46,735									
Solyc08g023490	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SZL2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	9,126	7,220	5,015	5,054	6,546									
Solyc08g023493	Stem-specific TSJT1 (AHRD V3.3 *** A0A0B0N6F5_GOSAR)						IPR029055 (G3DSA:3.60.20.GENE3D	0,696	0,611	0,653	0,362	0,467									
Solyc08g023497	LSD1-like 3 (AHRD V3.3 --* AT4G16310.5)							0,245	0,121	0,172	0,295	0,259									
Solyc08g023500	Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 *** AT1G30300.4)		F:GO:0016787	F:hydrolase activity			IPR036866 (G3DSA:3.60.15.GENE3D	13,905	14,958	11,912	9,590	12,464									
Solyc08g023510	Serine incorporator 4 (AHRD V3.3 *** A0A1D1XYQ2_9ARAE)						PTHR38226 (PANTHER)	0,000	0,000	0,197	0,407	0,379									
Solyc08g023530	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G05260.1)							2,178	1,964	1,364	1,776	1,524									
Solyc08g023540	LOW QUALITY:homeobox-leucine zipper protein 17 (AHRD V3.3 --* AT2G01430.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,047	1,036	0,834	0,826	1,199									
Solyc08g023570	WD repeat-containing protein 48 (AHRD V3.3 *-* A0A1D1XI50_9ARAE)		F:GO:0043130; P:GO	F:ubiquitin binding; P:positive regulation of protein deubiquitinati			IPR021772 (PFAM); mobidb-lite (MOB	0,637	0,802	0,675	0,701	0,752									
Solyc08g023580	WD repeat-containing protein 48 (AHRD V3.3 *-* A0A151TXJ1_CAJCA)						IPR021772 (PFAM); mobidb-lite (MOB	4,008	3,580	4,790	4,441	4,832									
Solyc08g023585	DUF4283 domain protein (AHRD V3.3 --* G7IZV0_MEDTR)						IPR025558 (PFAM); PTHR34427 (PAN	0,240	0,116	0,264	0,240	0,187									
Solyc08g023590	Transducin/WD40 repeat protein (AHRD V3.3 *-* A0A072VMJ6_MEDTR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (PF	4,171	3,994	4,698	5,161	5,414									
Solyc08g023593	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 --* C1E4X3_MICCC)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	1,856	1,551	2,663	1,874	1,885									
Solyc08g023597	Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 --* A0A151TS47_CAJCA)							0,038	0,041	0,025	0,076	0,023									
Solyc08g023600	marneral synthase (AHRD V3.3 --* AT5G42600.1)						PS51257 (PROSITE_PROFILES)	0,037	0,118	0,071	0,025	0,094									
Solyc08g023630	U11/U12 small nuclear ribonucleoprotein 25 kDa (AHRD V3.3 *-* A0A0B0PAC5_GOSAR)		P:GO:0000398; C:GO	P:mRNA splicing, via spliceosome; C:U12-type spliceosomal co			G3DSA:3.10.20.90 (GENE3D); IPR04	0,000	0,000	0,000	0,025	0,000									
Solyc08g023640	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151RRH8_CAJCA)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR002885 (PFAM); IPR002885 (PFA	1,888	1,966	1,311	1,157	1,226									
Solyc08g023650	LOW QUALITY:Xanthine/uracil permease family protein (AHRD V3.3 --* AT5G62890.4)						mobidb-lite (MOBIDB_LITE)	0,605	0,655	0,471	0,362	0,424									
Solyc08g023660	Major latex-like protein (AHRD V3.3 *** B5THI3_PANGI)		P:GO:0006952	P:defense response			IPR023393 (G3DSA:3.30.530.GENE3	0,561	0,330	0,000	0,000	0,000									
Solyc08g028670	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast			IPR008543 (PFAM); IPR008543 (PAN	0,000	0,000	0,000	0,022	0,000									
Solyc08g028690	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	5,939	10,570	4,127	4,150	8,929	0,858	0,010	1,101	0,003			up	up	
Solyc08g028700	Delta-9 acyl-lipid desaturase 1 (AHRD V3.3 --* ADS1_ARATH)							0,000	0,019	0,000	0,000	0,000									
Solyc08g028780	LOW QUALITY:DUF868 family protein (AHRD V3.3 *** G7J9W6_MEDTR)		C:GO:0005886	C:plasma membrane			IPR008586 (PFAM); IPR008586 (PAN	28,549	37,135	2,973	2,551	4,346									
Solyc08g028850	LOW QUALITY:NAC domain-containing protein, putative (AHRD V3.3 --* B9T476_R NAC076		F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM) NAC	0,059	0,000	0,000	0,047	0,046									
Solyc08g028880	30S ribosomal protein S2, chloroplastic (AHRD V3.3 *** RR2_SOLLC)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001865 (PFAM); G3DSA:3.40.50.1	0,021	0,102	0,025	0,173	0,189									
Solyc08g028890	ribosomal protein S2 (AHRD V3.3 *-* ATCG00160.1)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:translation; C:small ribos			G3DSA:3.40.50.10490 (GENE3D); IPF	0,000	0,021	0,000	0,000	0,000									
Solyc08g028910	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	SSF64484 (SUPERFAMILY)	0,000	0,144	0,025	0,125	0,000									
Solyc08g028915	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLBU)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA polymerase		0,019	0,000	0,022	0,000	0,000									
Solyc08g028920	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_GUIAB)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	PTHR34995 (PANTHER)	0,000	0,021	0,025	0,000	0,000									
Solyc08g028940	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLBU)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	IPR007081 (PFAM); IPR007083 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc08g028950	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLTU)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA po	IPR007083 (PFAM); IPR038120 (G3D	0,057	0,100	0,000	0,075	0,023									
Solyc08g028970	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT1G50440.4)		C:GO:0016020	C:membrane				3,162	2,786	5,501	6,600	5,705									
Solyc08g028977	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* U3R7P8_9ASTE)		F:GO:0016740	F:transferase activity			mobidb-lite (MOBIDB_LITE)	0,000	0,061	0,000	0,025	0,023									
Solyc08g029000	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	LOX8	F:GO:0005515; F:GO	F:protein binding; F:	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS); IPR013819 (PF	0,021	0,060	0,658	0,143	0,262									
Solyc08g029050	TOPLESS 6	TPL6	F:GO:0005515; P:GO	F:protein binding; P:regulation of transcription, DNA-templated			IPR015943 (G3DSA:2.130.10.GENE3	57,805	42,942	19,662	17,348	17,010									
Solyc08g029053	Unknown protein (AHRD V3.3)							0,019	0,043	0,000	0,025	0,000									
Solyc08g029090	B3 domain-containing protein family (AHRD V3.3 *-* A0A151RF19_CAJCA)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM) B3	17,141	12,637	5,781	3,993	6,536									
Solyc08g029110	Protein MEMO1 (AHRD V3.3 *** A0A1D1YE82_9ARAE)						IPR002737 (PFAM); G3DSA:3.40.830	23,360	19,761	28,246	31,965	25,064									
Solyc08g029115	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK1 (AHRD V3.3 --* LERK1_ORYSJ)							2,217	1,608	2,384	2,243	2,309									
Solyc08g029130	chromatin remodeling factor CHD3 (PICKLE) (AHRD V3.3 *** AT2G25170.4)		F:GO:0005506; F:GO	F:iron ion binding; F:ATP binding			IPR001650 (PFAM); IPR038718 (G3D	80,581	72,303	91,626	89,899	87,082									
Solyc08g029150	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XC37_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR011990 ((	10,825	9,899	11,451	10,689	11,419									
Solyc08g029170	Hexosyltransferase (AHRD V3.3 *** K4CJX9_SOLLC)		P:GO:0006486; F:GO	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR002659 (PFAM); IPR025298 (PFA	35,375	31,581	35,372	30,151	29,475									
Solyc08g029190	Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repeat-containing protein (AHRD		F:GO:0005515	F:protein binding			IPR000270 (PFAM); IPR011990 (G3D	26,413	25,001	28,232	35,506	30,903									
Solyc08g029200	S-acyltransferase (AHRD V3.3 *** K4CJY2_SOLLC)		C:GO:0005783; C:GO	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM); PTHR22883:SF2	18,821	16,021	24,625	26,689	23,176									
Solyc08g029220	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XK41_CYNCS)						IPR001623 (PRINTS); IPR001623 (PF	24,376	24,298	29,483	26,597	25,938									
Solyc08g029230	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** G7JCS6_MEDTR)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM); IPR021109 (G3D	17,510	17,036	19,703	19,318	18,769									
Solyc08g029240	G patch domain-containing protein TGH homolog (AHRD V3.3 --* TGHH_ORYSJ)							0,299	0,160	0,265	0,510	0,331									
Solyc08g029348	Ribosomal protein S1 (AHRD V3.3 *-* A0A142BZ25_ZIZJJ)		C:GO:0016020; C:GO	C:membrane; C:intracellular organelle; C:cytoplasmic part				0,000	0,000	0,000	0,000	0,023									
Solyc08g029360	LOW QUALITY:MATH domain and coiled-coil domain-containing protein At2g05420 (AHRD V3.3 --* MCC05_ARATH)							1,239	1,034	0,852	1,014	1,084									
Solyc08g029400	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast			IPR008543 (PANTHER)	0,000	0,043	0,025	0,000	0,000									
Solyc08g029404	Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 --* AT4G37110.4)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane				0,000	0,041	0,000	0,025	0,000									
Solyc08g036410	LOW QUALITY:arabinogalactan protein 12 (AHRD V3.3 --* AT3G13520.1)							0,277	0,214	0,150	0,199	0,165									
Solyc08g036520	Diphosphomevalonate decarboxylase (AHRD V3.3 --* A0A0N6YKZ0_NOTNI)		P:GO:0006811; F:GO	P:ion transport; F:lipid binding; F:proton transmembrane transporter activity; P:ATP synthesis coupled p				1,025	0,904	2,720	3,162	2,598									
Solyc08g036560	Phosphate transporter (AHRD V3.3 --* D5KXH7_PEA)							6,760	7,252	9,816	9,194	9,369									
Solyc08g036570	Glutaredoxin (AHRD V3.3 *** A0A103XEV9_CYNCS)		F:GO:0009055; F:GO	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR011905 (TIGRFAM); G3DSA:3.40.:	0,019	0,039	0,000	0,000	0,000									
Solyc08g036600	Transducin/WD40 repeat protein (AHRD V3.3 *-* G7L4S7_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	8,741	10,746	15,005	13,498	13,300									
Solyc08g036610	Meiotic recombination protein DMC1 homolog (AHRD V3.3 *-* DMC1_SOYBN)		F:GO:0000150; F:GO	F:recombinase activity; F:nucleotide binding; F:DNA binding; F:/			G3DSA:1.10.150.20 (GENE3D); mobic	0,175	0,304	0,168	0,188	0,187									
Solyc08g036615	ABC-2 type transporter family protein (AHRD V3.3 --* AT4G25750.1)							0,571	0,785	0,832	0,852	0,724									
Solyc08g036620	Jasmonate zim-domain protein (AHRD V3.3 *** G7LE60_MEDTR)		C:GO:0005634; P:GO	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (PFAM); IPR018467 (PFA	0,141	0,722	0,223	0,050	0,330									
Solyc08g036625	Jasmonate ZIM-domain protein 12a (AHRD V3.3 *-* T1WMW5_TOBAC)		C:GO:0005634; P:GO	C:nucleus; P:response to wounding; P:regulation of defense response; P:regulation of jasmonic acid me				0,021	0,227	0,050	0,025	0,072									
Solyc08g036630	LOW QUALITY:O-acetyltransferase family protein (AHRD V3.3 --* AT5G46340.1)							0,078	0,018	0,075	0,119	0,141									
Solyc08g036640	Jasmonate zim-domain protein (AHRD V3.3 *** G7LE60_MEDTR)		C:GO:0005634; P:GO	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (PFAM); IPR018467 (PFA	0,268	2,367	0,742	0,297	0,613									
Solyc08g036660	Jasmonate zim-domain protein (AHRD V3.3 *** G7IP70_MEDTR)		C:GO:0005634; P:GO	C:nucleus; P:response to wounding; P:regulation of defense res			IPR018467 (PFAM); IPR010399 (PFA	0,021	0,454	0,125	0,072	0,046									
Solyc08g041662	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 --* A0A061FD65_THECC)		F:GO:0003677; F:GO	F:DNA binding; F:protein dimerization activity			IPR037220 (SUPERFAMILY)	0,000	0,018	0,000	0,000	0,000									
Solyc08g041665	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061G8Z6_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM)	0,349	0,164	0,000	0,000	0,000									
Solyc08g041670	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** A0A072V6V2_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,037	0,120	0,000	0,000	0,000									
Solyc08g041700	LOW QUALITY:F-box protein (AHRD V3.3 *** A0A072VIK4_MEDTR)		F:GO:0005515	F:protein binding			IPR001810 (PROSITE_PROFILES); II	0,356	0,866	0,072	0,047	0,165									
Solyc08g041710	transmembrane protein (AHRD V3.3 *** AT2G25270.1)		C:GO:0005886; C:GO	C:plasma membrane; C:plasmodesma; C:integral component of			IPR040283 (PANTHER); PTHR31414::	39,245	34,388	6,501	4,029	5,078									
Solyc08g041740	LOW QUALITY:4-hydroxy-3-methylbut-2-enyl diphosphate synthase (AHRD V3.3 --* AT5G60600.5)		C:GO:0000943; F:GO	C:retrotransposon r	EC:2.1.1.43	Histone-lysine N-methyltransferase		0,057	0,180	0,000	0,025	0,047									
Solyc08g041750	Post-SET domain-containing protein (AHRD V3.3 *-* A0A103XZM4_CYNCS)		F:GO:0016740	F:transferase activity				0,040	0,099	0,000	0,000	0,023									
Solyc08g041760	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein (AHRD V3.3 --* AT5G12440		C:GO:0000943; C:GO	C:retrotransposon nucleocapsid; C:nucleus; F:methyltransferase activity; F:transferase activity; F:histo				0,021	0,175	0,000	0,000	0,023									
Solyc08g041770	Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *** AT5G25265.1)		C:GO:0016021	C:integral component of membrane			PTHR31485 (PANTHER); PTHR31485	16,082	19,107	7,971	7,038	11,810									
Solyc08g041780	Neurochondrin (AHRD V3.3 *** A0A0B0NUA0_GOSAR)						IPR008709 (PFAM); IPR008709 (PAN	62,259	60,463	79,088	75,178	82,485									
Solyc08g041800	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 --* CLPP_CUSGR)							1,066	0,883	0,697	0,612	0,798									
Solyc08g041810	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT5G14895.1)						PTHR33168 (PANTHER); PTHR33168	0,021	0,000	0,000	0,000	0,024									
Solyc08g041820	Homeobox protein knotted-1, putative (AHRD V3.3 *** B9RNZ6_RICCO)		F:GO:0003677; C:GO	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR005540 (PFAM) TALE	45,825	53,668	29,239	30,916	31,325									
Solyc08g041850	minichromosome maintenance 8 (AHRD V3.3 --* AT3G09660.3)							0,000	0,000	0,000	0,025	0,000									
Solyc08g041855	Homogentisate phytyltransferase (AHRD V3.3 *** W8NZU5_ELAOL)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity, trans			IPR000537 (PFAM); PTHR43009:SF1	0,000	0,000	0,000	0,000	0,024									
Solyc08g041860	serine/arginine repetitive matrix-like protein (AHRD V3.3 *-* AT4G32020.1)						PF15365 (PFAM); mobidb-lite (MOBID	305,144	103,983	115,683	265,288	133,368	-1,527	0,000			1,200	0,000	down		up
Solyc08g041870	Aspartate aminotransferase (AHRD V3.3 *** K4CK47_SOLLC)		P:GO:0006520; F:GO	P:cellular amino acid metabolic process; F:transaminase activit			IPR000796 (PRINTS); IPR004839 (PF	217,677	257,509	458,876	444,997	471,940									
Solyc08g041890	Importin subunit alpha (AHRD V3.3 *** K4CK49_SOLLC)		F:GO:0005515; C:GO	F:protein binding; C:nucleus; C:cytoplasm; P:protein import into			IPR024931 (PIRSF); IPR011989 (G3D	187,791	186,141	105,945	96,853	108,919									
Solyc08g041920	LOW QUALITY:serine/threonine protein kinase 2 (AHRD V3.3 --* AT3G08720.4)							0,975	1,809	1,833	1,888	2,452									
Solyc08g041930	LOW QUALITY:flocculation protein (AHRD V3.3 --* AT2G39950.1)							1,374	1,916	3,421	3,222	4,357									
Solyc08g041980	ER membrane protein complex subunit-like protein (AHRD V3.3 *** G7JAF8_MEDTR)		F:GO:0030246	F:carbohydrate binding			IPR019008 (PFAM); G3DSA:2.60.40.1	39,923	39,507	53,068	51,328	46,792									
Solyc08g042000	Sucrose-phosphate synthase (AHRD V3.3 *** SPSA_SPIOL)		P:GO:0005985; F:GO	P:sucrose metaboli	EC:2.4.1.14; EC:2.4.	Sucrose-phosphate s	IPR012819 (TIGRFAM); G3DSA:3.40.!	2,444	6,563	1,969	2,389	2,286	1,445	0,001					up		
Solyc08g042010	Exostosin family protein (AHRD V3.3 *** A0A061GIR4_THECC)		P:GO:0006486; F:GO	P:protein glycosylation; F:transferase activity, transferring glycc			IPR040911 (PFAM); IPR004263 (PAN	0,783	2,164	0,315	0,122	0,163									
Solyc08g042030	Kinesin-like protein (AHRD V3.3 *** V4T5G4_9ROSI)		F:GO:0003777; F:GO	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR036961 (G3	1,630	1,942	0,907	0,443	0,892									
Solyc08g042040	Kinesin-like protein (AHRD V3.3 *-* R0GV12_9BRAS)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,841	4,019	2,127	1,574	2,282									
Solyc08g042050	RNA helicase DEAD25	DEAD25	F:GO:0003723; F:GO	F:RNA binding; F:he	EC:3.6.1.15	Nucleoside-triphosph	IPR011545 (PFAM); IPR001650 (PFA	96,342	120,903	199,460	183,920	225,971									
Solyc08g042060	SET domain-containing protein (AHRD V3.3 --* AT2G23380.2)							0,220	0,334	0,143	0,267	0,071									
Solyc08g042070	arginine-rich cyclin 1 (AHRD V3.3 --* AT2G26430.4)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,037	0,000	0,073	0,023									
Solyc08g042080	Multiple chloroplast division site 1, putative (AHRD V3.3 *** A0A061FEL2_THECC)		C:GO:0009507; P:GO	C:chloroplast; P:chloroplast fission			mobidb-lite (MOBIDB_LITE); mobidb-lit	10,002	10,852	17,409	15,201	15,808									
Solyc08g042100	U-box domain-containing 12 (AHRD V3.3 *** A0A0B0MP20_GOSAR)		F:GO:0005515	F:protein binding			IPR011989 (G3DSA:1.25.10.GENE3D	7,267	7,047	0,473	0,270	0,234									
Solyc08g042120	Phox domain-containing family protein (AHRD V3.3 --* B9HAF8_POPTR)		F:GO:0035091	F:phosphatidylinositol binding				1,338	1,341	1,698	2,159	2,174									
Solyc08g042130	Phox (PX) domain-containing protein (AHRD V3.3 *** AT4G32160.1)		F:GO:0035091	F:phosphatidylinositol binding			IPR001683 (PFAM); IPR036871 (G3D	14,365	12,516	16,784	19,020	17,187									
Solyc08g042140	translation initiation factor 3 subunit I (AHRD V3.3 *** AT1G54680.4)		F:GO:0004222; F:GO	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	PTHR33471:SF4 (PANTHER); PTHR3:	8,959	8,548	11,822	11,086	12,996									
Solyc08g042143	Phox domain-containing family protein (AHRD V3.3 *-* B9HAF8_POPTR)		F:GO:0035091	F:phosphatidylinositol binding			PTHR10555:SF207 (PANTHER); IPR0	0,000	0,000	0,049	0,022	0,072									
Solyc08g042147	LOW QUALITY:Plant-specific transcription factor YABBY family protein (AHRD V3.3 --* AT2G45190.2)						IPR025558 (PFAM); mobidb-lite (MOB	0,060	0,021	0,096	0,097	0,072									
Solyc08g043140	Calcium-dependent ARF-type GTPase activating protein family (AHRD V3.3 *** AT3G07940.1)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS); IPR001164 (PF	0,573	0,471	0,071	0,075	0,163									
Solyc08g043170	delta 1-pyrroline-5-carboxylate synthetase	pro2	F:GO:0004350; C:GO	F:glutamate-5-semi	EC:1.2.1.41	Glutamate-5-semiald	IPR001057 (PRINTS); IPR015590 (PF	65,765	71,206	61,554	62,553	64,508									
Solyc08g043180	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** A0A0F7GYT8_9ROSI)		F:GO:0005509; C:GO	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR016123 (G3DSA:3.40.1000.GENE	7,590	13,807	26,633	35,828	35,150	0,891	0,002			0,432	0,049	up		up
Solyc08g043190	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G05540.1)						mobidb-lite (MOBIDB_LITE)	0,061	0,055	0,125	0,119	0,188									
Solyc08g044260	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT1G02205.2)		F:GO:0005506; P:GO	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM); PTHR11863:SF4	2,374	1,932	1,901	1,707	1,709									
Solyc08g044265	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT1G02205.5)		F:GO:0000170; F:GO	F:sphingosine hydroxylase activity; F:iron ion binding; C:endopl			IPR021940 (PFAM); PTHR11863 (PAN	7,265	6,065	12,130	13,942	13,201									
Solyc08g044270	Glutamate synthase, putative (AHRD V3.3 *-* B9RII5_RICCO)		P:GO:0006537; F:GO	P:glutamate biosynthetic process; F:glutamate synthase activity			IPR002932 (PFAM); IPR013785 (G3D	0,546	0,668	0,447	0,815	0,868									
Solyc08g044280	LOW QUALITY:Adenine nucleotide alpha hydrolase-like domain kinase (AHRD V3.3 --* A0A072V3K5_MEDTR)							0,000	0,076	0,000	0,000	0,000									
Solyc08g044332	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:3.40.395.10 (GENE3D); IPR0	0,019	0,000	0,000	0,000	0,000									
Solyc08g044334	LOW QUALITY:DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 *-* G7L3J8_MEDTR)		F:GO:0003676; F:GO	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR001650 (PFAM); G3DSA:3.40.50.3	0,019	0,000	0,000	0,069	0,069									
Solyc08g044336	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			IPR001611 (PFAM); IPR032675 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc08g044340	LOW QUALITY:Glutamate receptor (AHRD V3.3 *-* G5EKP3_SOLLC)		F:GO:0004970; C:GO	F:ionotropic glutamate receptor activity; C:plasma membrane; P			PTHR43891 (PANTHER); PTHR43891	0,019	0,000	0,000	0,000	0,024									
Solyc08g044345	Prefoldin chaperone subunit family protein (AHRD V3.3 *** A0A061F0A6_THECC)		P:GO:0006457; C:GO	P:protein folding; C:prefoldin complex; F:unfolded protein bindinc			IPR002777 (PFAM); IPR009053 (G3D	5,765	6,888	7,789	8,433	7,987									
Solyc08g044350	Sodium/sulfate cotransporter 2 (AHRD V3.3 --* SLT2_CHLRE)							0,000	0,018	0,022	0,000	0,000									
Solyc08g044355	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (AHRD V3.3 *-* W9S9V0_9ROSA)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR001986 (PFAM); IPR036968 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc08g044360	PIF1-like helicase (AHRD V3.3 *-* G7JL89_MEDTR)		P:GO:0000723; F:GO	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR025476 (PFAM); IPR010285 (PFA	0,019	0,000	0,022	0,000	0,000									
Solyc08g044370	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						IPR015410 (PFAM); mobidb-lite (MOB	0,283	0,203	0,025	0,099	0,000									
Solyc08g044375	Replication factor-A carboxy-terminal domain protein (AHRD V3.3 --* A0A072U9L2_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D); IPR0	0,019	0,064	0,068	0,100	0,072									
Solyc08g044400	SacI-like domain protein/WW domain protein (AHRD V3.3 *** G7JNP0_MEDTR)		F:GO:0005515; F:GO	F:protein binding; F:phosphoric ester hydrolase activity			IPR002013 (PFAM); IPR001202 (PFA	86,400	81,479	84,596	86,729	84,722									
Solyc08g044460	cytochrome P450, family 82, subfamily F, polypeptide 1 (AHRD V3.3 --* AT2G25160.2)							0,506	0,892	0,025	0,025	0,071									
Solyc08g044510	Beta-glucosidase (AHRD V3.3 *** L0ASF2_POPTO)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); IPR001360 (PF	3,031	1,771	0,389	0,051	0,095									
Solyc08g045640	Remorin family protein (AHRD V3.3 *** B9GJG3_POPTR)						IPR005516 (PFAM); mobidb-lite (MOB	21,600	18,729	13,079	12,250	12,218									
Solyc08g045710	LOW QUALITY:ATP synthase subunit alpha (AHRD V3.3 --* ATCG00120.1)		F:GO:0000166; C:GO	F:nucleotide binding; C:mitochondrial proton-transporting ATP sy			G3DSA:3.40.50.300 (GENE3D)	0,019	0,019	0,000	0,000	0,046									
Solyc08g045750	mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT5G19480.4)							3,102	2,709	1,902	2,008	1,888									

Solyc08g045780	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RVL0_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	24,219	22,342	24,765	24,384	27,987									
Solyc08g045850	pentatricopeptide repeat-containing protein		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	40,615	37,032	79,558	75,918	73,019									
Solyc08g045880	LOW QUALITY:Protein YIPF (AHRD V3.3 --* A0A0D9V2T1_9ORYZ)							0,000	0,018	0,025	0,000	0,000									
Solyc08g047885	calcium-dependent lipid-binding family protein (AHRD V3.3 --* AT1G48090.6)							0,019	0,000	0,000	0,000	0,000									
Solyc08g048080	LOW QUALITY:Polyketide cyclase/dehydrase and lipid transport superfamily protein (AHRD V3.3 --* AT5G49800.2)							0,000	0,000	0,025	0,022	0,024									
Solyc08g048190	LOW QUALITY:phosphotransferases/inositol or phosphatidylinositol kinase (AHRD V3.3 --* AT4G36080.3)							0,000	0,000	0,025	0,047	0,047									
Solyc08g048240	Bifunctional protein FolD (AHRD V3.3 *** W9T0H0_9ROSA)		F:GO:0004488: P:G(	F:methylenetetrahv	EC:1.5.1.5	Methylenetetrahydrol	IPR000672 (PRINTS): IPR020630 (PF	18,304	16,404	15,215	14,018	15,102									
Solyc08g048250	Peroxisomal (S)-2-hydroxy-acid oxidase (AHRD V3.3 *** GOX_SPIOL)		F:GO:0010181: F:G(	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR012133 (PIRSF): IPR000262 (PFA	17,287	17,241	48,584	51,259	43,438									
Solyc08g048280	Transporter (AHRD V3.3 *-* A0A0K9P6N2_ZOSMR)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): PTH	0,075	0,000	0,025	0,000	0,000									
Solyc08g048290	inositol transporter 2	INT2	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): IPR005828 (PF	22,243	16,890	9,959	8,751	9,692									
Solyc08g048300	cinnamyl-alcohol dehydrogenase (AHRD V3.3 *-* AT1G72680.1)		F:GO:0008270: F:G(	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduct			G3DSA:3.40.50.720 (GENE3D): PTHF	0,021	0,036	0,000	0,000	0,046									
Solyc08g048370	TCP transcription factor 29	TCP29					IPR017887 (PFAM: TCP	7,120	7,835	5,004	5,097	4,408									
Solyc08g048390	TCP transcription factor 24	TCP24					IPR017887 (PFAM: TCP	37,580	41,537	18,722	17,465	22,861									
Solyc08g048400	RNA helicase, ATP-dependent, SK12/DOB1 protein (AHRD V3.3 --* AT3G46960.3)							4,918	5,213	2,172	1,844	2,364									
Solyc08g048430	F-box family protein (AHRD V3.3 *** B9H2A8_POPTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	43,042	47,885	57,608	54,261	53,866									
Solyc08g048435	LINE-1 reverse transcriptase isogeny (AHRD V3.3 *-* A0A151QW83_CAJCA)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane				0,252	0,672	0,137	0,265	0,519									
Solyc08g048450	ornithine aminotransferase	oat	F:GO:0004587: F:G(	F:ornithine-oxo-acic	EC:2.6.1.13	Ornithine aminotrans	IPR015421 (G3DSA:3.40.640.GENE3I	36,833	34,011	107,420	113,694	105,397									
Solyc08g048500	RNA-binding KH domain protein (AHRD V3.3 *** G7IP63_MEDTR)		F:GO:0003723	F:RNA binding			G3DSA:3.30.310.210 (GENE3D): IPR(	50,043	48,003	64,046	67,019	66,970									
Solyc08g048510	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* AT3G20810.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,081	0,064	0,147	0,173	0,282									
Solyc08g048520	LOW QUALITY:Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT4G18372.2)		C:GO:0031417	C:NatC complex			G3DSA:2.30.30.100 (GENE3D): PTHF	0,037	0,021	0,000	0,000	0,024									
Solyc08g048525	protein phosphatase 2A subunit A3 (AHRD V3.3 --* AT1G13320.3)							0,782	0,942	2,927	2,233	2,402									
Solyc08g048540	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT4G18372.2)		C:GO:0031417	C:NatC complex			IPR001163 (PFAM): G3DSA:2.30.30.1	1,895	2,001	2,770	3,213	2,433									
Solyc08g048545	NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 --* A0A199VVJ6_ANACO)							0,363	0,374	0,266	0,388	0,424									
Solyc08g048550	Protease Do-like protein (AHRD V3.3 *** G7IP65_MEDTR)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): G3DSA:2.40.1(	16,940	22,273	21,924	20,970	23,430									
Solyc08g048570	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 --* A0A067GG63_CITSI)							0,000	0,000	0,025	0,000	0,000									
Solyc08g059660	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT4G32285.2)		F:GO:0005545: C:G(	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR014712 (G3DSA:1.20.58.GENE3D	224,382	212,491	139,480	136,135	135,530									
Solyc08g059700	Histone acetyltransferase (AHRD V3.3 *** A0A0B0NK56_GOSAR)						G3DSA:1.10.246.20 (GENE3D): mobic	0,021	0,072	0,000	0,025	0,000									
Solyc08g059710	EEIG1/EHBP1 N-terminal domain-containing protein (AHRD V3.3 *** A0A103XZJ5_CYNCS)						IPR019448 (PFAM): mobidb-lite (MOB	0,136	0,588	0,583	1,144	0,588									
Solyc08g059730	Serine/threonine-protein kinase (AHRD V3.3 *** K4CKL7_SOLLC)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR024171 (PIRSF): G3DSA:3.30.200	5,663	3,447	1,696	1,580	2,070									
Solyc08g059750	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G30630.1)		F:GO:0005524: F:G(	F:ATP binding; F:kinase activity			IPR010488 (PFAM): PTHR31153:SF9	0,019	0,041	0,121	0,075	0,024									
Solyc08g059760	Peroxidase (AHRD V3.3 *** A0A0V0I4D2_SOLCH)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR002207 (PF	19,200	18,394	16,011	16,509	18,253									
Solyc08g059800	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT4G32330.4)						IPR027329 (PFAM): mobidb-lite (MOB	24,666	21,537	5,844	5,374	6,504									
Solyc08g060810	EIN3-binding F-box protein 2	EBF1	F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR032675 (G3D	196,614	109,486	363,776	409,865	288,820	-0,817	0,005					down		
Solyc08g060830	Unknown protein (AHRD V3.3)							12,819	13,290	17,262	16,040	16,286									
Solyc08g060840	FAR1 (AHRD V3.3 *** A0A178UYQ0_ARATH)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR007527 (PFAM: FAR1	38,235	34,776	46,439	52,967	48,557									
Solyc08g060845	terpene synthase 14 (AHRD V3.3 --* AT1G61680.2)							7,513	6,386	7,093	8,611	7,923									
Solyc08g060860	DUF4050 family protein (AHRD V3.3 *** G7JE31_MEDTR)						IPR025124 (PFAM): mobidb-lite (MOB	11,469	12,059	15,641	16,403	15,949									
Solyc08g060920	IDS4-like	ail	P:GO:0016036	P:cellular response to phosphate starvation			IPR004331 (PFAM): PTHR10783:SF8	25,986	22,367	37,370	30,233	32,310									
Solyc08g060940	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT4G32390.1)		C:GO:0005768: C:G(	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM): mobidb-lite (MOB	67,301	69,179	59,757	60,099	52,564									
Solyc08g060960	LOW QUALITY:BnaC06g12010D protein (AHRD V3.3 *-* A0A078F401_BRANA)						PTHR33527 (PANTHER): PTHR33527	0,000	0,018	0,000	0,000	0,000									
Solyc08g060970	polygalacturonase AF118567	PG64 (Pgcat)	F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	3,441	9,642	1,166	0,865	1,817	1,513	0,001					up		
Solyc08g061000	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RV50_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	64,085	77,628	81,978	76,891	77,552									
Solyc08g061010	Major facilitator superfamily protein (AHRD V3.3 *** AT2G26690.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): PTHR11654:SF8	2,604	3,430	0,022	0,047	0,000									
Solyc08g061037	Laccase (AHRD V3.3 --* O24043_LIRTU)		P:GO:0006508: F:G(	P:proteolysis; F:cysteine-type peptidase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc08g061060	Barwin-like endoglucanase (AHRD V3.3 *** A0A103XZL4_CYNCS)	PNPL2	C:GO:0016021	C:integral component of membrane			IPR009009 (PFAM): IPR036908 (G3D	0,000	0,019	0,000	0,220	0,048									
Solyc08g061063	EG45-like domain containing protein (AHRD V3.3 *-* A0A151TT40_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR036908 (G3DSA:2.40.40.GENE3D	0,000	0,000	0,025	0,022	0,000									
Solyc08g061090	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT4G32400.1)		F:GO:0022857: P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS): IPR018108 (PF	37,994	38,986	48,508	46,122	43,116									
Solyc08g061100	Cellulose synthase (AHRD V3.3 *** M1BV52_SOLTU)		C:GO:0016020: F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (I	IPR013083 (G3DSA:3.30.40.GENE3D	1209,000	1003,934	437,296	379,630	440,480									
Solyc08g061130	BZIP transcription factor (AHRD V3.3 *** L0MZN5_MALDO)	HY5	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (PFAM: bZIP	6,477	8,993	41,670	42,172	36,194									
Solyc08g061140	overexpressor of cationic peroxidase 3 (AHRD V3.3 *** AT5G11270.1)		F:GO:0003677	F:DNA binding			IPR001356 (PFAM: HB-other	15,107	16,202	30,204	32,589	32,020									
Solyc08g061160	LOW QUALITY:BnaC09g16480D protein (AHRD V3.3 *** A0A078G2W2_BRANA)		C:GO:0005739: C:G(	C:mitochondrion; C:ribosome; C:chloroplast				0,136	0,518	0,247	0,591	0,430									
Solyc08g061180	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 --* B9SZC0_RICCO)		C:GO:0009507: P:G(	C:chloroplast; P:embryo development ending in seed dormancy				0,338	0,060	0,218	0,199	0,023									
Solyc08g061190	LOW QUALITY:proteolysis 6 (AHRD V3.3 --* AT5G02310.3)							0,061	0,062	0,068	0,249	0,093									
Solyc08g061210	LOW QUALITY:CW-type Zinc Finger (AHRD V3.3 --* AT4G15730.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,835	3,631	2,171	2,187	2,684									
Solyc08g061220	Tomato G protein alpha-subunit	tga1	F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001019 (PRINTS): IPR002976 (PF	18,372	21,491	11,091	10,931	13,021									
Solyc08g061230	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT4G33180.1)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,554	0,628	0,270	0,347	0,236									
Solyc08g061240	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G33180.1)		F:GO:0016787	F:hydrolase activity			IPR000073 (PRINTS): IPR000073 (PF	1,033	0,944	0,633	0,347	0,684									
Solyc08g061250	Kinase family protein (AHRD V3.3 *** U5GAR5_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	3,589	4,423	1,157	2,627	1,326					1,183	0,008			up
Solyc08g061260	G-protein coupled receptor 1 (AHRD V3.3 *** A0A097PPA8_SOLLC)		F:GO:0004888: P:G(	F:transmembrane signaling receptor activity; P:cell surface rece			IPR022340 (PRINTS): IPR022343 (PF	7,340	5,774	9,864	9,987	9,409									
Solyc08g061265	G-protein coupled receptor 1 (AHRD V3.3 *-* A0A097PPA8_SOLLC)		P:GO:0000278: F:G(	P:mitotic cell cycle; F:transmembrane signaling receptor activity			IPR022343 (PRINTS): IPR022340 (PF	7,711	7,057	10,379	11,841	8,885									
Solyc08g061270	DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)						IPR012876 (PFAM): IPR012876 (PAN	8,017	9,338	126,511	122,712	92,599			-0,453	0,038				down	
Solyc08g061273	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3-like protein (AHRD V3.3 --* AT1G17770.1)		F:GO:0003677	F:DNA binding			IPR017956 (PRINTS): mobidb-lite (MO	0,019	0,060	0,000	0,000	0,000									
Solyc08g061277	alpha-L-fucosidase 1 (AHRD V3.3 --* AT2G28100.1)							0,000	0,018	0,000	0,000	0,000									
Solyc08g061320	CTC-interacting domain 7 (AHRD V3.3 *** AT2G26280.3)						IPR013899 (PFAM): G3DSA:3.30.137(	251,341	284,165	337,373	348,865	331,181									
Solyc08g061323	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *** A0A061FD65_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM): IPR025525 (PFA	4,088	4,239	3,617	5,508	4,411									
Solyc08g061375	RING/FYVE/PHD-type zinc finger family protein (AHRD V3.3 --* AT1G29800.2)							0,348	0,405	0,510	0,870	0,567									
Solyc08g061380	WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)							0,281	0,172	0,330	0,287	0,186									
Solyc08g061390	LOW QUALITY:DNA repair protein rhp54 (AHRD V3.3 *-* A0A151S5C7_CAJCA)		F:GO:0005524	F:ATP binding			IPR038718 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc08g061410	LOW QUALITY:Chromatin remodeling 31, putative (AHRD V3.3 *-* A0A061FRH7_THECC)		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	0,021	0,018	0,025	0,000	0,000									
Solyc08g061450	exosome complex exonuclease (AHRD V3.3 *** AT5G25500.1)						PTHR37763 (PANTHER)	2,194	2,840	2,509	1,979	1,788									
Solyc08g061480	Chalcone--flavonone isomerase (AHRD V3.3 *** A0A1D1XWC4_9ARAE)	CHI	F:GO:0016872	F:intramolecular lyase activity			IPR016087 (PFAM): IPR016088 (G3D	20,211	37,203	25,199	33,813	26,483					0,427	0,039			up
Solyc08g061500	myosin (AHRD V3.3 *** AT4G33200.1)		F:GO:0003774: F:G(	F:motor activity; F:ε	EC:3.6.1.15	Nucleoside-triphosph	IPR000048 (PFAM): IPR002710 (PFA	25,651	21,094	32,170	33,905	34,940									
Solyc08g061510	myosin (AHRD V3.3 *-* AT4G33200.4)		F:GO:0003774: F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.58.530 (GENE3D): IPR0(	0,038	0,064	0,118	0,022	0,047									
Solyc08g061520	myosin (AHRD V3.3 *-* AT4G33200.3)		F:GO:0003774: F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): G3DSA:1.20.12	10,838	8,223	12,604	13,078	13,383									
Solyc08g061560	Receptor protein kinase (AHRD V3.3 *** A0A0U5BM22_RORAQ)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR013210 (PFAM): IPR032675 (G3D	25,717	21,497	0,568	0,397	0,633									
Solyc08g061570	P-type ATPase (AHRD V3.3 *-* F8WLD4_CITUN)		F:GO:0005524: C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR43520:SF10 (PANTHER): PTHR4	0,220	0,144	0,000	0,000	0,023									
Solyc08g061580	P-type ATPase (AHRD V3.3 *-* F4K8C8_ARATH)		F:GO:0005524: C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR43520 (PANTHER): PTHR43520	0,383	0,558	0,144	0,219	0,141									
Solyc08g061590	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SGW5_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	121,296	91,329	36,696	41,664	35,586									
Solyc08g061610	P-type ATPase of Arabidopsis 2 (AHRD V3.3 *** AT5G21930.2)		F:GO:0000166: C:G(	F:nucleotide binding	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): G3DSA:2.70.150	46,573	62,278	13,506	11,802	18,652									
Solyc08g061630	YGGT family protein (AHRD V3.3 *** B9HD03_POPTR)		C:GO:0016020	C:membrane			IPR003425 (PFAM): IPR003425 (PAN	3,727	6,109	1,812	1,982	3,477			0,926	0,019				up	
Solyc08g061635	F-box/LRR protein (AHRD V3.3 *-* AT2G06040.1)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	0,222	0,264	0,044	0,048	0,000									
Solyc08g061778	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 --* AT3G15520.3)						PTHR36014 (PANTHER)	7,095	7,531	5,538	6,353	8,190			0,564	0,039				up	
Solyc08g061800	BnaC08g32970D protein (AHRD V3.3 *-* A0A078CHK0_BRANA)						PTHR36014 (PANTHER)	2,894	2,334	2,373	1,968	3,404									
Solyc08g061820	F-box / LRR-repeat protein (AHRD V3.3 *** F8WLC8_CITUN)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	88,850	67,880	77,977	80,859	74,941									
Solyc08g061830	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase 22 (AHRD V3.3 *-* A0A061GQ99_THECC)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,039	0,000	0,000	0,000									
Solyc08g061850	Ribosomal protein S3 family protein (AHRD V3.3 *** AT5G35530.1)		F:GO:0003723: F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR004044 (PFAM): IPR005703 (TIGF	141,552	165,769	155,102	144,612	145,257									
Solyc08g061880	Peroxisome biogenesis factor 10 (AHRD V3.3 *-* B9U2H6_TOBAC)		C:GO:0005779: F:G(	C:integral component of peroxisomal membrane; F:zinc ion binding; P:protein import into peroxisome ma				5,506	4,606	7,789	7,568	7,812									
Solyc08g061890	E3 ubiquitin-protein ligase RBBP6 (AHRD V3.3 *** A0A1D1Z3E3_9ARAE)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	13,886	9,834	16,993	21,446	19,273									
Solyc08g061900	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_SILLA)		C:GO:0005886: F:G(	C:plasma membrane	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	PTHR45564 (PANTHER)	0,021	0,039	0,025	0,000	0,000									
Solyc08g061903	Auxin response factor (AHRD V3.3 --* M5VPK1_PRUPE)							1,471	0,661	0,333	0,148	0,308									
Solyc08g061910	Trihelix transcription factor GT-2-like protein (AHRD V3.3 --* A0A0B0NUX7_GOSAR)							2,938	2,624	0,610	0,655	0,517									
Solyc08g061920	cytokinin oxidase/dehydrogenase 3		P:GO:0009690: F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroger	IPR006094 (PFAM): IPR016169 (G3D	0,019	0,097	0,000	0,000	0,000									
Solyc08g061930	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ5_SOLLC)		P:GO:0009690: F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroger	IPR016169 (G3DSA:3.30.465.GENE3I	1,029	1,086	0,121	0,000	0,117									
Solyc08g061950	LOW QUALITY:Rhomboid-related intramembrane serine protease family protein (AHRD V3.3 --* AT5G38510.3)							2,113	1,567	1,638	1,724	1,627									
Solyc08g061960	Ribosomal protein S3 family protein (AHRD V3.3 *** AT5G35530.1)		F:GO:0003723: F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR004044 (PFAM): IPR005703 (TIGF	259,812	277,480	242,505	217,810	224,721									
Solyc08g061970	putative spermine synthase	spe4	F:GO:0003824	F:catalytic activity			IPR035246 (PFAM): G3DSA:3.40.50.1	8,326	6,616	0,025	0,050	0,000									
Solyc08g061980	Mechanosensitive ion channel family protein (AHRD V3.3 *** G7J8E6_MEDTR)		C:GO:0016020: P:G(	C:membrane; P:transmembrane transport			IPR016688 (PIRSF): IPR006685 (PFA	28,092	18,305	7,037	5,887	8,161									
Solyc08g062180	Protein BIG GRAIN 1 (AHRD V3.3 *-* A0A199VVQ2_ANACO)		P:GO:0009734	P:auxin-activated signaling pathway			PTHR33541:SF2 (PANTHER): IPR039	0,833	1,114	0,212	0,477	0,378									
Solyc08g062190	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (AHRD V3.3 *** A0A097PLA		P:GO:0006807	P:nitrogen compound metabolic process			IPR003010 (PFAM): IPR036526 (G3D	45,236	46,296	86,107	80,018	83,374									
Solyc08g062200	Plant regulator RWP-RK family protein (AHRD V3.3 *-* AT1G64530.1)		C:GO:0005886	C:plasma membrane			IPR003035 (PFAM: Nin-like	0,000	0,018	0,000	0,000	0,000									
Solyc08g062210	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRINT: NF-YA	38,008	51,452	40,201	39,653	43,167									
Solyc08g062220	Glycosyltransferase (AHRD V3.3 *** K4CL11_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	0,232	1,782	0,421	1,083	0,447									
Solyc08g062250	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:2.40.50.140 (GENE3D): IPR0	0,670	0,655	0,331	0,383	0,541									
Solyc08g062260	LOW QUALITY:PIF1-like helicase (AHRD V3.3 *** A0A072VE64_MEDTR)		P:GO:0000723: F:G(	P:telomere mainten	EC:3.6.1.15	Nucleoside-triphosph	IPR010285 (PFAM): G3DSA:3.40.50.3	0,000	0,000	0,000	0,000	0,024									
Solyc08g062275	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *-* A0A0V0IG10_SOLCH)		F:GO:0003824	F:catalytic activity			IPR016039 (G3DSA:3.40.47.GENE3D	0,233	0,279	0,096	0,221	0,190									
Solyc08g062280	Alpha-L-fucosidase 1 (AHRD V3.3 *-* W9SQK3_9ROSA)		F:GO:0004560: P:G(	F:alpha-L-fucosidas	EC:3.2.1.51	Alpha-L-fucosidase	G3DSA:3.20.20.80 (GENE3D): mobidb	0,021	0,103	0,068	0,025	0,024									
Solyc08g062290	Light-independent protochlorophyllide reductase subunit B (AHRD V3.3 --* CHLB_CI POR-B							3,442	5,645	1,297	1,783	2,593			0,986	0,014				up	
Solyc08g062330	Ankyrin repeat family protein (AHRD V3.3 *** F8WLA0_CITUN)		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	3,112	12,670	0,538	1,229	1,322	2,046	0,003					up		
Solyc08g062340	Heat-shock protein, putative (AHRD V3.3 *** B9RQT7_RICCO)	Hsp17.3B	P:GO:0006457: P:G(	P:protein folding; P:response to heat; P:response to salt stress;			IPR002068 (PFAM): IPR008978 (G3D	44,547	36,228	828,551	818,775	898,110									
Solyc08g062360	Ankyrin repeat family protein (AHRD V3.3 *** F8WLA0_CITUN)		F:GO:0005515	F:protein binding			IPR026961 (PFAM): IPR036770 (G3D	1,225	3,094	0,813	1,837	3,365			2,023	0,000	1,153	0,027		up	up
Solyc08g062370	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G78550.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,598	0,496	0,312	0,148	0,118									
Solyc08g062380	LOW QUALITY:2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* A		F:GO:0008168: F:G(	F:methyltransferase activity; F:oxidoreductase activity; P:methylation; F:metal ion binding; F:dioxygena				0,077	0,000	0,025	0,000	0,000									
Solyc08g062383	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G78550.1)		F:GO:0008168: F:G(	F:methyltransferase activity; F:oxidoreductase activity; P:methy			IPR027443 (G3DSA:2.60.120.GENE3I	0,099	0,124	0,000	0,000	0,023									
Solyc08g062420	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** G7I747_MEDTR)						IPR024752 (PFAM): PTHR31704 (PAI	13,003	15,012	16,999	15,961	15,921									
Solyc08g062450	Heat-shock protein, putative (AHRD V3.3 *** B9RQT7_RICCO)	Hsp17.6D	P:GO:0006457: P:G(	P:protein folding; P:response to heat; P:response to salt stress;			IPR002068 (PFAM): IPR008978 (G3D	91,612	57,574	280,872	211,777	298,519									
Solyc08g062490	WRKY transcription factor 50	WRKY50	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM: WRKY	0,468	1,810	0,494	0,987	0,635	1,956	0,042					up		
Solyc08g062500	EEIG1/EHBP1 protein amino-terminal domain protein (AHRD V3.3 *** AT5G20610.1)		P:GO:0009902	P:chloroplast relocation			IPR019448 (PFAM): mobidb-lite (MOB	48,398	61,941	50,340	50,564	51,464									
Solyc08g062510	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072UAM9_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (PFAM: HD-ZIP	0,000	0,000	0,000	0,000	0,024									
Solyc08g062560	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G26180.5)		F:GO:0008168	F:methyltransferase activity			IPR023267 (PRINTS): G3DSA:3.30.7(	36,805	39,493	42,833	44,660	41,421									
Solyc08g062570	Glutathione s-transferase, putative (AHRD V3.3 *-* B9R999_RICCO)	GSTU28	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): G3DS/	0,019	0,021	0,000	0,000	0,000									
Solyc08g062580	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151SLA5_CAJCA)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (PFA	0,019	0,041	0,000	0,025	0,626									
Solyc08g062585	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151U161_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAI	0,056	0,018	0,000	0,000	0,000									
Solyc08g062600	Exostosin family protein (AHRD V3.3 *** AT1G74680.1)		P:GO:0006486: F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): IPR004263 (PAN	0,000	0,059	0,000	0,000	0,000									
Solyc08g062610	(S)-coclaurine N-methyltransferase (AHRD V3.3 *** W9QPZ2_9ROSA)		F:GO:0008168: P:G(	F:methyltransferase activity; P:lipid biosynthetic process; P:met			G3DSA:3.40.50.150 (GENE3D): PF02	35,479	34,373	76,052	79,198	89,515									
Solyc08g062620	Protein phosphatase 2C (AHRD V3.3 *-* I3XLL9_CUCSA)						IPR007918 (PFAM): PS51808 (PROSI	1,983	2,486	3,267	2,592	3,198									
Solyc08g062630	aminopeptidase M1 (AHRD V3.3 *** AT4G33090.1)		P:GO:0006508: F:G(	P:proteolysis; F:metallopeptidase activity; F:zinc ion binding			IPR001930 (PRINTS): PF17900 (PFAI	144,498	134,873	189,680	176,951	186,788									
Solyc08g062640	Protein phosphatase 2C (AHRD V3.3 *-* G5DC07_FRAAN)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	8,200	10,380	7,080	6,350	6,291									
Solyc08g062650	Protein phosphatase 2c (AHRD V3.3 *** F8WL78_CITUN)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	20,773	23,402	16,764	14,942	16,756									
Solyc08g062660	Ran binding protein-1	ranbp1	P:GO:0046907	P:intracellular transport			IPR011993 (G3DSA:2.30.29.GENE3D	111,763	115,848	98,929	87,995	84,872									
Solyc08g062670	Protein kinase (AHRD V3.3 *** Q41383_SPIOL)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): G3DS	26,834	28,159	53,798	46,032	46,489									
Solyc08g062680	LOW QUALITY:Harbinger transposase-derived nuclease (AHRD V3.3 *-* A0A103Y2W0_CYNCS)						IPR027806 (PFAM): PTHR22930 (PAI	32,165	11,011	9,504	26,813	17,054	-1,523	0,000	0,839	0,018	1,494	0,000	down	up	up
Solyc08g062690	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein (AHRD V3.3 --* AT2G05160.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	73,403	23,100	22,089	61,619	36,928	-1,643	0,000	0,738	0,033	1,480	0,000	down	up	up
Solyc08g062700	Peptidyl-prolyl cis-trans isomerase, putative (AHRD V3.3 *** B9RQS7_RICCO)		P:GO:0000413: F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR002130 (PF	36,537	42,031	50,095	47,410	46,517									
Solyc08g062703	Long-chain fatty alcohol dehydrogenase family protein (AHRD V3.3 --* AT4G28570.2)							0,000	0,043	0,000	0,025	0,023									
Solyc08g062760	LOW QUALITY:villin 4 (AHRD V3.3 --* AT4G30160.4)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:kinase acti			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,184	0,236	0,025	0,047	0,023									
Solyc08g062770	Methyltransferase (AHRD V3.3 *** F8WL68_CITUN)						G3DSA:3.40.50.150 (GENE3D): IPR0	11,774	10,264	12,676	13,950	13,369									
Solyc08g062780	bHLH transcription factor 089	bHLH089	F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM: bHLH	0,180	0,121	0,099	0,201	0,188									
Solyc08g062800	RNA helicase DEAD26	DEAD26	F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	181,965	190,364	164,767	154,594	152,723									
Solyc08g062810	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 *** I3SBP3_MEDTR)						IPR021899 (PFAM): mobidb-lite (MOB	0,098	0,224	0,000	0,025	0,046									
Solyc08g062820	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** K4CL66_SOLLC)		C:GO:0005634: C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): IPR0:	27,267	30,770	44,979	45,772	44,058									
Solyc08g062825	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072TVC2_MEDTR)						IPR025558 (PFAM): IPR040256 (PAN	0,061	0,000	0,047	0,049	0,095									

Solyc08g062850	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GC	F:ATP binding; C:chloroplast		IPR008543 (PFAM): IPR008543 (PAN	0,000	0,043	0,072	0,022	0,046									
Solyc08g062860	Mitochondrial substrate carrier family protein (AHRD V3.3 *** U5G8Q5_POPTR)		F:GO:0022857; P:GC	F:transmembrane transporter activity; P:transmembrane transpo		IPR002067 (PRINTS): IPR018108 (PF	17,415	29,802	13,048	14,097	14,135									
Solyc08g062870	LOW QUALITY:Frigida-like protein (AHRD V3.3 --* AT5G27220.4)					mobidb-lite (MOBIDB_LITE)	0,364	0,472	0,118	0,199	0,117									
Solyc08g062910	Elongation factor 2 (AHRD V3.3 *** EF2_ARATH)		F:GO:0003924; F:GC	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.30.70	331,575	366,291	280,121	239,111	252,888									
Solyc08g062920	elongation factor 2	elf2	F:GO:0003924; F:GC	F:GTPase activity; EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.30.70	0,000	0,059	0,000	0,000	0,071									
Solyc08g062930	Calmodulin binding protein, putative (AHRD V3.3 *** B9RQR7_RICCO)		F:GO:0005516	F:calmodulin binding		PTHR31250:SF1 (PANTHER): PTHR3	0,201	0,497	0,090	0,076	0,211									
Solyc08g062940	SUN-like protein 22	SUN22	F:GO:0005515	F:protein binding		IPR025064 (PFAM): G3DSA:1.20.5.1	0,199	0,213	0,025	0,000	0,000									
Solyc08g062960	SolycHsfA2	HSF-18	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati		IPR000232 (PRIN HSF	47,748	31,853	64,071	66,461	70,600									
Solyc08g062970	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)		F:GO:0009055; F:GC	F:electron transfer activity; F:protein disulfide oxidoreductase a		IPR011905 (TIGRFAM): G3DSA:3.40.	3,201	2,741	0,643	0,643	0,871									
Solyc08g063000	Nucleosome assembly protein 1-like 1 (AHRD V3.3 *** A0A0B2RMX0_GLYSO)		C:GO:0005634; P:GC	C:nucleus; P:nucleosome assembly		G3DSA:3.30.1120.90 (GENE3D): IPR	30,984	26,046	7,143	6,126	7,719									
Solyc08g063010	ADP,ATP carrier protein, putative (AHRD V3.3 *** B9RRQ6_RICCO)		F:GO:0022857	F:transmembrane transporter activity		IPR018108 (PFAM): IPR023395 (G3D	3,606	4,300	4,874	5,070	4,730									
Solyc08g063020	LOW QUALITY:isoamylase 1 (AHRD V3.3 --* AT2G39930.3)						0,040	0,018	0,025	0,025	0,000									
Solyc08g063040	Zinc-finger protein		F:GO:0003676	F:nucleic acid binding		IPR022755 (PFAM C2H2	0,944	1,137	6,931	10,952	7,875					0,667	0,021			up
Solyc08g063045	Zinc finger family protein (AHRD V3.3 --* A0A0K9PZ45_ZOSMR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:DNA-binding transcription factor activit		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,924	0,928	6,768	11,998	8,205					0,835	0,002			up
Solyc08g063050	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** G7J7N5_MEDTR)		F:GO:0004222; F:GC	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	PR00830 (PRINTS): IPR003959 (PFA	78,878	70,937	112,398	109,644	110,095									
Solyc08g063070	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G11910.4)					IPR029058 (G3DSA:3.40.50.GENE3D	17,613	17,744	31,357	31,238	30,020									
Solyc08g063080	UDP-sulfoquinovose synthase (AHRD V3.3 *** C0LIR3_SOLLC)		F:GO:0003824; F:GC	F:catalytic activity; F:coenzyme binding		G3DSA:3.90.25.10 (GENE3D): IPR00	49,482	70,329	111,948	110,850	128,186	0,534	0,035					up		
Solyc08g063090	Sphingolipid delta-8 desaturase (AHRD V3.3 *** A4GK73_TOBAC)		P:GO:0006629; C:GC	P:lipid metabolic process; C:integral component of membrane; F		IPR036400 (G3DSA:3.10.120.GENE3	31,419	22,728	10,814	14,284	13,399									
Solyc08g063130	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT5G05320.1)		F:GO:0071949	F:FAD binding		PR00420 (PRINTS): IPR002938 (PFA	0,103	0,314	0,022	0,050	0,331									
Solyc08g065130	LOB domain-containing protein, putative (AHRD V3.3 *-* B9SN30_RICCO)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane		PTHR31301 (PAN LBD	0,021	0,000	0,025	0,050	0,000									
Solyc08g065140	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT1G17620.1)		C:GO:0005886; C:GC	C:plasma membrane; C:integral component of membrane		IPR004864 (PFAM): mobidb-lite (MOB	8,983	6,629	3,022	1,651	2,187					-0,873	0,033			down
Solyc08g065150	cotton fiber (DUF761) (AHRD V3.3 -** AT1G61260.1)		C:GO:0016021	C:integral component of membrane		IPR008480 (PFAM): IPR025520 (PFA	32,986	20,518	14,554	12,152	14,319	-0,658	0,020					down		
Solyc08g065160	Mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** T2DMK4_PHAVU)		F:GO:0003712; P:GC	F:transcription coregulator activity; P:regulation of transcription		IPR019145 (PFAM): mobidb-lite (MOB	73,435	64,749	72,954	69,567	69,854									
Solyc08g065190	zinc transporter (AHRD V3.3 *** AT1G10970.2)		F:GO:0005385; C:GC	F:zinc ion transmembrane transporter activity; C:integral compo		IPR003689 (PFAM): IPR004698 (TIGF	33,816	33,014	87,445	86,792	63,699			-0,460	0,043				down	
Solyc08g065210	LOW QUALITY:Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 --* A0A072UDV5_MEDTR)					PTHR37265:SF1 (PANTHER): PTHR3	2,337	2,053	0,391	0,532	0,843									
Solyc08g065220	glycine decarboxylase p-protein		F:GO:0004375; P:GC	F:glycine dehydrog EC:1.4.4.2	Glycine dehydrogena	IPR015421 (G3DSA:3.40.640.GENE3	247,609	261,845	198,717	166,327	225,549									
Solyc08g065245	Zinc-finger homeodomain protein 1 (AHRD V3.3 --* ZHD1_ORYSJ)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,059	0,090	0,122	0,024									
Solyc08g065250	Kinase family protein (AHRD V3.3 *** B9HDN3_POPTR)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR001245 (PRINTS): PF14381 (PFAI	19,033	20,024	27,133	29,368	26,689									
Solyc08g065260	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 --* CLPP_GOSBA)		C:GO:0016021	C:integral component of membrane		IPR009631 (PFAM): mobidb-lite (MOB	4,751	4,191	9,339	7,925	9,367									
Solyc08g065265	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *** A0A061FD65_THECC)		F:GO:0003677; F:GC	F:DNA binding; F:protein dimerization activity		IPR008906 (PFAM): IPR025525 (PFA	0,042	0,059	0,150	0,022	0,000									
Solyc08g065310	cell wall invertase 2 (AHRD V3.3 --* AT3G52600.3)					mobidb-lite (MOBIDB_LITE): mobidb-lit	43,295	42,579	44,890	52,291	47,119									
Solyc08g065320	green ripe-like 1	GRL1	C:GO:0016021	C:integral component of membrane		IPR008496 (PFAM): PTHR20921:SF1	7,478	8,139	22,145	28,135	22,487									
Solyc08g065330	Calcineurin B, putative (AHRD V3.3 *** B9RRT2_RICCO)		F:GO:0005509	F:calcium ion binding		PR00450 (PRINTS): G3DSA:1.10.238	3,984	3,464	7,004	10,059	6,944									
Solyc08g065350	Histone deacetylase, putative (AHRD V3.3 *** B9RRT4_RICCO)		C:GO:0005634; F:GC	C:nucleus; F:NAD-d EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS): IPR023801 (PF	35,096	29,070	27,322	25,866	29,250									
Solyc08g065360	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NUN8_ZOSMR)		P:GO:0006812; F:GC	P:cation transport; F:solute:proton antiporter activity; C:integral		IPR006153 (PFAM): IPR038770 (G3D	53,915	34,448	14,848	16,685	15,291	-0,618	0,018					down		
Solyc08g065370	LOW QUALITY:Photosystem II D2 protein (AHRD V3.3 *-* PSBD_CRYJA)		P:GO:0009772; F:GC	P:photosynthetic electron transport in photosystem II; F:electro		IPR000484 (PFAM): IPR000484 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc08g065380	Myb transcription factor family protein, putative (AHRD V3.3 *** A0A061GL43_THECC)		F:GO:0003677	F:DNA binding		IPR006447 (TIGRI MYB_related	0,061	0,019	0,000	0,000	0,000									
Solyc08g065420	bell-like homeodomain protein 4	bl4	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated		IPR008422 (PFAM TALE	6,748	6,513	0,172	0,092	0,117									
Solyc08g065430	Pollen specific protein sf21, putative (AHRD V3.3 *** B9RRU1_RICCO)		C:GO:0016021; P:GC	C:integral component of membrane; P:regulation of auxin polar t		IPR004142 (PFAM): IPR029058 (G3D	34,726	47,528	4,607	1,715	3,477									
Solyc08g065440	Activating transcription factor 7-interacting 1 (AHRD V3.3 *** A0A0B0MF55_GOSAR)					PTHR35505 (PANTHER): PTHR35505	4,049	5,053	3,022	3,050	2,450									
Solyc08g065470	Mitochondrial ATP synthase subunit G protein (AHRD V3.3 *** AT4G29480.1)		C:GO:0000276; F:GC	C:mitochondrial proton-transporting ATP synthase complex, cou		IPR006808 (PFAM): IPR006808 (PAN	3,043	2,476	3,136	2,880	2,633									
Solyc08g065480	Ferrochelatase (AHRD V3.3 *** K4CLC8_SOLLC)	FC	F:GO:0004325; P:GC	F:ferrochelatase ac EC:4.99.1.1	Protoporphyrin ferroc	IPR001015 (TIGRFAM): G3DSA:3.40.	56,305	101,689	52,877	55,171	54,717	0,878	0,022					up		
Solyc08g065490	Serine hydroxymethyltransferase (AHRD V3.3 *** M0ZQ61_SOLTU)		F:GO:0004372; P:GC	F:glycine hydroxym EC:2.1.2.1	Glycine hydroxymeth	IPR015421 (G3DSA:3.40.640.GENE3	29,666	34,802	45,385	44,555	44,505									
Solyc08g065540	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)		F:GO:0004722; P:GC	F:protein serine/thr EC:3.1.3.16	Protein-serine/threon	IPR001932 (PFAM): IPR036457 (G3D	0,042	0,098	0,022	0,094	0,024									
Solyc08g065560	Core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 --* AT4G31350.4)						0,040	0,000	0,000	0,000	0,024									
Solyc08g065570	Vacuolar processing enzyme (AHRD V3.3 *** Q9SMD0_SOLLC)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): IPR001096 (PF	2,661	8,321	0,065	0,025	0,071									
Solyc08g065590	Vacuolar processing enzyme (AHRD V3.3 *** Q9SMD0_SOLLC)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): G3DSA:3.40.50	0,120	1,313	0,050	0,050	0,024									
Solyc08g065600	Vacuolar-processing enzyme (AHRD V3.3 *** VPE_VICSA)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		G3DSA:3.40.50.1460 (GENE3D): G3D	0,189	0,019	0,046	0,045	0,071									
Solyc08g065610	Vacuolar processing enzyme (AHRD V3.3 *** V9M6Z0_9ROSA)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): IPR001096 (PI	209,656	238,575	1379,464	1317,733	1385,427									
Solyc08g065625	cytochrome b (AHRD V3.3 *-* AT2G07727.1)		F:GO:0009055; C:GC	F:electron transfer activity; C:membrane; P:respiratory electron		IPR005797 (PFAM): IPR027387 (G3D	0,019	0,000	0,094	0,072	0,046									
Solyc08g065640	PITH domain-containing protein 1 (AHRD V3.3 *** A0A0B2SR38_GLYSO)					IPR037047 (G3DSA:2.60.120.GENE3	29,411	30,086	50,293	52,908	51,465									
Solyc08g065700	Flavin-containing monooxygenase (AHRD V3.3 *** M1DQI5_SOLTU)		F:GO:0000166; F:GC	F:nucleotide binding; F:monooxygenase activity; F:coenzyme bi		IPR036188 (G3DSA:3.50.50.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc08g065710	Vacuolar-processing enzyme (AHRD V3.3 *** VPE_CITSI)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): G3DSA:1.10.13	0,000	0,000	0,000	0,025	0,000									
Solyc08g065740	Vacuolar processing enzyme (AHRD V3.3 *** Q9SMD0_SOLLC)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): PIRSF500139 (	0,037	0,250	0,000	0,000	0,000									
Solyc08g065760	Ribosomal protein L28 (AHRD V3.3 *** A0A103XZR0_CYNCS)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation		IPR037147 (G3DSA:2.30.170.GENE3	35,197	37,186	40,015	36,261	36,121									
Solyc08g065780	Vacuolar processing enzyme (AHRD V3.3 *** Q9SMD0_SOLLC)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): IPR001096 (PF	10,099	34,536	1,030	0,231	0,694									
Solyc08g065790	vacuolar processing enzyme	vpe	P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity		IPR001096 (PRINTS): PIRSF500139 (	36,544	65,144	1,221	0,253	0,673									
Solyc08g065820	Transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 *-* AT3G07610.1)		F:GO:0008168; P:GC	F:methyltransferase activity; P:methylation		IPR003347 (PFAM): G3DSA:2.60.120	13,122	14,978	8,289	8,133	9,356									
Solyc08g065830	Transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 *-* AT3G07610.1)		F:GO:0008168; P:GC	F:methyltransferase activity; P:methylation		mobidb-lite (MOBIDB_LITE): mobidb-lit	2,466	1,889	0,979	1,267	1,624									
Solyc08g065840	DUF1639 family protein (AHRD V3.3 *-* A0A072VEU0_MEDTR)		C:GO:0016021	C:integral component of membrane		IPR012438 (PFAM): mobidb-lite (MOB	24,324	18,926	47,184	37,555	38,638									
Solyc08g065850	Arabinogalactan peptide 14 (AHRD V3.3 -** AGP14_ARATH)						39,687	26,097	9,210	13,005	10,705									
Solyc08g065860	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT5G11730.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:membrane		IPR003406 (PFAM): PTHR31042:SF5	14,816	12,209	16,021	17,080	15,499									
Solyc08g065870	EARLY FLOWERING 3 (AHRD V3.3 *** A0A088PY80_9ROSI)		P:GO:2000028	P:regulation of photoperiodism, flowering		mobidb-lite (MOBIDB_LITE): mobidb-lit	21,542	14,843	18,388	18,713	20,178									
Solyc08g065880	3'-5' exonuclease domain-containing protein-like (AHRD V3.3 *** Q2V9B5_SOLTU)		F:GO:0003723; P:GC	F:RNA binding; P:nucleobase-containing compound metabolic p		IPR002562 (PFAM): G3DSA:3.30.420	74,786	63,684	110,969	83,143	84,445			-0,397	0,046	-0,413	0,014		down	down
Solyc08g065890	Clathrin interactor EPSIN 1 (AHRD V3.3 *** A0A0B2QBN6_GLYSO)		P:GO:0006623; F:GC	P:protein targeting to vacuole; F:clathrin binding		IPR013809 (PFAM): IPR008942 (G3D	155,628	106,464	113,583	100,427	105,301									
Solyc08g065900	Vacuolar protein sorting-associated protein 32 homolog 1 (AHRD V3.3 *** VP321_ARATH)		P:GO:0007034	P:vacuolar transport		IPR005024 (PFAM): G3DSA:1.10.287	95,455	95,131	115,016	120,343	115,645									
Solyc08g065910	blind-like5	R2R3MYB34	F:GO:0003677	F:DNA binding		IPR001005 (PFAM MYB	0,000	0,077	0,000	0,000	0,000									
Solyc08g065940	Zinc finger CCCH domain-containing protein (AHRD V3.3 *** R4QQJ8_CUCME)		F:GO:0046872	F:metal ion binding		IPR000571 (PFAM): G3DSA:4.10.100	108,367	76,910	61,027	37,296	42,131			-0,537	0,001	-0,706	0,000		down	down
Solyc08g065970	Sigma factor (AHRD V3.3 *** A0A0G2STQ0_9ROSI)	SIG3	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:DNA-templated tra		IPR000943 (PRINTS): IPR036388 (G3	17,487	13,470	7,683	5,646	9,175									
Solyc08g065980	glycine-rich protein (AHRD V3.3 *** AT4G32920.3)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	95,225	87,285	105,710	111,499	106,950									
Solyc08g065990	cytosolic Fe-S cluster assembly factor nar1		C:GO:0005634; C:GC	C:nucleus; C:cytosol; F:4 iron, 4 sulfur cluster binding; P:respon		G3DSA:3.40.950.20 (GENE3D): IPR0	28,775	23,867	34,301	33,035	31,685									
Solyc08g066000	Tetratricopeptide repeat-like superfamily protein isoform 1 (AHRD V3.3 *-* A0A061GK97_THECC)		P:GO:0006336	P:DNA replication-independent nucleosome assembly		mobidb-lite (MOBIDB_LITE): mobidb-lit	11,191	10,005	13,016	11,563	11,489									
Solyc08g066010	Tetratricopeptide repeat-like superfamily protein isoform 1 (AHRD V3.3 *** A0A061GK97_THECC)		F:GO:0005515; P:GC	F:protein binding; P:DNA replication-independent nucleosome a		IPR011990 (G3DSA:1.25.40.GENE3D	32,001	24,033	29,208	31,254	30,397									
Solyc08g066020	Long chain base biosynthesis protein 1 (AHRD V3.3 *-* LCB1_ARATH)		F:GO:0003824; P:GC	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha		IPR015421 (G3DSA:3.40.640.GENE3	5,323	16,659	5,770	5,968	6,088	1,673	0,000					up		
Solyc08g066030	Caveolin-1 (AHRD V3.3 *** A0A0B0P1B2_GOSAR)		C:GO:0016021	C:integral component of membrane		PTHR35465 (PANTHER)	46,228	37,282	29,758	30,731	25,120									
Solyc08g066040	Oleosin (AHRD V3.3 *** A0A0D2V8E6_GOSRA)		C:GO:0012511; C:GC	C:monolayer-surrounded lipid storage body; C:integral compone		IPR000136 (PFAM): PTHR33203:SF3	10,477	3,942	1,406	1,281	1,134									
Solyc08g066050	Protein kinase (AHRD V3.3 *** A0A059LJJ8_9CHLO)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		PIRSF000654 (PIRSF): G3DSA:3.30.2	0,292	0,426	0,000	0,047	0,000									
Solyc08g066060	LOW QUALITY:chromatin remodeling factor CHD3 (PICKLE) (AHRD V3.3 --* AT2G25170.4)					mobidb-lite (MOBIDB_LITE): mobidb-lit	5,840	6,148	4,110	3,880	3,922									
Solyc08g066070	leucine zipper Z12127		C:GO:0000145; P:GC	C:exocyst; P:exocytosis		G3DSA:1.20.1280.170 (GENE3D): IPI	81,782	79,257	41,328	48,892	52,156									
Solyc08g066100	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** A0A0V0IM90_SOLCH)		F:GO:0003872; F:GC	F:6-phosphofructok EC:2.7.1.11	6-phosphofructokinas	IPR022953 (PRINTS): IPR000023 (PF	64,134	63,462	45,209	21,473	38,455					-1,071	0,000			down
Solyc08g066110	Profilin (AHRD V3.3 *** PROF_CAPAN)		F:GO:0003785; C:GC	F:actin monomer binding; C:cytoskeleton; C:cell cortex; P:seque		IPR005455 (PRINTS): IPR005455 (PF	158,154	150,398	184,218	158,737	158,285									
Solyc08g066120	polyribonucleotide nucleotidyltransferase (AHRD V3.3 *** AT3G03710.1)		F:GO:0003723; F:GC	F:RNA binding; F:pc EC:2.7.7.8	Polyribonucleotide nu	G3DSA:2.40.50.140 (GENE3D): IPR0	24,215	23,106	31,580	29,462	33,971									
Solyc08g066140	Polyribonucleotide nucleotidyltransferase (AHRD V3.3 *-* W9R4G3_9ROSA)		F:GO:0003723; F:GC	F:RNA binding; F:pc EC:2.7.7.8	Polyribonucleotide nu	IPR004088 (PFAM): IPR027408 (G3D	0,122	0,061	0,218	0,047	0,212									
Solyc08g066150	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT3G44480.5)						0,767	0,792	0,813	1,000	1,057									
Solyc08g066160	Early nodulin 93 (AHRD V3.3 *** G7I281_MEDTR)		C:GO:0005739; C:GC	C:mitochondrion; C:integral component of membrane		IPR005050 (PFAM): PTHR33605:SF3	24,670	23,082	35,072	30,262	30,539									
Solyc08g066170	Early nodulin-93 (AHRD V3.3 *** A0A1D1XFG2_9ARAE)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane		IPR005050 (PFAM): PTHR33605:SF3	0,019	0,000	0,000	0,000	0,000									
Solyc08g066180	endoribonuclease YbeY-like		F:GO:0004222; P:GC	F:metalloendopeptic EC:3.4.24	Acting on peptide bor	PR00119 (PRINTS): IPR023214 (G3D	24,535	26,105	7,613	5,804	8,944									
Solyc08g066190	Myb domain-containing protein (AHRD V3.3 *-* W9SD24_9ROSA)		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.60 MYB_related	0,040	0,019	0,025	0,045	0,000									
Solyc08g066200	Poly(A) polymerase (AHRD V3.3 *** A0A0B2Q923_GLYSO)		F:GO:0003723; F:GC	F:RNA binding; F:pc EC:2.7.7.19	Polynucleotide adeny	IPR007010 (PFAM): IPR002934 (PFA	125,734	118,267	143,813	145,116	143,987									
Solyc08g066220	Histidine decarboxylase (AHRD V3.3 *** W0KR26_TOBAC)		F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR015421 (G3DSA:3.40.640.GENE3	0,000	0,000	0,000	0,025	0,000									
Solyc08g066240	Histidine decarboxylase (AHRD V3.3 *** DCHS_SOLLC)	hdc	F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR015421 (G3DSA:3.40.640.GENE3	0,531	0,722	1183,681	1822,290	816,720									
Solyc08g066245	Histidine decarboxylase (AHRD V3.3 *-* DCHS_SOLLC)		F:GO:0003824	F:catalytic activity		IPR015421 (G3DSA:3.40.640.GENE3	0,021	0,021	18,841	46,139	18,581					1,299	0,000			up
Solyc08g066250	Histidine decarboxylase (AHRD V3.3 *** DCHS_SOLLC)		F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR002129 (PFAM): IPR015421 (G3D	0,000	0,000	12,787	32,842	11,722					1,369	0,000			up
Solyc08g066260	Histidine decarboxylase (AHRD V3.3 *** DCHS_SOLLC)		F:GO:0016831; P:GC	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F		IPR015421 (G3DSA:3.40.640.GENE3	0,000	0,021	6,116	4,238	4,340									
Solyc08g066270	kinase family with leucine-rich repeat domain-containing protein (AHRD V3.3 *** AT5G25930.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		PR00019 (PRINTS): G3DSA:3.30.200	0,229	0,286	0,000	0,000	0,000									
Solyc08g066290	low-molecular-weight cysteine-rich 2 (AHRD V3.3 --* AT4G10595.1)					mobidb-lite (MOBIDB_LITE): mobidb-lit	3,336	3,886	5,711	5,034	5,388									
Solyc08g066310	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9PZN1_ZOSMR)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		PR00019 (PRINTS): IPR032675 (G3D	1,170	8,346	0,340	0,537	0,732	2,852	0,000					up		
Solyc08g066320	kinase family with leucine-rich repeat domain-containing protein (AHRD V3.3 *** AT5G25930.1)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		PR00019 (PRINTS): G3DSA:1.10.510	0,600	3,574	0,072	0,119	0,399	2,587	0,010					up		
Solyc08g066330	LEY17225 cyclin-dependent protein kinase A-1	cdc2a1	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (PFAM): PIRSF000654 (P	49,814	46,098	7,668	4,348	5,527									
Solyc08g066350	Histidine phosphotransfer protein (AHRD V3.3 *** A0A061GBY7_THECC)		P:GO:0000160	P:phosphorelay signal transduction system		IPR008207 (PFAM): IPR036641 (G3D	0,040	0,037	0,000	0,073	0,023									
Solyc08g066360	Malic enzyme (AHRD V3.3 *** A0A0V0IM81_SOLCH)		F:GO:0004471; F:GC	F:malate dehydrog EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS): IPR037062 (G3	9,354	22,649	17,232	18,666	17,443	1,303	0,000					up		
Solyc08g066370	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)					IPR019557 (PFAM): mobidb-lite (MOB	0,079	0,021	0,550	1,208	0,306									
Solyc08g066390	Sequence-specific DNA-binding transcription factor (AHRD V3.3 *** G7LDQ2_MEDTR)		F:GO:0003682	F:chromatin binding		IPR032001 (PFAM): G3DSA:2.30.30.1	9,972	9,385	4,001	4,350	5,072									
Solyc08g066400	Casein kinase I protein (AHRD V3.3 *** A0A061GK62_THECC)		F:GO:0004672; P:GC	F:protein kinase activity; P:protein phosphorylation; P:peptidyl-a		G3DSA:1.10.510.10 (GENE3D): PTHF	0,628	0,533	0,000	0,025	0,000									
Solyc08g066410	Protein kinase family protein (AHRD V3.3 *-* AT2G25760.2)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR000719 (PFAM): G3DSA:1.10.510	0,536	0,373	0,000	0,025	0,000									
Solyc08g066420	LOW QUALITY:Lachrymatory-factor synthase, putative (AHRD V3.3 *** B9RS03_RICCO)		F:GO:0004864; C:GC	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm		IPR023393 (G3DSA:3.30.530.GENE3	0,219	0,504	0,288	0,338	0,306									
Solyc08g066440	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GK57_THECC)		C:GO:0005783; C:GC	C:endoplasmic reticulum; C:Golgi apparatus; C:membrane		IPR000073 (PRINTS): IPR029058 (G3	66,551	91,347	35,981	47,308	51,435									
Solyc08g066490	Receptor protein kinase CLAVATA1, putative (AHRD V3.3 *** B9RRZ6_RICCO)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc		IPR001611 (PFAM): IPR032675 (G3D	12,136	16,138	2,277	1,229	2,064									
Solyc08g066500	Homeobox leucine-zipper protein (AHRD V3.3 *** Q8H964_ZINVI)		F:GO:0003677; F:GC	F:DNA binding; F:lipid binding		IPR023393 (G3DS HD-ZIP	16,344	26,500	3,197	1,599	3,962									
Solyc08g066510	GATA transcription factor (AHRD V3.3 *** K4CLM7_SOLLC)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; F:zinc ion		IPR000679 (PFAM GATA	0,037	0,018	0,000	0,000	0,000									
Solyc08g066520	nuclear fusion defective 6 (AHRD V3.3 --* AT2G20585.7)		P:GO:0006952	P:defense response		PTHR33156 (PANTHER): IPR033252 (	3,772	4,490	3,545	3,556	3,800									
Solyc08g066530	Acid phosphatase 1 (AHRD V3.3 *** W9S6E0_9ROSA)		F:GO:0003993; P:GC	F:acid phosphatase EC:3.1.3.2	Acid phosphatase	IPR005519 (PFAM): PTHR31284 (PAI	1,666	2,453	0,214	0,124	0,141									
Solyc08g066540	Peptidyl-tRNA hydrolase, putative (AHRD V3.3 *** B9RRZ0_RICCO)		F:GO:0004045	F:aminoacyl-tRNA h EC:3.1.1.29; EC:3.1.	Aminoacyl-tRNA hydr	IPR002833 (PFAM): IPR023476 (G3D	9,188	9,123	13,105	12,020	12,275									
Solyc08g066550	RING/U-box superfamily protein (AHRD V3.3 --* AT1G35330.1)		F:GO:0008270; F:GC	F:zinc ion binding; F:ubiquitin protein ligase activity		IPR013083 (G3DSA:3.30.40.GENE3D	0,040	0,137	0,000	0,022	0,023									
Solyc08g066560	LOW QUALITY:protein serine/threonine kinase (AHRD V3.3 --* AT3G51270.4)						0,000	0,043	0,076	0,000	0,000									
Solyc08g066570	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G11580.1)					IPR000408 (PRINTS): IPR000408 (PF	13,736	10,040	15,528	12,416	14,265									
Solyc08g066580	nuclear pore complex Nup85-like protein (AHRD V3.3 *** AT4G32910.1)		P:GO:0006406; P:GC	P:mRNA export from nucleus; P:protein import into nucleus; P:re		IPR011502 (PFAM): IPR011502 (PAN	41,707	41,607	43,728	45,793	42,789									
Solyc08g066600	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *** A0A103XZP5_CYNCS)					PF05664 (PFAM): mobidb-lite (MOBID	91,085	69,124	40,320	40,505	38,969									
Solyc08g066610	EPIDERMAL PATTERNING FACTOR-like protein 9 (AHRD V3.3 *** A0A0B2PPB1_GLYSO)		P:GO:2000123	P:positive regulation of stomatal complex development		IPR038572 (G3DSA:2.20.25.GENE3D	1,790	2,694	0,448	0,176	0,561									
Solyc08g066620	cystathionine beta-lyase (AHRD V3.3 *-* AT3G57050.5)		F:GO:0030170	F:pyridoxal phosphate binding		IPR000277 (PFAM): PTHR11808:SF5	36,325	30,872	32,129	32,619	32,936									
Solyc08g066630	LOW QUALITY:F-box/LRR-repeat protein 4 (AHRD V3.3 *-* A0A1D1XF78_9ARAE)		P:GO:0006511; C:GC	P:ubiquitin-dependent protein catabolic process; C:integral com		IPR032675 (G3DSA:3.80.10.GENE3D	1,750	1,607	1,611	1,166	1,245									
Solyc08g066635	LOW QUALITY:BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THE		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM): PTHR23272 (PAI	0,021	0,037	0,000	0,000	0,000									
Solyc08g066640	Transcriptional regulatory plant protein, putative (AHRD V3.3 *** A0A072VD14_MEDTR)		C:GO:0009507	C:chloroplast		IPR017856 (G3DSA:1.10.10.GENE3D	5,169	5,315	6,403	6,169	6,337									
Solyc08g066650	Carotenoid Cleavage Dioxygenase 8	CCD8	F:GO:0016702; P:GC	F:oxidoreductase a EC:1.13.11	Acting on single donc	IPR004294 (PFAM): IPR004294 (PAN	0,121	0,348	0,000	0,025	0,000									
Solyc08g066660	Ethylene-responsive transcription factor TINY (AHRD V3.3 *** TINY_ARATH)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec		IPR001471 (PRIN ERF	0,040	0,019	0,000	0,025	0,000									
Solyc08g066670	Exostosin family protein (AHRD V3.3 *** AT4G32790.3)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc		IPR040911 (PFAM): PTHR11062:SF1	3,718	2,115	1,868	2,228	1,577									
Solyc08g066680	Exostosin family protein (AHRD V3.3 *** AT5G25820.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc		IPR040911 (PFAM): mobidb-lite (MOB	19,551	13,313	37,841	41,369	32,263									
Solyc08g066690	Exostosin family protein (AHRD V3.3 *** AT5G25820.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glycc		IPR040911 (PFAM): mobidb-lite (MOB	38,373	29,020	1560,774	1701,667	1548,549									
Solyc08g066700	Exosome complex exonuclease RRP46 homolog (AHRD V3.3 *** EXOS5_ARATH)		C:GO:0000176; C:GC	C:nuclear exosome (RNase complex); C:cytoplasmic exosome (		IPR001247 (PFAM): IPR027408 (G3D	20,591	16,383	588,633	633,771	514,619									
Solyc08g066710	Carotenoid 9,10(9',10')-cleavage dioxygenase 1, putative isoform 1 (AHRD V3.3 *-* A0A061GK16_THECC)		F:GO:0016702; P:GC	F:oxidoreductase a EC:1.13.11	Acting on single donors with incorporation of molecular oxyge		0,196	0,279	0,000	0,069	0,164									
Solyc08g066720	Carotenoid cleavage dioxygenase (AHRD V3.3 *** B6UEM5_MAIZE)		F:GO:0016702; P:GC	F:oxidoreductase a EC:1.13.11	Acting on single donc	IPR004294 (PFAM): PTHR10543:SF3	0,963	1,754	0,249	0,696	0,776									
Solyc08g066730	N6-adenosine-methyltransferase MT-A70-like protein (AHRD V3.3 *** W9QTM1_9ROSA)		F:GO:0008168; C:GC	F:methyltransferase activity; C:chloroplast; P:embryo developm		IPR007757 (PFAM): mobidb-lite (MOB	73,008	44,289	56,721	49,451	52,066	-0,694	0,004					down		
Solyc08g066740	Early nodulin-like protein 1 (AHRD V3.3 *** A0A151U5D7_CAJCA)		F:GO:0009055	F:electron transfer activity		IPR008972 (G3DSA:2.60.40.GENE3D	12,042	6,544	1,744	1,584	1,629	-0,848	0,031					down		
Solyc08g066750	Major facilitator superfamily domain-containing protein (AHRD V3.3 *** A0A0K9PJ16_ZOSMR)		F:GO:0015098; P:GC	F:molybdate ion transmembrane transporter activity; P:molybda		G3DSA:1.20.1250.20 (GENE3D): IPR	49,353	39,025	29,771	27,549	27,072									
Solyc08g066760	Ankyrin repeat family protein, putative (AHRD V3.3 *-* A0A061GJP2_THECC)		F:GO:0005515	F:protein binding		IPR002110 (PFAM): IPR036770 (G3D	4,156	1,761	0,530	1,082	0,821	-1,213	0,010					down		
Solyc08g066770	Ankyrin repeat family protein, putative (AHRD V3.3 *** A0A061GJP2_THECC)		F:GO:0005515	F:protein binding		IPR026961 (PFAM): IPR036770 (G3D	0,019	0,043	0,000	0,000	0,047									
Solyc08g066790	Phospholipase D (AHRD V3.3 *** M1AKN6_SOLTU)		F:GO:0004630; F:GC	F:phospholipase D EC:3.1.4.4	Phospholipase D	G3DSA:3.30.870.10 (GENE3D): IPR0	14,942	24,869	22,553	26,959	24,390	0,760	0,024					up		
Solyc08g066800	phospholipase D	tpld	F:GO:0004630; F:GC	F:phospholipase D EC:3.1.4.4	Phospholipase D	IPR000008 (PFAM): IPR035892 (G3D	229,896	135,263	364,280	341,130	361,692	-0,738	0,010					down		
Solyc08g066810	Glycosyl hydrolase family 5 protein (AHRD V3.3 *** D7KPG3_ARALL)		F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		G3DSA:3.20.20.80 (GENE3D): IPR00	19,059	12,492	35,367	27,953	32,431									
Solyc08g066820	Choline/ethanolamine kinase family protein (AHRD V3.3 *** B9MTI9_POPTR),Pfam:PF01633		C:GO:0005886; P:GC	C:plasma membrane; P:phospholipid biosynthetic process; F:kir		G3DSA:3.90.1200.10 (GENE3D): G3D	24,793	24,234	34,788	37,510	37,166									
Solyc08g066840	tonoplast intrinsic protein 4.1	TIP4.1	F:GO:0015267; C:GC	F:channel activity; C:membrane; P:transmembrane transport		IPR000425 (PRINTS): IPR023271 (G3	18,060	10,574	4,328	1,253	2,658					-1,777	0,000			down

Solyc08g066850	Lactoylglutathione lyase (AHRD V3.3 *** K4CLR1_SOLLC)		F:GO:0004462: F:G(	F:lactoylglutathione	EC:4.4.1.5	Lactoylglutathione ly	IPR029068 (G3DSA:3.10.180.GENE3I	6,005	7,259	5,941	5,184	8,399									
Solyc08g066860	LOW QUALITY:Auxin canalization protein (AHRD V3.3 *** G7ZWI5_MEDTR)						IPR013666 (PFAM): IPR011993 (G3D	0,553	0,313	0,137	0,094	0,214									
Solyc08g066870	Casein kinase I-like protein (AHRD V3.3 *-* G7KPU7_MEDTR)		F:GO:0004674: F:G(	F:protein serine/thre	EC:2.7.11	Transferring phosphorus-containing groups		14,218	16,016	14,149	18,173	15,146									
Solyc08g066875	Casein kinase family protein (AHRD V3.3 *** B9ILR0_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	21,217	22,368	19,206	23,641	21,646									
Solyc08g066880	Bark storage protein A (AHRD V3.3 *** A0A151TDP1_CAJCA)		F:GO:0003824: P:G(	F:catalytic activity; P:nucleoside metabolic process			G3DSA:3.40.50.1580 (GENE3D): IPR(	0,000	0,018	0,072	0,022	0,000									
Solyc08g066900	Bark storage protein A (AHRD V3.3 *-* A0A0B2QEI9_GLYSO)		F:GO:0003824: P:G(	F:catalytic activity; P:nucleoside metabolic process			G3DSA:3.40.50.1580 (GENE3D): IPR(	0,000	0,021	0,000	0,000	0,047									
Solyc08g066920	ATP/ADP transporter (AHRD V3.3 *-* A0A0X9Q301_MENSP)		F:GO:0003774: F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR001609 (PF	2,423	2,387	0,921	1,631	1,385									
Solyc08g066940	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	17,215	10,816	11,887	12,533	12,139									
Solyc08g066950	1-deoxy-D-xylulose-5-phosphate synthase (AHRD V3.3 *** A0A161ZT20_DAUCA)		F:GO:0008661: P:G(	F:1-deoxy-D-xylulos	EC:2.2.1.7	1-deoxy-D-xylulose-5	IPR005475 (PFAM): IPR005477 (TIGF	29,229	23,451	36,657	32,793	36,011									
Solyc08g066980	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT4G32272.2)		P:GO:0008643: C:G(	P:carbohydrate transport; C:integral component of membrane			IPR004853 (PFAM): PTHR44680:SF2	17,004	21,092	21,538	25,197	22,987									
Solyc08g066990	Potassium channel (AHRD V3.3 *** O24382_SOLTU)		F:GO:0005249: F:G(	F:voltage-gated potassium channel activity; F:protein binding; P			IPR002110 (PRINTS): IPR003938 (PF	0,420	0,320	0,115	0,025	0,047									
Solyc08g067000	Serine/arginine repetitive matrix protein 2 isoform 1 (AHRD V3.3 --* A0A061DPI3_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,562	0,843	0,215	0,100	0,305									
Solyc08g067020	Cytochrome b-c1 complex subunit 7 (AHRD V3.3 *** QCR7_SOLTU)		C:GO:0005750: P:G(	C:mitochondrial respiratory chain complex III; P:mitochondrial el			IPR003197 (PFAM): IPR036544 (G3D	95,398	98,489	192,031	168,679	170,895									
Solyc08g067030	transmembrane protein, putative (Protein of unknown function, DUF642) (AHRD V3.3 *** AT5G11420.1)						IPR008979 (G3DSA:2.60.120.GENE3I	685,381	450,488	12,504	4,111	11,601					-1,602	0,000			down
Solyc08g067040	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061FYJ3_THECC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	51,721	48,519	55,400	53,661	52,199									
Solyc08g067050	Arginine N-methyltransferase family protein (AHRD V3.3 *** B9NAU7_POPTR)		P:GO:0006479: F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): PF06	6,911	6,820	1,389	1,287	1,575									
Solyc08g067060	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GWC7_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	28,165	24,639	22,782	27,355	25,127									
Solyc08g067070	cytosine-5 DNA methyltransferaseL	METL	F:GO:0008168	F:methyltransferase activity			IPR001525 (PRINTS): IPR001525 (PF	6,830	4,830	7,957	9,256	8,980									
Solyc08g067090	cyclophilin-like protein	pi2.1	P:GO:0000413: F:G(	P:protein peptidyl-pi	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR002130 (PF	61,845	60,434	58,694	52,177	53,776									
Solyc08g067095	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *-* G7JB56_MEDTR)		P:GO:0000413: F:G(	P:protein peptidyl-pi	EC:5.2.1.8	Peptidylprolyl isomer:	mobidb-lite (MOBIDB_LITE): mobidb-lit	76,391	82,259	79,665	64,285	70,552									
Solyc08g067100	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT5G10770.1)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	67,226	67,196	51,861	50,801	61,397									
Solyc08g067120	DnaJ P58IPK-like protein (AHRD V3.3 *-* AT5G03160.1)		C:GO:0005788: C:G(	C:endoplasmic reticulum lumen; C:integral component of membr:			PTHR45188 (PANTHER)	0,038	0,000	0,025	0,000	0,024									
Solyc08g067123	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAI	0,019	0,000	0,025	0,000	0,023									
Solyc08g067130	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)						IPR019557 (PFAM): mobidb-lite (MOB	0,078	0,060	0,000	0,025	0,023									
Solyc08g067140	CW-type zinc finger protein (AHRD V3.3 *-* E9NZV0_PHAVU)		F:GO:0008270	F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,142	0,210	0,046	0,022	0,069									
Solyc08g067145	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 --* AT1G70180.4)		F:GO:0008270	F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,022	0,000	0,000									
Solyc08g067150	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 *-* AT3G22780.1)						IPR005172 (PFAM_CPP	25,568	25,425	59,234	79,800	63,445					0,434	0,037			up
Solyc08g067160	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A061GQK2_THECC)		F:GO:0016787	F:hydrolase activity			IPR003140 (PFAM): IPR029058 (G3D	85,585	65,419	36,574	23,214	42,589									
Solyc08g067170	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TCY2_CAJCA)						IPR011989 (G3DSA:1.25.10.GENE3D	0,021	0,018	0,000	0,000	0,000									
Solyc08g067180	Zinc finger family protein (AHRD V3.3 *** B9IKV1_POPTR)		F:GO:0046872	F:metal ion binding			G3DSA:4.10.1060.10 (GENE3D): IPR(	2,559	2,570	0,261	0,092	0,071									
Solyc08g067185	Malate dehydrogenase [NADP], chloroplastic (AHRD V3.3 --* MDHP_SPIOL)							0,241	0,200	0,097	0,139	0,142									
Solyc08g067190	Anaphase-promoting complex subunit 5 (AHRD V3.3 *** A0A151QXF2_CAJCA)		F:GO:0005515: C:G(	F:protein binding; C:anaphase-promoting complex			IPR026000 (PFAM): IPR011990 (G3D	4,606	4,698	2,008	1,771	2,226									
Solyc08g067200	Dicer-like protein 3 (AHRD V3.3 *-* X4Y6L7_SOLLC)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			IPR011545 (PFAM): G3DSA:3.40.50.3	3,685	3,023	3,447	3,030	2,757									
Solyc08g067210	Dicer-like 3	DCL3	F:GO:0004525: F:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	G3DSA:2.170.260.10 (GENE3D): G3D	22,764	20,480	16,490	18,031	18,409									
Solyc08g067230	MADS box transcription factor (AHRD V3.3 *** G3EIU8_9SOLA)		F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN1_MIKC_MADS	0,042	0,057	0,022	0,000	0,000									
Solyc08g067240	BRCT domain-containing DNA repair protein (AHRD V3.3 *** A0A061GLS5_THECC)						IPR036420 (G3DSA:3.40.50.GENE3D	5,896	5,993	2,472	1,910	2,233									
Solyc08g067245	BRCT domain-containing DNA repair protein (AHRD V3.3 *-* A0A061GLS5_THECC)						IPR001357 (PFAM): IPR036420 (G3D	1,622	2,011	0,816	0,775	0,754									
Solyc08g067250	DNA cross-link repair 1A (AHRD V3.3 *** A0A0B0N3I1_GOSAR)		F:GO:0005515	F:protein binding			IPR011084 (PFAM): G3DSA:1.10.150	7,822	7,102	1,739	1,698	2,425									
Solyc08g067260	3-ketoacyl-CoA synthase (AHRD V3.3 *** A0A0V0IHH6_SOLCH)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013747 (PFAM): IPR012392 (PIRS	149,703	86,713	115,548	137,390	121,535									
Solyc08g067270	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** A0A061GLU2_THECC)						PTHR37256 (PANTHER)	2,229	2,562	1,975	2,384	2,327									
Solyc08g067280	squamosa promoter binding protein-like 7 (AHRD V3.3 --* AT5G18830.3)							0,607	0,386	0,353	0,672	0,467									
Solyc08g067290	RING/U-box superfamily protein (AHRD V3.3 *** AT5G20910.1)		C:GO:0005634: C:G(	C:nucleus; C:cytosol; P:ubiquitin-dependent protein catabolic pr			IPR001841 (PFAM): IPR013083 (G3D	13,755	13,093	23,642	23,992	24,602									
Solyc08g067300	F-box family protein (AHRD V3.3 *** AT4G33160.2)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	12,811	1,448	4,579	8,509	3,140	-3,112	0,000			0,897	0,008	down		up
Solyc08g067310	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CLV7_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.310.80 (GENE3D): G3DS	0,040	0,064	2,376	1,292	4,148									
Solyc08g067320	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41447_SOLTU)		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	1,020	4,491	0,146	0,471	0,566	2,163	0,001					up		
Solyc08g067330	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4CLV9_SOLLC)		P:GO:0009765: C:G(	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	0,019	0,211	0,000	0,000	0,046									
Solyc08g067340	WRKY transcription factor 46	WRKY46	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036576 (G3DS_WRKY	5,718	15,930	1,145	7,682	5,614			2,286	0,000	2,740	0,000		up	up
Solyc08g067360	WRKY transcription factor 45	WRKY45	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM_WRKY	0,100	0,507	0,046	0,248	0,186									
Solyc08g067370	Isoflavone reductase family protein (AHRD V3.3 *-* B9H4C4_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	25,391	21,755	17,716	11,404	15,160					-0,630	0,032			down
Solyc08g067380	LOW QUALITY:NBS-LRR disease resistance protein (AHRD V3.3 --* G7IA97_MEDTR)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,217	0,220	0,168	0,264	0,258									
Solyc08g067390	EG45-like domain containing protein (AHRD V3.3 *** A0A0B2PHN1_GLYSO)	PNPL3					IPR009009 (PFAM): IPR036908 (G3D	0,302	1,411	0,140	0,147	0,140	2,235	0,000					up		
Solyc08g067410	3-ketoacyl-CoA synthase (AHRD V3.3 *** A0A023PMK5_TOBAC)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR016039 (G3D	11,428	21,139	1,402	1,535	1,686	0,915	0,001					up		
Solyc08g067420	Carbon catabolite repressor-like protein (AHRD V3.3 *-* A0A072VDG6_MEDTR)						IPR036691 (G3DSA:3.60.10.GENE3D	26,945	26,538	33,547	35,435	34,321									
Solyc08g067425	Carbon catabolite repressor-like protein (AHRD V3.3 *-* G7I6D2_MEDTR)						IPR036691 (G3DSA:3.60.10.GENE3D	11,061	8,786	12,837	13,161	12,555									
Solyc08g067430	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** AT2G25605.1)		F:GO:0003899: P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA pc	PTHR35716 (PANTHER): PTHR35716	3,119	3,180	6,025	6,343	5,682									
Solyc08g067440	N-acetyltransferase NAT13 (AHRD V3.3 *** A0A151RZY9_CAJCA)		P:GO:0007064: F:G(	P:mitotic sister chrc	EC:2.3.1.5	Arylamine N-acetyltra	IPR000182 (PFAM): G3DSA:3.40.630	0,182	0,138	0,191	0,146	0,186									
Solyc08g067450	Kinase-like protein (AHRD V3.3 *** O49669_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): PIRSF000654 (P	0,178	0,204	0,264	0,409	0,188									
Solyc08g067460	Pre-mRNA-splicing factor syf2 (AHRD V3.3 *** A0A0B0NDC2_GOSAR)		C:GO:0000974: C:G(	C:Prp19 complex; C:catalytic step 2 spliceosome; C:post-mRNA			IPR013260 (PFAM): mobidb-lite (MOB	1,202	1,233	1,100	1,098	0,827									
Solyc08g067470	Zeaxanthin epoxidase, chloroplastic (AHRD V3.3 *-* ZEP_ONCHC)		F:GO:0071949	F:FAD binding			PR00420 (PRINTS): IPR036188 (G3D	20,801	25,471	17,808	20,170	17,269									
Solyc08g067480	V-type proton ATPase proteolipid subunit (AHRD V3.3 *** A0A1D1XX18_9ARAE)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR000245 (PRINTS): G3DSA:1.20.12	17,785	19,748	24,765	28,574	23,842									
Solyc08g067490	LOW QUALITY:CW-type Zinc Finger (AHRD V3.3 *-* AT3G62900.3)		F:GO:0008270	F:zinc ion binding			G3DSA:3.30.40.100 (GENE3D): IPR0'	0,099	0,000	0,000	0,025	0,023									
Solyc08g067500	Non-specific lipid-transfer protein (AHRD V3.3 *** K4CLX6_SOLLC)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,019	0,076	0,000	0,000	0,000									
Solyc08g067510	Non-specific lipid-transfer protein (AHRD V3.3 *** Q93YX9_DAVIN)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc08g067530	Non-specific lipid-transfer protein (AHRD V3.3 *** K4CLX9_SOLLC)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,141	0,200	0,047	0,000	0,000									
Solyc08g067540	Non-specific lipid-transfer protein (AHRD V3.3 *** K4CLY0_SOLLC)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,585	0,613	0,000	0,000	0,000									
Solyc08g067550	Non-specific lipid-transfer protein (AHRD V3.3 *** K4CLY1_SOLLC)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,000	0,061	0,000	0,025	0,000									
Solyc08g067560	SUMO activating enzyme 1B (AHRD V3.3 --* AT5G50680.2)							0,021	0,000	0,000	0,000	0,000									
Solyc08g067570	LOW QUALITY:CW-type Zinc Finger (AHRD V3.3 *-* AT3G62900.3)		F:GO:0008270	F:zinc ion binding			IPR011124 (PFAM): G3DSA:3.30.40.1	0,379	0,500	2,172	1,797	2,265									
Solyc08g067580	phytochrome interacting factor 3 (AHRD V3.3 --* AT1G09530.6)							0,601	0,531	0,243	0,244	0,119									
Solyc08g067590	CW-type Zinc Finger (AHRD V3.3 *-* AT3G62900.3)		F:GO:0008270	F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,016	0,798	15,752	18,355	15,023									
Solyc08g067595	Ribonuclease H-like protein (AHRD V3.3 --* A0A061FNB8_THECC)		F:GO:0003676: F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis				0,559	0,563	9,709	9,251	9,224									
Solyc08g067605	Lecithin-cholesterol acyltransferase-like 4 (AHRD V3.3 --* LCAT4_ARATH)							0,000	0,021	0,000	0,000	0,023									
Solyc08g067610	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG44	F:GO:0005524: C:G(	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR029481 (PFAM): G3DSA:3.40.50.3	1,667	4,139	6,888	10,231	25,876			1,900	0,022				up	
Solyc08g067620	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG45	F:GO:0005524: C:G(	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): IPR029481 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc08g067630	histone deacetylase-like protein (AHRD V3.3 *** AT2G25625.2)						mobidb-lite (MOBIDB_LITE): PTHR372	0,857	1,488	1,413	1,992	2,585									
Solyc08g067640	LOW QUALITY:Zinc finger C-x8-C-x5-C-x3-H type family protein (AHRD V3.3 --* AT1G21580.8)							0,976	1,088	0,101	0,119	0,070									
Solyc08g067650	LOW QUALITY:Ribonuclease H-like superfamily protein (AHRD V3.3 --* AT3G09510.1)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3I	0,079	0,057	0,000	0,124	0,072									
Solyc08g067670	LOW QUALITY:DNA-binding bromodomain-containing protein (AHRD V3.3 --* AT1G58025.2)							3,649	4,184	1,546	1,881	2,306									
Solyc08g067690	Homeobox-leucine zipper protein HOX7 (AHRD V3.3 --* HOX7_ORYSJ)							0,000	0,018	0,000	0,000	0,000									
Solyc08g067730	RING/U-box superfamily protein (AHRD V3.3 --* AT1G30860.1)							0,101	0,215	0,346	0,338	0,326									
Solyc08g067740	ribosomal protein L5 (AHRD V3.3 --* AT3G25520.3)							3,837	3,253	5,198	6,756	6,001									
Solyc08g067760	MLO-like protein (AHRD V3.3 *** K4CM00_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	0,040	0,000	0,025	0,097	0,000									
Solyc08g067770	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GNC5_THECC)		C:GO:0005886: F:G(	C:plasma membrane; F:zinc ion binding; C:integral component o			IPR001841 (PFAM): IPR013083 (G3D	70,592	110,761	70,871	72,034	83,262									
Solyc08g067790	SPOC domain/transcription elongation factor S-II, putative (AHRD V3.3 *** G7JBQ4_MEDTR)		P:GO:0006351	P:transcription, DNA-templated			IPR036575 (G3DSA:1.10.472.GENE3I	73,349	78,779	77,236	79,754	75,976									
Solyc08g067795	DNAJ heat shock family protein (AHRD V3.3 *** AT5G25530.1)		P:GO:0006457: F:G(	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS): IPR002939 (PF	0,077	0,126	0,093	0,048	0,071									
Solyc08g067800	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT1G21770.1)		F:GO:0016740	F:transferase activity			G3DSA:3.40.630.30 (GENE3D): IPR0:	8,592	8,123	11,634	12,173	10,629									
Solyc08g067805	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,325	0,232	0,194	0,306	0,187									
Solyc08g067810	CTC-interacting domain protein, putative (AHRD V3.3 *** G7I5S9_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:1.10.8.10 (GENE3D): mobidb-l	23,554	25,269	32,026	32,167	30,354									
Solyc08g067820	RNA-binding 48 (AHRD V3.3 *** A0A0B0P6M7_GOSAR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	14,026	11,401	15,036	15,705	14,213									
Solyc08g067830	Transmembrane protein 18 (AHRD V3.3 *** A0A0B2RE88_GLYSO)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:pollen germination; P:pollen tube grc			IPR026721 (PFAM): PTHR22593 (PAI	11,746	12,715	18,007	17,043	16,257									
Solyc08g067840	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** A0A0F7GYP2_9ROSI)		F:GO:0005509: C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR002683 (PFAM): IPR016123 (G3D	10,801	12,168	11,994	12,572	15,969									
Solyc08g067860	embryo defective 2410 (AHRD V3.3 *** AT2G25660.3)		C:GO:0016021: C:G(	C:integral component of membrane; C:apoplast			IPR007452 (PFAM): mobidb-lite (MOB	46,602	46,170	131,836	147,787	130,824									
Solyc08g067870	embryo defective 2410 (AHRD V3.3 *** AT2G25660.3)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	23,810	20,089	58,664	74,775	66,277									
Solyc08g067880	Copper ion binding protein (AHRD V3.3 *** A0A0K9PL91_ZOSMR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	32,089	31,744	28,923	27,921	29,282									
Solyc08g067885	Copper ion binding protein (AHRD V3.3 *** A0A0K9PL91_ZOSMR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc08g067890	Copper ion binding protein (AHRD V3.3 *** A0A0K9PL91_ZOSMR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,061	0,075	0,076	0,023									
Solyc08g067900	copper ion binding protein (AHRD V3.3 *-* AT4G32610.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,168	7,454	10,144	9,764	8,935									
Solyc08g067910	Syntaxin, putative (AHRD V3.3 *** B9RPA3_RICCO)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport			IPR000727 (PFAM): G3DSA:1.20.5.11	76,575	77,351	84,635	84,226	80,261									
Solyc08g067920	Enhancer of polycomb-like transcription factor protein, putative isoform 1 (AHRD V3.3 *** A0A061GQB3_TH		P:GO:0006342: P:G(	P:chromatin silencing; P:histone deacetylation; C:protein-contai			IPR019542 (PFAM): mobidb-lite (MOB	46,305	44,518	61,130	59,604	58,095									
Solyc08g067930	ARF GTPase activator (AHRD V3.3 *** G7L8Z4_MEDTR)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (PF	0,116	0,000	0,025	0,000	0,000									
Solyc08g067940	To encode a PR protein, Belongs to the plant thionin family with the following members:, putative (AHRD V3.3 -** A0A061GI20_THECC)						IPR038975 (PANTHER): PTHR36312:!	0,241	0,454	0,000	0,000	0,000									
Solyc08g067950	50S ribosomal protein L17 (AHRD V3.3 *** A0A151T5E2_CAJCA)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036373 (G3DSA:3.90.1030.GENE:	172,591	148,998	103,741	107,232	99,545									
Solyc08g067960	RING finger and CHY zinc finger protein (AHRD V3.3 *** G7JNA1_MEDTR)		F:GO:0008270	F:zinc ion binding			IPR039512 (PFAM): IPR008913 (PFA	540,167	400,972	681,577	686,666	747,316									
Solyc08g067970	Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 *** A0A061GBF7_THECC)						IPR007650 (PFAM): PTHR33059:SF1!	6,756	8,364	10,548	7,348	8,431									
Solyc08g067980	Polyamine-modulated factor 1-binding protein 1 (AHRD V3.3 *** A0A061GKH1_THECC)						PTHR36800 (PANTHER)	0,115	0,039	0,000	0,000	0,000									
Solyc08g067990	Subtilisin-like protease (AHRD V3.3 *** W9R6D5_9ROSA)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	12,619	13,822	0,341	0,224	0,187									
Solyc08g067995	vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-like protein (AHF		F:GO:0004672: F:G(	F:protein kinase activity; F:protein serine/threonine kinase activ			PTHR34892 (PANTHER)	0,000	0,021	0,022	0,047	0,047									
Solyc08g068000	Potassium channel (AHRD V3.3 *** B6ECZ4_TOBAC)		F:GO:0005249: P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra			IPR003938 (PRINTS): IPR005821 (PF	0,040	0,043	0,025	0,000	0,000									
Solyc08g068010	zinc finger FYVE domain protein (AHRD V3.3 *** AT2G25730.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	27,218	26,517	33,160	34,323	33,462									
Solyc08g068013	zinc finger FYVE domain protein (AHRD V3.3 *-* AT2G25730.4)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,241	5,312	7,680	8,451	8,327									
Solyc08g068017	Zinc finger FYVE domain-containing protein 26 (AHRD V3.3 *-* A0A151SQY5_CAJCA)						PTHR35478 (PANTHER)	1,291	1,013	1,192	1,514	1,389									
Solyc08g068030	Zinc finger FYVE domain-containing protein 26 (AHRD V3.3 *-* A0A151SQY5_CAJCA)						PTHR35478 (PANTHER)	1,183	0,881	1,071	1,481	1,203									
Solyc08g068040	zinc finger FYVE domain protein (AHRD V3.3 *-* AT2G25730.3)						PTHR35478 (PANTHER)	10,548	8,700	11,275	12,754	13,030									
Solyc08g068050	Remodeling and spacing factor 1 (AHRD V3.3 *** A0A151SQU5_CAJCA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,349	5,094	2,907	1,499	2,906									
Solyc08g068060	transmembrane protein (AHRD V3.3 *** AT4G32680.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	12,570	12,818	15,729	14,953	12,899									
Solyc08g068070	hemoglobin 3 (AHRD V3.3 *** AT4G32690.1)		F:GO:0019825: F:G(	F:oxygen binding; F:heme binding			IPR001486 (PFAM): IPR012292 (G3D	23,273	19,913	23,460	21,238	20,263									
Solyc08g068080	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT5G14895.1)						PTHR33168 (PANTHER): PTHR33168	0,061	0,043	0,000	0,000	0,023									
Solyc08g068090	hemoglobin 3 (AHRD V3.3 *** AT4G32690.1)		F:GO:0019825: F:G(	F:oxygen binding; F:heme binding			IPR001486 (PFAM): IPR012292 (G3D	0,000	0,019	0,000	0,069	0,120									
Solyc08g068100	bZIP transcription factor (DUF630 and DUF632) (AHRD V3.3 *** AT2G27090.2)		P:GO:0071249	P:cellular response to nitrate			IPR006868 (PFAM): IPR006867 (PFA	158,869	117,331	47,995	36,430	45,289					-0,396	0,013			down
Solyc08g068120	DNA polymerase theta (AHRD V3.3 *** A0A0B2Q221_GLYSO)		F:GO:0003677: F:G(	F:DNA binding; F:DI	EC:2.7.7.7	DNA-directed DNA pc	IPR002298 (PRINTS): G3DSA:3.30.70	1,580	1,267	0,358	0,248	0,376									
Solyc08g068150	BURP domain-containing protein (AHRD V3.3 *** B2ZPK7_SOLLC)						IPR004873 (PFAM): mobidb-lite (MOB	129,418	113,908	172,122	290,058	183,232					0,755	0,000			up
Solyc08g068160	Flavin-containing monooxygenase (AHRD V3.3 *** K4CM40_SOLLC)		F:GO:0004499: F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.'	Flavin-containing mo	PR00469 (PRINTS): PR00368 (PRINT	0,941	1,450	0,071	0,000	0,094									
Solyc08g068180	Ribosomal protein L37 (AHRD V3.3 *** K4CM42_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR011331 (G3DSA:2.20.25.GENE3D	132,946	147,395	112,136	106,388	106,597									
Solyc08g068190	Aldehyde dehydrogenase (AHRD V3.3 *** Q1AFF6_VITPS)		F:GO:0016620: P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR016162 (G3DSA:3.40.605.GENE3I	0,021	0,039	0,025	0,074	0,000									
Solyc08g068200	P-loop containing nucleoside triphosphate hydrolases superfamily protein		F:GO:0005525	F:GTP binding			IPR019987 (TIGRFAM): IPR006073 (F	21,649	19,062	35,806	31,842	34,138									
Solyc08g068210	Beta-adaptin-like protein (AHRD V3.3 *** G8Z247_SOLLC)		P:GO:0006886: P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR011989 (G3DSA:1.25.10.GENE3D	117,354	105,348	123,299	124,135	123,422									
Solyc08g068220	50S ribosomal protein L27 (AHRD V3.3 *** B7FGL1_MEDTR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001684 (PRINTS): G3DSA:2.40.50	21,874	25,421	32,913	28,361	29,394									
Solyc08g068230	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2SBT0_GLYSO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	0,600	1,760	0,387	0,685	1,462	1,551	0,047	1,887	0,000			up	up	
Solyc08g068240	Phosphate transporter PHO1-like protein (AHRD V3.3 *** G7JWG7_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR004331 (PFAM): IPR004342 (PFA	0,000	0,041	0,000	0,000	0,000									
Solyc08g068250	Receptor protein kinase (AHRD V3.3 *-* T2C4B6_BRAJU)		F:GO:0004252: F:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM): IPR035952 (G3D	0,546	0,337	0,343	0,293	0,306									
Solyc08g068270	Rhomboid-like protein (AHRD V3.3 *** K4CM51_SOLLC)		F:GO:0004252: C:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM): IPR035952 (G3D	0,280	0,512	0,386	0,389	0,400									
Solyc08g068290	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM): PTHR14255 (PAI	29,797	48,771	91,357	104,598	100,908	0,740	0,003					up		
Solyc08g068300	Coiled-coil domain-containing protein 25 (AHRD V3.3 *** A0A151TDR8_CAJCA)		P:GO:0008150	P:biological_process			IPR008532 (PFAM): mobidb-lite (MOB	105,553	94,124	121,739	120,728	114,136									
Solyc08g068310	La-like protein (AHRD V3.3 *** W9RMR2_9ROSA)		F:GO:0003723: C:G(	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprote			IPR002344 (PRINTS): IPR014886 (PF	66,586	64,829	60,808	57,808	53,193									
Solyc08g068320	Myb (AHRD V3.3 *** Q948S5_TOBAC)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(_MYB	10,158	10,140	2,746	2,053	2,448									
Solyc08g068330	Aspartate aminotransferase (AHRD V3.3 *** K4CM57_SOLLC)		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR000796 (PRINTS): IPR015421 (G3	87,890	74,814	307,822	284,463	281,116									
Solyc08g068340	Eukaryotic translation initiation factor 3 subunit L (AHRD V3.3 *** K4CM58_SOLLC)		F:GO:0003743: C:G(	F:translation initiation factor activity; C:eukaryotic translation in			IPR019382 (PFAM): IPR019382 (PAN	92,823	96,957	85,539	79,679	83,984									
Solyc08g068350	Pericentriolar material 1 protein (AHRD V3.3 *** A0A1D1XL49_9ARAE)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	22,465	19,200	9,955	11,156	15,186			0,602	0,029				up	
Solyc08g068370	ENTH/VHS/GAT family protein (AHRD V3.3 *** A0A061GKP2_THECC)		C:GO:0005622: P:G(	C:intracellular; P:intracellular protein transport			IPR038425 (G3DSA:1.20.58.GENE3D	58,431	65,702	68,909	70,037	68,966									
Solyc08g068380	NAC domain containing protein 82 (AHRD V3.3 --* AT5G09330.5)	NAC077	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS_NAC	2,672	1,784	1,479	1,203	1,249									
Solyc08g068390	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857: C:G(	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	IPR001753 (PFAM): IPR006176 (PFA	12,801	36,623	12,513	13,471	15,758	1,543	0,000					up		

Solyc08g068400	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G25770.3)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity			IPR029058 (G3DSA:3.40.50.GENE3D	24,202	26,563	20,957	20,317	20,435									
Solyc08g068410	flowering time control protein-related / FCA gamma-like protein (AHRD V3.3 --* AT2G47310.1)		P:GO:0009910: P:G(	P:negative regulation of flower development; P:negative regulat			mobidb-lite (MOBIDB_LITE)	0,651	1,062	0,298	0,050	0,588									
Solyc08g068420	L-gulonolactone oxidase (AHRD V3.3 *** A0A151T9K5_CAJCA)		F:GO:0003885: C:G(	F:D-arabinono-1,4-l	EC:1.1.3.37	D-arabinono-1,4-lact	IPR016169 (G3DSA:3.30.465.GENE3	6,489	6,425	1,854	0,856	1,723									
Solyc08g068430	Beta-1,3-glucuronyltransferase, putative (AHRD V3.3 *** B9RS38_RICCO)		F:GO:0015018: C:G(	F:galactosylgalacto	EC:2.4.1.17; EC:2.4.	Glucuronosyltransfer	IPR005027 (PFAM): IPR029044 (G3D	26,060	23,846	17,042	16,881	18,598									
Solyc08g068440	Lipoyl synthase (AHRD V3.3 *-* W9RNC4_9ROSA)		P:GO:0009107: F:G(	P:lipoate biosynthet	EC:2.8.1.8	Lipoyl synthase	IPR003698 (PANTHER): PTHR10949:	0,019	0,041	0,046	0,047	0,046									
Solyc08g068450	LOW QUALITY:Serine/threonine-protein phosphatase 2A regulatory subunit delta isoform (AHRD V3.3 --* A0A1D1YJ73_9ARAE)							0,000	0,000	0,022	0,000	0,000									
Solyc08g068460	LOW QUALITY:CK25 (AHRD V3.3 *** Q1W1G0_TOBAC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,701	0,939	0,025	0,000	0,048									
Solyc08g068470	LOW QUALITY:F-box/kelch-repeat protein (AHRD V3.3 *** W9SF98_9ROSA)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	0,021	0,000	0,000	0,000	0,000									
Solyc08g068490	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT4G03400.2)						IPR004993 (PFAM): PTHR31901:SF1	0,019	0,000	0,000	0,000	0,000									
Solyc08g068500	F-box/FBD/LRR-repeat protein (AHRD V3.3 *** W9RF70_9ROSA)						IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc08g068510	F-box protein (AHRD V3.3 *** A0A072USG8_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,040	0,043	0,000	0,025	0,000									
Solyc08g068520	F-box/RNI-like superfamily protein (AHRD V3.3 *-* AT3G58860.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	1,223	0,857	0,732	0,557	0,495									
Solyc08g068530	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** G7IHX4_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	3,107	3,128	4,712	4,494	3,447									
Solyc08g068540	B3 domain-containing protein (AHRD V3.3 *** W9QJE4_9ROSA)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	4,377	3,686	4,240	5,094	4,116									
Solyc08g068545	B3 domain-containing transcription factor VRN1 (AHRD V3.3 *-* A0A0B2QZW5_GLYSO)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM): IPR015300 (G3D	2,904	2,197	2,398	3,182	2,975									
Solyc08g068570	Tocopherol cyclase (AHRD V3.3 *** F1BPV7_SOLPN)	VTE1	F:GO:0009976	F:tocopherol cyclase activity			IPR025893 (PFAM): mobidb-lite (MOB	3,335	4,020	3,105	4,428	3,909									
Solyc08g068580	Phospholipase D Z (AHRD V3.3 *** A0A0K1R0A7_VITVI)		F:GO:0003824	F:catalytic activity			IPR025202 (PFAM): G3DSA:3.30.870	9,269	9,552	8,768	8,329	8,825									
Solyc08g068590	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT2G46910.1)		C:GO:0010287	C:plastoglobule			IPR006843 (PFAM): PTHR31906:SF6	15,938	19,191	27,385	28,806	32,809									
Solyc08g068600	Aromatic amino acid decarboxylase 1B (AHRD V3.3 *** Q1KSC5_SOLLC)		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015421 (G3DSA:3.40.640.GENE3	64,169	16,034	3,409	15,145	9,374	-1,974	0,000	1,449	0,001	2,137	0,000	down	up	up
Solyc08g068610	Decarboxylase family protein IPR002129 Pyridoxal phosphate-dependent decarboxylase		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR002129 (PFAM): IPR015422 (G3D	1,191	1,030	0,318	0,193	0,353									
Solyc08g068620	Decarboxylase family protein IPR002129 Pyridoxal phosphate-dependent decarboxylase		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR002129 (PFAM): IPR015422 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc08g068630	Decarboxylase family protein IPR002129 Pyridoxal phosphate-dependent decarboxylase		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015422 (G3DSA:3.90.1150.GENE	0,080	0,344	0,025	0,116	0,142									
Solyc08g068640	Decarboxylase family protein IPR002129 Pyridoxal phosphate-dependent decarboxylase		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015422 (G3DSA:3.90.1150.GENE	1,918	1,106	0,000	0,050	0,071									
Solyc08g068660	Histidine decarboxylase (AHRD V3.3 *-* W0KR26_TOBAC)		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			PTHR11999:SF116 (PANTHER): PTHF	4,072	6,917	0,188	0,551	0,397									
Solyc08g068670	Aromatic amino acid decarboxylase 1B (AHRD V3.3 *** Q1KSC5_SOLLC)		F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR015421 (G3DSA:3.40.640.GENE3	0,117	0,000	0,000	0,000	0,047									
Solyc08g068680	aromatic amino acid decarboxylase 1A	AADC1A	F:GO:0016831: P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F			IPR002129 (PFAM): IPR015422 (G3D	20,104	19,353	3,224	9,887	7,136			1,140	0,009	1,613	0,000		up	up
Solyc08g068690	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): IPR039534 (PTH	237,751	258,497	38,805	35,922	61,503									
Solyc08g068700	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): mobidb-lite (MOB	29,707	49,778	2,121	1,303	4,458	0,772	0,006					up		
Solyc08g068710	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): PTHR10545 (PAN	0,309	0,938	0,025	0,025	0,188									
Solyc08g068730	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): PTHR10545 (PAN	0,322	0,727	0,165	0,172	0,209									
Solyc08g068770	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): PTHR10545 (PAN	1,327	2,040	0,075	0,051	0,211									
Solyc08g068780	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT7-8	tht7d8	F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): IPR039534 (PTH	2,155	2,319	0,116	0,369	0,492									
Solyc08g068790	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): G3DSA:3.40.630	1,511	1,285	0,834	2,403	1,274					1,501	0,001			up
Solyc08g068800	Glutathione peroxidase (AHRD V3.3 *** A0A068UHC8_COFCA)	GPX	F:GO:0004602: P:G(	F:glutathione peroxi	EC:1.11.1.9; EC:1.1	Glutathione peroxida	G3DSA:3.40.30.10 (GENE3D): IPR00	0,123	0,396	0,074	0,098	0,189									
Solyc08g068810	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9RNT9_RICCO)		F:GO:0008270: P:G(	F:zinc ion binding; F	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR013083 (G3DSA:3.30.40.GENE3D	7,003	9,873	7,239	6,330	6,703									
Solyc08g068820	Zinc finger CCCH domain-containing protein 18 (AHRD V3.3 *** A0A0B2PY90_GLYSO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:metal ion binding			IPR000467 (PFAM): IPR041367 (PFA	4,546	3,108	7,261	6,345	6,491									
Solyc08g068840	Transcription factor IIIB subunit (AHRD V3.3 --* A0A1D1ZC65_9ARAE)		P:GO:0006351	P:transcription, DNA-templated			G3DSA:1.20.5.650 (GENE3D): IPR01	3,466	3,480	4,145	3,602	3,383									
Solyc08g068850	Proton pump interactor 1 (AHRD V3.3 *-* D5L6G0_SOLTU)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:plasma membrane; P:regulation of c			IPR029669 (PTHR32219:PANTHER):	0,076	0,244	0,050	0,094	0,071									
Solyc08g068860	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061GIP5_THECC)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	0,237	0,853	0,218	0,656	0,872									
Solyc08g068870	aspartate protease family protein		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	0,057	0,390	0,370	0,663	1,458									
Solyc08g068880	enhanced disease resistance-like protein (DUF1336) (AHRD V3.3 *** AT5G10750.1)						IPR009769 (PFAM): mobidb-lite (MOB	48,456	35,680	55,274	57,144	52,966									
Solyc08g068920	Protein kinase superfamily protein (AHRD V3.3 *** AT5G24970.3)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM): PTHR10566 (PAN	10,315	11,769	14,187	13,926	14,401									
Solyc08g068925	Protein kinase superfamily protein (AHRD V3.3 *-* AT5G24970.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PTHR10566:SF70 (PANTHER): PTHR	3,212	3,364	3,919	4,073	4,233									
Solyc08g068930	Transmembrane protein, putative (AHRD V3.3 *** A0A072V1M8_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35755 (PANTHER)	3,672	3,831	4,204	4,528	4,481									
Solyc08g068940	LOW QUALITY:TSA: Wollemia nobilis Ref_Wollemi_Transcript_13512_1189 transcribed RNA sequence (AHRD V3.3 --* A0A0C9QQX4_9SPER)							0,042	0,018	0,047	0,050	0,094									
Solyc08g068960	Histidine kinase 5 (AHRD V3.3 *** W9RFB6_9ROSA)		F:GO:0000155: P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR003661 (PF	1,694	1,926	0,886	0,921	1,010									
Solyc08g068970	Oxidative stress 3, putative isoform 2 (AHRD V3.3 *-* A0A061GIQ6_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,811	1,370	0,100	0,050	0,000									
Solyc08g068990	Pathogenesis-related protein 1 (AHRD V3.3 *** A0MZ69_MUSAC)		C:GO:0005615	C:extracellular space			IPR002413 (PRINTS): IPR001283 (PF	0,038	0,079	0,000	0,000	0,024									
Solyc08g069000	Mg2+ transporter protein, CorA-like/Zinc transport protein ZntB (AHRD V3.3 *** A0A118JVW7_CYNCS)		C:GO:0016020: P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:1.20.58.340 (GENE3D): G3DS	29,134	38,794	19,394	16,997	17,884									
Solyc08g069010	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RNM2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	4,957	10,361	2,661	3,980	6,938	1,091	0,023	1,365	0,006			up	up	
Solyc08g069030	aminolevulinic acid dehydratase	HEMB/ALAD	F:GO:0004655: P:G(	F:porphobilinogen s	EC:4.2.1.24	Porphobilinogen synt	IPR001731 (PRINTS): IPR001731 (PF	98,806	140,476	176,953	191,102	210,389	0,535	0,045					up		
Solyc08g069040	Peroxidase (AHRD V3.3 *** K4CMC4_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	7,356	6,262	2,379	2,599	3,020									
Solyc08g069050	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** D7LIB1_ARALL)		P:GO:0016579: F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	21,705	21,660	38,847	43,230	39,290									
Solyc08g069060	Hexosyltransferase (AHRD V3.3 *-* K4CMC6_SOLLC)		P:GO:0006486: F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR025298 (PFAM): PTHR11214:SF2	1,423	2,577	16,518	19,531	13,764									
Solyc08g069065	Hexosyltransferase (AHRD V3.3 *** K4CMC6_SOLLC)		P:GO:0006486: F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			G3DSA:3.90.550.50 (GENE3D): IPR0	12,497	22,255	146,981	166,487	126,343									
Solyc08g069080	Splicing factor 3B, subunit 5 (AHRD V3.3 *** A0A103XPM0_CYNCS)		P:GO:0000398	P:mRNA splicing, via spliceosome			IPR009846 (PFAM): IPR017089 (PIRS	10,332	10,976	18,187	20,624	16,026									
Solyc08g069100	LOW QUALITY:Exocyst complex exo70-like protein (AHRD V3.3 *** G7I5R5_MEDTR)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): G3DSA:1.20.128	9,300	10,411	11,868	14,270	12,084									
Solyc08g069110	NAD-dependent epimerase/dehydratase family protein (AHRD V3.3 *** AT1G53500.1)		F:GO:0008460: P:G(	F:dTDP-glucose 4,6	EC:4.2.1.46	dTDP-glucose 4,6-de	G3DSA:3.40.50.720 (GENE3D): IPR0	0,431	0,796	0,212	0,701	0,258									
Solyc08g069120	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *** B9RNP5_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR000504 (PFAM): IPR012677 (G3D	27,666	21,789	28,247	27,830	27,939									
Solyc08g069125	nitrile specifier protein 3 (AHRD V3.3 --* AT3G16390.2)		C:GO:0000943	C:retrotransposon nucleocapsid				4,896	5,991	5,874	5,223	5,180									
Solyc08g069130	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT5G43822.1)						IPR029159 (PFAM): IPR038985 (PAN	1,610	2,193	2,372	2,324	2,335									
Solyc08g069140	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216: P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR000595 (PFAM): IPR005821 (PFA	1,406	1,754	0,191	0,599	0,611									
Solyc08g069160	sequence-specific DNA binding transcription factor (AHRD V3.3 *** AT4G31270.1)						PF13837 (PFAM): Trihelix	7,977	8,867	11,986	9,920	10,314									
Solyc08g069170	Receptor protein kinase, putative (AHRD V3.3 *** B9RHT1_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:1.10.510.10 (GENE3D): IPR0	0,038	0,000	0,000	0,022	0,046									
Solyc08g069180	Kinase (AHRD V3.3 *** D7LHK4_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	1,468	2,277	0,499	0,483	0,496									
Solyc08g069200	LOW QUALITY:Chlorophyll synthase, chloroplastic (AHRD V3.3 --* CHLG_AVESA)							0,098	0,205	0,025	0,025	0,046									
Solyc08g069230	DnaJ (AHRD V3.3 *** A0A0B0NWN0_GOSAR)						PTHR10168 (PANTHER): PTHR10168	1,717	3,293	0,236	0,245	1,086									
Solyc08g074240	40S ribosomal protein S6 (AHRD V3.3 *** K4CME5_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014401 (PIRSF): IPR001377 (PFA	314,763	298,217	218,771	185,144	200,145									
Solyc08g074250	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT5G35450.2)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,000	0,019	0,022	0,122	0,000									
Solyc08g074260	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,118	0,078	0,168	0,073	0,118									
Solyc08g074270	Cryptochrome DASH, chloroplastic/mitochondrial (AHRD V3.3 *** CRYD_SOLLC)		F:GO:0003913: P:G(	F:DNA photolyase a	EC:4.1.99	Carbon-carbon lyase	IPR002081 (PRINTS): IPR006050 (PF	6,014	7,470	6,980	7,091	7,983									
Solyc08g074280	ABC1 family protein (AHRD V3.3 *** AT5G24810.1)						IPR001466 (PFAM): G3DSA:3.40.710	28,334	27,364	32,297	33,054	35,408									
Solyc08g074290	myosin heavy chain-like protein (AHRD V3.3 *** AT4G31340.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR343	161,719	150,216	246,678	244,036	233,429									
Solyc08g074300	NAC domain-containing protein (AHRD V3.3 *-* I6YR01_9CARY)	NAC078	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,000	0,081	0,025	0,025	0,023									
Solyc08g074303	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 --* AT2G37760.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,019	0,072	0,025	0,000									
Solyc08g074307	Photosystem I reaction center subunit III (AHRD V3.3 *-* I3SN70_MEDTR)		C:GO:0009538: P:G(	C:photosystem I reaction center; P:photosynthesis			IPR036577 (G3DSA:1.10.8.GENE3D):	0,081	0,308	0,050	0,097	0,187									
Solyc08g074340	WD repeat domain phosphoinositide-interacting 3 (AHRD V3.3 *** A0A0B0P0U0_GOSAR)		F:GO:0005515	F:protein binding			PTHR11227 (PANTHER): PTHR11227	0,118	0,041	0,068	0,048	0,000									
Solyc08g074350	NAC domain-containing protein 78 (AHRD V3.3 --* A0A1D1YBD8_9ARAE)							1,823	1,076	0,600	0,700	0,635									
Solyc08g074355	Sodium Bile acid symporter family (AHRD V3.3 --* AT3G56160.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,025	0,022	0,000									
Solyc08g074360	N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein (AHRD V3.3 *** AT3G58130.2)		F:GO:0000225: P:G(	F:N-acetylglucosam	EC:3.5.1.89	N-acetylglucosaminyl	IPR024078 (G3DSA:3.40.50.GENE3D	1,666	0,999	1,984	2,545	2,001									
Solyc08g074370	DDB1-and CUL4-associated factor like 1 (AHRD V3.3 *** A0A0B2Q9I5_GLYSO)		F:GO:0005515: P:G(	F:protein binding; P:protein ubiquitination			IPR003737 (PFAM): IPR015943 (G3D	79,518	71,078	110,353	113,125	108,508									
Solyc08g074390	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SPT8_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM): G3DSA:3.20.20.8	21,702	16,030	10,708	8,485	13,039									
Solyc08g074400	keratin-associated protein (DUF1218) (AHRD V3.3 *** AT4G31130.1)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane			IPR009606 (PFAM): PTHR31769 (PAN	0,000	0,041	0,025	0,000	0,000									
Solyc08g074410	tRNA synthetase (AHRD V3.3 *** C1N232_MICPC)		F:GO:0004830: F:G(	F:tryptophan-tRNA l	EC:6.1.1.2	Tryptophan--tRNA lig	IPR002306 (PRINTS): G3DSA:1.10.24	69,892	66,367	77,605	73,847	78,465									
Solyc08g074420	Coiled-coil domain-containing protein, putative (AHRD V3.3 *** B9RY29_RICCO)						IPR007590 (PFAM): mobidb-lite (MOB	30,864	31,622	49,715	50,193	50,067									
Solyc08g074450	(RAP Annotation release2) Galactose-binding like domain containing protein (AHRD V3.3 *** Q10RT4_ORYSJ)						IPR018971 (PFAM): PTHR34131 (PAN	7,723	9,402	9,223	10,562	11,548									
Solyc08g074480	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *** A0A0B2P545_GLYSO)						G3DSA:1.10.110.10 (GENE3D): IPR0	958,693	804,350	267,877	228,489	233,610									
Solyc08g074490	Glycosyltransferase (AHRD V3.3 --* M5XW04_PRUPE)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	0,040	0,099	0,000	0,000	0,000									
Solyc08g074495	Glycosyltransferase (AHRD V3.3 *** A0A022RAZ3_ERYGU)		C:GO:0000139: C:G(	C:Golgi membrane; C:integral component of membrane; F:transf			IPR005069 (PFAM): PTHR44478 (PAN	0,037	0,057	0,000	0,000	0,000									
Solyc08g074500	TATA-binding protein associated factor-like protein (AHRD V3.3 *** A0A072UIT4_MEDTR)		F:GO:0005524	F:ATP binding			IPR011989 (G3DSA:1.25.10.GENE3D	36,324	35,379	38,026	39,161	38,789									
Solyc08g074510	TATA-binding protein associated factor-like protein (AHRD V3.3 *-* A0A072UIT4_MEDTR)		F:GO:0005524	F:ATP binding			PTHR36498 (PANTHER)	1,954	1,830	2,121	2,256	2,167									
Solyc08g074520	TATA-binding protein associated factor-like protein (AHRD V3.3 *-* G7JQD7_MEDTR)		F:GO:0005524	F:ATP binding			IPR011989 (G3DSA:1.25.10.GENE3D	17,858	13,925	15,815	17,181	17,325									
Solyc08g074550	Threonyl-tRNA synthetase (AHRD V3.3 *** AT5G26830.1)		F:GO:0004829: F:G(	F:threonine-tRNA lic	EC:6.1.1.3	Threonine--tRNA liga	IPR002320 (PRINTS): IPR004095 (PF	51,221	64,299	64,080	76,547	66,494									
Solyc08g074560	ABC1-like kinase 1		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM): G3DSA:1.10.510.	11,515	16,625	30,372	36,769	57,240			0,913	0,000				up	
Solyc08g074565	phloem protein 2-B13 (AHRD V3.3 --* AT1G56240.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,237	0,424	0,436	0,387	0,375									
Solyc08g074570	Protein MOS2, putative (AHRD V3.3 *** B9SAH9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR026822 (PFAM): IPR041330 (PFA	26,088	24,503	31,429	30,124	28,081									
Solyc08g074580	Cytoplasmic tRNA 2-thiolation protein 1 (AHRD V3.3 *** CTU1_ARATH)		F:GO:0000049: P:G(	F:tRNA binding; P:tRNA wobble uridine modification; P:tRNA thic			IPR014729 (G3DSA:3.40.50.GENE3D	26,095	25,621	40,698	40,135	39,433									
Solyc08g074600	ATP-dependent DNA helicase RecQ family protein (AHRD V3.3 *** G7K6R5_MEDTR)		F:GO:0000166: F:G(	F:nucleotide bindinc	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036388 (G3DSA:1.10.10.GENE3D	12,923	11,468	9,486	8,090	8,538									
Solyc08g074605	DNA helicase family protein (AHRD V3.3 *-* B9GZY0_POPTR)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,000	0,018	0,000	0,050	0,000									
Solyc08g074620	polyphenol oxidase precursor		F:GO:0004097: P:G(	F:catechol oxidase	EC:1.1.3; EC:1.1.3.1	Acting on diphenols a	IPR002227 (PRINTS): IPR016213 (PII	0,429	3,467	0,000	0,000	0,000									
Solyc08g074630	polyphenol oxidase precursor		F:GO:0004097: P:G(	F:catechol oxidase	EC:1.1.3; EC:1.1.3.1	Acting on diphenols a	IPR002227 (PRINTS): IPR022739 (PF	0,040	0,447	0,201	0,000	0,071									
Solyc08g074660	F-box/kelch-repeat protein SKIP25, putative (AHRD V3.3 *** G7K6R4_MEDTR)		F:GO:0005515	F:protein binding			PF13964 (PFAM): IPR015915 (G3DSA	0,455	0,458	0,583	0,365	0,423									
Solyc08g074670	Mediator of RNA polymerase II transcription subunit 28 (AHRD V3.3 *** G7LBD1_MEDTR)		P:GO:0006355: C:G(	P:regulation of transcription, DNA-templated; C:mediator comple			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,629	4,294	4,778	4,358	4,132									
Solyc08g074682	polyphenol oxidase precursor		F:GO:0004097: P:G(	F:catechol oxidase	EC:1.1.3; EC:1.1.3.1	Acting on diphenols a	IPR002227 (PRINTS): IPR008922 (G3	0,290	3,030	15,887	6,216	6,843			-1,216	0,035	-1,348	0,035		down	down
Solyc08g074683	polyphenol oxidase precursor		F:GO:0004097: P:G(	F:catechol oxidase	EC:1.1.3; EC:1.1.3.1	Acting on diphenols a	IPR002227 (PRINTS): IPR016213 (PII	0,512	2,763	0,175	0,025	0,117									
Solyc08g074700	LOW QUALITY:50S ribosomal protein L16, chloroplastic (AHRD V3.3 *-* Q332Q3_WHEAT)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR000114 (PRINTS): IPR036920 (G3	0,000	0,000	0,025	0,072	0,023									
Solyc08g074705	tubulin-tyrosine ligase (AHRD V3.3 --* AT3G18535.3)		F:GO:0005524	F:ATP binding				0,477	0,612	0,424	3,084	1,543					2,861	0,000			up
Solyc08g074710	LOW QUALITY:DNA repair protein rhp54 (AHRD V3.3 --* M8CMQ9_AEGTA)		F:GO:0005524	F:ATP binding			mobidb-lite (MOBIDB_LITE): PTHR107	0,019	0,055	0,050	0,097	0,024									
Solyc08g074715	Ripening related protein family (AHRD V3.3 *** A0A072TPZ5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR036908 (G3DSA:2.40.40.GENE3D	0,000	0,021	0,365	0,290	0,355									
Solyc08g074720	LOW QUALITY:Late embryogenesis abundant protein (AHRD V3.3 *** A0A075C704_9CARY)		C:GO:0005739	C:mitochondrion			IPR004926 (PFAM): mobidb-lite (MOB	0,000	0,000	0,215	0,148	0,119									
Solyc08g074730	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4CMJ1_SOLLC)		F:GO:0003950: P:G(	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosyltr	G3DSA:3.90.228.10 (GENE3D): IPR0	2,392	2,986	1,324	1,249	2,190									
Solyc08g074740	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4CMJ2_SOLLC)		F:GO:0003950: P:G(	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosyltr	IPR003034 (PFAM): IPR036930 (G3D	4,655	7,265	2,428	2,146	1,747									
Solyc08g074750	Zinc finger, C2H2 (AHRD V3.3 *** A0A103XIU1_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR026939 (G3DSA:4.10.1050.GENE	94,449	75,138	109,714	94,575	94,501									
Solyc08g074755	DCL protein (DUF3223) (AHRD V3.3 --* AT1G45230.2)							2,369	2,300	1,566	2,059	1,857									
Solyc08g074760	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9Q349_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:1.10.510.10 (GENE3D): G3DS	81,855	90,084	62,059	68,281	60,206									
Solyc08g074780	SH3 domain-containing protein (AHRD V3.3 *** AT4G34660.1)		F:GO:0005515	F:protein binding			IPR027267 (G3DSA:1.20.1270.GENE	7,596	7,200	9,319	10,584	9,516									
Solyc08g074790	Eukaryotic translation initiation factor 3 subunit G (AHRD V3.3 *** K4CMJ7_SOLLC)		F:GO:0003743: C:G(	F:translation initiation factor activity; C:eukaryotic translation in			IPR024675 (PFAM): PIRSF037949 (P	85,764	96,056	99,263	80,353	81,703									
Solyc08g074800	F-box/RNI/FBD-like domain protein (AHRD V3.3 --* G7I7L3_MEDTR)						PTHR44451:SF2 (PANTHER): PTHR4	11,925	9,793	7,476	9,588	9,013									
Solyc08g074830	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR006566 (PFAM): IPR032675 (G3D	11,054	9,791	14,093	15,221	13,576									
Solyc08g074835	F-box protein (AHRD V3.3 --* A0A0B2R4T3_GLYSO)						PTHR44451:SF2 (PANTHER): PTHR4	0,000	0,018	0,310	0,346	0,285									
Solyc08g074855	BZIP transcription factor family protein (AHRD V3.3 *-* D7LGH5_ARALL)		F:GO:0003677: C:G(	F:DNA binding; C:endoplasmic reticulum; P:response to stress;			PTHR37616 (PANTHER)	0,021	0,041	0,000	0,025	0,024									
Solyc08g074860	Eukaryotic translation initiation factor 3 subunit G (AHRD V3.3 *-* M1CY77_SOLTU)		F:GO:0003700: F:G(	F:DNA-binding transcription factor activity; F:translation initiatio			IPR012677 (G3DS bZIP	0,000	0,118	0,000	0,000	0,023									
Solyc08g074865	GATA transcription factor-like protein (AHRD V3.3 --* A0A0X7YHI0_SOLTU)							1,916	1,508	0,801	0,367	0,306									
Solyc08g074870	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)						IPR025521 (PFAM): IPR004314 (PFA	0,474	0,406	0,284	0,236	0,823									
Solyc08g074883	CURVATURE THYLAKOID protein (AHRD V3.3 --* AT1G52220.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,188	0,532	1,407	1,260	1,086									
Solyc08g074887	F-box/FBD/LRR protein (AHRD V3.3 --* A0A072V7K4_MEDTR)						PTHR44451:SF2 (PANTHER): PTHR4	2,551	2,302	2,350	2,595	2,884									
Solyc08g074890	U6 snRNA phosphodiesterase (AHRD V3.3 --* A0A0D2PGE3_GOSRA)							3,051	3,753	1,839	2,222	2,805									
Solyc08g074893	HSP20-like chaperones superfamily protein (AHRD V3.3 --* AT1G76780.3)						mobidb-lite (MOBIDB_LITE)	0,490	0,574	0,211	0,484	0,283									
Solyc08g074897	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** G7I7L0_MEDTR)						IPR032675 (G3DSA:3.80.10.GENE3D	3,592	4,611	2,857	4,111	3,743									
Solyc08g074910	F-box/FBD/LRR-repeat protein (AHRD V3.3 --* A0A0H4TD52_MOMCH)							0,993	1,310	0,811	1,294	1,343									
Solyc08g074920	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT5G33340.1)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	0,021	0,000	0,000	0,000	0,000									
Solyc08g074930	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061EZ29_THECC)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	0,019	0,097	0,000	0,000	0,000									
Solyc08g074940	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G64830.1)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032861 (PF	38,058	70,237	27,139	36,012	28,857									
Solyc08g074960	Major facilitator superfamily protein (AHRD V3.3 *** AT5G45275.1)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM): G3DSA:1.20.125	1,068	0,954	0,686	1,253	1,151									
Solyc08g074970	LOW QUALITY:Glycosyltransferase family protein (AHRD V3.3 *** G7L745_MEDTR)		C:GO:0016021: F:G(	C:integral component of membrane; F:transferase activity, trans			IPR028098 (PFAM): G3DSA:3.40.50.2	1,593	1,437	0,739	0,800	0,783									
Solyc08g074980	Kinase family protein (AHRD V3.3 *** B9H049_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRS	0,019	0,000	0,000	0,025	0,000									
Solyc08g074990	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): IPR004963 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc08g075000	(+)-neomenthol dehydrogenase (AHRD V3.3 --* MNR1_CAPAN)							0,399	0,460	0,553	0,661	0,330									
Solyc08g075010	Carbon catabolite repressor protein 4 like 4 (AHRD V3.3 *** A0A0B2PWB3_GLYSO)						IPR005135 (PFAM): IPR036691 (G3D	3,921	3,689	6,856	6,376	6,865									
Solyc08g075013	F-box/FBD-like domains containing protein (AHRD V3.3 --* AT5G38565.1)							0,969	1,156	1,247	1,396	1,366									
Solyc08g075017	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_AMBTC)							0,163	0,136	0,121	0,243	0,260									

Solyc08g075020	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): PTHR21562:SF4	10,251	11,089	109,091	156,609	141,287					0,525	0,003			up
Solyc08g075060	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): PTHR21562:SF4	0,042	0,058	0,000	0,025	0,000									
Solyc08g075070	Profilin family protein (AHRD V3.3 *** A0A061G6B4_THECC)						G3DSA:3.30.450.30 (GENE3D): IPR0	3,489	3,982	3,936	3,268	3,648									
Solyc08g075080	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GED0_THECC)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	12,324	5,273	0,115	0,189	0,094	-1,190	0,023					down		
Solyc08g075090	bHLH transcription factor144		P:GO:0000463; F:G	P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU			IPR005998 (TIGRI bHLH	106,796	115,879	85,874	74,817	80,708									
Solyc08g075100	initiation factor 4F subunit (DUF1350) (AHRD V3.3 *** AT3G43540.1)						IPR010765 (PFAM): PTHR34127:SF1	16,052	16,888	31,056	29,405	35,896									
Solyc08g075120	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9S1Q7_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			IPR005512 (PFAM): G3DSA:1.20.58.2	19,880	17,945	8,881	9,462	9,477									
Solyc08g075140	LOW QUALITY:BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): PTHR23272:SF3	0,000	0,019	0,000	0,000	0,000									
Solyc08g075150	Coiled-coil domain-containing 73 (AHRD V3.3 *** A0A0B0NIE5_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR36073 (PANTHER)	23,398	14,844	10,241	14,674	14,358									
Solyc08g075160	Bifunctional purine biosynthesis protein PurH (AHRD V3.3 *** A0A0B2PXS6_GLYSO)		F:GO:0003937; F:G	F:IMP cyclohydrola: EC:3.5.4.1; EC:2.1.2 IMP cyclohydrolase;			IPR024051 (G3DSA:3.40.140.GENE3	37,776	47,318	38,195	33,496	40,248									
Solyc08g075165	Cytochrome P450 (AHRD V3.3 *** S4UX03_SALMI)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR036396 (G3	0,101	0,138	0,191	0,122	0,070									
Solyc08g075190	LOW QUALITY:C2 and GRAM domain-containing protein At1g03370 (AHRD V3.3 --* C2GR1_ARATH)							0,869	0,589	0,619	0,943	0,727									
Solyc08g075200	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *-* A0A061E8W4_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	0,165	0,099	0,046	0,050	0,116									
Solyc08g075210	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G30280.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM): IPR023213 (G3D	58,411	59,229	133,683	86,602	111,751					-0,623	0,001			down
Solyc08g075230	LOW QUALITY:Late embryogenesis abundant (LEA)hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane			PTHR31852 (PANTHER): PTHR31852	1,663	1,541	0,498	0,597	0,399									
Solyc08g075240	Long-chain-alcohol oxidase (AHRD V3.3 *** K4CMP1_SOLLC)		F:GO:0046577; F:G	F:long-chain-alcoho	EC:1.1.3.2	Long-chain-alcohol o	IPR012400 (PIRSF): IPR036188 (G3D	3,193	2,163	0,046	0,050	0,070									
Solyc08g075250	Long-chain-alcohol oxidase (AHRD V3.3 *-* K4CMP1_SOLLC)		F:GO:0016614; F:G	F:oxidoreductase activity, acting on CH-OH group of donors; F:			IPR000172 (PFAM): IPR036188 (G3D	0,141	0,134	0,000	0,025	0,023									
Solyc08g075260	Long-chain-alcohol oxidase (AHRD V3.3 *-* A0A0V0IT17_SOLCH)		F:GO:0016614; F:G	F:oxidoreductase activity, acting on CH-OH group of donors; F:			IPR036188 (G3DSA:3.50.50.GENE3D	0,122	0,170	0,044	0,000	0,047									
Solyc08g075270	Long-chain-alcohol oxidase (AHRD V3.3 *-* K4CMP1_SOLLC)		F:GO:0016614; P:G	F:oxidoreductase activity, acting on CH-OH group of donors; P:			IPR036188 (G3DSA:3.50.50.GENE3D	0,199	0,097	0,044	0,025	0,024									
Solyc08g075280	Structural constituent of ribosome protein (AHRD V3.3 *** A0A072UL21_MEDTR)		C:GO:0009941; C:G	C:chloroplast envelope; C:integral component of membrane			IPR005134 (PFAM): PTHR31721 (PAN	35,142	22,783	96,856	63,356	81,829	-0,595	0,040			-0,609	0,000	down		down
Solyc08g075290	chitin synthase, putative (DUF1218) (AHRD V3.3 *** AT1G31720.2)		P:GO:0009808; C:G	P:lignin metabolic process; C:integral component of membrane			IPR009606 (PFAM): PTHR31769 (PAN	0,117	0,195	0,265	0,097	0,378									
Solyc08g075300	Decapping 5-like, putative isoform 5 (AHRD V3.3 *** A0A061GEA8_THECC)		C:GO:0016020; C:G	C:membrane; C:integral component of membrane			IPR019050 (PFAM): G3DSA:2.30.30.1	2,300	1,404	3,801	3,813	3,597									
Solyc08g075310	AP-4 complex subunit epsilon (AHRD V3.3 *** W9S8A1_9ROSA)		P:GO:0006886; P:G	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR002553 (PFAM): IPR011989 (G3D	119,428	126,634	119,909	123,567	118,991									
Solyc08g075320	Cytochrome P450 family ABA 8'-hydroxylase (AHRD V3.3 *** G7L7U3_MEDTR)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,487	0,137	13,612	23,031	16,156					0,762	0,024			up
Solyc08g075340	Glycosyltransferase-like protein (AHRD V3.3 *** A0A0K9NR32_ZOSMR)		C:GO:0005794; P:G	C:Golgi apparatus; P:protein glycosylation; C:integral componer			IPR005069 (PFAM): PTHR10994 (PAN	105,148	104,059	101,004	91,584	96,219									
Solyc08g075350	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JUV7_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	1,255	1,377	0,788	0,890	0,962									
Solyc08g075353	Plant invertase/pectin methylesterase inhibitor superfamily (AHRD V3.3 --* AT4G02320.1)							0,019	0,000	0,000	0,000	0,000									
Solyc08g075357	NIMA-related serine/threonine kinase 1 (AHRD V3.3 --* AT1G54510.5)							0,077	0,000	0,000	0,000	0,000									
Solyc08g075360	ABC transporter family protein (AHRD V3.3 *** A0A097P9S2_HEVBR)	ABCE2	F:GO:0005524; F:G	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013283 (PRINTS): IPR017896 (PF	1,837	2,544	1,794	1,716	2,325									
Solyc08g075370	Glycine-rich protein A3 (AHRD V3.3 *** A0A151QUZ1_CAJCA)		C:GO:0005886	C:plasma membrane			IPR006031 (PFAM): mobidb-lite (MOB	99,459	170,977	75,731	77,162	92,644									
Solyc08g075380	F-box family protein (AHRD V3.3 *** A0A061G875_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	72,211	66,736	78,744	73,111	74,331									
Solyc08g075390	nudix hydrolase homolog 3 (AHRD V3.3 *** AT1G79690.2)	IDI1	F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D): IPR03	57,805	51,229	82,852	84,112	80,120									
Solyc08g075400	SWIb domain-containing protein (AHRD V3.3 *** Q6V9I4_SOLCH)		F:GO:0005515	F:protein binding			IPR003121 (PFAM): IPR036885 (G3D	10,747	9,271	13,061	13,182	13,401									
Solyc08g075410	Ribosomal protein L2 (AHRD V3.3 *** Q8VZZ7_SOLLC)		F:GO:0003723; F:G	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR014722 (G3DSA:2.30.30.GENE3D	1,705	2,780	2,574	2,027	2,176									
Solyc08g075420	Ribosomal protein L2 (AHRD V3.3 *-* Q8VZZ7_SOLLC)		F:GO:0003714; F:G	F:transcription corepressor activity; F:structural constituent of r			IPR041670 (PFAM): IPR014722 (G3D	81,357	51,004	59,152	50,779	51,215	-0,645	0,035					down		
Solyc08g075430	ABC transporter family protein (AHRD V3.3 *** U5GKR9_POPTR)	ABCG22	F:GO:0005524; C:G	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	27,413	19,969	43,275	33,650	35,606									
Solyc08g075440	Conserved oligomeric Golgi complex subunit 6 (AHRD V3.3 *** W9S8X8_9ROSA)		P:GO:0006891; C:G	P:intra-Golgi vesicle-mediated transport; C:Golgi transport comp			IPR010490 (PFAM): mobidb-lite (MOB	40,698	39,720	44,056	45,545	41,682									
Solyc08g075450	WAT1-related protein (AHRD V3.3 *** K4CMR2_SOLLC)		C:GO:0016021; F:G	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	0,587	1,252	0,866	0,860	0,895									
Solyc08g075460	WAT1-related protein (AHRD V3.3 *** K4CMR3_SOLLC)		C:GO:0016021; F:G	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	3,158	4,293	3,288	4,530	4,096									
Solyc08g075470	WAT1-related protein (AHRD V3.3 *** K4CMR4_SOLLC)		C:GO:0016021; F:G	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): PTHR31218:SF7	5,159	4,850	1,281	2,331	2,681			1,043	0,015				up	
Solyc08g075480	9-cis-epoxycarotenoid dioxygenase, putative (AHRD V3.3 *** B9S1S9_RICCO)		F:GO:0016702; P:G	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR004294 (PFAM): PTHR10543:SF4	0,019	0,041	0,022	0,000	0,000									
Solyc08g075490	9-cis-epoxycarotenoid dioxygenase, putative (AHRD V3.3 *** B9S1S9_RICCO)		F:GO:0016702; P:G	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR004294 (PFAM): PTHR10543:SF4	36,459	25,162	1,005	0,792	1,618									
Solyc08g075500	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2R3S8_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,861	2,639	2,709	2,024	2,919									
Solyc08g075510	JmjC domain-containing protein (AHRD V3.3 *** A0A103XFS1_CYNCS),Pfam:PF13621		F:GO:0016706; P:G	F:2-oxoglutarate-de	EC:1.14.11	Acting on paired donc	IPR041667 (PFAM): G3DSA:2.60.120	6,036	4,409	5,858	5,555	5,775									
Solyc08g075520	UPF0162 protein XF_1494 (AHRD V3.3 *-* A0A1D1XBY2_9ARAE)						IPR032698 (PFAM): PTHR31350:SF4	35,502	27,387	23,476	21,890	25,948									
Solyc08g075530	Alpha glucosidase-like protein (AHRD V3.3 *** Q93Y12_ARATH)		F:GO:0004553; P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:2.60.40.1760 (GENE3D): IPR	118,539	104,058	130,324	108,358	124,331									
Solyc08g075540	alternative oxidase 1au	1au	F:GO:0009916; P:G	F:alternative oxidas	EC:1.1.3	Acting on diphenols a	IPR002680 (PFAM): IPR038659 (G3D	20,206	61,170	38,924	72,025	47,385	1,618	0,019			0,890	0,000	up		up
Solyc08g075550	alternative oxidase 1au	aox1b	F:GO:0009916; P:G	F:alternative oxidas	EC:1.1.3	Acting on diphenols a	IPR002680 (PIRSF): IPR002680 (PFA	0,291	0,497	0,233	0,190	0,163									
Solyc08g075560	Unknown protein (AHRD V3.3)							0,844	1,968	0,906	2,013	1,391	1,243	0,045					up		
Solyc08g075570	Sodium:solute symporter family protein (AHRD V3.3 *** G7K6S1_MEDTR)		F:GO:0015204; C:G	F:urea transmembrane transporter activity; C:integral componer			IPR001734 (PFAM): IPR031155 (PTH	1,158	0,449	0,190	0,098	0,071									
Solyc08g075580	DNA-directed RNA polymerase III subunit RPC6 (AHRD V3.3 *** A0A0B2Q204_GLYSO)		C:GO:0005666; P:G	C:RNA polymerase III complex; P:transcription by RNA polymera			IPR007832 (PFAM): IPR036388 (G3D	24,350	20,283	18,149	19,902	18,289									
Solyc08g075590	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CMS6_SOLLC)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc08g075610	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CMS8_SOLLC)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001611 (PFAM): IPR000719 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc08g075630	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)		F:GO:0005515; F:G	F:protein binding; F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	0,082	0,154	0,222	0,147	0,117									
Solyc08g075640	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)		F:GO:0005515; F:G	F:protein binding; F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	2,859	2,719	2,084	1,639	1,432									
Solyc08g075650	Formin-like protein (AHRD V3.3 *** K4CMT2_SOLLC)						IPR015425 (PFAM): G3DSA:1.20.58.2	36,075	27,408	25,352	22,886	25,590									
Solyc08g075670	Formin-like protein (AHRD V3.3 *-* A0A068UF08_COFCA)						IPR014020 (PFAM): G3DSA:2.60.40.1	21,450	14,286	12,161	13,035	13,628									
Solyc08g075680	Ribonuclease P protein subunit P38, related protein (AHRD V3.3 *** G7K6S6_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,734	2,168	0,656	0,682	0,519									
Solyc08g075690	Acyl-CoA-binding protein (AHRD V3.3 *** K7WVA0_SOLTU)		F:GO:0000062	F:fatty-acyl-CoA binding			IPR000582 (PRINTS): IPR014352 (G3	372,249	329,997	412,457	379,084	371,474									
Solyc08g075700	60S ribosomal protein L13 (AHRD V3.3 *** K4CMT7_SOLLC)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001380 (PFAM): PTHR11722:SF3	250,113	287,634	253,915	217,287	227,490									
Solyc08g075705	thioredoxin Y2 (AHRD V3.3 --* AT1G43560.1)							0,061	0,085	0,025	0,095	0,047									
Solyc08g075710	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)		C:GO:0016020; F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1740.10 (GENE3D): IPR	24,349	27,389	28,918	31,773	28,786									
Solyc08g075720	30S ribosomal protein S11 (AHRD V3.3 *-* A0A0B2QWJ9_GLYSO)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001971 (PFAM): IPR036967 (G3D	20,074	22,434	39,669	34,587	33,814									
Solyc08g075730	Anamorsin homolog (AHRD V3.3 *** K4CMU0_SOLLC)		C:GO:0005737; P:G	C:cytoplasm; P:iron-sulfur cluster assembly; F:iron-sulfur cluster			G3DSA:3.40.50.150 (GENE3D): IPR0	59,222	61,016	115,617	107,747	105,695									
Solyc08g075740	LOW QUALITY:male gametophyte defective 3 (AHRD V3.3 --* AT1G68990.2)							0,938	1,071	0,710	0,587	0,762									
Solyc08g075750	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4CMU2_SOLLC)		F:GO:0004252; P:G	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): G3DSA:3.90.22	28,660	38,954	138,197	171,791	153,261									
Solyc08g075760	CYCLOPS/IPD3-like protein		C:GO:0005634; P:G	C:nucleus; P:arbuscular mycorrhizal association; F:sequence-s			mobidb-lite (MOBIDB_LITE): mobidb-lit	11,608	6,343	4,358	2,975	4,328	-0,840	0,021					down		
Solyc08g075770	exopolysaccharide production negative regulator (AHRD V3.3 *** AT4G19140.1)		C:GO:0016021	C:integral component of membrane			PTHR36779 (PANTHER)	11,107	9,405	15,102	14,998	14,033									
Solyc08g075780	Ubiquitin-fold modifier 1 (AHRD V3.3 *** K4CMU5_SOLLC)		C:GO:0005634; C:G	C:nucleus; C:cytoplasm; P:protein K69-linked ufmylation			G3DSA:3.10.20.90 (GENE3D): IPR00	21,037	18,356	40,908	44,096	38,720									
Solyc08g075790	Vacuolar sorting-associated protein 62 (AHRD V3.3 *** A0A0B0MX79_GOSAR)						IPR009291 (PFAM): PTHR42656 (PAN	0,118	0,435	0,050	0,075	0,069									
Solyc08g075800	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** B9H5H2_POPTR)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): IPR025110 (PFA	9,129	4,250	2,453	3,829	2,063									
Solyc08g075810	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** B9H5H2_POPTR)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.40.50.1	13,930	12,938	39,076	43,217	35,336									
Solyc08g075820	RNA-dependent RNA polymerase6b	RDR6b	F:GO:0003676; F:G	F:nucleic acid bindi	EC:2.7.7.48	RNA-directed RNA pc	IPR012677 (G3DSA:3.30.70.GENE3D	0,255	0,254	0,330	0,589	0,497									
Solyc08g075825	RNA-dependent RNA polymerase (AHRD V3.3 *** K4CMU9_SOLLC)		F:GO:0003968	F:RNA-directed 5'-3	EC:2.7.7.48	RNA-directed RNA pc	IPR007855 (PFAM): IPR007855 (PAN	1,401	1,009	1,074	0,976	0,894									
Solyc08g075850	50S ribosomal protein L24 (AHRD V3.3 *** W9QWA0_9ROSA)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR003256 (PFAM): IPR005824 (PFA	20,865	21,870	31,011	27,576	27,687									
Solyc08g075860	zinc finger B-box protein (AHRD V3.3 *** AT5G45410.5)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	192,278	238,125	227,201	227,376	250,974									
Solyc08g075870	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G19120.2)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	496,657	656,000	474,378	447,787	450,315									
Solyc08g075880	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT2G18196.1)		P:GO:0030001; F:G	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0	9,753	11,032	0,830	0,300	0,492									
Solyc08g075890	MAP kinase (AHRD V3.3 *** I7ENF6_TOBAC)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	149,560	152,480	210,190	209,530	204,760									
Solyc08g075900	LOW QUALITY:B3 domain-containing protein (AHRD V3.3 *-* A0A0B2NQY0_GLYSO)		F:GO:0003677	F:DNA binding			IPR015300 (G3DSA:2.40.330.GENE3	0,019	0,000	0,000	0,000	0,000									
Solyc08g075910	RING/U-box superfamily protein (AHRD V3.3 *** AT3G56580.3)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR001841 (PFAM): IPR039525 (PFA	15,112	13,010	9,849	7,168	9,511									
Solyc08g075920	Protein BREVIS RADIX (AHRD V3.3 *** A0A0B2R5Q1_GLYSO)						IPR027988 (PFAM): IPR013591 (PFA	2,055	2,620	0,090	0,116	0,093									
Solyc08g075925	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT1G08260.2)							0,080	0,043	0,000	0,000	0,000									
Solyc08g075930	Kinesin-like protein (AHRD V3.3 *-* G7K6T5_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,184	1,853	1,662	1,466	1,336									
Solyc08g075940	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** K4CMW1_SOLLC)		F:GO:0003677; F:G	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR037033 (G3DSA:2.40.270.GENE3	52,966	37,347	21,027	22,402	31,223			0,567	0,004				up	
Solyc08g075950	Growth-regulating factor (AHRD V3.3 *** A0A072TW62_MEDTR)		F:GO:0005524; C:G	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-tem			IPR014977 (PFAM GRF	1,726	2,600	0,870	1,010	0,562									
Solyc08g075960	MOB kinase activator-like 1A (AHRD V3.3 *** MOB1A_ARATH)		C:GO:0005634; C:G	C:nucleus; C:early endosome; C:trans-Golgi network; C:plasma			IPR036703 (G3DSA:1.20.140.GENE3	120,840	116,943	98,646	108,114	102,380									
Solyc08g075970	Transmembrane protein 45B (AHRD V3.3 *** A0A151THE3_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR006904 (PFAM): PTHR16007:SF4	23,704	24,493	79,522	91,394	76,242									
Solyc08g075980	LOW QUALITY:NBS-LRR resistance protein (AHRD V3.3 *-* B6E013_SOLBU)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,000	0,021	0,101	0,050	0,024									
Solyc08g075990	LOW PSII ACCUMULATION protein (DUF1995) (AHRD V3.3 *** AT5G48790.1)		C:GO:0009507; P:G	C:chloroplast; P:photosystem II assembly			IPR018962 (PFAM): PTHR34051:SF1	4,982	6,683	4,059	3,787	5,201									
Solyc08g076000	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)		F:GO:0005515; F:G	F:protein binding; F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	2,019	1,704	1,306	2,215	1,816									
Solyc08g076010	Myb family transcription factor family protein (AHRD V3.3 *** B9GZU3_POPTR)		F:GO:0003677	F:DNA binding			IPR025756 (PFAM G2-like	1,456	1,423	1,042	1,563	1,082									
Solyc08g076020	COBW domain-containing protein 2 (AHRD V3.3 *** A0A1D1YXT1_9ARAE)						G3DSA:3.40.50.300 (GENE3D): IPR0	13,985	14,412	16,212	15,375	15,359									
Solyc08g076025	Tudor/PWWP/MBT superfamily protein (AHRD V3.3 *** G7K6J4_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,618	0,925	0,552	0,481	0,727									
Solyc08g076030	TOPLESS 2	TPL2	F:GO:0005515; P:G	F:protein binding; P:regulation of transcription, DNA-templated			IPR001680 (PFAM): IPR015943 (G3D	69,503	67,584	54,538	60,966	61,243									
Solyc08g076040	5'-AMP-activated protein kinase subunit gamma-3, putative (AHRD V3.3 *** A0A061GE25_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,100	0,060	0,000	0,050	0,023									
Solyc08g076050	Serine/Threonine kinase family protein (AHRD V3.3 *** G7L990_MEDTR)		F:GO:0004674; F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): IPR0	0,928	2,712	2,478	5,000	4,818			0,954	0,003	1,009	0,002		up	up
Solyc08g076060	Serine/Threonine kinase family protein (AHRD V3.3 *** G7L990_MEDTR)		F:GO:0004674; F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): IPR0	126,638	83,060	48,511	52,413	59,393	-0,581	0,032					down		
Solyc08g076080	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CMX5_SOLLC)		F:GO:0004553; C:G	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	G3DSA:2.60.120.200 (GENE3D): IPR	0,142	0,229	2,442	4,087	2,356									
Solyc08g076090	UV-B-induced protein, chloroplastic (AHRD V3.3 *** A0A199W567_ANACO)						IPR008479 (PFAM): PTHR31808:SF6	10,964	13,102	67,272	62,812	68,017									
Solyc08g076100	GBF9G-box binding	gbf9	F:GO:0003700; P:G	F:DNA-binding transcription factor activity; P:regulation of transc			IPR012900 (PFAM bZIP	29,448	32,017	40,092	42,162	37,873									
Solyc08g076120	MIP18 family protein (AHRD V3.3 *** A0A0B2S844_GLYSO)		P:GO:0106035	P:protein maturation by [4Fe-4S] cluster transfer			IPR002744 (PFAM): IPR034904 (G3D	1,472	1,810	2,685	2,136	2,139									
Solyc08g076130	E2F/DP family winged-helix DNA-binding domain-containing protein (AHRD V3.3 *** AT4G19003.6)		C:GO:0000814; P:G	C:ESCRT II complex; P:multivesicular body sorting pathway			IPR036388 (G3DSA:1.10.10.GENE3D	14,120	14,427	25,027	22,294	21,441									
Solyc08g076140	Phosphomevalonate kinase (AHRD V3.3 *** A9YZY5_9BORA)		F:GO:0004631; F:G	F:phosphomevalona	EC:2.7.4.2	Phosphomevalonate	IPR013750 (PFAM): IPR006204 (PFA	25,693	28,783	43,068	41,771	40,113									
Solyc08g076150	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5GMW9_POPTR)		F:GO:0005515; F:G	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (PFA	0,019	0,077	0,000	0,050	0,024									
Solyc08g076160	Guanine nucleotide-binding protein alpha-2 subunit (AHRD V3.3 *** W9S534_9ROSA)		F:GO:0003924; P:G	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR001019 (PRINTS): IPR011025 (G3	48,048	42,723	73,252	69,367	70,988									
Solyc08g076170	LOW QUALITY:50S ribosomal protein L22, chloroplastic (AHRD V3.3 -** RK22_CHLAT)							0,957	1,671	0,071	0,144	0,094									
Solyc08g076180	Cystic fibrosis transmembrane conductance regulator (AHRD V3.3 *** A0A0B0NAP2_GOSAR)						PTHR34196 (PANTHER): PTHR34196	14,169	10,898	17,809	16,737	15,461									
Solyc08g076190	Dimerizations, putative (AHRD V3.3 *** A0A061GE03_THECC)						PTHR35761 (PANTHER)	0,476	0,611	0,069	0,122	0,163									
Solyc08g076200	RNA helicase DEAD27	DEAD27	F:GO:0003676; F:G	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	146,659	131,876	120,088	118,281	111,859									
Solyc08g076210	Secretory carrier-associated membrane protein (AHRD V3.3 *** G7K9I4_MEDTR)		P:GO:0015031; C:G	P:protein transport; C:integral component of membrane			IPR007273 (PFAM): PTHR10687:SF1	36,891	43,547	25,342	24,046	24,633									
Solyc08g076220	Phosphoribulokinase (AHRD V3.3 *** K4CMY9_SOLLC)		F:GO:0005524; P:G	F:ATP binding; P:ca	EC:2.7.1.19	Phosphoribulokinase	IPR006082 (PRINTS): IPR006083 (PF	141,901	342,930	39,578	55,612	144,924	1,301	0,000	1,869	0,000			up	up	
Solyc08g076230	GAGA-binding transcriptional activator (AHRD V3.3 *** H1ZN90_SOLLC)		F:GO:0003700; C:G	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR010409 (PFAM BBR-BPC	10,326	6,561	7,107	8,196	6,917									
Solyc08g076250	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	21,240	11,677	0,124	0,048	0,000									
Solyc08g076253	Cytochrome P450 (AHRD V3.3 *-* Q9M7M3_CAPAN)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PFAM): IPR036396 (G3D	0,728	0,238	0,046	0,047	0,000									
Solyc08g076257	Cytochrome P450 (AHRD V3.3 *-* A0A103XWG4_CYNCS)		F:GO:0005506; F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR036396 (G3	2,237	0,934	0,140	0,120	0,261									
Solyc08g076290	Inner membrane yohK (AHRD V3.3 *** A0A0B0N2P7_GOSAR)		P:GO:0009658; C:G	P:chloroplast organization; C:chloroplast inner membrane; P:res			IPR007300 (PFAM): PTHR30249:SF0	2,959	11,769	0,653	0,654	0,682	2,016	0,003					up		
Solyc08g076300	4-coumarate--CoA ligase family protein (AHRD V3.3 *** B9GZT7_POPTR)	4CL	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.40.50.1	6,388	7,464	12,351	10,748	10,230									
Solyc08g076310	ERD (Early-responsive to dehydration stress) family protein (AHRD V3.3 *** G7K880_MEDTR)		C:GO:0016020	C:membrane			IPR027815 (PFAM): IPR003864 (PFA	19,402	18,643	14,961	14,148	14,713									
Solyc08g076320	Cellulose synthase (AHRD V3.3 *** A0A118JX74_CYNCS)		C:GO:0016020; F:G	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR013083 (G3DSA:3.30.40.GENE3D	202,655	132,575	145,243	217,225	176,371	-0,586	0,034			0,583	0,000	down		up
Solyc08g076335	40S ribosomal S30-like protein (AHRD V3.3 *** G7JW33_MEDTR)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR006846 (PFAM): mobidb-lite (MOB	0,019	0,041	0,000	0,000	0,000									
Solyc08g076340	40S ribosomal protein S30 (AHRD V3.3 *** W9QWZ6_9ROSA)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR006846 (PFAM): mobidb-lite (MOB	10,014	11,606	10,438	9,146	8,186									
Solyc08g076350	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G32190.1)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,311	0,696	0,050	0,047	0,070									
Solyc08g076360	gamma-tocopherol methyltransferase	VTE4	F:GO:0008168; P:G	F:methyltransferase activity; P:methylation			IPR013216 (PFAM): G3DSA:3.40.50.1	22,843	32,522	31,611	33,165	43,737	0,537	0,037	0,465	0,003			up	up	
Solyc08g076370	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GZI9_POPTR)		F:GO:0003677; F:G	F:DNA binding; F:lipid binding			IPR002913 (PFAM HD-ZIP	0,588	0,970	0,022	0,076	0,023									
Solyc08g076390	Lysine-specific demethylase (AHRD V3.3 *** A0A199VZ18_ANACO)		P:GO:0006338; F:G	P:chromatin remodeling; F:methyltransferase activity; P:methyla			G3DSA:2.60.120.650 (GENE3D): IPR	106,501	109,160	40,003	65,074	64,715			0,691	0,029	0,703	0,016		up	up
Solyc08g076400	Myb family transcription factor family protein (AHRD V3.3 *** U5GMY7_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	1,784	1,681	2,293	3,137	2,238									
Solyc08g076410	Shikimate kinase (AHRD V3.3 *** A0A151RA83_CAJCA)		F:GO:0000287; F:G	F:magnesium ion bi	EC:2.7.1.71	Shikimate kinase	G3DSA:3.40.50.300 (GENE3D): IPR0	7,066	6,431	5,584	6,764	7,733									
Solyc08g076420	Poly [ADP-ribose] polymerase (AHRD V3.3 *** A0A0V0IXP4_SOLCH)		F:GO:0003950	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylt	G3DSA:3.90.228.10 (GENE3D): IPR0	136,808	169,719	90,084	101,316	92,442									
Solyc08g076430	Survival motor neuron (AHRD V3.3 *** A0A0B0NST2_GOSAR)		C:GO:0005634	C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,265	6,199	8,164	7,891	6,643									
Solyc08g076440	Programmed cell death protein 2 (AHRD V3.3 *** A0A0B0NZT2_GOSAR)		C:GO:0005737	C:cytoplasm			IPR002893 (PFAM): G3DSA:3.30.60.1	20,007	24,910	19,713	18,018	19,116									
Solyc08g076450	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G32220.1)		F:GO:0003954; C:G	F:NADH dehydroge	EC:1.6.99.3	NADH dehydrogenas	IPR016040 (PFAM): G3DSA:3.40.50.7	49,815	64,399	126,700	106,610	131,659									
Solyc08g076460	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 (AHRD V3.3 *** DAD1_SOLL		F:GO:0004579; C:G	F:dolichyl-diphosph	EC:2.4.1.119	Glycosyltransferases	IPR003038 (PFAM): IPR003038 (PIRS	42,840	42,206	43,950	44,482	39,074									
Solyc08g076470	glycerol-3-phosphate acyltransferase	gpat	F:GO:0004366; P:G	F:glycerol-3-phosph	EC:2.3.1.15	Glycerol-3-phosphate	IPR023083 (PFAM): IPR016222 (PIRS	14,707	29,611	25,512	25,857	34,412	1,035	0,000	0,427	0,036			up	up	
Solyc08g076480	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT2G35490.1)						IPR006843 (PFAM): mobidb-lite (MOB	178,560	202,319	223,374	162,779	246,173					-0,453	0,007			down
Solyc08g076490	LOW QUALITY:MAP kinase kinase kinase 64	MAPKKK64	F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	1,716	2,202	1,155	1,473	1,268									
Solyc08g076497	RNAse E/G-like protein (AHRD V3.3 --* AT2G04270.9)							1,326	1,328	0,318	0,514	0,257									
Solyc08g076500	LOW QUALITY:proline iminopeptidase (AHRD V3.3 --* AT2G14260.4)							0,000	0,000	0,025	0,000	0,000									
Solyc08g076510	envelope glycoprotein (AHRD V3.3 *** AT1G32260.1)						mobidb-lite (MOBIDB_LITE): PTHR359	12,929	11,265	21,477	21,173	20,308									
Solyc08g076520	Transmembrane protein, putative (AHRD V3.3 *** G7KCF0_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35297 (PANTHER): PTHR35297	11,956	6,827	0,576	0,688	1,055	-0,779	0,025					down		
Solyc08g076530	RNA-binding family protein isoform 1 (AHRD V3.3 *** A0A061G6K6_THECC)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	17,004	17,764	5,921	6,311	6,700									

Solyc08g076540	Syntaxin-like protein (AHRD V3.3 *** Q3HRZ4_SOLTU)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			G3DSA:1.20.58.70 (GENE3D): IPR00	135,026	131,059	131,501	134,877	121,949									
Solyc08g076550	Phosphomannomutase (AHRD V3.3 *** K4CN17_SOLLC)		F:GO:0004615; C:G(	F:phosphomannomu	EC:5.4.2.8	Phosphomannomutas	IPR005002 (PFAM): IPR023214 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc08g076570	Phosphatidylinositol-glycan biosynthesis class X protein, putative (AHRD V3.3 *** A0A061GDT5_THECC)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:GPI anchor biosynthetic			IPR013233 (PFAM): IPR040039 (PAN	5,797	5,243	5,544	6,359	5,820									
Solyc08g076580	valine-tRNA ligase (AHRD V3.3 *** AT1G32310.1)		F:GO:0010997; P:G(	F:anaphase-promoting complex binding; P:negative regulation o			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,571	3,789	3,455	2,689	3,221									
Solyc08g076590	SolycHsfA1c	HSF-15	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRINT HSF	1,801	2,184	1,526	1,495	1,915									
Solyc08g076610	Cell cycle checkpoint protein RAD1 (AHRD V3.3 *-* W9RDU4_9ROSA)		P:GO:0000077; C:G(	P:DNA damage checkpoint; C:nucleus			IPR003021 (PFAM): G3DSA:3.70.10.1	2,790	2,093	0,762	0,739	0,963									
Solyc08g076620	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03230.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032861 (PFAM): IPR032799 (PFA	2,888	5,398	0,000	0,000	0,000	0,928	0,046					up		
Solyc08g076645	heptahelical transmembrane protein2 (AHRD V3.3 --* AT4G30850.2)							0,357	0,301	0,365	0,538	0,330									
Solyc08g076650	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** Q2A970_BRAOL)		F:GO:0003824; P:G(	F:catalytic activity; P:trehalose biosynthetic process			G3DSA:3.40.50.2000 (GENE3D): IPR(	208,873	168,434	200,848	175,859	191,303									
Solyc08g076660	RNA-binding family protein, putative (AHRD V3.3 *** A0A061G5L3_THECC)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	32,033	30,327	36,842	33,840	32,543									
Solyc08g076670	SNARE associated Golgi protein family (AHRD V3.3 *** AT4G17790.1)		C:GO:0016021	C:integral component of membrane			IPR032816 (PFAM): PTHR43220:SF6	10,009	7,416	20,603	18,891	17,030									
Solyc08g076680	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9R9U2_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	14,458	12,287	11,887	13,188	11,790									
Solyc08g076685	homeobox-leucine zipper protein ATHB-8 (AHRD V3.3 --* AT4G32880.1)							2,044	1,157	1,453	1,745	1,797									
Solyc08g076690	high mobility group B2 (AHRD V3.3 --* AT1G20693.3)							9,004	8,461	8,757	7,494	7,620									
Solyc08g076720	ABC transporter B family-like protein (AHRD V3.3 *** G7KDP1_MEDTR)	ABCB13	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	98,678	60,523	6,647	7,656	9,141									
Solyc08g076730	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT4G17940.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	52,692	40,575	22,484	16,642	20,719									
Solyc08g076740	ER-based factor for assembly of V-ATPase (AHRD V3.3 *-* AT5G52980.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:vacuolar proton-transporting V-type ATPase complex assembly				3,736	3,413	5,675	5,816	4,575									
Solyc08g076760	LOW QUALITY:Retrotransposon protein, putative, Ty3-gypsy subclass (AHRD V3.3 --* Q339R7_ORYSJ)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3	0,257	0,080	0,190	0,169	0,143									
Solyc08g076770	ER-based factor for assembly of V-ATPase (AHRD V3.3 *** AT5G52980.1)		P:GO:0070072	P:vacuolar proton-transporting V-type ATPase complex assemb			IPR021013 (PANTHER)	14,744	13,363	23,059	25,701	22,643									
Solyc08g076780	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *-* B9S247_RICCO)	CCR	P:GO:0008152; F:G(	P:metabolic process; F:oxidoreductase activity, acting on the C			G3DSA:3.40.50.720 (GENE3D): PTHF	0,019	0,018	0,295	0,388	0,282									
Solyc08g076790	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *** B9S247_RICCO)	CCR	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	0,886	0,732	16,668	22,899	17,819					0,460	0,012			up
Solyc08g076800	LOW QUALITY:arginine/serine-rich splicing factor 35 (AHRD V3.3 --* AT4G25500.8)							0,084	0,099	2,726	3,101	2,041									
Solyc08g076810	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G17920.1)		P:GO:0006506; C:G(	P:GPI anchor biosynthetic process; C:integral component of me			G3DSA:3.40.50.720 (GENE3D): IPR0(	10,814	8,130	12,322	12,634	11,696									
Solyc08g076820	bHLH transcription factor146		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM bHLH	0,237	0,095	0,000	0,000	0,000									
Solyc08g076830	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GAA2_THECC)		C:GO:0016021; P:G(	C:integral component of membrane; P:protein ubiquitination			IPR013083 (G3DSA:3.30.40.GENE3D	8,360	4,316	29,719	17,947	20,817	-0,925	0,037			-0,722	0,000	down		down
Solyc08g076840	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G35410.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	12,076	13,775	18,070	18,863	19,399									
Solyc08g076850	Tetraspanin family protein (AHRD V3.3 *** AT5G46700.1)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	0,105	0,117	0,000	0,048	0,000									
Solyc08g076860	PLATZ transcription factor family protein (AHRD V3.3 *** G7KDS6_MEDTR)						IPR006734 (PFAM): mobidb-lite (MOB	110,648	111,733	114,726	99,507	92,322									
Solyc08g076870	LOW QUALITY:DUF740 family protein (AHRD V3.3 *** G7KDT4_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR341	3,447	2,415	1,910	1,493	1,955									
Solyc08g076880	Nodulin26-like intrinsic protein 31 (AHRD V3.3 --* K4C978_SOLLC)							62,386	57,193	71,509	51,787	63,399					-0,464	0,021			down
Solyc08g076885	Unknown protein (AHRD V3.3)						PR01228 (PRINTS): mobidb-lite (MOB	24,384	18,522	2,555	1,811	2,631									
Solyc08g076890	Glycine-rich cell wall structural protein 2 (AHRD V3.3 --* GRP2_ORYSI)							9,835	9,738	1,946	1,521	2,350									
Solyc08g076910	Ubiquitin carboxyl-terminal hydrolase-like protein (AHRD V3.3 *** G7KF27_MEDTR)		P:GO:0016579; F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D): IPR00	11,744	13,600	9,735	10,371	10,360									
Solyc08g076915	Serine-threonine protein kinase, plant-type, putative (AHRD V3.3 --* B9SHV6_RICCO)		F:GO:0003856; P:G(	F:3-dehydroquinate	EC:4.2.3.4	3-dehydroquinate syı	PTHR33563:SF3 (PANTHER): IPR002	0,019	0,043	0,068	0,148	0,140									
Solyc08g076920	Arf gtpase-activating protein, putative (AHRD V3.3 *** B9SNV8_RICCO)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR038508 (G3	67,711	70,872	88,783	89,259	80,352									
Solyc08g076930	jasmonic acid 3	Ja3	F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	274,998	115,845	121,638	232,512	129,526	-1,221	0,000			0,938	0,000	down		up
Solyc08g076950	Unknown protein (AHRD V3.3)							0,553	0,465	0,277	0,261	0,141									
Solyc08g076960	Abscisic acid receptor PYL1 (AHRD V3.3 *** M1BH64_SOLTU)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm			IPR019587 (PFAM): IPR023393 (G3D	2,472	1,330	2,924	2,701	2,020									
Solyc08g076970	Acetylornithine deacetylase (AHRD V3.3 *** ARGE_ARATH)		F:GO:0016787	F:hydrolase activity			IPR011650 (PFAM): IPR002933 (PFA	147,365	191,039	281,971	270,291	278,447									
Solyc08g076980	Acetylornithine deacetylase (AHRD V3.3 *** ARGE_ARATH)		F:GO:0016787	F:hydrolase activity			IPR011650 (PFAM): IPR002933 (PFA	0,042	0,037	0,807	0,215	0,356									
Solyc08g076990	Acetylornithine deacetylase (AHRD V3.3 *** ARGE_ARATH)		F:GO:0016787	F:hydrolase activity			IPR002933 (PFAM): G3DSA:3.40.630	58,236	57,164	91,638	85,923	83,668									
Solyc08g077000	LOW QUALITY:Zinc finger, C2H2 (AHRD V3.3 *** A0A103XFH7_CYNCS)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM): C2H2	0,000	0,018	0,000	0,000	0,000									
Solyc08g077010	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A0K9P144_ZOSMR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	0,019	0,018	0,000	0,000	0,023									
Solyc08g077020	Auxin responsive SAUR protein (AHRD V3.3 *** A0A118K7G8_CYNCS)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR35296:SF2	5,111	5,041	1,866	5,469	3,603					1,534	0,000			up
Solyc08g077030	AT hook motif DNA-binding family protein (AHRD V3.3 *** AT4G17950.1)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	22,390	30,004	22,343	19,945	20,030									
Solyc08g077040	phospholipid hydroperoxide glutathione peroxidase (AHRD V3.3 *** AT4G17960.1)						PTHR35750 (PANTHER)	10,162	11,599	12,792	13,111	11,414									
Solyc08g077050	Ferredoxin family protein (AHRD V3.3 *** B9N2P1_POPTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:iron-sulfur cluster binding			IPR001041 (PFAM): IPR012675 (G3D	30,550	45,699	35,978	40,166	47,785	0,609	0,017					up		
Solyc08g077060	Zinc finger, LSD1-type (AHRD V3.3 *** A0A103XQX8_CYNCS)		P:GO:0034051; P:G(	P:negative regulation of plant-type hypersensitive response; P:ı			IPR005735 (PFAM LSD	155,038	162,379	13,674	4,255	14,617					-1,681	0,000			down
Solyc08g077070	Protein NAP1 (AHRD V3.3 --* NCKP1_ARATH)							0,795	0,683	0,605	0,453	0,565									
Solyc08g077080	Glycosyltransferase (AHRD V3.3 *** E5L3R9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,098	0,138	0,050	0,047	0,117									
Solyc08g077090	Eyes absent-like protein (AHRD V3.3 *** A0A097PQS8_SOLLC)		F:GO:0004725; P:G(	F:protein tyrosine p	EC:3.1.3.16; EC:3.1.	Protein-serine/threor	IPR038102 (G3DSA:3.40.50.GENE3D	8,990	9,046	11,967	11,683	11,612									
Solyc08g077100	RING/U-box superfamily protein (AHRD V3.3 *** AT2G35330.2)						IPR013083 (G3DSA:3.30.40.GENE3D	8,833	10,657	0,594	0,481	0,518									
Solyc08g077110	NAC domain protein, (AHRD V3.3 *** A0A061GAH7_THECC)	NAC079	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	2,752	14,504	3,642	3,008	3,908	2,422	0,000					up		
Solyc08g077150	Protein phosphatase 2C (AHRD V3.3 *** A0A124SBW4_CYNCS)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): PTHR13832:SF2	33,149	31,885	39,011	37,594	35,293									
Solyc08g077170	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	1,452	1,351	0,072	0,050	0,000									
Solyc08g077180	Pyruvate kinase (AHRD V3.3 *** K4CN78_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS): IPR015806 (G3	56,027	56,744	65,480	59,797	54,520									
Solyc08g077190	LOW QUALITY:MATE efflux family protein (AHRD V3.3 --* AT4G38380.5)							0,518	0,681	0,671	0,576	0,776									
Solyc08g077200	Ribose-phosphate pyrophosphokinase (AHRD V3.3 *** G7JHM7_MEDTR)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	IPR005946 (PFAM): IPR005946 (TIGF	9,020	9,596	15,797	17,272	17,316									
Solyc08g077210	inositol-1,4,5-triphosphate-5-phosphatase 1	5pt1	F:GO:0004439; F:G(	F:phosphatidylinosit	EC:3.1.3.36	Phosphoinositide 5-p	IPR036691 (G3DSA:3.60.10.GENE3D	67,435	61,385	18,054	25,609	31,407			0,793	0,000				up	
Solyc08g077220	Tetraspanin family protein (AHRD V3.3 *** A0A072UPD9_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR018499 (PFAM): mobidb-lite (MOB	99,819	97,407	117,194	113,480	110,046									
Solyc08g077230	two-component response regulator-like APRR2-like	APRR2-LIKE	P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:DNA binding			IPR001789 (PFAM ARR-B	6,444	10,721	40,291	72,268	49,026	0,761	0,042			0,847	0,000	up		up
Solyc08g077240	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G18030.1)		F:GO:0008168	F:methyltransferase activity			IPR004159 (PFAM): G3DSA:3.40.50.1	581,536	478,771	272,787	218,415	267,842									
Solyc08g077250	Inner nuclear membrane Man1 (AHRD V3.3 *** A0A0B0P5D6_GOSAR)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			G3DSA:1.10.10.1180 (GENE3D): IPR(	16,834	13,570	22,404	24,106	20,397									
Solyc08g077260	Vacuolar protein sorting 55 (AHRD V3.3 *** B9N2S0_POPTR)		C:GO:0005768; C:G(	C:endosome; C:vacuole; C:integral component of membrane; P:			IPR007262 (PFAM): IPR007262 (PAN	0,362	0,238	0,340	0,442	0,402									
Solyc08g077270	Phosphoacetylglucosamine mutase family protein (AHRD V3.3 *** B9MTY0_POPTR)		F:GO:0004610; P:G(	F:phosphoacetylglu	EC:5.4.2.3	Phosphoacetylglucos	G3DSA:3.30.310.50 (GENE3D): G3DS	17,393	16,051	13,992	14,955	14,406									
Solyc08g077280	allyl alcohol dehydrogenase-like protein (AHRD V3.3 *** AT3G59840.1)		C:GO:0009941	C:chloroplast envelope			mobidb-lite (MOBIDB_LITE)	21,163	22,982	27,523	23,220	25,677									
Solyc08g077290	Myb family transcription factor (AHRD V3.3 *** D7MWS4_ARALL)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): G3DSA	21,276	28,700	33,780	35,776	30,002									
Solyc08g077300	UMP-CMP kinase (AHRD V3.3 *** K4CN90_SOLLC)		F:GO:0004127; F:G(	F:cytidylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS): PF00406 (PFA	26,998	21,218	50,563	50,880	50,325									
Solyc08g077310	RNA-binding protein, putative (AHRD V3.3 *** A0A072U387_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR041591 (PFA	112,010	96,290	123,862	128,338	123,797									
Solyc08g077320	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A0B2QIA0_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,791	1,896	1,295	1,203	0,939									
Solyc08g077330	Expansin-like protein (AHRD V3.3 *** W9SU42_9ROSA)	EXLB1	C:GO:0005576	C:extracellular region			IPR007118 (PRINTS): IPR009009 (PF	0,316	0,305	0,681	0,690	1,200									
Solyc08g077340	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)						IPR006566 (PFAM): IPR032675 (G3D	1,150	1,224	0,481	0,438	0,801									
Solyc08g077350	Haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** B9MTX7_POPTR)		F:GO:0016787	F:hydrolase activity			IPR006439 (PRINTS): IPR023214 (G3	27,687	26,416	20,717	16,869	16,425									
Solyc08g077370	Purine permease (AHRD V3.3 *** G7IK92_MEDTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): PTHR31376:SF16 (	0,021	0,000	0,050	0,025	0,094									
Solyc08g077380	Purine permease (AHRD V3.3 *** A0A072UNZ2_MEDTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): PTHR31376:SF16 (	0,040	0,021	0,000	0,025	0,047									
Solyc08g077385	LOW QUALITY:Intron maturase, type II family protein (AHRD V3.3 *** AT5G46920.1)		P:GO:0006397	P:mRNA processing			IPR024937 (PFAM): mobidb-lite (MOB	7,510	8,630	8,231	6,466	6,829									
Solyc08g077400	LOW QUALITY:Invertase/pectin methylesterase inhibitor family protein (AHRD V3.3 *** B9MVC0_POPTR)		F:GO:0004857	F:enzyme inhibitor activity			IPR035513 (G3DSA:1.20.140.GENE3	0,000	0,039	0,050	0,051	0,024									
Solyc08g077410	Cytochrome c oxidase subunit 6B (AHRD V3.3 *** A0A151TJ10_CAJCA)		C:GO:0005739	C:mitochondrion			IPR036549 (G3DSA:1.10.10.GENE3D	0,944	1,307	0,520	0,834	0,352									
Solyc08g077420	Regulator of nonsense transcripts 1-like protein (AHRD V3.3 *** W9SU51_9ROSA)		P:GO:0000184; F:G(	P:nuclear-transcribe	EC:3.6.1.15	Nucleoside-triphosph	IPR006935 (PFAM): IPR041679 (PFA	91,267	87,109	88,893	93,305	93,083									
Solyc08g077430	Glycine-rich protein (AHRD V3.3 *** D7MQL9_ARALL)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	148,716	120,053	120,916	120,754	114,270									
Solyc08g077440	Lon protease homolog 2, peroxisomal (AHRD V3.3 *** K4CNA3_SOLLC)		F:GO:0004176; F:G(	F:ATP-dependent p	EC:3.4.21; EC:3.6.1.	Acting on peptide bor	PR00830 (PRINTS): IPR004815 (TIGF	126,273	152,898	170,786	171,935	181,645									
Solyc08g077450	electron carrier/iron ion-binding protein (AHRD V3.3 *** AT1G32730.1)						mobidb-lite (MOBIL SRS	21,187	20,741	21,646	21,894	21,496									
Solyc08g077460	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT1G32740.1)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			IPR017066 (PIRSF): PF13920 (PFAM	121,146	70,422	228,046	195,541	191,296	-0,753	0,015					down		
Solyc08g077470	Reticulon family protein (AHRD V3.3 *** AT1G78895.1)		C:GO:0016021	C:integral component of membrane			IPR003388 (PFAM): PTHR10994:SF9	16,510	11,171	21,865	21,539	19,030									
Solyc08g077480	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT4G17670.1)		F:GO:0016874	F:ligase activity			IPR007650 (PFAM): mobidb-lite (MOB	38,607	38,206	20,393	11,353	19,566					-0,843	0,002			down
Solyc08g077483	calcium-dependent lipid-binding family protein (AHRD V3.3 --* AT1G48090.6)		C:GO:0005773; C:G(	C:vacuole; C:Golgi apparatus; P:protein targeting to vacuole; C:plasmodesma; C:integral component of				0,019	0,021	0,022	0,073	0,046									
Solyc08g077487	Vacuolar protein sorting-associated protein, putative (AHRD V3.3 *-* B9RUS0_RICCO)		C:GO:0016021	C:integral component of membrane			IPR026854 (PFAM): IPR026847 (PAN	0,000	0,000	0,025	0,022	0,000									
Solyc08g077490	pleckstrin homology (PH) domain-containing protein (AHRD V3.3 *-* AT4G17140.3)		C:GO:0016021	C:integral component of membrane			IPR026854 (PFAM): IPR031646 (PFA	0,063	0,039	0,147	0,125	0,187									
Solyc08g077500	Pleckstrin (PH) domain-containing protein isoform 1 (AHRD V3.3 *** A0A061G2P4_THECC)						IPR001849 (PFAM): IPR011993 (G3D	82,147	68,333	125,716	146,530	137,974									
Solyc08g077510	poly(U)-specific endoribonuclease-B protein (AHRD V3.3 *** AT4G17100.1)		F:GO:0004521	F:endoribonuclease activity			IPR018998 (PFAM): mobidb-lite (MOB	78,593	78,393	157,503	149,162	137,192									
Solyc08g077520	Centromere O (AHRD V3.3 *** A0A0B0P617_GOSAR)		C:GO:0000776; P:G(	C:kinetochore; P:centromere complex assembly			IPR018464 (PFAM): PTHR14582 (PAN	21,597	20,719	31,764	29,118	28,991									
Solyc08g077530	Beta-amylase (AHRD V3.3 *** K4CNB2_SOLLC)		P:GO:0000272; F:G(	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS): G3DSA:3.20.2(	23,823	31,989	21,781	18,010	24,882									
Solyc08g077540	pumilio 6 (AHRD V3.3 --* AT4G25880.5)							4,957	3,503	6,963	8,613	6,149									
Solyc08g077550	Novel plant snare, putative (AHRD V3.3 *** B9RUR4_RICCO)		C:GO:0005886; C:G(	C:plasma membrane; C:cell plate; C:integral component of mem			G3DSA:1.20.5.110 (GENE3D): IPR00	2,930	3,307	0,390	0,332	0,213									
Solyc08g077560	Kinase family protein (AHRD V3.3 *** B9MTV7_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRS	99,102	108,910	42,494	65,278	49,286					0,621	0,037			up
Solyc08g077570	LOW QUALITY:DNA repair protein rhp54 (AHRD V3.3 *-* M8CMQ9_AEGTA)		F:GO:0005524	F:ATP binding			PTHR10799 (PANTHER): PTHR10799	0,057	0,096	0,000	0,000	0,000									
Solyc08g077575	LOW QUALITY:SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 *-* AT2G1		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	0,000	0,037	0,000	0,000	0,000									
Solyc08g077580	LOW QUALITY:chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR001650 (PFAM): G3DSA:3.40.50.3	0,019	0,036	0,000	0,000	0,000									
Solyc08g077600	LOW QUALITY:chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR000330 (PFAM): IPR038718 (G3D	0,000	0,019	0,000	0,000	0,000									
Solyc08g077610	chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR038718 (G3DSA:3.40.50.GENE3D	0,000	0,115	0,000	0,000	0,000									
Solyc08g077630	Kinase family protein (AHRD V3.3 *** B9MTV7_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	0,078	0,186	0,068	0,050	0,023									
Solyc08g077640	DNA repair protein rhp54 (AHRD V3.3 *-* M8CMQ9_AEGTA)		F:GO:0005524	F:ATP binding			PTHR10799:SF858 (PANTHER): PTHF	0,019	0,019	0,025	0,022	0,024									
Solyc08g077650	chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): PTHF	0,021	0,000	0,022	0,025	0,000									
Solyc08g077660	LOW QUALITY:DNA repair protein rhp54 (AHRD V3.3 *-* N1R0A5_AEGTA)		F:GO:0005524	F:ATP binding			PTHR10799 (PANTHER): PTHR10799	0,000	0,000	0,025	0,000	0,000									
Solyc08g077670	LOW QUALITY:chromatin remodeling 31 (AHRD V3.3 *-* AT1G05490.1)		F:GO:0005524	F:ATP binding			IPR000330 (PFAM): IPR038718 (G3D	0,019	0,021	0,000	0,025	0,024									
Solyc08g077680	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** G7K0U4_MEDTR)		F:GO:0003779	F:actin binding			IPR011684 (PFAM): mobidb-lite (MOB	71,025	110,003	115,168	136,538	115,303									
Solyc08g077690	Chromatin remodeling 31, putative (AHRD V3.3 *** A0A061FRH7_THECC)		F:GO:0005524	F:ATP binding			IPR038718 (G3DSA:3.40.50.GENE3D	15,893	10,227	17,186	18,437	18,466									
Solyc08g077700	Eukaryotic translation initiation factor 4G-like protein (AHRD V3.3 *** A0A072TL86_MEDTR)		F:GO:0003723; F:G(	F:RNA binding; F:protein binding			IPR016021 (G3DSA:1.25.40.GENE3D	0,190	0,097	0,000	0,050	0,047									
Solyc08g077710	60S ribosomal protein L37a (AHRD V3.3 *** RL37A_GOSHI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR011331 (G3DSA:2.20.25.GENE3D	85,337	93,183	70,347	61,088	65,172									
Solyc08g077720	60S ribosomal protein L37a (AHRD V3.3 *** RL37A_GOSHI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002674 (TIGRFAM): IPR011331 ((	126,030	130,340	81,467	70,530	75,951									
Solyc08g077730	Phosphatidylinositol-4-phosphate 5-kinase 5-like protein (AHRD V3.3 *** A0A0B0PLQ6_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR003409 (PFAM): G3DSA:2.20.110	20,256	17,171	21,789	17,765	19,561									
Solyc08g077740	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT2G33170.2)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,257	0,570	0,256	0,478	0,400									
Solyc08g077750	Glycine-rich family protein (AHRD V3.3 *** B9MTU7_POPTR)						IPR013961 (PFAM): mobidb-lite (MOB	37,848	35,806	62,965	58,728	56,552									
Solyc08g077760	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G41750.2)							5,317	10,890	0,536	0,512	0,937									
Solyc08g077770	Calcineurin B-like protein (AHRD V3.3 *** A1XCM9_POPEU)		F:GO:0005509	F:calcium ion binding			PR00450 (PRINTS): G3DSA:1.10.238	12,540	13,068	9,367	8,588	8,422									
Solyc08g077780	Protein kinase (AHRD V3.3 *** Q39868_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	27,020	40,326	50,772	60,771	46,139									
Solyc08g077790	peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** AT4G17070.1)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR029000 (G3DSA:2.40.100.GENE3	28,145	35,902	17,272	15,588	18,040									
Solyc08g077800	DNA repair endonuclease UVH1 (AHRD V3.3 *** XPF_ARATH)		F:GO:0003677; F:G(	F:DNA binding; F:nuclease activity			G3DSA:1.10.150.20 (GENE3D): IPR0(	13,294	13,465	15,851	18,319	15,612									
Solyc08g077827	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT5G37380.9)							1,685	1,570	1,764	2,226	1,599									
Solyc08g077830	Deoxyhypusine hydroxylase (AHRD V3.3 *** K4CNE2_SOLLC)		P:GO:0008612; F:G(	P:peptidyl-lysine mc	EC:1.14.99.29	Deoxyhypusine monc	PF13646 (PFAM): IPR011989 (G3DS/	17,404	16,536	23,833	24,656	24,092									
Solyc08g077840	ureidoglycine aminohydrolase (AHRD V3.3 *** AT4G17050.1)		P:GO:0000256; P:G(	P:allantoin catabolic	EC:3.5.3.26	(S)-ureidoglycine ami	IPR014710 (G3DSA:2.60.120.GENE3	6,948	7,116	17,482	17,369	14,557									
Solyc08g077850	tRNA/rRNA methyltransferase family protein (AHRD V3.3 *** D7M9H6_ARALL)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; F:RNA methyltransferase ac			IPR001537 (PFAM): IPR029026 (G3D	21,992	20,818	15,420	16,159	15,232									
Solyc08g077860	meiotic serine proteinase	tmp	F:GO:0004252; P:G(	F:serine-type endoı	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR000209 (PF	0,308	0,226	0,022	0,050	0,071									
Solyc08g077870	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G22670.1)							10,107	6,415	1,069	0,930	2,263									
Solyc08g077880	High molecular mass early light-inducible HV58, chloroplastic (AHRD V3.3 *** A0A0B0NUU8_GOSAR)		C:GO:0009535	C:chloroplast thylakoid membrane			mobidb-lite (MOBIDB_LITE): PTHR141	110,397	150,212	55,528	57,627	94,243			0,760	0,000				up	
Solyc08g077890	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4CNE8_SOLLC)		F:GO:0004252; P:G(	F:serine-type endoı	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): IPR023562 (PF	107,521	135,082	175,252	170,570	190,401									
Solyc08g077900	Expansin-like protein (AHRD V3.3 *** W9S0F1_9ROSA)	EXLB2	C:GO:0005576	C:extracellular region			IPR007118 (PRINTS): IPR036749 (G3	0,019	0,072	0,245	0,454	0,259									
Solyc08g077910	Expansin-like protein (AHRD V3.3 *** W9S0F1_9ROSA)	EXLB4	C:GO:0005576	C:extracellular region			IPR007118 (PRINTS): IPR007117 (PF	0,100	0,182	0,194	0,366	0,116									
Solyc08g077920	Isocitrate dehydrogenase [NAD] subunit, mitochondrial (AHRD V3.3 *** K4CNF1_SOLLC)		F:GO:0004449; P:G(	F:isocitrate dehydrc	EC:1.1.1.41	Isocitrate dehydroge	IPR004434 (TIGRFAM): G3DSA:3.40.	16,294	17,183	26,662	23,258	21,894									
Solyc08g077930	Isocitrate dehydrogenase [NAD] subunit, mitochondrial (AHRD V3.3 *** K4CNF2_SOLLC)		F:GO:0004449; P:G(	F:isocitrate dehydrc	EC:1.1.1.41	Isocitrate dehydroge	G3DSA:3.40.718.10 (GENE3D): IPR0	38,059	35,197	61,052	53,706	51,503									
Solyc08g077940	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6 (AHRD V3.3 *** W9S0E6_9ROSA)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR036987 (G3DSA:2.30.280.GENE3	1,660	2,130	0,047	0,120	0,211									
Solyc08g077955	transcription factor IIIB (AHRD V3.3 *-* AT4G17010.1)						PTHR35749 (PANTHER)	0,118	0,096	0,025	0,073	0,000									
Solyc08g077960	GATA transcription factor, putative (AHRD V3.3 *** B9SYZ6_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR038108 (G3DS GATA	13,039	10,003	12,228	12,349	11,798									
Solyc08g077970	transcription factor IIIB (AHRD V3.3 *** AT4G17010.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,917	2,343	0,966	1,019	0,561									
Solyc08g077980	Bax inhibitor	bi1	C:GO:0016021	C:integral component of membrane			IPR006214 (PFAM): PTHR23291:SF7	68,834	68,833	123,779	148,687	133,361									
Solyc08g077990	Kinase like protein (AHRD V3.3 *-* Q0WPK0_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	3,243	3,016	0,650	0,468	0,590									
Solyc08g078000	Vesicle-associated protein 2-1 (AHRD V3.3 *** W9S0E2_9ROSA)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR000535 (PFAM): IPR016763 (PIRS	17,140	15,366	16,241	16,084	14,854									
Solyc08g078010	Ribosomal protein L19 family protein (AHRD V3.3 *** AT4G17560.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001857 (PRINTS): IPR038657 (G3	8,753	14,266	10,172	12,502	15,466	0,735	0,022	0,601	0,004			up	up	
Solyc08g078020	LOW QUALITY:Methionine rich arabinogalactan (AHRD V3.3 *** Q52QJ6_SOLLC)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): mobidb-lite (MOB	1,830	1,517	1,240	1,428	1,575									
Solyc08g078030	Transferase, putative (AHRD V3.3 *** B9T0L5_RICCO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	0,262	0,079	0,025	0,051	0,070									
Solyc08g078040	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT2G35660.1)		F:GO:0071949	F:FAD binding			PR00420 (PRINTS): IPR036188 (G3D	18,974	13,116	12,146	24,493	16,717					1,014	0,000			up

Solyc08g078060	transmembrane protein (AHRD V3.3 *** AT5G61630.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR341	0,203	0,219	0,072	0,047	0,189									
Solyc08g078070	small GTP-binding protein A	rab1a	F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR005225 (TIGF	78,075	116,392	94,977	136,440	109,621					0,525	0,001			up
Solyc08g078080	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XFF0_CYNCS)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR032867 (PFAI	1,125	1,061	1,311	1,291	1,229									
Solyc08g078083	DDT domain superfamily (AHRD V3.3 --* AT1G18950.3)							0,328	0,178	0,295	0,268	0,165									
Solyc08g078087	Malate synthase, glyoxysomal (AHRD V3.3 --* MASY_MAIZE)							0,021	0,000	0,025	0,000	0,024									
Solyc08g078090	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GB30_THECC)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.50.12520 (GENE3D): IPF	33,861	17,702	15,854	15,449	16,710	-0,908	0,000					down		
Solyc08g078100	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			IPR002293 (PFAM): IPR002293 (PIRS	7,334	6,062	4,345	4,334	4,051									
Solyc08g078110	Gibberellin 20 oxidase, putative (AHRD V3.3 *-* B9T282_RICCO)		F:GO:0045486; F:GC	F:naringenin 3-dioxy	EC:1.14.11; EC:1.14	Acting on paired don	IPR027443 (G3DSA:2.60.120.GENE3I	0,021	0,021	0,022	0,000	0,000									
Solyc08g078115	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 *-* AT1G05380.3)		F:GO:0016491; F:GC	F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduc			IPR027443 (G3DSA:2.60.120.GENE3I	0,019	0,098	0,000	0,000	0,023									
Solyc08g078120	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* A0A072VQ30_MEDTR)		F:GO:0046872	F:metal ion binding			IPR032308 (PFAM): IPR013083 (G3D	0,178	0,060	0,025	0,025	0,000									
Solyc08g078130	Methylglutaconyl-CoA hydratase (AHRD V3.3 *** B4FQA8_MAIZE)		F:GO:0003824	F:catalytic activity			G3DSA:3.90.226.10 (GENE3D): IPR0(	18,795	16,965	26,475	23,961	25,093									
Solyc08g078140	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** K4CNH3_SOLLC)		F:GO:0004843; C:GC	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001578 (PRINTS): IPR001578 (PF	2,947	3,447	6,017	7,071	5,509									
Solyc08g078150	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HYB0_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	25,409	26,542	24,051	24,577	26,072									
Solyc08g078155	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT5G06940.1)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane; F:kinase acti			IPR032675 (G3DSA:3.80.10.GENE3D	0,464	0,189	0,022	0,000	0,023									
Solyc08g078170	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A024CAT9_BRAJU)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,176	0,286	0,516	0,165	0,375									
Solyc08g078180	Ethylene Response Factor A.1	ERF-A_1	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,264	0,494	0,785	0,465	0,401									
Solyc08g078190	ethylene-responsive transcription factor	ERF.B13	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	71,974	14,531	19,515	38,112	13,253	-2,282	0,000			0,968	0,000	down		up
Solyc08g078200	Plasma membrane ATPase (AHRD V3.3 *** M1DGA0_SOLTU)		F:GO:0000166; F:GC	F:nucleotide binding	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR001757 (PRINTS): PR00119 (PRIN	0,000	0,062	0,000	0,000	0,000									
Solyc08g078203	PPPDE thiol peptidase family protein, putative (AHRD V3.3 *** A0A061GB44_THECC)						G3DSA:3.90.1720.30 (GENE3D): IPR(	49,453	44,845	34,182	31,002	33,045									
Solyc08g078207	RING-H2 finger protein ATL22 (AHRD V3.3 *** A0A0B2SEF9_GLYSO)		C:GO:0016021	C:integral component of membrane			PTHR27009 (PANTHER): PTHR27009	0,199	0,136	0,237	0,171	0,260									
Solyc08g078210	Nudix hydrolase (AHRD V3.3 *** A0A061G4C5_THECC)		F:GO:0016787	F:hydrolase activity			IPR003293 (PRINTS): IPR040618 (PF	16,343	11,194	7,932	6,120	9,469									
Solyc08g078230	SWIM zinc finger family protein (AHRD V3.3 *** AT1G60560.1)		F:GO:0008270	F:zinc ion binding			PTHR33977 (PANTHER): PTHR33977	46,251	42,743	44,724	40,410	46,713									
Solyc08g078240	Mediator of RNA polymerase II transcription subunit 32 (AHRD V3.3 *** G7J6I0_MEDTR)		P:GO:0006355; P:GC	P:regulation of transcription, DNA-templated; P:cold acclimation			mobidb-lite (MOBIDB_LITE): IPR0332	38,781	32,612	55,906	45,518	50,796									
Solyc08g078250	Palmitoyl protein thioesterase containing protein, expressed (AHRD V3.3 *-* Q10T54_ORYSJ)		C:GO:0016021; F:GC	C:integral component of membrane; F:palmitoyl hydrolase activi			IPR029058 (G3DSA:3.40.50.GENE3D	71,686	67,658	116,847	116,243	118,252									
Solyc08g078270	Protein-tyrosine phosphatase mitochondrial 1-like protein (AHRD V3.3 *** W9SEA4_9ROSA)		P:GO:0006470; F:GC	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR029021 (G3DSA:3.90.190.GENE3I	26,332	30,425	29,684	27,673	28,504									
Solyc08g078280	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SZP7_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	2,148	2,113	1,454	1,658	1,580									
Solyc08g078290	LOW QUALITY:Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *** A0A061G512_THE(		C:GO:0016021	C:integral component of membrane			IPR008480 (PFAM): mobidb-lite (MOB	4,473	4,261	2,507	2,904	2,849									
Solyc08g078300	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MUS1_POPTR)		F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000047 (PRIN HD-ZIP	22,754	24,061	2,531	1,587	3,050									
Solyc08g078310	DUF1639 family protein (AHRD V3.3 *** G7JHQ0_MEDTR)						IPR012438 (PFAM): mobidb-lite (MOB	10,586	16,710	7,267	5,991	6,757									
Solyc08g078320	E3 ubiquitin-protein ligase HOS1 (AHRD V3.3 *** G7JXE3_MEDTR)		F:GO:0004842; C:GC	F:ubiquitin-protein transferase activity; C:nucleus; C:cytoplasm;			IPR025151 (PFAM): mobidb-lite (MOB	76,394	66,427	49,368	42,362	47,309									
Solyc08g078330	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G16765.6)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	0,021	0,060	0,000	0,025	0,000									
Solyc08g078340	MYB transcription factor (AHRD V3.3 *** T2DNE9_PHAVU)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB_related	20,526	27,742	13,506	15,824	18,732									
Solyc08g078360	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072TMP1_MEDTR)		C:GO:0016020; C:GC	C:membrane; C:integral component of membrane			PTHR34115:SF5 (PANTHER): PTHR3	0,019	0,000	0,000	0,000	0,000									
Solyc08g078370	pfkB-like carbohydrate kinase family protein (AHRD V3.3 *** AT4G28706.1)		F:GO:0016301	F:kinase activity			IPR002139 (PRINTS): IPR011611 (PF	19,140	23,906	32,345	32,194	30,423									
Solyc08g078380	O-fucosyltransferase family protein (AHRD V3.3 *** AT4G17430.1)		P:GO:0006004; C:GC	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): PTHR36050 (PAN	7,460	8,141	10,477	8,445	8,192									
Solyc08g078390	peroxisomal acyl-CoA oxidase 1A	acx1a	F:GO:0003997; C:GC	F:acyl-CoA oxidase	EC:1.3.3.6	Acyl-CoA oxidase	IPR002655 (PFAM): G3DSA:2.40.110	117,011	193,015	142,226	136,107	141,325	0,747	0,030					up		
Solyc08g078400	peroxisomal acyl-CoA oxidase 1A	acx1b	F:GO:0003997; C:GC	F:acyl-CoA oxidase	EC:1.3.3.6	Acyl-CoA oxidase	G3DSA:1.20.140.10 (GENE3D): G3DS	0,000	0,039	0,025	0,000	0,000									
Solyc08g078410	ethylene-responsive transcription factor (AHRD V3.3 *-* AT5G07580.1)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,021	0,000	0,000	0,000	0,000									
Solyc08g078420	ethylene-responsive transcription factor (AHRD V3.3 *-* AT5G07580.1)		F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,021	0,000	0,000	0,000	0,000									
Solyc08g078430	U4/U6 small nuclear ribonucleoprotein Prp31 (AHRD V3.3 *** A0A0B0PVX3_GOSAR)		P:GO:0000244; C:GC	P:spliceosomal tri-snRNP complex assembly; C:U4/U6 x U5 tri-s			IPR029012 (G3DSA:1.10.287.GENE3I	80,144	82,088	118,070	112,071	110,100									
Solyc08g078440	Sphingomyelin phosphodiesterase 4 (AHRD V3.3 *** A0A0B0PYY0_GOSAR)		F:GO:0050290	F:sphingomyelin ph	EC:3.1.4.41	Sphingomyelin phosp	IPR024129 (PFAM): PTHR31801 (PAN	43,068	64,267	53,924	51,558	54,614									
Solyc08g078450	Exostosin family protein (AHRD V3.3 *** AT4G16745.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyc			IPR040911 (PFAM): PTHR11062:SF5	0,200	0,076	17,091	26,850	16,736					0,655	0,001			up
Solyc08g078460	Oxidoreductase family protein (AHRD V3.3 *** AT4G17370.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR000683 (PFAM): G3DSA:3.30.360	0,813	0,728	178,337	222,937	202,045									
Solyc08g078470	FHA domain-containing protein (AHRD V3.3 *-* W9R6B4_9ROSA)		F:GO:0005515	F:protein binding			G3DSA:2.60.200.20 (GENE3D): IPR0(	4,283	3,676	3,506	3,546	3,829									
Solyc08g078480	transmembrane protein (AHRD V3.3 *** AT4G16695.1)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane			PTHR37749 (PANTHER)	7,583	7,551	11,058	10,271	9,926									
Solyc08g078490	formyltetrahydrofolate deformylase (AHRD V3.3 *** AT5G47435.2)		P:GO:0006189; F:GC	P:'de novo' IMP bio	EC:3.5.1.1	Formyltetrahydrofolat	IPR004810 (PRINTS): IPR002376 (PF	2,777	2,528	5,515	5,718	6,199									
Solyc08g078500	auxin canalization protein (DUF828) (AHRD V3.3 *** AT4G17350.1)						IPR008546 (PFAM): IPR013666 (PFAI	2,486	3,323	3,171	2,722	2,576									
Solyc08g078510	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)						IPR004182 (PFAM): mobidb-lite (MOB	168,662	231,408	138,054	239,577	161,751					0,798	0,000			up
Solyc08g078520	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G47380.4)						IPR006869 (PFAM): IPR025757 (PFAI	1,357	1,740	3,830	6,176	3,965									
Solyc08g078530	Agenet-like domain-containing protein (AHRD V3.3 *** A0A103XFP8_CYNCS)						IPR008395 (PFAM): mobidb-lite (MOB	190,787	148,303	274,756	277,729	277,592									
Solyc08g078540	O-fucosyltransferase family protein (AHRD V3.3 *** AT4G16650.2)		P:GO:0006004; C:GC	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	2,429	2,060	3,495	3,027	3,372									
Solyc08g078550	Metalloendoproteinase 1, putative (AHRD V3.3 *** B9T8P6_RICCO)		F:GO:0004222; P:GC	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR021190 (PRINTS): IPR002477 (PF	0,360	0,347	3,132	3,437	3,442									
Solyc08g078560	nuclear fusion defective 6 (AHRD V3.3 --* AT2G20585.7)		C:GO:0005739	C:mitochondrion			PTHR33156:SF9 (PANTHER): PTHR3	13,726	14,603	15,528	16,100	15,221									
Solyc08g078580	WAT1-related protein (AHRD V3.3 *** A0A0V0IGS4_SOLCH)		C:GO:0016021; F:GC	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): IPR030184 (PAN	0,335	0,423	0,000	0,000	0,116									
Solyc08g078590	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9IBW4_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	0,000	0,021	0,000	0,000	0,000									
Solyc08g078600	DNA-directed RNA polymerase III subunit RPC5 (AHRD V3.3 *** A0A0B0N397_GOSAR)		F:GO:0003899; C:GC	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA p	IPR006886 (PFAM): mobidb-lite (MOB	18,549	15,797	27,955	29,067	24,620									
Solyc08g078610	Zinc knuckle family protein (AHRD V3.3 *** B9I9G6_POPTR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	55,162	53,557	52,722	50,359	49,599									
Solyc08g078620	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHU8_9ROSA)		F:GO:0003676; P:GC	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR002562 (PFAM): IPR036397 (G3D	0,376	0,414	0,149	0,150	0,187									
Solyc08g078630	transmembrane protein (AHRD V3.3 *** AT5G18250.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,497	6,632	7,604	7,837	7,081									
Solyc08g078640	Pectinesterase (AHRD V3.3 *** K4CNM3_SOLLC)		F:GO:0030599; P:GC	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	0,171	0,139	0,000	0,000	0,000									
Solyc08g078650	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 *** AT2G35710.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyc			IPR022751 (PFAM): IPR029044 (G3D	1,763	2,212	40,027	48,321	31,931									
Solyc08g078660	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9SSF5_RICCO)		C:GO:0009536; P:GC	C:plastid; P:vegetative to reproductive phase transition of meris			IPR001623 (PRINTS): IPR001623 (PF	18,553	19,085	24,979	24,986	23,936									
Solyc08g078670	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061G3B8_THECC)		F:GO:0004190; P:GC	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032799 (PF	151,660	48,853	10,808	19,527	15,311	-1,607	0,000			0,853	0,004	down		up
Solyc08g078680	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT5G47510.4)						G3DSA:1.10.8.20 (GENE3D): IPR036	0,080	0,197	0,022	0,000	0,023									
Solyc08g078690	putative vesicle-associated protein		C:GO:0005789	C:endoplasmic reticulum membrane			IPR013783 (G3DSA:2.60.40.GENE3D	6,217	5,782	5,192	4,657	5,692									
Solyc08g078695	Heat-shock protein, putative (AHRD V3.3 *** B9SSG1_RICCO)						IPR002068 (PFAM): IPR008978 (G3D	30,882	17,624	120,009	132,683	125,869									
Solyc08g078710	Heat-shock protein, putative (AHRD V3.3 *-* B9R9S7_RICCO)	Hsp21.5B					IPR008978 (G3DSA:2.60.40.GENE3D	0,040	0,000	0,000	0,025	0,000									
Solyc08g078720	Heat-shock protein, putative (AHRD V3.3 *-* B9R9S7_RICCO)	Hsp18.2					IPR002068 (PFAM): IPR008978 (G3D	23,325	26,763	24,776	16,328	20,890					-0,599	0,002			down
Solyc08g078730	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT2G35730.1)		P:GO:0030001; F:GC	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	0,000	0,019	0,050	0,022	0,000									
Solyc08g078750	Leukocyte receptor cluster member 1 (AHRD V3.3 *** A0A0B0N472_GOSAR)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,009	5,381	4,124	4,952	3,926									
Solyc08g078753	DEAD-box ATP-dependent RNA helicase 41 (AHRD V3.3 *-* A0A0B2NZE8_GLYSO)		F:GO:0003676; F:GC	F:nucleic acid binding; F:zinc ion binding			G3DSA:3.30.60.220 (GENE3D): IPR0(	14,984	13,431	10,266	9,402	11,445									
Solyc08g078757	squamosa promoter binding protein-like 15 (AHRD V3.3 --* AT3G57920.1)							0,101	0,099	0,050	0,122	0,118									
Solyc08g078770	LOW QUALITY:Plant/MNJ7-17 protein, putative (AHRD V3.3 *** G7JIX8_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35307 (PANTHER): PS51257 (P	0,342	0,195	0,122	0,139	0,237									
Solyc08g078780	LOW QUALITY:Plant/MNJ7-17 protein, putative (AHRD V3.3 *** G7JIY0_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35307 (PANTHER)	15,428	20,760	9,744	12,393	11,345									
Solyc08g078785	Peroxidase superfamily protein (AHRD V3.3 --* AT4G11290.1)							0,358	0,529	0,074	0,045	0,093									
Solyc08g078790	transmembrane protein (AHRD V3.3 *** AT4G25225.2)						IPR027854 (PFAM): IPR027854 (PAN	1,820	2,426	3,566	3,417	3,180									
Solyc08g078800	GRAS family transcription factor (AHRD V3.3 *** A0A061GBD8_THECC)	GRAS					IPR005202 (PFAM GRAS	20,010	23,389	8,384	10,110	8,765									
Solyc08g078810	indeterminate(ID)-domain 16 (AHRD V3.3 --* AT1G25250.3)							3,546	3,070	1,289	1,528	1,107									
Solyc08g078820	Autophagy-related protein (AHRD V3.3 *** K4CNP1_SOLLC)		C:GO:0005737; P:GC	C:cytoplasm; P:autophagy			IPR004241 (PFAM): G3DSA:3.10.20.9	18,239	17,264	129,769	145,192	114,039									
Solyc08g078830	LOW QUALITY:DEAD-box ATP-dependent RNA helicase 56-like protein (AHRD V3.3 -** A0A0B0PLQ2_GOSAR)							0,061	0,145	0,000	0,047	0,000									
Solyc08g078840	root meristem growth factor (AHRD V3.3 --* AT4G16515.1)						PTHR34961 (PANTHER): PTHR34961	1,905	3,875	0,097	0,073	0,094									
Solyc08g078845	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein (AHRD V3.3 *-* AT4G16510.2)		F:GO:0140101	F:catalytic activity, acting on a tRNA			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,507	0,471	0,069	0,158	0,047									
Solyc08g078850	lactate dehydrogenase	ldh1	F:GO:0004459; C:GC	F:L-lactate dehydro	EC:1.1.1.27	L-lactate dehydroger	IPR001557 (PRINTS): IPR011304 (TI(	20,513	50,939	7,722	2,093	3,782	1,334	0,002			-1,880	0,004	up		down
Solyc08g078860	NADH dehydrogenase 1 beta subcomplex subunit 8 (AHRD V3.3 *** A0A061GBE7_THECC)		C:GO:0044425	C:membrane part			IPR038863 (PANTHER)	53,715	55,144	97,539	80,423	83,755									
Solyc08g078870	14 kDa proline-rich protein DC2.15, putative (AHRD V3.3 *** B9RD76_RICCO)						IPR027923 (PFAM): G3DSA:1.10.110	0,842	4,584	3,539	3,775	2,224	2,467	0,000					up		
Solyc08g078880	Cation/H(+) antiporter 15 (AHRD V3.3 *** W9QLT0_9ROSA)		P:GO:0006812; F:GC	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	0,216	1,096	0,050	0,101	0,163									
Solyc08g078890	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *-* AT1G62500.1)						PR01217 (PRINTS): G3DSA:1.10.110	11,930	10,521	0,000	0,602	0,023									
Solyc08g078900	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)						IPR027923 (PFAM): G3DSA:1.10.110	0,058	0,412	0,072	0,025	0,000									
Solyc08g078910	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)						IPR027923 (PFAM): G3DSA:1.10.110	0,019	0,000	0,000	0,000	0,000									
Solyc08g078940	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT1G12100.1)						IPR027923 (PFAM): G3DSA:1.10.110	0,000	0,000	0,025	0,000	0,000									
Solyc08g078950	NIT1	nit1	C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	5,657	5,967	0,478	0,606	0,679									
Solyc08g078960	Oxysterol-binding family protein (AHRD V3.3 *** U5GRI5_POPTR)						G3DSA:2.40.160.120 (GENE3D): PF1	15,903	19,019	6,441	6,725	8,955									
Solyc08g078980	Sec-independent protein translocase protein TatC (AHRD V3.3 --* A0A1D1XXF3_9ARAE)							0,040	0,000	0,025	0,050	0,000									
Solyc08g078990	Phosphatidic acid phosphatase (AHRD V3.3 *** A0A0K9NN47_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR000326 (PFAM): G3DSA:1.20.144	2,372	2,396	4,028	4,872	3,776									
Solyc08g079000	Terpenoid cyclases/Protein prenyltransferases superfamily protein (AHRD V3.3 --* AT3G14540.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,037	0,000	0,000	0,023									
Solyc08g079020	Adenine phosphoribosyltransferase-like protein (AHRD V3.3 *** G7JW03_MEDTR)		F:GO:0003999; C:GC	F:adenine phosphor	EC:2.4.2.7	Adenine phosphoribo	IPR005764 (TIGRFAM): G3DSA:3.40.5	35,756	21,890	21,264	21,637	18,651									
Solyc08g079030	Low-density lipoprotein receptor-related 11 (AHRD V3.3 *** A0A0B0PKY1_GOSAR)						IPR008581 (PFAM): mobidb-lite (MOB	0,733	0,560	0,140	0,256	0,257									
Solyc08g079040	Exostosin family protein (AHRD V3.3 *** AT4G22580.1)		P:GO:0006486; F:GC	P:protein glycosylation; F:transferase activity, transferring glyc			IPR040911 (PFAM): PTHR11062:SF5	25,967	23,110	16,473	16,526	16,232									
Solyc08g079050	transcription factor (AHRD V3.3 *** AT4G22600.1)		P:GO:0006351; F:GC	P:transcription, DNA-templated; F:sequence-specific DNA bindi			IPR025422 (PFAM): PTHR22952:SF2	0,332	0,200	0,071	0,022	0,142									
Solyc08g079060	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4CNR5_SOLLC)		F:GO:0003824; P:GC	F:catalytic activity; P:trehalose biosynthetic process			IPR023214 (G3DSA:3.40.50.GENE3D	81,394	88,207	127,902	108,792	134,597									
Solyc08g079080	symbol=lin9	lin9	F:GO:0004575	F:sucrose alpha-glu	EC:3.2.1.2; EC:3.2.1	Alpha-glucosidase; S	IPR013189 (PFAM): IPR013148 (PFAI	2,629	2,051	0,674	0,586	0,584									
Solyc08g079090	Monocopper oxidase-like protein SKU5 (AHRD V3.3 *** SKU5_ARATH)		F:GO:0005507; F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR011706 (PFAM): IPR001117 (PFAI	179,327	159,578	60,295	54,119	87,818									
Solyc08g079100	CRABS CLAW 1b	YABBY1b	P:GO:0007275	P:multicellular organism development			IPR006780 (PFAM YABBY	9,234	11,895	1,841	2,368	1,963									
Solyc08g079110	Thylakoid lumenal protein (AHRD V3.3 *** G7KG97_MEDTR)						G3DSA:2.160.20.100 (GENE3D): IPR(	14,124	23,169	22,987	30,773	38,255	0,741	0,010	0,732	0,000	0,425	0,019	up	up	up
Solyc08g079120	NAC domain protein, (AHRD V3.3 *** A0A061G3J0_THECC)	NAC080	F:GO:0003677; P:GC	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,077	0,037	0,000	0,000	0,000									
Solyc08g079130	Small auxin up-regulated RNA66	SAUR66	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	0,019	0,000	0,025	0,000	0,000									
Solyc08g079140	Small auxin up-regulated RNA67	SAUR67	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF4	1,829	1,667	0,513	0,471	0,772									
Solyc08g079150	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G22620.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	3,127	1,141	0,050	0,025	0,140	-1,413	0,014					down		
Solyc08g079160	Vacuolar-processing enzyme (AHRD V3.3 *** VPE_SOYBN)		P:GO:0006508; F:GC	P:proteolysis; F:peptidase activity			IPR001096 (PRINTS): G3DSA:1.10.13	15,453	19,827	1,499	5,631	0,231									
Solyc08g079170	Heat shock protein STI (AHRD V3.3 *** W9R4M6_9ROSA)		F:GO:0005515	F:protein binding			PF13414 (PFAM): IPR011990 (G3DSA	475,346	355,958	454,589	467,943	485,150									
Solyc08g079180	Elongation factor G, chloroplastic (AHRD V3.3 *** K4CNS6_SOLLC)		F:GO:0003746; F:GC	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.40.50	48,992	78,327	75,610	67,854	114,240	0,704	0,009	0,592	0,000			up	up	
Solyc08g079190	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)						G3DSA:1.10.110.10 (GENE3D): IPR0	0,000	0,361	0,000	0,000	0,000									
Solyc08g079200	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)						G3DSA:1.10.110.10 (GENE3D): IPR0	0,038	0,000	0,000	0,000	0,047									
Solyc08g079210	LOW QUALITY:Esterase/lipase/thioesterase family protein (AHRD V3.3 --* AT3G26820.2)							0,021	0,000	0,000	0,000	0,000									
Solyc08g079235	Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** G7KG88_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (TIGRFAM): IPR035513 ((	21,369	32,140	29,174	39,819	47,488			0,699	0,049				up	
Solyc08g079240	(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB (AHRD V3.3 *** A0A0B0NEC9_GOSAR)		C:GO:0009570	C:chloroplast stroma			PTHR36333 (PANTHER)	14,868	31,521	10,742	12,463	22,943	1,111	0,000	1,089	0,000			up	up	
Solyc08g079250	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** C0KHK1_9CARY)		C:GO:0016021	C:integral component of membrane			IPR016140 (PFAM): G3DSA:1.10.110	0,473	0,545	0,075	0,142	0,117									
Solyc08g079255	Lipid transfer protein (AHRD V3.3 *** I3SGW1_MEDTR)		C:GO:0016020	C:membrane			IPR016140 (PFAM): G3DSA:1.10.110	83,293	78,650	68,963	64,220	55,781									
Solyc08g079260	Tetratricopeptide repeat-containing family protein (AHRD V3.3 *** U5GMD7_POPTR)		F:GO:0046983	F:protein dimerization activity			IPR011990 (G3DSA:1.25.40.GENE3D	231,441	223,370	270,472	252,158	271,110									
Solyc08g079270	R2R3MYB transcription factor 42	R2R3MYB42	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,686	0,399	0,044	0,122	0,119									
Solyc08g079280	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	31,941	31,373	19,112	13,453	28,356			0,565	0,002	-0,502	0,049		up	down
Solyc08g079285	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,099	0,195	0,118	0,150	0,237									
Solyc08g079300	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,040	0,000	0,000	0,025	0,000									
Solyc08g079310	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,734	1,106	0,536	0,320	0,918									
Solyc08g079313	Cytochrome P450, putative (AHRD V3.3 *-* B9RBQ8_RICCO)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3I	0,000	0,000	0,000	0,025	0,023									
Solyc08g079317	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR036396 (G3	0,076	0,021	0,000	0,000	0,047									
Solyc08g079330	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	1,555	1,460	0,000	0,025	0,000									
Solyc08g079350	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	9,506	6,303	0,025	0,051	0,000									
Solyc08g079370	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	6,338	7,032	0,000	0,025	0,000									
Solyc08g079420	Cytochrome P450 (AHRD V3.3 *-* A0A118JTP4_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	2,727	3,001	1,054	1,085	2,297									
Solyc08g079430	partialcopper-containing amine oxidase	cuao	F:GO:0005507; F:GC	F:copper ion bindin	EC:1.4.3.21	Primary-amine oxida	IPR015798 (PFAM): G3DSA:3.10.450	313,603	175,215	263,106	210,301	219,097	-0,813	0,005					down		
Solyc08g079440	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE5	F:GO:0003824; C:GC	F:catalytic activity; C:endosome; C:trans-Golgi network; C:integ			PR01713 (PRINTS): IPR016040 (PFAI	11,509	8,635	10,669	9,793	10,227									
Solyc08g079450	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G12230.1)						IPR000073 (PFAM): IPR029058 (G3D	40,479	30,713	46,476	47,360	43,432									
Solyc08g079460	Receptor-like kinase (AHRD V3.3 *** A0A191UPW4_CASSA)		F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PFAM): IPR013210 (PFAI	13,785	11,157	3,884	4,149	3,381									
Solyc08g079470	Glycine cleavage T-protein aminomethyltransferase (AHRD V3.3 *** A0A072V145_MEDTR)		F:GO:0005515	F:protein binding			IPR027266 (G3DSA:3.30.1360.GENE	13,441	13,124	18,190	19,255	18,554									
Solyc08g079480	DUF1442 family protein (AHRD V3.3 *** G7KG71_MEDTR)						G3DSA:3.40.50.150 (GENE3D): IPR0(	0,613	1,311	5,724	5,035	5,699									
Solyc08g079490	Class I peptide chain release factor (AHRD V3.3 *** AT1G62850.3)		F:GO:0003747; P:GC	F:translation release factor activity; P:translational termination			G3DSA:3.30.160.20 (GENE3D): IPR0(	10,486	10,373	16,621	19,911	19,218									
Solyc08g079500	Myeloid leukemia factor 1 (AHRD V3.3 *** A0A0B0Q1A9_GOSAR)						IPR019376 (PFAM): mobidb-lite (MOB	87,347	88,923	163,103	144,760	147,055									
Solyc08g079510	cyclin-dependent kinase-like protein (AHRD V3.3 *** AT1G12330.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,206	7,790	9,308	14,004	12,201					0,589	0,027			up
Solyc08g079520	SNARE-interacting protein KEULE (AHRD V3.3 *** KEULE_ARATH)		P:GO:0006904	P:vesicle docking involved in exocytosis			G3DSA:3.90.830.10 (GENE3D): G3DS	33,030	38,706	39,983	40,027	38,986									
Solyc08g079530	CPD photolyase (AHRD V3.3 *** Q9AVI6_CUCSA)		F:GO:0003904; P:GC	F:deoxyribodipyrimi	EC:4.1.99.3; EC:4.1.	Deoxyribodipyrimidin	IPR008148 (TIGRFAM): G3DSA:1.10.5	6,668	9,716	5,981	5,171	9,128			0,600	0,037				up	

Solyc08g079545	F5O11.10 isoform 1 (AHRD V3.3 *** A0A061G506_THECC)						IPR007021 (PFAM): PTHR32166 (PAN	23,369	19,806	0,475	0,196	0,259									
Solyc08g079570	sterol C4-methyl oxidase 1-2 (AHRD V3.3 *** AT4G22756.1)		F:GO:0005506: P:G(	F:iron ion binding: P:lipid biosynthetic process: F:oxidoreductas			IPR006694 (PFAM): PTHR11863 (PAN	8,921	8,041	7,825	7,327	7,930									
Solyc08g079590	Pentatricopeptide (PPR) repeat-containing protein-like (AHRD V3.3 *** Q6ETC2_ORYSJ)						mobidb-lite (MOBIDB_LITE): IPR0403!	4,533	4,470	1,473	1,735	2,495									
Solyc08g079600	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)						IPR040358 (PANTHER): PTHR33270:	1,113	2,877	0,268	0,712	1,008	1,385	0,022					up		
Solyc08g079610	Nucleotide excision repair, TFIIH, subunit TTDA (AHRD V3.3 *** AT1G12400.2)		C:GO:0000439: P:G(	C:transcription factor TFIIH core complex: P:nucleotide-excisior			IPR035935 (G3DSA:3.30.70.GENE3D	33,314	26,860	32,837	28,049	28,656									
Solyc08g079620	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4CNW2_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): IPR023562 (PF	31,159	43,445	55,439	54,915	60,345	0,507	0,045					up		
Solyc08g079630	AT hook, DNA-binding motif-containing protein (AHRD V3.3 *** A0A103XG23_CYNCS)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): G3DSA:3.30.133	7,147	6,903	2,961	2,983	3,209									
Solyc08g079640	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103XK68_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	2,712	2,814	2,357	1,524	1,695									
Solyc08g079650	ACT domain-containing family protein (AHRD V3.3 *** B9N3K8_POPTR)						G3DSA:3.30.70.260 (GENE3D): IPR0(	24,691	14,687	6,766	8,802	8,344	-0,724	0,012					down		
Solyc08g079660	ATP-dependent Clp protease (AHRD V3.3 *** G7KG47_MEDTR)		P:GO:0019538	P:protein metabolic process			IPR004176 (PFAM): IPR036628 (G3D	22,869	30,972	38,929	39,699	42,620									
Solyc08g079670	TVP38/TMEM64 family membrane protein (AHRD V3.3 *** A0A0B2P9N9_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR032816 (PFAM): PTHR12677:SF2	28,244	19,667	31,903	32,567	35,407									
Solyc08g079680	YCF49-like protein (AHRD V3.3 *** AT4G22830.1)		C:GO:0016021	C:integral component of membrane			IPR019634 (PFAM): IPR019634 (PAN	1,607	1,125	0,616	0,393	0,661									
Solyc08g079690	Homeobox-leucine zipper protein HOX9, putative (AHRD V3.3 *** A0A061DUZ5_THECC)						PTHR33601:SF2 (PANTHER): IPR039	19,635	12,124	4,307	3,835	4,359	-0,665	0,016					down		
Solyc08g079700	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** V5PZR5_9CARY)		F:GO:0003677: F:G(	F:DNA binding; F:zinc ion binding			IPR002653 (PFAM): IPR000058 (PFA	150,526	39,232	61,667	150,630	67,458	-1,914	0,000			1,291	0,000	down		up
Solyc08g079710	Kinesin-like protein (AHRD V3.3 *** K4CNX1_SOLLC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR011989 (G3	9,652	7,998	2,396	3,489	3,436									
Solyc08g079720	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TPA5_MEDTR)		F:GO:0003680	F:AT DNA binding			IPR005175 (PFAM): G3DSA:3.30.133	0,019	0,039	0,000	0,000	0,024									
Solyc08g079730	Protein DETOXIFICATION (AHRD V3.3 *** K4CNX3_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport: F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	7,894	10,355	5,286	3,114	6,030					-0,762	0,032			down
Solyc08g079750	1-aminocyclopropane-1-carboxylate synthase family protein (AHRD V3.3 *** B9GV\	ACS12	F:GO:0003824: P:G(	F:catalytic activity: P:biosynthetic process: F:pyridoxal phospha			PR00753 (PRINTS): IPR015422 (G3D	7,427	5,594	17,239	20,211	21,430									
Solyc08g079760	Cell cycle regulated microtubule associated protein (AHRD V3.3 *** AT4G22860.1)		C:GO:0005819: C:G(	C:spindle: C:microtubule: P:activation of protein kinase activity:			IPR027330 (PFAM): mobidb-lite (MOB	2,434	2,515	0,557	0,584	0,779									
Solyc08g079770	S-type anion channel (AHRD V3.3 *** A0A1C3RMF1_MEDTR)		P:GO:0006873: F:G(	P:cellular ion homeostasis: F:voltage-gated anion channel activ			IPR004695 (PFAM): IPR038665 (G3D	0,000	0,019	0,000	0,000	0,000									
Solyc08g079780	Blue copper protein, putative (AHRD V3.3 *** B9RBW4_RICCO)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	0,000	0,043	0,025	0,000	0,000									
Solyc08g079790	Nucleotide-sugar transporter family protein (AHRD V3.3 *** A0A061G5R7_THECC)		C:GO:0005794: F:G(	C:Golgi apparatus: F:pyrimidine nucleotide-sugar transmembran			IPR004853 (PFAM): PTHR44010 (PAN	7,765	5,836	1,281	1,244	1,150									
Solyc08g079800	Growth-regulating factor (AHRD V3.3 *-* B6UGM8_MAIZE)		F:GO:0005524: C:G(	F:ATP binding: C:nucleus: P:regulation of transcription, DNA-ten			IPR014977 (PFAM_GRF	0,019	0,019	0,000	0,000	0,000									
Solyc08g079810	obscurin-like protein (AHRD V3.3 *** AT1G73970.1)						PTHR36337 (PANTHER)	10,212	9,161	13,581	16,326	14,499									
Solyc08g079820	Nudix hydrolase (AHRD V3.3 *** A0A061G560_THECC)		F:GO:0016787	F:hydrolase activity			IPR000086 (PFAM): G3DSA:3.90.79.1	8,879	18,536	15,279	15,797	22,248	1,090	0,001	0,540	0,048			up	up	
Solyc08g079830	copper/zinc superoxide dismutase copper chaperone precursor	ccs	P:GO:0006801: P:G(	P:superoxide metabolic process: P:metal ion transport: F:metal			IPR036423 (G3DSA:2.60.40.GENE3D	10,452	9,912	34,263	30,476	27,968									
Solyc08g079840	subtilisin-like endoprotease	prp69	F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:2.60.40	3,181	5,445	0,187	0,246	0,164									
Solyc08g079850	P69F P69D protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	0,417	0,668	0,025	0,025	0,047									
Solyc08g079860	P69C protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR041469 (PF	0,038	0,104	0,022	0,122	0,046									
Solyc08g079870	subtilisin	p69b	F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	16,612	52,941	2,086	5,168	10,977	1,697	0,000	2,376	0,000	1,298	0,006	up	up	up
Solyc08g079880	P69C protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.30	0,241	0,100	0,245	0,332	0,422									
Solyc08g079890	P69e protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR041469 (PF	2,628	3,249	8,622	12,909	11,220									
Solyc08g079900	subtilisin-like protease		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	0,000	0,699	0,261	0,844	0,831									
Solyc08g079910	P69e protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	0,000	0,041	0,050	0,121	0,024									
Solyc08g079920	P69f protein		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	0,115	0,000	0,000	0,000	0,000									
Solyc08g079930	subtilisin-like protease		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): G3DSA:3.50.30	0,000	0,021	0,000	0,000	0,000									
Solyc08g079970	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR041469 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc08g079980	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR041469 (PF	0,264	6,103	0,194	0,073	0,188	4,519	0,000					up		
Solyc08g080000	Transmembrane protein, putative (AHRD V3.3 *-* A0A072U537_MEDTR)		F:GO:0005515	F:protein binding			IPR036872 (G3DSA:1.10.418.GENE3I	13,790	18,703	6,594	7,140	8,750									
Solyc08g080010	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR010259 (PF	2,450	1,926	0,888	1,258	0,920									
Solyc08g080030	Glyoxylate reductase (AHRD V3.3 *** A0A0B0NZ21_GOSAR)		F:GO:0016616: F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			G3DSA:3.40.50.720 (GENE3D): IPR0(	10,628	8,736	12,934	11,688	12,547									
Solyc08g080040	Anthocyanidin synthase (AHRD V3.3 *** A0A0A1E1Z9_9SOLA)	ANS	F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	2,812	1,978	1,889	2,015	1,676									
Solyc08g080050	PGRL1A transmembrane protein (AHRD V3.3 *** A0A0F7GZP2_9ROSI)		C:GO:0009535: P:G(	C:chloroplast thylakoid membrane: P:photosynthetic electron tra			PTHR31032:SF1 (PANTHER): IPR039	53,827	90,403	20,248	25,363	56,574	0,775	0,002	1,476	0,000			up	up	
Solyc08g080060	Expansin-like protein (AHRD V3.3 *** Q0WT83_ARATH)	EXPA17	C:GO:0005576: P:G(	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	0,019	0,036	0,022	0,000	0,023									
Solyc08g080070	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT4G22900.1)		C:GO:0016021	C:integral component of membrane			IPR010605 (PFAM): IPR010605 (PAN	0,097	0,151	0,025	0,022	0,046									
Solyc08g080080	WD40 repeat-containing protein (AHRD V3.3 *** A0A103XFY3_CYNCS)		F:GO:0005515: F:G(	F:protein binding: F:anaphase-promoting complex binding: F:ubi(			IPR024977 (PFAM): IPR015943 (G3D	21,863	13,641	25,594	29,070	21,906	-0,652	0,019					down		
Solyc08g080090	STAY-GREEN-like protein (AHRD V3.3 *** AT4G11910.1)	SGR	F:GO:0005515: C:G(	F:protein binding: C:chloroplast: P:chlorophyll catabolic process			IPR024438 (PFAM): PTHR31750:SF4	26,322	21,079	556,961	560,839	472,796									
Solyc08g080110	Protein FAM63A (AHRD V3.3 *** A0A151TJL9_CAJCA)		F:GO:0004843: F:G(	F:thiol-dependent u(	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR033979 (PFAM): mobidb-lite (MOB	31,562	30,423	35,058	35,420	32,680									
Solyc08g080120	Homeobox protein knotted-1, putative (AHRD V3.3 *** B9RC00_RICCO)	thox2	F:GO:0003677: C:G(	F:DNA binding: C:nucleus: P:regulation of transcription, DNA-ter			IPR005541 (PFAM_TALE	26,365	25,117	30,870	32,189	28,973									
Solyc08g080130	phospholipase PLDb1	pldb1	F:GO:0004630: F:G(	F:phospholipase D	EC:3.1.4.4	Phospholipase D	IPR011402 (PIRSF): IPR001736 (PFA	63,935	134,005	25,798	25,934	35,586									
Solyc08g080140	3,5-epimerase/4-reductase (AHRD V3.3 *** I3SMF8_MEDTR)		F:GO:0008830: F:G(	F:dTDP-4-dehydror	EC:5.1.3.13: EC:1.1.	dTDP-4-dehydrorhan	G3DSA:3.40.50.720 (GENE3D): IPR0;	249,907	211,072	34,635	24,807	34,772									
Solyc08g080150	TCP transcription factor 20	TCP20	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR017887 (PFAM_TCP	14,823	9,105	3,554	3,193	3,129									
Solyc08g080160	Hydroxymethylglutaryl-CoA synthase (AHRD V3.3 *-* F5CLC5_CATRO)		F:GO:0004421: P:G(	F:hydroxymethylglut	EC:2.3.3.1	Hydroxymethylglutary	IPR013746 (PFAM): IPR016039 (G3D	1,104	0,772	0,025	0,025	0,047									
Solyc08g080170	Hydroxymethylglutaryl-CoA synthase, putative (AHRD V3.3 *** B9RC08_RICCO)		F:GO:0004421: P:G(	F:hydroxymethylglut	EC:2.3.3.1	Hydroxymethylglutary	IPR010122 (TIGRFAM): IPR016039 ((	77,291	65,714	31,182	22,572	28,357									
Solyc08g080180	LOW QUALITY:Molybdenum cofactor sulfurase (AHRD V3.3 *** A0A0B2Q7C8_GLYSO)		F:GO:0003824	F:catalytic activity			IPR015422 (G3DSA:3.90.1150.GENE:	4,043	2,848	0,867	0,624	1,176									
Solyc08g080190	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G12570.1)		F:GO:0016614: F:G(	F:oxidoreductase activity, acting on CH-OH group of donors: F:			IPR036188 (G3DSA:3.50.50.GENE3D	0,741	0,829	0,072	0,025	0,116									
Solyc08g080200	SPX domain-containing family protein (AHRD V3.3 *** B9GW54_POPTR)		C:GO:0016021: F:G(	C:integral component of membrane: F:oxidoreductase activity, a			IPR000172 (PFAM): G3DSA:3.30.410	58,885	55,636	74,017	91,273	76,151									
Solyc08g080220	DNA-directed RNA polymerase subunit (AHRD V3.3 *** A0A0V0J1K4_SOLCH)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.6	DNA-directed RNA p(	PF11523 (PFAM): IPR007083 (PFAM)	23,032	17,114	24,800	28,414	24,912									
Solyc08g080225	ATP-dependent Clp protease (AHRD V3.3 --* AT1G33360.1)							1,635	1,291	2,016	1,813	1,550									
Solyc08g080230	Modifier of rudimentary (Mod(r)) protein (AHRD V3.3 --* AT2G36680.4)							0,038	0,083	0,122	0,097	0,095									
Solyc08g080240	NADH dehydrogenase 1 alpha subcomplex subunit 8 (AHRD V3.3 *** A0A0K9PKB1_ZOSMR)		C:GO:0005747: P:G(	C:mitochondrial respiratory chain complex I: P:mitochondrial ele			IPR010625 (PFAM): PTHR13344:SF2	0,308	0,406	0,463	0,612	0,447									
Solyc08g080250	APO protein 1 (AHRD V3.3 *** F4I896_ARATH)		F:GO:0003723	F:RNA binding			IPR023342 (PFAM): PTHR10388:SF5	2,471	2,840	6,367	5,858	5,553									
Solyc08g080260	Nuclear pore complex protein Nup50 (AHRD V3.3 *** A0A0B2RK82_GLYSO)		P:GO:0046907	P:intracellular transport			IPR000156 (PFAM): IPR011993 (G3D	17,237	17,971	24,859	25,850	25,498									
Solyc08g080270	UDP-galactose transporter (AHRD V3.3 *** M4QC22_PRUPE)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM): PTHR10778:SF1!	0,633	0,437	0,737	1,041	0,542									
Solyc08g080280	FAM91 carboxy-terminus protein (AHRD V3.3 --* AT1G35220.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,422	0,904	0,046	0,120	0,047									
Solyc08g080290	Dehydration responsive element binding transcription factor (AHRD V3.3 *** W6FIY4_9ROSA)		F:GO:0003677: F:G(	F:DNA binding: F:DNA-binding transcription factor activity: P:rec			IPR036955 (G3DS_ERF	0,347	0,715	0,344	0,488	0,537									
Solyc08g080320	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** BAG2_ARATH)		F:GO:0051087	F:chaperone binding			IPR000626 (PFAM): IPR003103 (PFA	0,596	0,502	0,230	0,289	0,236									
Solyc08g080340	Membrane bound O-acyl transferase family protein (AHRD V3.3 *** B9GW66_POPTR)		C:GO:0016021: F:G(	C:integral component of membrane: F:transferase activity, trans			IPR004299 (PFAM): PTHR13906 (PAN	14,408	11,631	6,062	5,128	5,763									
Solyc08g080360	F-box protein PP2-B1		F:GO:0005515	F:protein binding			IPR025886 (PFAM): PTHR31960:SF2	21,244	50,428	21,739	19,957	23,983	1,274	0,000					up		
Solyc08g080370	N2-acetylornithine aminotransferase (AHRD V3.3 *** A0A0G2SJJ3_SOLLC)		P:GO:0006525: F:G(	P:arginine metabolic process: F:transaminase activity: F:pyrido			IPR005814 (PFAM): IPR015422 (G3D	45,403	39,185	45,759	43,945	46,109									
Solyc08g080375	DEAD-box ATP-dependent RNA helicase 13 (AHRD V3.3 --* A0A1D1YAB5_9ARAE)							0,740	0,707	0,717	0,622	0,775									
Solyc08g080380	Cytochrome P450 (AHRD V3.3 *** A0A0N9HM28_9MAGN)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	7,357	7,588	4,644	5,464	7,005									
Solyc08g080390	Cytochrome P450 (AHRD V3.3 *** A0A0N9HM28_9MAGN)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	13,034	8,970	26,956	25,031	24,929									
Solyc08g080400	GRAS family transcription factor (AHRD V3.3 *** A0A061G628_THECC)	GRAS	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR005202 (PFAM_GRAS	2,037	1,441	2,938	3,615	3,168									
Solyc08g080410	UBX domain-containing protein		F:GO:0005515	F:protein binding			PF14555 (PFAM): G3DSA:1.10.8.10 ((	85,015	102,204	154,485	146,146	143,848									
Solyc08g080420	GPI transamidase subunit PIG-U (AHRD V3.3 *** AT1G63110.1)		P:GO:0016255: C:G(	P:attachment of GPI anchor to protein: C:GPI-anchor transamid			IPR009600 (PFAM): IPR009600 (PAN	46,936	40,653	67,996	68,896	63,337									
Solyc08g080430	Cytochrome P450 family protein (AHRD V3.3 *** B9GKM6_POPTR)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	0,105	0,233	0,100	0,000	0,023									
Solyc08g080440	Generative cell specific-1 (AHRD V3.3 *-* A0A061G636_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,113	0,157	0,000	0,000	0,024									
Solyc08g080450	Generative cell specific-1 (AHRD V3.3 *** A0A061G636_THECC)		C:GO:0016021	C:integral component of membrane			IPR018928 (PFAM): IPR040326 (PAN	0,037	0,077	0,025	0,000	0,000									
Solyc08g080460	MAP kinase kinase kinase 65	MAPKKK65	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PRINTS): IPR000014 (PF	0,000	0,061	0,000	0,000	0,000									
Solyc08g080470	SUN-like protein 23	SUN23	F:GO:0005515	F:protein binding			IPR000048 (PFAM): IPR025064 (PFA	49,682	86,004	45,119	53,766	57,281	0,819	0,005					up		
Solyc08g080480	Monomeric alpha-amylase inhibitor (AHRD V3.3 --* C4P627_TRIDC)		F:GO:0045735	F:nutrient reservoir activity			IPR000617 (PRINTS): IPR016140 (PF	84,246	109,620	8,815	19,405	1,298									
Solyc08g080490	Grain softness protein (AHRD V3.3 -** G8CLQ8_9POAL)		F:GO:0045735	F:nutrient reservoir activity			IPR000617 (PRINTS): IPR016140 (PF	1452,814	1480,606	38,091	87,036	4,936									
Solyc08g080500	Rhomboid-like protein (AHRD V3.3 *** K4CP50_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR035952 (G3DSA:1.20.1540.GENE:	95,287	136,921	100,535	101,529	100,976									
Solyc08g080510	Replication factor C subunit 2 (AHRD V3.3 *** RFC2_ARATH)		F:GO:0003677: F:G(	F:DNA binding; F:ATP binding; P:DNA replication			G3DSA:1.10.8.60 (GENE3D): G3DSA:	12,166	20,297	10,183	8,701	9,705	0,765	0,005					up		
Solyc08g080520	DNA topoisomerase 4 subunit B (DUF810) (AHRD V3.3 *** AT4G11670.2)						PF05664 (PFAM): IPR008528 (PANTH	26,483	25,121	36,970	42,946	38,332									
Solyc08g080540	SolycHsfB2b	HSF-10	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR000232 (PRIN_HSF	23,911	9,300	12,840	20,847	14,275	-1,335	0,000			0,699	0,005	down		up
Solyc08g080550	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9RC60_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	16,228	18,181	36,372	30,272	36,017									
Solyc08g080560	CASP-like protein (AHRD V3.3 *** V4TQ43_9ROSI)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR33573 (PAN	0,212	0,094	0,275	0,322	0,096									
Solyc08g080570	UDP-glucose 4-epimerase (AHRD V3.3 *** GALE1_PEA)		F:GO:0003978: P:G(	F:UDP-glucose 4-e(	EC:5.1.3.2	UDP-glucose 4-epim(	G3DSA:3.90.25.10 (GENE3D): IPR00!	66,650	76,307	187,821	235,082	215,953									
Solyc08g080580	Myb (AHRD V3.3 *** Q948S4_TOBAC)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM_MYB	4,622	3,739	4,034	3,982	3,904									
Solyc08g080585	Thaumatin-like protein (AHRD V3.3 *** TLP_ACTDE)						IPR001938 (PRINTS): IPR001938 (PII	0,261	0,776	0,466	0,488	0,166									
Solyc08g080620	PR-5x	pr5	C:GO:0005737: P:G(	C:cytoplasm: P:killing of cells of other organism: P:defense resp			IPR001938 (PRINTS): IPR037176 (G3	0,021	0,018	0,000	0,000	0,023									
Solyc08g080630	Ethylene-responsive proteinase inhibitor 1 (AHRD V3.3 *** IER1_SOLLC)		F:GO:0004867: P:G(	F:serine-type endopeptidase inhibitor activity: P:response to wo			IPR000864 (PRINTS): IPR000864 (PF	0,534	0,511	21,647	12,711	10,348									
Solyc08g080640	Osmotin-like protein (Fragment) IPR017949 Thaumatin, conserved site IPR00193	np24	C:GO:0005737: P:G(	C:cytoplasm: P:killing of cells of other organism: P:defense resp			IPR001938 (PRINTS): IPR037176 (G3	4,221	4,359	190,228	161,880	159,032									
Solyc08g080650	Osmotin-like protein (Fragment) IPR001938 Thaumatin, pathogenesis-related	PRP23	C:GO:0005737: P:G(	C:cytoplasm: P:killing of cells of other organism: P:defense resp			IPR001938 (PRINTS): IPR001938 (PII	49,498	28,673	382,390	190,793	239,052					-1,001	0,001			down
Solyc08g080660	Osmotin-like protein (AHRD V3.3 *** OLPA_TOBAC)		P:GO:0006952: P:G(	P:defense response; P:response to biotic stimulus			IPR001938 (PRINTS): IPR001938 (PII	0,310	0,299	1,476	0,932	0,805									
Solyc08g080670	Pathogenesis-related 5-like protein	PR-5	P:GO:0006952: P:G(	P:defense response; P:response to biotic stimulus			IPR001938 (PRINTS): IPR037176 (G3	0,240	0,175	11,796	9,775	6,829									
Solyc08g080680	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** A0A0K9PV75_ZOSMR)						IPR035892 (G3DSA:2.60.40.GENE3D	10,539	10,531	13,165	12,312	8,891			-0,572	0,044				down	
Solyc08g080690	Methyl-CpG-binding domain protein (AHRD V3.3 *-* A0A072U5A2_MEDTR)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			G3DSA:3.30.890.10 (GENE3D): G3DS	111,111	76,219	100,227	96,133	103,696									
Solyc08g080700	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)						IPR004314 (PFAM): PTHR31589:SF2	1,056	0,908	0,000	0,000	0,000									
Solyc08g080720	Selenoprotein H (AHRD V3.3 *-* A0A0B0P3H0_GOSAR)		C:GO:0005737	C:cytoplasm			IPR011893 (TIGRFAM): IPR011893 (F	8,783	10,734	15,029	11,486	12,190									
Solyc08g080730	Tetraspanin family protein (AHRD V3.3 *** A0A072TVY8_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	2,634	1,988	0,882	0,702	0,568									
Solyc08g080745	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)						IPR025521 (PFAM): IPR004314 (PFA	0,197	0,483	0,000	0,000	0,000									
Solyc08g080750	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)						IPR007612 (PFAM): IPR038595 (G3D	2,528	3,123	0,749	1,172	1,390									
Solyc08g080770	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)						IPR007612 (PFAM): IPR038595 (G3D	0,000	0,000	0,151	0,124	0,094									
Solyc08g080780	Myosin heavy chain-related protein, putative (AHRD V3.3 *** A0A061GCE0_THECC)		P:GO:0016539	P:intein-mediated protein splicing			IPR019448 (PFAM): mobidb-lite (MOB	62,194	44,396	18,892	17,690	20,243									
Solyc08g080790	LOW QUALITY:carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)						IPR004314 (PFAM): IPR025521 (PFA	0,058	0,019	0,000	0,000	0,000									
Solyc08g080810	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)						IPR025521 (PFAM): IPR004314 (PFA	0,019	0,079	0,000	0,000	0,000									
Solyc08g080830	Receptor kinase, putative (AHRD V3.3 *** B9RC93_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR032675 (G3DSA:3.80.10.GENE3D	33,964	33,247	10,439	11,672	16,246									
Solyc08g080840	LOW QUALITY:carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)						IPR004314 (PFAM): PTHR31589:SF2	0,059	0,134	0,000	0,000	0,000									
Solyc08g080850	Serine/threonine-protein kinase RIO1 (AHRD V3.3 *** K4CP83_SOLLC)		F:GO:0004674	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR017407 (PIRSF): G3DSA:1.10.510	18,763	21,205	17,849	17,363	17,151									
Solyc08g080860	patatin-like phospholipase domain protein (AHRD V3.3 *** AT1G76980.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,871	0,713	2,421	3,063	2,154									
Solyc08g080870	heavy metal atpase 5 (AHRD V3.3 *** AT1G63440.1)		F:GO:0000166: P:G(	F:nucleotide bindinc	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (PRIN	0,122	0,117	0,022	0,025	0,023									
Solyc08g080880	LOW QUALITY:F-box/RNI-like/FBD-like domains-containing protein (AHRD V3.3 --* AT1G16930.3)							0,000	0,019	0,000	0,000	0,000									
Solyc08g080890	heavy metal atpase 5 (AHRD V3.3 *** AT1G63440.1)		F:GO:0000166: C:G(	F:nucleotide bindinc	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	PR00119 (PRINTS): PR00943 (PRINT	2,984	1,895	0,239	0,126	0,234									
Solyc08g080900	Glutathione S-transferase family protein (AHRD V3.3 *** B9GKJ1_POPTR)	GSTT2	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	29,712	43,879	48,678	45,497	48,424	0,589	0,045					up		
Solyc08g080910	Glutathione S-transferase family protein (AHRD V3.3 *** B9GKJ1_POPTR)	GSTT3	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	10,867	12,443	19,472	21,227	18,794									
Solyc08g080920	Phosphopantothenoylcysteine decarboxylase (AHRD V3.3 *** W9RGR9_9ROSA)		F:GO:0003824	F:catalytic activity			IPR003382 (PFAM): IPR036551 (G3D	16,284	14,389	25,155	25,472	24,493									
Solyc08g080930	Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *** W9R3A3_9ROSA)		P:GO:0006486: F:G(	P:protein glycosylation: F:transferase activity, transferring glyco			IPR040911 (PFAM): PTHR11062:SF4	0,040	0,000	0,000	0,000	0,000									
Solyc08g080940	glutathione peroxidase like encoding 1	gpxle1	F:GO:0004602: P:G(	F:glutathione peroxi	EC:1.11.1.9: EC:1.1	Glutathione peroxida	IPR000889 (PRINTS): IPR000889 (PII	124,375	164,325	317,295	366,769	330,636									
Solyc08g080950	Ripening related protein family (AHRD V3.3 *** G7L3L3_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR036908 (G3DSA:2.40.40.GENE3D	0,000	0,000	0,071	0,022	0,023									
Solyc08g080960	AT hook motif DNA-binding family protein, putative (AHRD V3.3 *** A0A061G6C0_THECC)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	14,730	10,842	45,245	45,715	40,388									
Solyc08g080970	Periplasmic binding protein-like II (AHRD V3.3 --* I0Z2M4_COCSC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,037	0,000	0,000	0,000	0,000									
Solyc08g080980	Weak chloroplast movement under blue light 1-like protein (AHRD V3.3 --* A0A0B0MKQ7_GOSAR)							1,089	1,400	1,692	2,247	1,415									
Solyc08g080990	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G18000.1)		F:GO:0003677	F:DNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,395	0,204	0,100	0,025	0,047									
Solyc08g081000	Transcription factor jumonji (JmjC) domain protein (AHRD V3.3 *** G7KC35_MEDTR)		F:GO:0003677	F:DNA binding			IPR001606 (PFAM): IPR013083 (G3D	48,700	42,826	51,154	57,997	55,058									
Solyc08g081010	gamma-glutamylcysteine synthetase 1	gsh1	F:GO:0004357: P:G(	F:glutamate-cystein	EC:6.3.2.2	Glutamate--cysteine	IPR011556 (TIGRFAM): IPR006336 (F	70,806	71,608	540,224	599,149	475,271									
Solyc08g081020	LOW QUALITY:carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *-* AT5G18460.1)						IPR004314 (PFAM): PTHR31589 (PAN	0,097	0,135	0,000	0,000	0,000									
Solyc08g081030	LOW QUALITY:Haloacid dehalogenase-like hydrolase superfamily protein (AHRD V3.3 *** A0A061EYI4_THE		F:GO:0016787	F:hydrolase activity			IPR023214 (G3DSA:3.40.50.GENE3D	41,641	64,756	96,521	79,411	88,131	0,663	0,010					up		
Solyc08g081040	RNA polymerase I largest subunit (AHRD V3.3 --* D0VYF6_9POAL)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR007175 (PFAM): mobidb-lite (MOB	1,218	1,184	0,553	0,318	0,449									
Solyc08g081050	Bromo-adjacent-like (BAH) domain protein (AHRD V3.3 *** G7KC24_MEDTR)		F:GO:0003682: P:G(	F:chromatin binding; P:transcription, DNA-templated			IPR003618 (PFAM): IPR001025 (PFA	16,375	13,882	19,376	18,299	17,410									
Solyc08g081060	DUF3527 domain protein (AHRD V3.3 *** A0A072UCU8_MEDTR)						IPR021916 (PFAM): mobidb-lite (MOB	14,690	11,862	5,615	5,193	6,575									
Solyc08g081070	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT4G11440.2)		F:GO:0022857	F:transmembrane transporter activity			IPR023395 (G3DSA:1.50.40.GENE3D	24,916	17,387	7,843	5,066	6,571									
Solyc08g081080	structural maintenance of chromosomes-like protein, putative (DUF3531) (AHRD V3.3 *** AT5G08400.2)						IPR021920 (PFAM): PTHR33102 (PAN	9,439	10,569	13,637	12,371	13,194									
Solyc08g081100	Kinesin-like protein (AHRD V3.3 *-* A0A059CH08_EUCGR)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	9,039	9,090	8,065	9,380	8,712									
Solyc08g081120	Kinesin-like protein (AHRD V3.3 *** A0A061G4H7_THECC)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR036961 (G3DSA:3.40.850.GENE3I	7,101	7,049	5,931	7,843	5,881									
Solyc08g081130	Myc-type, basic helix-loop-helix (BHLH) domain-containing protein (AHRD V3.3 *-* A0A103XRA7_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	13,323	10,856	17,703	14,443	14,823									
Solyc08g081140	bHLH transcription factor 090	JAF13	F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM_bHLH	14,282	12,273	7,261	6,038	9,173									
Solyc08g081150	GMP synthase (AHRD V3.3 *** W8TFM6_TOBAC)		F:GO:0003922: F:G(	F:GMP synthase (g	EC:6.3.5.2	GMP synthase (gluta	IPR014729 (G3DSA:3.40.50.GENE3D	22,369	23,312	8,539	6,315	7,386									
Solyc08g081155	GMP synthase (AHRD V3.3 *** W8TFM6_TOBAC)		F:GO:0003922: F:G(	F:GMP synthase (g	EC:6.3.5.2	GMP synthase (gluta	PR00097 (PRINTS): PR00096 (PRINT	23,560	20,387	9,156	6,809	7,471									

Solyc08g081160	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein (AHRD V3.3 *** A0A072TN99_MEDTR)				IPR025486 (PFAM): IPR022212 (PFA	19,836	16,964	9,396	7,525	10,242									
Solyc08g081170	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase (AHRD V3.3 *** W9QPL2_9ROSA	F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:regulation of cell shape; P:biosy	G3DSA:3.40.1390.10 (GENE3D): IPR(	17,296	15,914	100,518	101,864	91,205									
Solyc08g081180	Signal peptide peptidase-like protein (AHRD V3.3 *** A0A072UBU3_MEDTR)		F:GO:0004190; C:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR007369 (PFAM): G3DSA:3.50.30.3	69,329	42,709	154,725	176,156	144,991	-0,670	0,011					down		
Solyc08g081190	plasma membrane intrinsic protein 1.5	PIP1.5	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS): IPR023271 (G3	635,068	369,493	1289,652	1284,217	1138,702	-0,753	0,020					down		
Solyc08g081195	heavy metal atpase 3 (AHRD V3.3 --* AT4G30120.2)					2,025	1,527	5,335	3,286	3,093									
Solyc08g081200	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G11410.1)		F:GO:0016630; P:G(	F:protochlorophyllid EC:1.3.1.33 Protochlorophyllide r	IPR002347 (PRINTS): IPR002347 (PF	31,383	31,958	27,148	28,496	27,978									
Solyc08g081210	MAP kinase kinase kinase 66	MAPKKK66	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:1.10.510	17,271	18,941	9,722	11,471	10,443									
Solyc08g081220	Cytochrome P450 (AHRD V3.3 *** A0A103XJH9_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR001128 (PRINTS): IPR002401 (PF	184,461	115,637	0,099	0,150	0,047									
Solyc08g081230	BTB/POZ domain-containing protein (AHRD V3.3 *** W9R367_9ROSA)		F:GO:0005515; P:G(	F:protein binding; P:protein homooligomerization	IPR015943 (G3DSA:2.130.10.GENE3I	40,572	25,901	13,973	21,306	13,524					0,610	0,010			up
Solyc08g081240	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** A0A061GCL9_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	49,543	73,404	50,034	55,226	57,446									
Solyc08g081250	Peptidase M1 family aminopeptidase N (AHRD V3.3 *** A0A072TU77_MEDTR)		P:GO:0006508	P:proteolysis	IPR035414 (PFAM): IPR027268 (G3D	324,894	312,014	489,716	477,845	458,063									
Solyc08g081260	Disease resistance protein (TIR-NBS class) (AHRD V3.3 *** A0A061FNY9_THECC)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding	IPR002182 (PFAM): G3DSA:3.40.50.3	1,213	1,761	0,090	0,360	0,258									
Solyc08g081265	Flowering-promoting factor 1-like protein 3 (AHRD V3.3 --* FLP3_ORYSJ)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,253	0,218	0,171	0,259	0,167									
Solyc08g081270	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A072TMX8_MEDTR)		F:GO:0005524; P:G(	F:ATP binding; P:ubiquitin-dependent protein catabolic process;	IPR016135 (G3DSA:3.10.110.GENE3I	18,333	16,354	39,016	39,657	36,010									
Solyc08g081280	CDK activating kinase (AHRD V3.3 *** A7M6H0_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:3.30.200	15,438	16,770	42,888	54,131	41,058					0,339	0,049			up
Solyc08g081290	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** A0A118JWJ3_CYNCS)		F:GO:0003677	F:DNA binding	IPR001606 (PFAM): IPR036431 (G3D	20,588	17,499	18,940	17,849	17,729									
Solyc08g081300	RING/U-box superfamily protein (AHRD V3.3 *** AT5G41350.2)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:cytosol; P:protein ubic	IPR013083 (G3DSA:3.30.40.GENE3D	19,256	17,540	28,727	33,535	26,577									
Solyc08g081310	histone deacetylase complex subunit (AHRD V3.3 *** AT1G19330.2)		F:GO:0005515	F:protein binding	IPR038291 (G3DSA:1.10.720.GENE3I	82,502	47,709	28,256	33,438	34,293	-0,762	0,006					down		
Solyc08g081320	Beta-adaptin-like protein (AHRD V3.3 *** K4CPC9_SOLLC)		P:GO:0006886; P:G(	P:intracellular protein transport; P:vesicle-mediated transport; C	IPR016342 (PIRSF): IPR008152 (PFA	250,717	207,703	170,354	171,226	173,015									
Solyc08g081330	GPN-loop GTPase 1 (AHRD V3.3 *** A0A0B0MIT7_GOSAR)		F:GO:0003924	F:GTPase activity EC:3.6.1.15 Nucleoside-triphosph	IPR004130 (PFAM): G3DSA:3.40.50.3	76,308	66,497	92,536	81,530	83,172									
Solyc08g081340	DNA repair helicase XPB1-like protein (AHRD V3.3 *** AT5G41370.1)		F:GO:0003677; F:G(	F:DNA binding; F:A EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	PR00851 (PRINTS): IPR032830 (PFA	78,220	70,987	140,201	140,475	132,627									
Solyc08g081350	LOW QUALITY:Zinc finger protein CONSTANS-LIKE 3 (AHRD V3.3 *** W9QPI7_9ROSA)		F:GO:0005515	F:protein binding	IPR010402 (PFAM): PTHR31319 (PAN	0,061	0,083	0,049	0,145	0,117									
Solyc08g081360	PLAC8 family protein (AHRD V3.3 *** AT4G23470.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,078	0,054	0,147	0,073	0,070									
Solyc08g081380	BTB/POZ domain-containing protein (AHRD V3.3 *** AT1G63850.1)		F:GO:0005515	F:protein binding	G3DSA:3.30.710.10 (GENE3D): mobic	0,019	0,000	0,000	0,000	0,000									
Solyc08g081385	BEL1-like homeodomain 2 (AHRD V3.3 *-* AT4G36870.4)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	G3DSA:1.10.10.60 (GENE3D): IPR00(	6,415	7,261	6,233	6,584	6,358									
Solyc08g081390	Phosphoglycerate mutase family protein (AHRD V3.3 *** A0A061G5H4_THECC)		F:GO:0003824	F:catalytic activity	IPR029033 (G3DSA:3.40.50.GENE3D	1,150	1,374	0,097	0,248	0,424									
Solyc08g081400	Homeobox protein BEL1 like (AHRD V3.3 *-* A0A0B2QVN2_GLYSO)	bl3	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-templated	TALE	3,064	3,584	2,543	3,725	3,136									
Solyc08g081410	Golgin candidate 6 (AHRD V3.3 *** W9SQ07_9ROSA)		C:GO:0000139; P:G(	C:Golgi membrane; P:intracellular protein transport; F:protein tra	IPR006955 (PFAM): IPR011989 (G3D	99,788	85,642	118,483	110,408	113,929									
Solyc08g081420	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)		C:GO:0016021	C:integral component of membrane	G3DSA:3.90.550.50 (GENE3D): IPR0(	52,230	36,446	21,463	20,167	23,942									
Solyc08g081430	Import inner membrane translocase subunit tim21, mitochondrial, putative (AHRD V3.3 *** B9RD27_RICCO)		C:GO:0005744; P:G(	C:TIM23 mitochondrial import inner membrane translocase com	IPR013261 (PFAM): IPR038552 (G3D	13,855	14,017	18,918	20,198	19,027									
Solyc08g081440	LOW QUALITY:Pentatricopeptide repeat-containing protein, mitochondrial (AHRD V3.3 --* A0A0B2R362_GLYSO)					0,000	0,000	0,050	0,000	0,024									
Solyc08g081450	Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *-* AT5G41470.1)		C:GO:0016021	C:integral component of membrane	G3DSA:3.10.450.50 (GENE3D): PTHR	0,257	0,374	0,313	0,100	0,236									
Solyc08g081457	IQ-domain 28 (AHRD V3.3 --* AT1G14380.7)					0,061	0,107	0,320	0,196	0,286									
Solyc08g081470	3-isopropylmalate dehydratase large subunit (AHRD V3.3 *** A0A0B0Q086_GOSAR)		P:GO:0043622	P:cortical microtubule organization	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,769	5,299	0,047	0,022	0,164	1,612	0,002					up		
Solyc08g081480	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G23500.1)	PG56-1	F:GO:0004650; P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3I	1,557	2,235	1,548	2,229	2,044									
Solyc08g081490	mitogen-activated protein kinase 7	mapk7			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,124	0,050	0,025	0,000									
Solyc08g081495	Mitogen-activated protein kinase (AHRD V3.3 *** A0A0V0I7N7_SOLCH)		F:GO:0003677; F:G(	F:DNA binding; F:protein kinase activity; F:ATP binding; P:prote	IPR000719 (PFAM): IPR001005 (PFA	3,632	8,651	2,870	3,481	3,433	1,276	0,004					up		
Solyc08g081500	LETHM1	R2R3MYB103/THM1	F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 MYB	0,000	0,019	0,000	0,000	0,000									
Solyc08g081520	LOW QUALITY:Plant/F1M20-13 protein (AHRD V3.3 *** A0A072TUL8_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR008511 (PFAM): PTHR31509 (PAN	1,290	2,134	0,982	1,645	1,932									
Solyc08g081530	monodehydroascorbate reductase	mdhar	F:GO:0016491; F:G(	F:oxidoreductase activity; F:flavin adenine dinucleotide binding;	PR00411 (PRINTS): PR00368 (PRINT	61,579	55,742	94,803	88,759	89,044									
Solyc08g081540	1-aminocyclopropane-1-carboxylate synthase 1A	ACS1B	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	PR00753 (PRINTS): IPR004839 (PFA	1,361	1,715	3,255	3,657	3,537									
Solyc08g081550	1-aminocyclopropane-1-carboxylate synthase (AHRD V3.3 *-* Q96579_SOLLC)	ACS1A	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	PR00753 (PRINTS): IPR015421 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc08g081555	1-aminocyclopropane-1-carboxylate synthase (AHRD V3.3 *-* Q96579_SOLLC)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	PR00753 (PRINTS): IPR004839 (PFA	22,390	21,420	68,047	76,986	81,003									
Solyc08g081560	LOW QUALITY:DNA-directed RNA polymerase subunit alpha (AHRD V3.3 *-* RPOA_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA p(	IPR011773 (PANTHER): IPR036603 (	0,000	0,081	0,025	0,124	0,118									
Solyc08g081570	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (AHRD V3.3 *** K4CPF3_S(	MCS	F:GO:0008685; P:G(	F:2-C-methyl-D-ery EC:4.6.1.12 2-C-methyl-D-erythrit	IPR003526 (PFAM): IPR036571 (G3D	23,699	29,580	33,362	32,965	40,079									
Solyc08g081580	D111/G-patch domain-containing protein (AHRD V3.3 *** AT1G63980.2)		F:GO:0003676	F:nucleic acid binding	IPR000467 (PFAM): mobidb-lite (MOB	117,499	111,166	107,065	110,616	102,362									
Solyc08g081590	DNA topoisomerase 6 subunit A (AHRD V3.3 *** TOP6A_ARATH)		P:GO:0000737; F:G(	P:DNA catabolic process, endonucleolytic; F:DNA binding; F:cat	IPR002815 (PRINTS): IPR013048 (PF	0,019	0,000	0,000	0,000	0,000									
Solyc08g081610	WRKY family transcription factor, putative (AHRD V3.3 *** A0A061G6N0_THECC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (PFAM WRKY	0,019	0,264	0,075	0,000	0,024									
Solyc08g081620	LEU13054 endo-1,4-beta-glucanase precursor	cel1	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	1,502	2,386	21,927	46,869	30,475					1,097	0,000			up
Solyc08g081630	WRKY transcription factor 56	WRKY56	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR003657 (PFAM WRKY	0,358	0,294	0,312	0,271	0,353									
Solyc08g081640	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G11270.2)		F:GO:0005515	F:protein binding	IPR001680 (PFAM): IPR015943 (G3D	51,508	38,604	53,180	52,701	52,313									
Solyc08g081650	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RJN8_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PFAM AP2	2,820	3,373	1,580	1,292	1,977									
Solyc08g081660	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 --* NDHH_ORYNI)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; C:nucleus; P:regulation of transcription, DNA		0,000	0,018	0,047	0,148	0,071									
Solyc08g081670	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RJN8_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR036955 (G3DS AP2	5,861	5,474	6,993	8,025	6,460									
Solyc08g081680	Protein LURP-one-related 17 (AHRD V3.3 *** A0A0B2R169_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR007612 (PFAM): IPR038595 (G3D	0,000	0,136	0,134	0,098	0,233									
Solyc08g081690	NADPH oxidase	rboh1	F:GO:0004601; F:G(	F:peroxidase activi EC:1.11.1.7 Peroxidase	IPR000778 (PRINTS): G3DSA:1.10.23	8,839	7,701	1,272	2,570	3,761			1,536	0,000				up	
Solyc08g081700	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycofamily protein, putative (AHRD V3.3		C:GO:0016021	C:integral component of membrane	PTHR31852 (PANTHER): PTHR31852	0,299	0,405	0,047	0,095	0,119									
Solyc08g081710	membrane-associated kinase regulator (AHRD V3.3 *** AT1G64080.1)		C:GO:0005886	C:plasma membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,515	0,936	0,315	0,294	0,141									
Solyc08g081730	Reticulon-like protein (AHRD V3.3 *** K4CPG9_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me	IPR003388 (PFAM): mobidb-lite (MOB	238,685	226,224	198,443	167,990	173,437									
Solyc08g081740	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G64110.5)		F:GO:0005524	F:ATP binding	G3DSA:3.40.50.300 (GENE3D): G3DS	1,836	1,209	0,578	0,842	0,286									
Solyc08g081750	CAAX amino terminal protease family protein (AHRD V3.3 *** AT5G60750.1)		C:GO:0016020	C:membrane	IPR003675 (PFAM): PTHR43592 (PAN	7,433	10,840	15,673	17,067	16,154									
Solyc08g081760	Loricrin-like (AHRD V3.3 *** A0A0K9PKU0_ZOSMR)				PTHR31827 (PANTHER): PTHR31827	430,159	313,409	244,912	244,019	249,632									
Solyc08g081770	GDT1-like protein (AHRD V3.3 *** G7KAQ7_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR001727 (PFAM): IPR001727 (PAN	9,313	12,841	19,073	21,595	23,158									
Solyc08g081780	Dirigent protein		C:GO:0016021; C:G(	C:integral component of membrane; C:apoplast	IPR004265 (PFAM): PTHR21495 (PAN	0,000	0,000	0,000	0,025	0,046									
Solyc08g081790	Dirigent protein (AHRD V3.3 *** K4CPH5_SOLLC)		C:GO:0048046	C:apoplast	IPR004265 (PFAM): PTHR21495 (PAN	0,801	0,399	0,599	0,427	0,545									
Solyc08g081810	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR006153 (PFAM): IPR038770 (G3D	0,445	0,336	2,275	2,633	2,202									
Solyc08g081820	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR038770 (G3DSA:1.20.1530.GENE	7,950	6,400	3,563	1,350	2,846					-1,389	0,004			down
Solyc08g081830	Intracellular protein transporter USO1-like protein (AHRD V3.3 *** G7KAQ1_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	11,521	8,953	13,760	15,086	16,125									
Solyc08g081840	BTB/POZ domain-containing POB1-like protein (AHRD V3.3 *** A0A0B0N127_GOSAR)		C:GO:0005634; P:G(	C:nucleus; P:response to red light	IPR011705 (PFAM): G3DSA:1.25.40.4	5,018	4,576	3,699	4,019	4,138									
Solyc08g081850	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT4G23720.1)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane	IPR010605 (PFAM): IPR010605 (PAN	0,042	0,171	0,565	1,305	0,771									
Solyc08g081890	ABC transporter family protein (AHRD V3.3 *** U5FPJ5_POPTR)	ABCC7	F:GO:0005524; C:G(	F:ATP binding; C:in EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	24,076	15,391	80,463	93,505	71,421									
Solyc08g081900	Translation initiation factor 2 (AHRD V3.3 *** A0A097PN59_SOLLC)		F:GO:0003743; F:G(	F:translation initiati EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR000178 (TIGRFAM): IPR038495 ((	63,295	52,581	103,071	95,318	100,061									
Solyc08g081910	V-type proton ATPase subunit E (AHRD V3.3 *** VATE_CITUN)		P:GO:0015991; C:G(	P:ATP hydrolysis c(EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR002842 (PFAM): IPR038495 (G3D	5,499	5,357	10,821	10,474	10,574									
Solyc08g081920	beta 1,3-glycosyltransferase-like protein 1	AJ457975	P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR002659 (PFAM): PTHR11214:SF2	30,478	25,847	35,083	32,457	31,938									
Solyc08g081925	Hexosyltransferase (AHRD V3.3 *-* Q8RW34_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR002659 (PFAM): IPR002659 (PAN	26,006	22,221	30,886	29,010	28,757									
Solyc08g081930	Aldose 1-epimerase, putative (AHRD V3.3 *** B9RCN0_RICCO)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:isomerase activity; F:carb	IPR025532 (PIRSF): IPR014718 (G3D	16,681	16,531	13,158	15,848	15,465									
Solyc08g081940	LRR receptor-like kinase (AHRD V3.3 *** A0A072TUR7_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): IPR032675 (G3D	25,921	13,322	3,435	2,646	3,087									
Solyc08g081950	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A0K9P4K6_ZOSMR)		F:GO:0004839; F:G(	F:ubiquitin activatin EC:6.2.1.45 E1 ubiquitin-activatin	IPR016135 (G3DSA:3.10.110.GENE3I	520,726	456,549	377,681	349,538	364,133									
Solyc08g081960	Solanum Lycopersicum Cytokinin Response Factor 2	CRF2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,337	0,094	0,047	0,126	0,234									
Solyc08g081990	Ubiquitin ligase protein cop1, putative isoform 1 (AHRD V3.3 *** A0A061G5T1_THECC)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR015943 (G3	41,505	35,427	29,710	32,655	36,301									
Solyc08g082000	Homeobox-leucine zipper HOX24 (AHRD V3.3 *-* A0A0B0P867_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	10,073	8,650	7,620	7,814	8,525									
Solyc08g082010	Myosin heavy chain-like protein (AHRD V3.3 *** Q9FJ35_ARATH)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): mobidb-lite (MOB	70,447	45,456	50,440	51,813	45,508	-0,605	0,022					down		
Solyc08g082020	Mitochondrial substrate carrier family protein (AHRD V3.3 *** B9I8V0_POPTR)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS): IPR018108 (PF	32,435	33,980	63,728	64,366	59,779									
Solyc08g082040	Extra-large G-like protein (AHRD V3.3 *** G7L422_MEDTR)				IPR021480 (PFAM): mobidb-lite (MOB	6,316	8,099	3,610	4,457	4,575									
Solyc08g082050	UBX domain-containing protein (AHRD V3.3 *** M1CVT0_SOLTU)		F:GO:0005515	F:protein binding	G3DSA:3.40.30.10 (GENE3D): IPR00	0,019	0,076	0,000	0,022	0,000									
Solyc08g082060	Trichome birefringence-like protein (AHRD V3.3 *** A0A072TUJ8_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR026057 (PFAM): IPR025846 (PFA	17,130	11,323	4,394	3,907	4,961									
Solyc08g082070	High mobility group family protein (AHRD V3.3 *** B9GL80_POPTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus	IPR036910 (G3DSA:1.10.30.GENE3D	0,712	1,102	0,217	0,389	0,305									
Solyc08g082080	Amino acid transporter family protein (AHRD V3.3 *** B9GL79_POPTR)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:plasma membrane; F	IPR013057 (PFAM): PTHR22950:SF2	20,109	15,214	44,961	42,668	39,859									
Solyc08g082090	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** AT5G41810.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	140,101	48,546	27,407	85,804	49,668	-1,505	0,000	0,854	0,025	1,646	0,000	down	up	up
Solyc08g082100	WD40 repeat nucleoporin similar to SEH1 (AHRD V3.3 *** D7UPM8_LOTJA)		F:GO:0005198; F:G(	F:structural molecule activity; F:protein binding; P:positive regul	IPR001680 (PFAM): IPR015943 (G3D	11,698	11,660	14,755	13,393	12,223									
Solyc08g082110	WRKY transcription factor 54	WRKY54	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR036576 (G3DS WRKY	0,037	0,082	0,000	0,000	0,141									
Solyc08g082120	Methanol inducible protein (AHRD V3.3 *** D1MAX5_NICBE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	11,499	7,461	24,446	4,671	11,894			-1,044	0,019	-2,387	0,000		down	down
Solyc08g082130	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_CUCSA)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,400	0,309	0,175	0,048	0,189									
Solyc08g082150	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT5G41850.1)				IPR000073 (PFAM): IPR029058 (G3D	0,000	0,041	0,000	0,000	0,000									
Solyc08g082160	Subtilisin-like protease (AHRD V3.3 *-* W9RY25_9ROSA)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity	IPR010259 (PFAM): PTHR37379 (PAN	8,650	14,426	0,140	0,212	0,070									
Solyc08g082165	Ankyrin repeat family protein (AHRD V3.3 --* AT3G12360.2)					1,249	0,831	6,385	5,329	4,598									
Solyc08g082170	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A097PQY8_SOLLC)	PG49	F:GO:0004650; P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3I	103,358	98,509	191,211	205,536	172,570									
Solyc08g082180	Abscisic acid receptor PYL9-like protein (AHRD V3.3 *** V5L1G0_SOLNI)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR019587 (PFAM): IPR023393 (G3D	29,859	38,733	35,217	22,611	28,599					-0,634	0,007			down
Solyc08g082190	diacylglycerol kinase 5 (AHRD V3.3 --* AT2G20900.4)				mobidb-lite (MOBIDB_LITE)	368,607	438,685	446,323	518,377	532,526									
Solyc08g082200	DNA primase (AHRD V3.3 *** K4CPL6_SOLLC)		F:GO:0003896; P:G(	F:DNA primase acti EC:2.7.7.6 DNA-directed RNA p(	IPR002755 (PFAM): IPR014052 (TIGF	2,770	2,112	0,942	0,286	0,631									
Solyc08g082210	AP2/EREBP transcription factor		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,871	4,659	29,326	24,715	25,502	2,444	0,000					up		
Solyc08g082230	cation/H+ exchanger 20 (AHRD V3.3 --* AT3G53720.2)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	11,492	11,072	20,452	19,072	18,097									
Solyc08g082240	transmembrane protein (AHRD V3.3 *-* AT1G64385.2)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR342	7,582	7,400	13,256	11,799	10,209									
Solyc08g082250	endo-beta-1,4-D-glucanase (Cel8)	cel8	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	188,765	173,421	101,940	121,400	109,643									
Solyc08g082260	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)		F:GO:0004722; P:G(	F:protein serine/thr EC:3.1.3.16 Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	0,246	0,830	0,220	0,377	0,046									
Solyc08g082270	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT4G23840.1)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	6,879	6,388	10,715	10,124	9,002									
Solyc08g082280	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0G2SJB5_SALMI)		F:GO:0003824; C:G(	F:catalytic activity; C:integral component of membrane; F:memb	IPR001708 (PFAM): G3DSA:3.40.50.1	72,325	89,551	42,813	43,374	55,210									
Solyc08g082290	Mitochondrial inner membrane protein OXA1 (AHRD V3.3 *** A0A0B2PLM6_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase activ	IPR001708 (PFAM): mobidb-lite (MOB	7,496	8,727	10,747	8,884	8,894									
Solyc08g082300	Mitochondrial inner membrane OXA1-like protein (AHRD V3.3 *** A0A0B0MD66_GOSAR)		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase activ	IPR001708 (PANTHER): PTHR12428:	0,318	0,266	0,380	0,533	0,354									
Solyc08g082310	RING/U-box superfamily protein (AHRD V3.3 *** AT5G53110.1)		F:GO:0030247	F:polysaccharide binding	IPR013083 (G3DSA:3.30.40.GENE3D	9,983	13,028	2,900	2,736	3,219									
Solyc08g082320	PHD finger family protein (AHRD V3.3 *** A9PBM1_POPTR)		F:GO:0008270; F:G(	F:zinc ion binding; F:ubiquitin protein ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	15,908	17,607	19,594	17,959	19,162									
Solyc08g082330	Defensin-like protein 113 (AHRD V3.3 --* DF113_ARATH)					0,265	0,353	0,358	0,175	0,235									
Solyc08g082335	F-box protein (AHRD V3.3 --* W9RW78_9ROSA)					0,195	0,161	0,165	0,075	0,140									
Solyc08g082340	Glycerol-3-phosphate acyltransferase 3 (AHRD V3.3 *** A0A151RWP0_CAJCA)		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR002123 (PFAM): PTHR23063 (PAN	50,749	50,437	54,331	48,345	49,042									
Solyc08g082345	Bardet-biedl syndrome 3 (AHRD V3.3 --* C1EFH9_MICCC)					6,354	5,984	9,733	11,292	11,630									
Solyc08g082350	F-box family protein (AHRD V3.3 *** B9H429_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): IPR005174 (PFA	1,414	1,061	0,784	0,532	0,706									
Solyc08g082355	PHD finger transcription factor (AHRD V3.3 --* AT5G58610.9)					0,235	0,121	0,639	0,751	0,470									
Solyc08g082360	Plastid 30S ribosomal protein S3 (AHRD V3.3 --* RR3_CUSGR)					0,000	0,000	0,000	0,000	0,024									
Solyc08g082370	LOW QUALITY:calpain-type cysteine protease family (AHRD V3.3 --* AT1G55350.6)				mobidb-lite (MOBIDB_LITE): PTHR357	1,706	1,769	0,297	0,315	0,328									
Solyc08g082380	LOW QUALITY:Nucleosome assembly protein 1-3 (AHRD V3.3 --* NAP1C_ORYSJ)				PTHR36782 (PANTHER)	0,021	0,000	0,000	0,000	0,000									
Solyc08g082390	Coatomer subunit gamma-1 (AHRD V3.3 *** A0A1D1ZH87_9ARAE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	7,024	8,141	8,605	8,376	10,636									
Solyc08g082410	LOW protein: zinc finger CCCH domain protein (AHRD V3.3 *-* AT5G53440.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	88,803	82,642	91,921	86,724	91,813									
Solyc08g082420	Pleckstrin-like (PH) domain protein (AHRD V3.3 *** A0A072TUV8_MEDTR)				IPR011993 (G3DSA:2.30.29.GENE3D	9,121	8,781	11,937	15,188	13,700									
Solyc08g082430	Nucleoside diphosphate kinase (AHRD V3.3 *** K4CPN9_SOLLC)		F:GO:0004550; P:G(	F:nucleoside diphos EC:2.7.4.6 Nucleoside-diphosph	IPR001564 (PRINTS): IPR034907 (PF	80,438	81,056	37,810	27,320	40,442									
Solyc08g082440	UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU)		F:GO:0003978; P:G(	F:UDP-glucose 4-e EC:5.1.3.2 UDP-glucose 4-epim	PR01713 (PRINTS): IPR016040 (PFA	22,929	26,888	35,307	39,217	43,610									
Solyc08g082450	GDSL esterase/lipase family (AHRD V3.3 *** A0A151SCU2_CAJCA)		P:GO:0006629	P:lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	12,168	9,941	7,881	7,303	6,888									
Solyc08g082460	Kinase (AHRD V3.3 *-* A0A059Q131_9POAL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	PIRSF000654 (PIRSF): G3DSA:1.10.5	0,526	0,519	0,241	0,262	0,355									
Solyc08g082470	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane	IPR004864 (PFAM): PTHR31852 (PAN	2,817	2,390	4,400	6,244	3,979									
Solyc08g082480	Phosphatidylinositol 3-and 4-kinase family protein (AHRD V3.3 *** B9GL47_POPTR)		F:GO:0005515	F:protein binding	IPR000626 (PFAM): G3DSA:3.10.20.9	19,190	15,774	17,697	13,830	14,499									
Solyc08g082490	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2QVH8_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,461	0,411	0,533	0,322	0,352									
Solyc08g082500	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2QVH8_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,019	0,041	0,025	0,000	0,023									
Solyc08g082510	LOW QUALITY:F-box protein (AHRD V3.3 *** W9RW78_9ROSA)		F:GO:0005515	F:protein binding	IPR005174 (PFAM): G3DSA:1.20.128	0,042	0,241	0,050	0,025	0,023									
Solyc08g082530	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** W9SBH3_9ROSA)		F:GO:0004222; F:G(	F:metalloendopeptic EC:3.4.24 Acting on peptide bor	G3DSA:1.10.8.60 (GENE3D): G3DSA:	41,169	49,563	74,317	71,282	81,279									
Solyc08g082540	Galactose-binding protein (AHRD V3.3 *** AT4G23950.1)		C:GO:0005737; C:G(	C:cytoplasm; C:integral component of membrane; P:protein foldi	IPR012919 (PFAM): IPR008979 (G3D	12,551	12,264	35,487	40,744	29,923									
Solyc08g082560	F-box SKIP8-like protein (AHRD V3.3 *** A0A0B0PWH2_GOSAR)		F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D): IPR(	7,904	8,000	12,768	13,324	11,334									
Solyc08g082570	respiratory burst oxidase homolog A (AHRD V3.3 --* AT5G07390.2)					16,796	25,223	11,233	9,043	15,455	0,615	0,046	0,456	0,047			up	up	
Solyc08g082580	RNA polymerase II transcriptional coactivator KELP (AHRD V3.3 *** KELP_ARATH)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003173 (PFAM): G3DSA:1.10.10.6	34,990	37,110	35,665	31,288	32,740									
Solyc08g082590	Glutaredoxin (AHRD V3.3 *** A0A103XR19_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	G3DSA:3.40.30.10 (GENE3D): IPR00	3,514	4,451	1,794	1,864	3,101									
Solyc08g082610	DCD (Development and Cell Death) domain protein (AHRD V3.3 *** AT5G42050.1)				IPR013989 (PFAM): mobidb-lite (MOB	435,518	641,817	170,749	281,517	255,206			0,577	0,010	0,723	0,001		up	up
Solyc08g082620	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** O82520_CAPCH)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:transferase activity, transfe	IPR014031 (PFAM): IPR017568 (TIGF	16,451	16,005	0,068	0,050	0,141									
Solyc08g082630	Auxin Response Factor 9A	ARF9A	F:GO:0003677; F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran	IPR033389 (PFAM ARF	22,902	19,664	0,945	1,520	1,431									

Solyc08g082670	Cellulose synthase (AHRD V3.3 *** A0A118JUI8_CYNCS)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR029044 (G3DSA:3.90.550.GENE3	0,453	1,977	0,416	1,719	1,285									
Solyc08g082680	RING/U-box superfamily protein (AHRD V3.3 *** AT4G24015.1)		P:GO:0006511; C:G(	P:ubiquitin-dependent protein catabolic process; C:integral com			IPR001841 (PFAM); IPR013083 (G3D	2,762	3,102	0,983	0,782	1,197									
Solyc08g082685	Ribosomal protein S6 family protein (AHRD V3.3 *** D7KS90_ARALL)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR014717 (G3DSA:3.30.70.GENE3D	15,381	16,265	17,870	17,996	16,177									
Solyc08g082690	Ribosomal protein S6 (AHRD V3.3 *** A0A103XFW4_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR014717 (G3DSA:3.30.70.GENE3D	0,307	0,669	0,453	0,767	0,588									
Solyc08g082700	26S proteasome non-atpase regulatory subunit, putative (AHRD V3.3 *** B9RYN7_RICCO)		C:GO:0005838; P:G(	C:proteasome regulatory particle; P:proteolysis			G3DSA:1.25.40.990 (GENE3D); IPR0	86,109	81,876	113,823	114,876	108,650									
Solyc08g082710	Protein ABIL2, putative (AHRD V3.3 *** B9RSD0_RICCO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,579	3,158	0,699	0,661	0,636									
Solyc08g082720	DDE family endonuclease (AHRD V3.3 *-* AT4G10890.3)						IPR018838 (PFAM); PTHR28535 (PAN	0,947	0,626	0,109	0,167	0,303									
Solyc08g082730	BZIP transcription factor (AHRD V3.3 *** G7J8W4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR012458 (PFAM); PTHR31903:SF2	38,287	33,501	55,050	48,068	49,555									
Solyc08g082740	Signal recognition particle 19 kDa protein (AHRD V3.3 *** A0A061GDJ5_THECC)		P:GO:0006614; F:G(	P:SRP-dependent cotranslational protein targeting to membrane			IPR002778 (PFAM); IPR036521 (G3D	13,003	15,393	19,919	18,767	18,549									
Solyc08g082750	Plant regulator RWP-RK family protein (AHRD V3.3 *** G7IAL8_MEDTR)		F:GO:0005515	F:protein binding			IPR003035 (PFAM Nin-like	35,860	44,103	50,192	51,357	48,522									
Solyc08g082760	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4CPS2_SOLLC)		C:GO:0005743; P:G(	C:mitochondrial inner membrane; P:mitochondrial pyruvate trans			IPR005336 (PFAM); PTHR14154 (PAN	24,101	25,549	34,100	36,416	32,743									
Solyc08g082770	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4CPS3_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D); G3	11,578	11,020	0,585	0,352	0,046									
Solyc08g082780	Transmembrane protein, putative (AHRD V3.3 -** A0A072V1A4_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR344	6,805	4,601	0,025	0,150	0,047									
Solyc08g082790	mechanosensitive channel of small conductance-like 10 (AHRD V3.3 --* AT5G12080.3)						mobidb-lite (MOBIDB_LITE); PTHR344	0,142	0,369	0,075	0,050	0,071									
Solyc08g082810	Beta-amylase (AHRD V3.3 *** A0A0V0IFE3_SOLCH)		P:GO:0000272; F:G(	P:polysaccharide c	EC:3.2.1.2	Beta-amylase	IPR001554 (PRINTS); G3DSA:3.20.2(	12,119	13,540	21,781	19,092	18,367									
Solyc08g082830	Glutamine-dependent NAD(+) synthetase (AHRD V3.3 *** NADE_ARATH)		F:GO:0003952; F:G(	F:NAD+ synthase (	EC:6.3.5.1	NAD(+) synthase (glu	IPR003694 (TIGRFAM); IPR036526 ((	0,076	0,098	0,051	0,170	0,071									
Solyc08g082840	Glutamine-dependent NAD(+) synthetase (AHRD V3.3 *-* NADE_ARATH)		C:GO:0000506; F:G(	C:glycosylphosphat	EC:6.3.5.1; EC:2.4.1	NAD(+) synthase (glu	IPR001296 (PFAM); IPR014729 (G3D	6,946	7,495	7,229	7,647	7,497									
Solyc08g082850	ABC transporter family protein (AHRD V3.3 *** B9GL16_POPTR)	ABCF4	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); G3DSA:3.40.50.3	272,070	245,110	254,222	242,866	256,438									
Solyc08g082860	Trehalase (AHRD V3.3 *** K4CPT2_SOLLC)		F:GO:0004555; P:G(	F:alpha,alpha-treha	EC:3.2.1.28	Alpha,alpha-trehalase	IPR001661 (PRINTS); IPR012341 (G3	13,475	12,477	7,187	4,276	6,352									
Solyc08g082870	NAD(P)-binding Rossmann-fold superfamily protein						IPR002347 (PRINTS); IPR002347 (PF	21,236	16,066	21,555	21,061	21,428									
Solyc08g082880	Methyltransferase-like protein 17, mitochondrial (AHRD V3.3 *** A0A0B0PRZ2_GOSAR)		P:GO:0006412; F:G(	P:translation; F:methyltransferase activity			IPR015324 (PFAM); PTHR21320 (PAN	46,485	40,398	42,347	41,688	41,343									
Solyc08g082890	R2R3MYB transcription factor 9	R2R3MYB9	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 MYB	0,000	0,021	0,050	0,025	0,000									
Solyc08g082900	WD-repeat protein, putative (AHRD V3.3 *** B9RYR0_RICCO)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR015943 (G3	3,926	3,859	3,439	3,355	3,597									
Solyc08g082910	Dof zinc finger protein (AHRD V3.3 *** W9RTF5_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	4,177	4,681	2,160	2,032	2,097									
Solyc08g082920	ORMDL family protein (AHRD V3.3 *** AT5G42000.1)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR007203 (PIRSF); IPR007203 (PFA	10,937	8,425	13,048	12,046	9,567									
Solyc08g082930	Bhlh transcription factor, putative (AHRD V3.3 *-* B9RYR7_RICCO)		F:GO:0046983	F:protein dimerization activity			IPR025610 (PFAM); mobidb-lite (MOB	10,197	11,531	23,213	19,960	19,340									
Solyc08g082950	aluminum activated malate transporter family protein (AHRD V3.3 *** AT4G00910.1)		P:GO:0015743	P:malate transport			IPR020966 (PFAM); PTHR31086 (PAN	0,081	0,293	0,118	0,175	0,118									
Solyc08g082960	HIT zinc finger protein (AHRD V3.3 *** A0A072VFL0_MEDTR)		F:GO:0046872	F:metal ion binding			IPR007529 (PFAM); G3DSA:3.30.60.1	6,202	5,609	10,534	10,821	10,485									
Solyc08g082970	FAS-associated factor 2-B (AHRD V3.3 *** W9S3Z8_9ROSA)		F:GO:0005515	F:protein binding			PF14555 (PFAM); G3DSA:1.10.8.10 ((	37,570	37,839	67,115	61,926	60,556									
Solyc08g082980	MAP kinase kinase kinase 67	MAPKKK67	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:3.30.200	45,044	37,075	133,820	139,965	119,884									
Solyc08g082990	Oligopeptide transporter, putative (AHRD V3.3 *** B9RYS3_RICCO)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM); IPR004648 (TIGF	2,594	3,681	89,259	103,911	88,261									
Solyc08g083000	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase) (AHRD V3.3 --* AT5G04050.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,000	0,000	0,000	0,025	0,000									
Solyc08g083010	Homer (AHRD V3.3 *** A0A0B0PVA4_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR36383 (PANTHER)	1,535	2,087	4,551	5,392	6,282									
Solyc08g083030	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G27680.1)		F:GO:0005524	F:ATP binding			IPR003959 (PFAM); G3DSA:1.10.8.60	13,070	11,101	14,580	14,856	13,569									
Solyc08g083035	Zinc finger matrin-type protein 1, putative isoform 1 (AHRD V3.3 *** A0A061G3Y9_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR368	24,340	21,668	31,275	29,603	33,334									
Solyc08g083040	Kinase family protein (AHRD V3.3 *** D7M8X8_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	145,144	74,737	90,710	121,321	103,446	-0,932	0,000			0,422	0,018	down		up
Solyc08g083060	Yellow stripe-like transporter 1 (AHRD V3.3 *** T1Q4G6_ARAHY)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM); IPR004813 (TIGF	107,356	73,117	13,788	17,038	18,067									
Solyc08g083070	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase subunit (AHRD V3.3 *** A0A0B0MMV0		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	49,354	44,914	60,674	59,421	58,414									
Solyc08g083080	esterase/lipase/thioesterase family protein (AHRD V3.3 *-* AT3G50790.2)		F:GO:0016787	F:hydrolase activity				4,161	2,290	4,656	4,491	4,762									
Solyc08g083090	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)						IPR007493 (PFAM); PTHR31676:SF2(	2,173	1,938	3,251	2,904	3,153									
Solyc08g083100	Embryogenesis-associated EMB8 (AHRD V3.3 *-* A0A0B0P518_GOSAR)						PTHR10794 (PANTHER); IPR029058 (	1,976	0,994	2,183	2,402	1,788									
Solyc08g083110	Cystathionine gamma-synthase, putative (AHRD V3.3 *-* B9RYU1_RICCO)		F:GO:0003824; F:G(	F:catalytic activity; F:pyridoxal phosphate binding			IPR000277 (PFAM); IPR015421 (G3D	14,948	14,447	13,702	12,609	11,567									
Solyc08g083115	Cystathionine gamma-synthase, putative (AHRD V3.3 *** B9RYU1_RICCO)		F:GO:0003824; F:G(	F:catalytic activity; F:pyridoxal phosphate binding			IPR000277 (PIRSF); IPR000277 (PFA	40,177	45,079	43,257	38,998	35,576									
Solyc08g083120	ubiquitin-ribosomal fusion protein		F:GO:0003735; F:G(	F:structural constituent of ribosome; F:protein binding; C:riboso			IPR019956 (PRINTS); IPR038587 (G3	74,467	87,083	69,324	67,605	65,804									
Solyc08g083130	Homeobox-leucine zipper protein (AHRD V3.3 *** K4MNF8_MEDSA)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN HD-ZIP	0,021	0,079	0,123	0,025	0,024									
Solyc08g083140	Embryogenesis-associated EMB8 (AHRD V3.3 *** A0A0B0P518_GOSAR)						IPR012020 (PIRSF); IPR000073 (PFA	9,257	11,359	17,839	21,141	19,562									
Solyc08g083150	CHASE domain containing histidine kinase protein (AHRD V3.3 --* AT2G01830.6)							0,909	0,612	0,000	0,000	0,000									
Solyc08g083155	LOW QUALITY:Cytochrome P450, putative (AHRD V3.3 *-* A0A061E4E7_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3	0,061	0,000	0,000	0,000	0,000									
Solyc08g083170	LOW QUALITY:bHLH transcription factor 056		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	0,019	0,444	0,165	0,050	0,024									
Solyc08g083190	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061G3V4_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:hydrolase activity			IPR000073 (PRINTS); IPR000073 (PF	2,673	2,226	7,705	19,084	14,077			0,863	0,002	1,307	0,000		up	up
Solyc08g083200	ABC transporter A family member 1 (AHRD V3.3 *** A0A0B0NCE0_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR34970 (PANTHER)	6,992	8,251	7,284	6,409	7,962									
Solyc08g083210	endo-1,4-beta-glucanase (cel5)	cel5	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012341 (G3DSA:1.50.10.GENE3D	0,866	3,463	0,312	0,164	0,306	2,015	0,014					up		
Solyc08g083230	Growth-regulating factor (AHRD V3.3 *-* G7J891_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten			IPR014977 (PFAM GRF	0,748	0,543	0,075	0,195	0,234									
Solyc08g083240	SUN-like protein 24	SUN24	F:GO:0005515	F:protein binding			IPR000048 (PFAM); G3DSA:1.20.5.19	1,989	1,653	0,000	0,228	0,046									
Solyc08g083250	Purple acid phosphatase (AHRD V3.3 *-* K4CPW9_SOLLC)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR040974 (PFAM); PTHR22953:SF2	2,094	2,435	6,276	7,365	8,659									
Solyc08g083255	Purple acid phosphatase (AHRD V3.3 *** A0A0V0IIF1_SOLCH)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR029052 (G3DSA:3.60.21.GENE3D	19,290	22,187	48,544	49,658	63,281			0,380	0,024				up	
Solyc08g083260	snurportin-1 protein (AHRD V3.3 *** AT4G24880.1)		C:GO:0005634; C:G(	C:nucleus; C:cytoplasm; P:snRNA import into nucleus			G3DSA:3.30.470.30 (GENE3D); mobic	13,424	15,576	11,741	12,746	10,815									
Solyc08g083270	Hop-interacting protein THI143 (AHRD V3.3 *** G8Z252_SOLLC)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR002109 (PFAM); G3DSA:3.40.30.1	2,009	1,749	0,366	0,192	0,333									
Solyc08g083280	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9RYV6_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM); G3DSA:3.40.50.7	3,847	3,444	0,587	0,687	0,284									
Solyc08g083290	Zinc finger, FYVE/PHD-type (AHRD V3.3 *** A0A118JT98_CYNCS)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	40,278	38,548	53,309	50,901	49,007									
Solyc08g083300	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** S8CLS5_9LAMI)		F:GO:0004843; P:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.30.2230.10 (GENE3D); IPR(	14,972	14,841	19,898	21,551	19,648									
Solyc08g083310	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RYW1_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM); G3DSA:3.20.20.8	25,172	25,178	16,851	12,754	14,256									
Solyc08g083320	granule-bound starch synthase 1	STS1	F:GO:0004373	F:glycogen (starch)	EC:2.4.1.11	Glycogen(starch) syn	G3DSA:3.40.50.2000 (GENE3D); IPR(	276,943	320,551	140,036	110,903	188,757									
Solyc08g083325	Uricase-2 isozyme 2 (AHRD V3.3 --* URIC2_CANLI)						mobidb-lite (MOBIDB_LITE)	0,099	0,019	0,000	0,072	0,023									
Solyc08g083330	LOW QUALITY:StAR-related lipid transfer 7, mitochondrial (AHRD V3.3 *** A0A0B0NYG5_GOSAR)		F:GO:0008289	F:lipid binding			IPR002913 (PFAM); IPR023393 (G3D	197,211	246,196	262,717	289,054	282,421									
Solyc08g083350	Ribosomal protein L11 (AHRD V3.3 *** A0A124SHL6_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036796 (G3DSA:3.30.1550.GENE	45,891	72,767	43,532	48,595	64,020	0,692	0,004	0,554	0,000			up	up	
Solyc08g083360	Photosynthetic NDH subcomplex B 3 (AHRD V3.3 *** A0A0F7GXX2_9ROSI)		F:GO:0009055; F:G(	F:electron transfer activity; F:iron-sulfur cluster binding			IPR012675 (G3DSA:3.10.20.GENE3D	1,598	12,476	0,141	0,474	1,384	2,977	0,000					up		
Solyc08g083370	Soluble inorganic pyrophosphatase (AHRD V3.3 *** A0T3E7_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.1	Inorganic diphosphat	IPR036649 (G3DSA:3.90.80.GENE3D	0,470	0,647	0,072	0,025	0,072									
Solyc08g083380	Mitochondrial import inner membrane translocase subunit Tim13 (AHRD V3.3 *** A0A0B0NRT8_GOSAR)		C:GO:0005758; P:G(	C:mitochondrial intermembrane space; P:chaperone-mediated p			IPR035427 (G3DSA:1.10.287.GENE3	18,628	22,160	32,028	29,090	27,253									
Solyc08g083400	B3 domain-containing protein (AHRD V3.3 *-* W9RW19_9ROSA)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	4,417	4,749	3,739	3,091	2,676									
Solyc08g083410	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	17,967	14,171	0,025	0,025	0,000									
Solyc08g083450	Cytochrome P450 family protein (AHRD V3.3 *** A0A072UZE3_MEDTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,021	0,039	0,000	0,000	0,000									
Solyc08g083500	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	12,121	8,632	0,050	0,075	0,000									
Solyc08g083505	Cytochrome P450 (AHRD V3.3 *-* A0A118JTP4_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	1,307	0,456	0,124	0,076	0,071									
Solyc08g083510	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,867	0,662	0,000	0,000	0,000									
Solyc08g083520	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,209	0,233	0,025	0,000	0,023									
Solyc09g005000	Clade VI lectin receptor kinase (AHRD V3.3 *** K4CPZ0_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); IPR0(	0,139	0,018	0,044	0,025	0,047									
Solyc09g005010	Importin subunit beta-1 (AHRD V3.3 *** W9RG70_9ROSA)		P:GO:0006606; F:G(	P:protein import into nucleus; F:Ran GTPase binding; F:protein			IPR001494 (PFAM); IPR011989 (G3D	50,917	59,783	39,204	34,463	41,364									
Solyc09g005030	Homeodomain-like superfamily protein (AHRD V3.3 *-* AT2G40260.1)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 G2-like	0,954	1,380	0,731	0,892	0,848									
Solyc09g005050	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *-* A0A061F4Q5_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc09g005060	Phosphatidylethanolamine binding protein, putative (AHRD V3.3 *** B9SWX4_RICCO)						IPR005247 (TIGRFAM); IPR008914 (F	0,156	0,591	0,420	1,357	0,069									
Solyc09g005075	RNA polymerase II subunit B1 CTD phosphatase RPAP2-like protein (AHRD V3.3 --* AT5G26760.2)							0,000	0,000	0,022	0,000	0,000									
Solyc09g005080	verticillium wilt disease resistance 2	ve2	F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR032675 (G3D	26,134	53,641	8,058	11,826	13,721	1,061	0,003	0,764	0,007			up	up	
Solyc09g005100	Transcription factor bHLH140-like protein (AHRD V3.3 *** G7I746_MEDTR)		F:GO:0003824	F:catalytic activity			PF11969 (PFAM); IPR002589 (PFAM)	4,039	3,977	8,089	8,013	7,126									
Solyc09g005110	Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion binding; F:carboxy-lyase activity; F:thiamine p			G3DSA:3.40.50.1220 (GENE3D); IPR(	1,610	1,751	1,240	1,135	1,175									
Solyc09g005120	DnaJ domain-containing protein (AHRD V3.3 *** A0A103YM06_CYNCS)		C:GO:0005788; P:G(	C:endoplasmic reticulum lumen; P:response to heat; C:plasmod			IPR001623 (PRINTS); G3DSA:3.40.3(	24,628	13,893	32,123	39,927	32,963	-0,800	0,008					down		
Solyc09g005130	ARM repeat superfamily protein (AHRD V3.3 *** AT3G08960.3)		P:GO:0006886; F:G(	P:intracellular protein transport; F:Ran GTPase binding			IPR001494 (PFAM); mobidb-lite (MOB	24,494	25,573	23,600	23,604	24,451									
Solyc09g005132	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,019	0,000	0,000	0,022	0,024									
Solyc09g005134	DEAD-box ATP-dependent RNA helicase 26 (AHRD V3.3 --* RH26_ARATH)							0,000	0,000	0,000	0,092	0,000									
Solyc09g005136	DCD (Development and Cell Death) domain protein (AHRD V3.3 --* AT2G35140.6)							0,040	0,021	0,025	0,000	0,023									
Solyc09g005140	Zn-dependent exopeptidases superfamily protein (AHRD V3.3 --* AT1G67420.6)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,605	1,989	0,884	0,573	0,840									
Solyc09g005150	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			G3DSA:3.30.2160.10 (GENE3D); IPR(	0,152	0,116	0,000	0,000	0,000									
Solyc09g005160	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			G3DSA:3.30.2160.10 (GENE3D); G3D	0,115	0,116	0,047	0,048	0,023									
Solyc09g005170	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:2.10.25.10 (GENE3D); IPR00	0,042	0,060	0,137	0,000	0,000									
Solyc09g005180	L-gulonolactone oxidase (AHRD V3.3 *** A0A151SWE5_CAJCA)		F:GO:0003885; C:G(	F:D-arabinono-1,4-l	EC:1.1.3.37	D-arabinono-1,4-lact	IPR006094 (PFAM); IPR016169 (G3D	11,240	7,938	0,735	0,237	0,561									
Solyc09g005190	Kinase, putative (AHRD V3.3 *-* B9RJQ5_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,175	0,160	0,193	0,072	0,117									
Solyc09g005200	ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** AT1G65295.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR33786:SF1 (PANTHER); PTHR3	2,305	2,440	2,927	3,825	3,583									
Solyc09g005210	Protein LURP-one-related 12 (AHRD V3.3 *** A0A199W2R9_ANACO)						IPR007612 (PFAM); IPR038595 (G3D	0,040	0,085	0,075	0,047	0,000									
Solyc09g005220	Potassium channel (AHRD V3.3 *** S8DA85_9LAMI)		P:GO:0006810; F:G(	P:transport; F:ion transmembrane transporter activity; F:channe			G3DSA:1.10.287.70 (GENE3D); IPR0(	0,019	0,000	0,000	0,000	0,024									
Solyc09g005230	UPF0420 C16orf58-like protein (AHRD V3.3 *** G7KS93_MEDTR)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast envelope; P:response to UV-B; I			IPR006968 (PFAM); PTHR12770:SF2	9,468	7,003	5,182	4,282	5,649									
Solyc09g005250	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT3G51870.1)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS); IPR018108 (PF	11,517	13,825	18,539	19,839	19,929									
Solyc09g005260	Vacuolar cation/proton exchanger 3 (AHRD V3.3 *** A0A0B2SDY1_GLYSO)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004837 (PFAM); G3DSA:1.20.142	0,916	1,831	0,342	1,618	2,008									
Solyc09g005270	CRS1/YhbY (CRM) domain protein (AHRD V3.3 *** A0A072UMR2_MEDTR)		F:GO:0003723	F:RNA binding			IPR001890 (PFAM); IPR035920 (G3D	19,118	17,752	16,354	15,108	16,519									
Solyc09g005280	En/Spm transposon protein-like (AHRD V3.3 *-* Q9LH86_ARATH)						IPR004252 (PFAM); PTHR33499:SF1	17,071	12,836	16,482	14,572	13,268									
Solyc09g005290	LOW QUALITY:Nbs-lrr resistance protein, putative (AHRD V3.3 *** A0A061FEU3_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR002182 (PFA	4,145	3,791	2,246	2,576	2,346									
Solyc09g005300	mRNA cap guanine-N7 methyltransferase (AHRD V3.3 *** K4CQ20_SOLLC)		F:GO:0004482; C:G(	F:mRNA (guanine-N	EC:2.1.1.56	mRNA (guanine-N(7)-	IPR016899 (PIRSF); G3DSA:3.40.50.	11,997	13,229	15,637	12,986	13,278									
Solyc09g005310	LMBR1-like membrane protein (AHRD V3.3 *** AT5G01460.1)		C:GO:0016021	C:integral component of membrane			IPR006876 (PFAM); PTHR31652 (PAN	46,703	39,751	40,416	44,966	37,915									
Solyc09g005320	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01450.1)		C:GO:0016021	C:integral component of membrane			IPR032008 (PFAM); IPR013083 (G3D	28,989	17,368	9,588	5,663	8,677	-0,711	0,007			-0,757	0,015	down		down
Solyc09g005330	HEAT repeat-containing protein (AHRD V3.3 *** AT5G01400.3)		P:GO:0006396; P:G(	P:RNA processing; P:posttranscriptional gene silencing by RNA			IPR032460 (PFAM); IPR011989 (G3D	66,564	49,908	57,932	66,248	61,547									
Solyc09g005340	Symplekin, putative (AHRD V3.3 *-* B9SQ20_RICCO)		P:GO:0006396; P:G(	P:RNA processing; P:posttranscriptional gene silencing by RNA			IPR022075 (PFAM); mobidb-lite (MOB	53,534	48,486	55,942	57,428	55,831									
Solyc09g005350	DnaJ-like protein (AHRD V3.3 *** Q9SP09_TOBAC)		P:GO:0006457; F:G(	P:protein folding; F:unfolded protein binding			IPR001623 (PRINTS); IPR036869 (G3	37,890	33,711	45,472	40,680	40,582									
Solyc09g005360	PHD finger alfin-like protein (AHRD V3.3 *** A0A072UGM4_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR013083 (G3DSA:3.30.40.GENE3D	19,542	19,004	23,759	20,476	20,322									
Solyc09g005380	Peptide transporter, putative (AHRD V3.3 *** B9T6M4_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM); G3DSA:1.20.125	1,097	0,362	0,047	0,099	0,047									
Solyc09g005390	Thioesterase family protein (AHRD V3.3 *** D7KDD0_ARALL)		F:GO:0047617	F:acyl-CoA hydrolas	EC:3.1.2.2	Acyl-CoA hydrolase	G3DSA:3.10.129.10 (GENE3D); IPR0(	21,531	21,449	26,909	23,619	26,275									
Solyc09g005460	3-phosphoshikimate 1-carboxyvinyltransferase (AHRD V3.3 *-* G1FBT6_CAPAN)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR001986 (PFAM); IPR036968 (G3D	0,061	0,000	0,112	0,075	0,047									
Solyc09g005480	F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM); G3DSA:1.20.	14,232	15,506	11,585	13,601	10,453									
Solyc09g005490	LOW QUALITY:Ethylene-insensitive protein 2 (AHRD V3.3 *-* A0A142IX47_NICAT)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR001046 (PFAM); PTHR11706:SF3	0,359	0,391	0,147	0,195	0,256									
Solyc09g005510	LOW QUALITY:pathogenic type III effector avirulence factor Avr AvrRpt-cleavage: cleavage site protein (AHRD V3.3 --* AT5G48500.1)							0,772	0,576	0,477	0,685	0,564									
Solyc09g005520	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *-* A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR017451 (TIGF	1,080	1,070	0,606	0,965	0,754									
Solyc09g005523	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 *-* AT3G53520.4)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR001046 (PRINTS); G3DSA:3.40.5(	12,882	12,146	15,207	15,641	15,722									
Solyc09g005527	Ethylene-insensitive 2 (AHRD V3.3 *-* Q3S3T1_SOLLC)		F:GO:0005384; P:G(	F:manganese ion transmembrane transporter activity; P:ethylen			mobidb-lite (MOBIDB_LITE); mobidb-lit	3,435	3,260	3,770	3,543	3,425									
Solyc09g005530	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 *-* AT3G53520.4)		C:GO:0016021	C:integral component of membrane			IPR016040 (PFAM); G3DSA:3.40.50.7	0,021	0,079	0,050	0,116	0,166									
Solyc09g005540	Ethylene-insensitive 2 (AHRD V3.3 *-* Q3S3T1_SOLLC)		F:GO:0005384; P:G(	F:manganese ion transmembrane transporter activity; P:ethylene-activated signaling pathway; F:cadmiu				2,590	3,069	3,059	3,518	3,566									
Solyc09g005543	Ethylene-insensitive 2 (AHRD V3.3 *-* Q3S3T1_SOLLC)		F:GO:0005384; P:G(	F:manganese ion transmembrane transporter activity; P:ethylene-activated signaling pathway; F:cadmiu				2,106	2,035	1,759	1,562	1,811									
Solyc09g005547	Ethylene-insensitive protein 2 (AHRD V3.3 --* A0A142IX47_NICAT)		F:GO:0005384; P:G(	F:manganese ion transmembrane transporter activity; P:ethylene-activated signaling pathway; F:cadmiu				0,000	0,018	0,000	0,025	0,000									
Solyc09g005550	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9T5W7_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:3.30.200.20 (GENE3D); G3DS	63,201	62,208	62,064	62,791	57,063									
Solyc09g005560	Trihelix transcription factor GT-3b (AHRD V3.3 *** W9RYU5_9ROSA)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			PF13837 (PFAM); Trihelix	0,730	1,509	1,322	2,797	1,628					1,079	0,031			up
Solyc09g005570	ALC-interacting protein (AHRD V3.3 *-* G7JN31_MEDTR)						IPR032795 (PFAM); PTHR35499 (PAN	13,218	16,924	1,348	1,252	0,873									
Solyc09g005580	SelT-like protein (AHRD V3.3 *-* A0A0B2PRT5_GLYSO)						mobidb-lite (MOBIDB_LITE); IPR01938	72,581	56,206	63,682	59,482	63,077									
Solyc09g005600	Transducin family protein / WD-40 repeat family protein, putative isoform 5 (AHRD V3.3 *** A0A061EQ99_TI		F:GO:0005515; C:G(	F:protein binding; C:integral component of membrane; P:vesicle			IPR015943 (G3DSA:2.130.10.GENE3	43,049	37,604	50,907	49,940	49,458									
Solyc09g005610	transcription factor-like protein (AHRD V3.3 *** AT1G58330.1)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM); PTHR22952 (PAN	0,554	0,878	0,245	0,433	0,283									
Solyc09g005620	SIGRX1 protein (AHRD V3.3 *** E1UWA5_SOLLC)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR002109 (PFAM); IPR035901 (G3D	30,879	45,700	93,713	82,995	100,158	0,593	0,016					up		
Solyc09g005630	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT5G01360.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	0,059	0,149	0,044	0,000	0,000									
Solyc09g005640	Protein SCO1, mitochondrial-like protein (AHRD V3.3 *** A0A0B0PAY7_GOSAR)		F:GO:0005507; C:G(	F:copper ion binding; C:mitochondrial inner membrane; P:coppe			G3DSA:3.40.30.10 (GENE3D); IPR01	12,976	14,971	16,314	15,369	14,139									
Solyc09g005650	LOW QUALITY:HAT transposon superfamily protein, putative (AHRD V3.3 *** A0A061GGP8_THECC)		F:GO:0046983	F:protein dimerization activity			IPR007021 (PFAM); IPR008906 (PFA	0,021	0,000	0,000	0,000	0,000									
Solyc09g005660	HAT transposon superfamily protein, putative (AHRD V3.3 *** A0A061GGP8_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR003656 (PFAM); IPR007021 (PFA	15,404	12,789	17,325	17,949	16,971									
Solyc09g005670	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *-* A0A072UDV5_MEDTR)		F:GO:0046983	F:protein dimerization activity			IPR007021 (PFAM); IPR036691 (G3D	0,019	0,082	0,025	0,022	0,000									
Solyc09g005690	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2-like protein (AHRD V3.3 *** A0A0B0NZB0_GOSAR		F:GO:0016787; P:G(	F:hydrolase activity; P:phosphatidylinositol dephosphorylation			IPR005135 (PFAM); IPR036691 (G3D	1,103	1,189	0,270	0,247	0,330									
Solyc09g005700	diaminopimelate epimerase family protein (AHRD V3.3 *** AT3G53580.1)		F:GO:0008837; P:G(	F:diaminopimelate e	EC:5.1.1.7; EC:5.1.1	Diaminopimelate epi	G3DSA:3.10.310.10 (GENE3D); IPR0(	61,689	75,089	104,549	95,976	108,051									
Solyc09g005710	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061ES09_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,763	2,358	2,221	2,572	2,216									
Solyc09g005720	60S ribosomal protein L23A (AHRD V3.3 *** A0A0B2RCV3_GLYSO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR013025 (PFAM); IPR012677 (G3D	508,056	512,515	303,169	283,658	278,742									

Solyc09g005730	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)						IPR006476 (TIGRFAM): IPR006476 (F	5,582	1,661	6,823	5,471	6,716	-1,713	0,000					down		
Solyc09g005740	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G53560.2)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	28,655	29,907	58,484	49,056	50,169									
Solyc09g005750	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (AHRD V3.3 *** A0A0B0NEJ5_GOSAR)						IPR025486 (PFAM): IPR032795 (PFA	63,516	55,855	31,211	28,774	29,528									
Solyc09g005760	U3 small nucleolar RNA-associated protein, putative (AHRD V3.3 *** A0A061DSN9_THECC)		P:GO:0006364: C:G(	P:rRNA processing; C:small-subunit processome			PF04615 (PFAM): mobidb-lite (MOBID	139,942	103,790	74,128	68,740	73,964									
Solyc09g005765	T-complex protein 1 subunit zeta 1 (AHRD V3.3 --* TCPZA_ARATH)						mobidb-lite (MOBIDB_LITE)	24,460	9,470	0,000	0,000	0,023									
Solyc09g005770	F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): IPR001810 (F	7,639	6,424	6,262	7,254	5,412									
Solyc09g005780	LOW QUALITY:Sucrose-phosphate synthase 2 (AHRD V3.3 --* Q6EZE7_WHEAT)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,134	0,479	0,000	0,000	0,000									
Solyc09g005800	LOW QUALITY:cysteine-rich RLK (RECEPTOR-like protein kinase) 22 (AHRD V3.3 --* AT4G23300.1)							0,575	0,445	0,337	0,220	0,519									
Solyc09g005810	UDP-glucuronate decarboxylase protein 1 (AHRD V3.3 *** N0A417_POPTO)		C:GO:0005768: C:G(	C:endosome; C:trar	EC:4.1.1.35	UDP-glucuronate dec	G3DSA:3.90.25.10 (GENE3D): IPR01(	41,052	40,224	40,549	36,399	35,379									
Solyc09g005820	Bifunctional abietadiene synthase, chloroplastic (AHRD V3.3 --* LAS_ABIBA)							0,000	0,000	0,000	0,022	0,000									
Solyc09g005830	LOW QUALITY:ACI49	aci49	C:GO:0000145: P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): mobidb-lite (MOB	9,934	2,364	0,294	0,961	0,656	-2,049	0,000					down		
Solyc09g005840	LOW QUALITY:Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9HCA8_POPTR)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM): mobidb-lite (MOB	0,720	0,499	0,362	0,645	0,279									
Solyc09g005850	polysaccharide lyase family 6 protein		F:GO:0030570: P:G(	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR002022 (PF	14,959	13,494	13,214	14,252	14,097									
Solyc09g005860	ankyrin repeat-containing protein		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	29,754	46,589	7,153	7,837	11,338									
Solyc09g005870	Cytochrome c-type biogenesis protein CcmE (AHRD V3.3 *** A0A1D1XQ32_9ARAE)		C:GO:0005886: P:G(	C:plasma membrane; P:protein-heme linkage; P:cytochrome cor			G3DSA:2.40.50.140 (GENE3D): IPR0(	7,340	9,538	7,232	8,910	8,624									
Solyc09g005880	LOW QUALITY:Membrane-associated kinase regulator-like protein, putative (AHRD V3.3 *** A0A072VS60_I		C:GO:0005886: F:G(	C:plasma membrane; F:kinase inhibitor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,909	0,621	0,000	0,000	0,000									
Solyc09g005890	centrosomal protein of 135 kDa-like protein (AHRD V3.3 *** AT2G37370.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,595	0,590	0,356	0,800	0,376									
Solyc09g005910	Phosphatidate phosphatase LPIN2-like protein (AHRD V3.3 *** A0A0B2PEL3_GLYSO)		F:GO:0008195: P:G(	F:phosphatidate ph	EC:3.1.3.4	Phosphatidate phosp	IPR013209 (PFAM): IPR007651 (PFA	48,342	46,774	113,562	131,731	119,143									
Solyc09g005920	Lung seven transmembrane receptor family protein (AHRD V3.3 *** AT5G18520.1)		C:GO:0016021	C:integral component of membrane			IPR009637 (PFAM): PTHR21229:SF4	0,000	0,021	0,000	0,000	0,000									
Solyc09g005930	Ribosomal protein S24e family protein (AHRD V3.3 *** AT5G02740.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	20,754	19,912	25,348	30,481	24,497									
Solyc09g005940	Fatty acyl-CoA reductase (AHRD V3.3 *** K4CQ84_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			IPR013120 (PFAM): IPR033640 (PFA	0,000	0,018	0,000	0,000	0,000									
Solyc09g005960	Valine--trna ligase (AHRD V3.3 *** A0A0B0MMZ7_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR33780:SF3 (PANTHER): PTHR3	9,960	9,098	19,563	19,222	16,010									
Solyc09g005970	ABC transporter family protein (AHRD V3.3 *** B9ICA5_POPTR)	ABCG23	F:GO:0005524: C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	0,296	0,332	0,143	0,549	0,258									
Solyc09g005980	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *** B9SGV2_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR001878 (PFAM): IPR012677 (G3D	59,834	70,418	78,212	69,194	77,607									
Solyc09g005990	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SGU4_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,110	1,551	2,355	1,923	2,238									
Solyc09g006000	zinc/iron-chelating domain protein (AHRD V3.3 *** AT5G02710.3)						IPR005358 (PFAM): mobidb-lite (MOB	5,774	9,136	5,019	4,799	8,501			0,751	0,013				up	
Solyc09g006010	Pathogenesis-related protein 1 (AHRD V3.3 *** Q75QH2_CAPCH)		C:GO:0005576: P:G(	C:extracellular region; P:response to stimulus			IPR001283 (PRINTS): IPR014044 (PF	0,059	0,037	0,621	0,592	0,117									
Solyc09g007010	Pathogenesis-related protein 1 (AHRD V3.3 *** Q75QH2_CAPCH)		C:GO:0005615: P:G(	C:extracellular space; P:killing of cells of other organism; P:defe			IPR001283 (PRINTS): IPR035940 (G3	0,137	1,288	2,791	3,105	4,794									
Solyc09g007020	pathogenesis-related protein		C:GO:0005615: P:G(	C:extracellular space; P:killing of cells of other organism; P:defe			IPR001283 (PRINTS): IPR014044 (PF	0,000	0,096	0,143	0,075	0,164									
Solyc09g007030	Kinesin-like protein (AHRD V3.3 *** M0ZPI7_SOLTU)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	10,903	10,282	6,540	7,528	10,051									
Solyc09g007040	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7LUH3_ARALL)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,009	0,916	0,966	0,770	0,799									
Solyc09g007050	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JTY1_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,095	2,094	1,306	1,773	1,321									
Solyc09g007060	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061EZM8_THECC)		C:GO:0005737: P:G(	C:cytoplasm; P:protein ubiquitination; F:ligase activity; F:ubiquit			IPR001841 (PFAM): IPR013083 (G3D	0,566	1,127	0,417	0,220	0,188									
Solyc09g007070	Succinate dehydrogenase assembly factor 1, mitochondrial (AHRD V3.3 *** A0A0B0PRI9_GOSAR)						IPR008011 (PFAM): mobidb-lite (MOB	3,851	3,351	3,834	4,411	4,384									
Solyc09g007080	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G12620.2)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	14,084	13,926	21,934	21,089	19,287									
Solyc09g007100	bZIP transcription factor (DUF630 and DUF632) (AHRD V3.3 *** AT2G27090.2)		P:GO:0071249	P:cellular response to nitrate			IPR006867 (PFAM): IPR006868 (PFA	38,624	29,045	40,085	37,783	43,131									
Solyc09g007110	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** A0A0K9PPV4_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:3.30.200.20 (GENE3D): G3DS	11,204	10,105	3,649	4,706	4,042									
Solyc09g007120	TATA box-binding protein associated factor RNA polymerase I subunit B-like protein (AHRD V3.3 *** A0A072		F:GO:0001164: P:G(	F:RNA polymerase I CORE element sequence-specific DNA bin			mobidb-lite (MOBIDB_LITE): IPR0335	5,280	4,842	7,433	6,610	6,723									
Solyc09g007130	3-methyl-2-oxobutanoate hydroxymethyltransferase (AHRD V3.3 *** K4CQA3_SOLLC)		F:GO:0003864: P:G(	F:3-methyl-2-oxobu	EC:2.1.2.11	3-methyl-2-oxobutan	IPR040442 (G3DSA:3.20.20.GENE3D	7,734	11,349	12,375	9,494	12,549									
Solyc09g007140	Heat shock family protein (AHRD V3.3 *** B9MYM7_POPTR)	Hsp26.8	C:GO:0016021	C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,498	0,791	0,124	0,050	0,211									
Solyc09g007150	Glutathione S-transferase (AHRD V3.3 *** A0A096XCA4_BETPN)	GSTL2	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): PF1	0,061	0,060	0,000	0,050	0,072									
Solyc09g007160	Glutathione S-transferase (AHRD V3.3 *-* A0A096XCA4_BETPN)	GST	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:1.10.472	31,064	29,225	28,281	26,239	28,394									
Solyc09g007170	Protein kinase-like protein (AHRD V3.3 *** C6ZRY1_SOYBN)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:nucleobase-containir			IPR000850 (PRINTS): G3DSA:3.30.2(	28,046	28,245	24,793	23,010	23,906									
Solyc09g007180	Adenylate kinase		F:GO:0004017: F:G(	F:adenylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR000850 (PRINTS): IPR006259 (TI(	1,966	2,723	1,704	1,981	1,647									
Solyc09g007190	Thioredoxin superfamily protein (AHRD V3.3 *** AT2G37240.1)		P:GO:0055114	P:oxidation-reduction process			IPR032801 (PFAM): IPR032801 (PAN	16,283	22,761	21,563	19,900	34,035			0,655	0,000				up	
Solyc09g007200	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5GAL9_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	17,769	19,071	14,844	14,469	19,343									
Solyc09g007210	DNA topoisomerase 6 subunit A (AHRD V3.3 *** A0A0V0I1Z4_SOLCH)		P:GO:0000737: F:G(	P:DNA catabolic pr(	EC:3.6.1.3; EC:5.99.	Adenosinetriphospha	IPR002815 (PRINTS): IPR004085 (PF	30,995	25,536	24,220	20,349	20,581									
Solyc09g007220	LOW QUALITY:F-box protein (AHRD V3.3 *** W9QTH9_9ROSA)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	2,720	3,855	4,914	5,015	4,048									
Solyc09g007230	Zinc finger transcription factor 53	C3H53	F:GO:0046872	F:metal ion binding			IPR032378 (PFAM): mobidb-lite (MOB	86,742	85,239	119,447	125,547	111,999									
Solyc09g007240	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (AHRD V3.3 *** AT3G53470.1)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane; C:integral component of men			mobidb-lite (MOBIDB_LITE): PTHR360	1,303	1,883	1,395	2,437	2,117									
Solyc09g007250	60S ribosomal protein L4 (AHRD V3.3 *** RL4_PRUAR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002136 (PFAM): IPR025755 (PFA	285,911	322,210	252,328	226,115	239,355									
Solyc09g007260	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7IU38_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' AP2	3,732	2,578	0,782	0,522	0,800									
Solyc09g007270	Ascorbate peroxidase (AHRD V3.3 *** B9VRH6_CITMA)	APX3	F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002207 (PRINTS): IPR002016 (PF	652,697	499,211	1826,858	1610,048	1707,332									
Solyc09g007280	Kinase-like protein (AHRD V3.3 *** A0A0K9NJC4_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR024788 (PFAM): G3DSA:1.10.510	29,250	23,777	17,686	17,804	24,345									
Solyc09g007290	Nuclear transcription factor Y subunit B (AHRD V3.3 *** G7L1Q2_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	83,257	74,079	103,547	100,690	101,525									
Solyc09g007300	SITE-1 protease (AHRD V3.3 *** AT5G19660.3)		F:GO:0004252: P:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	26,498	21,370	31,066	32,308	31,187									
Solyc09g007310	E3 ubiquitin-protein ligase (AHRD V3.3 *** A0A072VW29_MEDTR)		F:GO:0004842	F:ubiquitin-protein transferase activity			IPR011989 (G3DSA:1.25.10.GENE3D	74,352	43,899	145,087	136,144	114,136	-0,734	0,002					down		
Solyc09g007330	minichromosome maintenance 8 (AHRD V3.3 *** AT3G09660.3)		F:GO:0003677: F:G(	F:DNA binding; F:ATP binding; P:DNA replication initiation			IPR001208 (PRINTS): IPR001208 (PF	3,419	3,144	1,063	0,344	0,612									
Solyc09g007340	Serine/threonine-protein kinase ATM (AHRD V3.3 *** A0A0B0N3M2_GOSAR)		F:GO:0003676	F:nucleic acid binding			G3DSA:2.30.30.140 (GENE3D): IPR0(	11,395	11,170	9,851	10,083	9,170									
Solyc09g007343	LOW QUALITY:F-box protein (AHRD V3.3 --* G7IWM2_MEDTR)						IPR005174 (PFAM)	0,181	0,181	0,365	0,580	0,214									
Solyc09g007347	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 --* AT3G29760.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,970	6,110	2,547	2,184	2,684									
Solyc09g007350	Ribosomal protein S12 (AHRD V3.3 *** A0A059LPB2_9CHLO)		F:GO:0003735: P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR006032 (PIRSF): G3DSA:2.40.50.	73,024	83,483	76,655	73,485	71,980									
Solyc09g007360	Interactor of constitutive active ROPs 2, chloroplastic-like protein (AHRD V3.3 *** A0A0B0PSX8_GOSAR)		F:GO:0051219	F:phosphoprotein binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,353	2,696	0,100	0,125	0,259									
Solyc09g007370	Ribonuclease P protein subunit p29 (AHRD V3.3 *** A0A0B2RS88_GLYSO)		F:GO:0000171: C:G(	F:ribonuclease MRI	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	mobidb-lite (MOBIDB_LITE): PTHR133	9,286	9,003	8,908	10,196	8,759									
Solyc09g007380	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G02970.1)		C:GO:0016021: F:G(	C:integral component of membrane; F:hydrolase activity			IPR000073 (PFAM): mobidb-lite (MOB	0,899	1,706	0,046	0,069	0,024									
Solyc09g007390	DNAJ protein, putative, expressed (AHRD V3.3 *** Q10DG4_ORYSJ)		C:GO:0001405: F:G(	C:PAM complex, Tim23 associated import motor; F:ATPase acti			IPR036869 (G3DSA:1.10.287.GENE3	10,266	10,618	18,069	15,664	15,445									
Solyc09g007410	SUN-like protein 25	SUN25	F:GO:0005515	F:protein binding			IPR000048 (PFAM): mobidb-lite (MOB	29,320	22,961	23,070	21,148	21,401									
Solyc09g007420	Glycosyltransferase (AHRD V3.3 *** I1Z1X6_TOBAC)		F:GO:0015018: C:G(	F:galactosylgalacto	EC:2.4.1.17; EC:2.4.	Glucuronosyltransfer	IPR005027 (PFAM): IPR029044 (G3D	0,732	0,511	0,068	0,098	0,071									
Solyc09g007430	Single-stranded DNA binding protein (AHRD V3.3 *** D7KGI0_ARALL)		F:GO:0003697	F:single-stranded DNA binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	8,316	8,542	9,512	7,354	7,927									
Solyc09g007440	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9S4I3_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			IPR011545 (PFAM): G3DSA:3.40.50.3	22,044	24,343	27,021	27,585	25,194									
Solyc09g007445	Phosphatidic acid phosphatase family protein isoform 1 (AHRD V3.3 *** A0A061ESH3_THECC)		F:GO:0016787	F:hydrolase activity			IPR000326 (PFAM): G3DSA:1.20.144	0,095	0,121	0,190	0,172	0,284									
Solyc09g007450	Phosphatidic acid phosphatase family protein isoform 1 (AHRD V3.3 *** A0A061ESH3_THECC)		F:GO:0016787	F:hydrolase activity			IPR000326 (PFAM): G3DSA:1.20.144	1,004	0,790	0,726	0,940	0,804									
Solyc09g007460	POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND protein (AHRD V3.3 *** AT3G09730.2)		P:GO:0008356	P:asymmetric cell division			PTHR33476:SF4 (PANTHER): IPR040	3,129	1,752	0,239	0,097	0,048									
Solyc09g007470	LOW QUALITY:Protamine P1 family protein (AHRD V3.3 *** G7L1S0_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,727	0,651	0,047	0,000	0,000									
Solyc09g007480	Fructose-bisphosphate aldolase, cytoplasmic isozyme (AHRD V3.3 --* ALF_MAIZE)						mobidb-lite (MOBIDB_LITE)	39,837	30,617	0,895	0,758	1,379									
Solyc09g007490	Cell number regulator-like protein (AHRD V3.3 *** G7L1S3_MEDTR)						IPR006461 (TIGRFAM): IPR006461 (F	129,657	147,389	157,875	155,917	157,747									
Solyc09g007500	DNA-binding protein S1FA, putative (AHRD V3.3 *** B9SGP8_RICCO)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			IPR006779 (PFAM S1Fa-like	52,782	42,675	46,617	47,911	43,801									
Solyc09g007510	Lectin receptor kinase-like protein (AHRD V3.3 *** B3XWM9_NICBE)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001220 (PFAM): G3DSA:1.10.510	12,633	8,574	3,481	4,300	4,951									
Solyc09g007520	Peroxidase (AHRD V3.3 *** K4CQE1_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,136	0,571	0,146	0,319	0,397									
Solyc09g007530	RING/U-box superfamily protein (AHRD V3.3 *** AT2G37150.15)		P:GO:0016567: F:G(	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga:			IPR001841 (PFAM): IPR013083 (G3D	66,766	57,542	169,351	175,161	145,130									
Solyc09g007535	chromatin remodeling 38 (AHRD V3.3 --* AT3G42670.4)							7,244	4,881	17,342	21,870	18,911									
Solyc09g007540	valyl-tRNA synthetase / valine-tRNA ligase (VALRS) (AHRD V3.3 *** AT1G14610.1)		F:GO:0002161: F:G(	F:aminoacyl-tRNA ε	EC:6.1.1.9; EC:3.1.1	Valine--tRNA ligase;	IPR002303 (PRINTS): IPR013155 (PF	296,576	250,243	199,100	184,691	200,615									
Solyc09g007550	Zinc finger family protein (AHRD V3.3 *** B9IJ27_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	3,960	8,751	0,902	0,891	0,707	1,175	0,008					up		
Solyc09g007560	50S ribosomal protein L5 (AHRD V3.3 *** B5TV71_CAMSI)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR031310 (PFAM): IPR031309 (PFA	67,202	108,218	99,484	105,783	130,297	0,715	0,016					up		
Solyc09g007570	Myb family transcription factor family protein (AHRD V3.3 *** B9H5N1_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI MYB_related	2,151	2,482	1,772	1,657	2,005									
Solyc09g007580	Myb family transcription factor family protein (AHRD V3.3 *** B9H5N1_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI MYB_related	0,115	0,059	0,000	0,000	0,000									
Solyc09g007620	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G53190.2)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	0,056	0,110	0,000	0,000	0,000									
Solyc09g007630	P58IPK	P58IPK	F:GO:0005515	F:protein binding			IPR001623 (PRINTS): IPR001623 (PF	19,007	14,668	26,415	31,005	27,542									
Solyc09g007640	Carboxypeptidase (AHRD V3.3 *** K4CQF3_SOLLC)		F:GO:0004185: P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	7,072	7,541	3,717	3,165	3,368									
Solyc09g007650	Fasciclin-like arabinogalactan protein (AHRD V3.3 *-* D5KXI3_EUCNI)		C:GO:0005886: P:G(	C:plasma membrane; P:plant-type secondary cell wall biogenesi			IPR000782 (PFAM): mobidb-lite (MOB	0,000	0,061	0,000	0,000	0,000									
Solyc09g007660	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7L2R9_MEDTR)		C:GO:0005886: P:G(	C:plasma membrane; P:plant-type secondary cell wall biogenesi			IPR036378 (G3DSA:2.30.180.GENE3	0,121	0,062	0,000	0,000	0,000									
Solyc09g007670	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G53390.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): mobidb-lite (MOB	10,589	7,606	8,560	9,851	9,374									
Solyc09g007680	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G60580.3)		F:GO:0008270	F:zinc ion binding			IPR013103 (PFAM): PF13920 (PFAM)	40,254	26,090	46,663	38,515	36,666	-0,598	0,036	-0,351	0,037			down	down	
Solyc09g007700	RING/U-box superfamily protein (AHRD V3.3 *** AT3G09770.1)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	6,158	5,167	5,604	6,429	5,944									
Solyc09g007710	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.2)		F:GO:0005515: P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR035897 (G3D	1,069	0,623	0,094	0,097	0,166									
Solyc09g007720	Ribosomal protein S7, mitochondrial (AHRD V3.3 --* RT07_BETVU)							0,461	0,199	0,441	0,263	0,349									
Solyc09g007730	Kinase family protein (AHRD V3.3 *** B9NAB5_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	3,449	9,574	2,573	2,907	3,593									
Solyc09g007740	LOW QUALITY:mediator of RNA polymerase II transcription subunit 19a-like protein (AHRD V3.3 --* AT5G12230.1)							0,000	0,039	0,100	0,097	0,023									
Solyc09g007750	Kinase family protein (AHRD V3.3 *** D7L8C6_ARALL)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (PFAM): G3DSA:1.10.510	2,512	2,542	2,903	3,590	2,782									
Solyc09g007760	plasma membrane intrinsic protein 2.10	PIP2.10	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	1,957	3,083	0,586	0,938	0,591									
Solyc09g007765	Aquaporin-like protein (AHRD V3.3 *-* A0A103XNC2_CYNCS)		F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	0,101	0,060	0,072	0,000	0,000									
Solyc09g007790	LOW QUALITY:Senescence regulator (AHRD V3.3 *** G7IRS7_MEDTR)						IPR007608 (PFAM): PTHR33083 (PAN	8,862	9,869	16,333	9,691	12,965					-0,747	0,003			down
Solyc09g007800	acyl-CoA-binding domain protein (AHRD V3.3 *** AT2G37195.2)		C:GO:0016021	C:integral component of membrane			PTHR37215 (PANTHER)	5,672	4,168	8,830	7,896	8,641									
Solyc09g007810	Auxin Response Factor 16A	ARF16A	F:GO:0003677: F:G(	F:DNA binding; F:protein binding; C:nucleus; P:regulation of tran			IPR015300 (G3DS ARF	12,944	15,440	13,243	11,141	13,543									
Solyc09g007820	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G03250.1)		F:GO:0005515	F:protein binding			IPR027356 (PFAM): IPR000210 (PFA	0,000	0,039	0,000	0,000	0,000									
Solyc09g007830	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** K4CQH2_SOLLC)		C:GO:0005634: C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			IPR005269 (TIGRFAM): IPR031100 (F	0,318	0,622	0,000	0,000	0,000									
Solyc09g007840	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005249: P:G(	F:voltage-gated potassium channel activity; P:potassium ion tra			IPR003938 (PRINTS): G3DSA:1.10.28	0,059	0,018	0,150	0,000	0,047									
Solyc09g007850	RNA binding protein (AHRD V3.3 *** Q39209_ARATH)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	116,081	206,365	163,280	137,610	239,536	0,858	0,000	0,550	0,022			up	up	
Solyc09g007860	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G04220.2)		F:GO:0008289	F:lipid binding			IPR035892 (G3DSA:2.60.40.GENE3D	60,004	54,873	48,988	43,433	48,815									
Solyc09g007870	ethylene signaling protein	EIN2	P:GO:0009873: C:G(	P:ethylene-activated signaling pathway; C:membrane; P:metal i(			IPR001046 (PRINTS): IPR001046 (PF	192,147	128,051	184,706	175,583	169,023	-0,558	0,035					down		
Solyc09g007880	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT1G31335.1)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	4,129	3,405	7,828	8,714	7,517									
Solyc09g007890	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL5_SOLLC)	PAL5D	C:GO:0005737: P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l			IPR024083 (G3DSA:1.10.275.GENE3	1,300	1,581	1,634	1,497	1,395									
Solyc09g007900	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL5_SOLLC)	PAL5C	C:GO:0005737: P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l			IPR023144 (G3DSA:1.10.274.GENE3	202,736	250,408	60,007	75,902	81,837									
Solyc09g007910	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL5_SOLLC)	PAL5B	C:GO:0005737: P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l			IPR024083 (G3DSA:1.10.275.GENE3	101,067	240,029	346,047	388,641	373,560									
Solyc09g007920	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL5_SOLLC)	PAL5A	C:GO:0005737: P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l			IPR024083 (G3DSA:1.10.275.GENE3	406,062	355,574	168,941	174,374	203,178									
Solyc09g007940	Adenosine kinase, putative (AHRD V3.3 *** B9T0A9_RICCO)		F:GO:0004001: P:G(	F:adenosine kinase	EC:2.7.1.2	Adenosine kinase	IPR001805 (PRINTS): IPR011611 (PF	7,563	12,064	0,211	0,172	0,211									
Solyc09g007950	transmembrane protein (AHRD V3.3 *** AT2G37035.1)		C:GO:0016021	C:integral component of membrane			PTHR36353 (PANTHER)	8,833	7,322	8,993	7,511	7,904									
Solyc09g007960	ATP binding microtubule motor family protein (AHRD V3.3 --* AT2G21300.5)							0,000	0,018	0,000	0,000	0,000									
Solyc09g007990	Telomere repeat-binding factor like-protein (AHRD V3.3 *-* A0A0K1SBG8_REHGL)		F:GO:0003677	F:DNA binding			G3DSA:1.10.246.2 MYB_related	24,306	21,403	36,304	39,029	34,404									
Solyc09g008000	ABC transporter G family-like protein (AHRD V3.3 *** A0A072UJT7_MEDTR)	ABCG62	F:GO:0005524: F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	0,177	0,336	0,075	0,092	0,094									
Solyc09g008010	Kinase family protein (AHRD V3.3 *** B9MTD8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): IPR001245 (F	27,796	68,561	20,084	26,371	29,230	1,326	0,001	0,539	0,018			up	up	
Solyc09g008020	OTU domain-containing protein (AHRD V3.3 *** A0A199VP67_ANACO)		F:GO:0004843: P:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.80 (GENE3D): IPR00:	34,668	26,797	99,014	120,203	85,875									
Solyc09g008030	TCP transcription factor 19	TCP19	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	3,889	3,074	2,227	2,752	2,158									
Solyc09g008040	Sigma factor (AHRD V3.3 *** A0A0G2STR6_9ROSI)	SIG6	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:DNA-templated tra			IPR000943 (PRINTS): IPR007630 (PF	11,274	12,565	12,834	14,344	16,543									
Solyc09g008050	Glycosyltransferase (AHRD V3.3 *** K4CQJ4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	18,108	17,999	18,259	15,845	15,655									
Solyc09g008060	Glycosyltransferase (AHRD V3.3 *** K4CQJ5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	5,140	11,035	0,119	0,098	0,142	1,131	0,004					up		
Solyc09g008070	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524: F:G(	F:ATP binding; F:hydrolase activity			IPR003959 (PFAM): G3DSA:1.10.8.6(	4,805	4,836	1,306	1,098	1,364									
Solyc09g008080	Ribosomal protein S5/Elongation factor G/III/V family protein (AHRD V3.3 --* AT1G56070.3)		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D): mobidt	1,443	1,682	0,813	1,436	1,505									
Solyc09g008090	Glycosyltransferase (AHRD V3.3 *** A0A0D5ZDE5_PANGI)		F:GO:0035251	F:UDP-glucosyltransferase activity			G3DSA:3.40.50.2000 (GENE3D): G3D	0,000	0,000	0,109	0,050	0,024									
Solyc09g008100	TSL-kinase interacting 1-like protein (AHRD V3.3 *** A0A0B0MZG4_GOSAR)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB_related	25,168	23,292	29,923	29,879	28,258									
Solyc09g008120	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9REC8_RICCO)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR007502 (PFAM): G3DSA:1.20.120	19,790	19,138	23,353	22,044	20,209									
Solyc09g008130	Phosphoglycerate kinase (AHRD V3.3 *** K4CQK2_SOLLC)		F:GO:0004618: P:G(	F:phosphoglycerate	EC:2.7.2.3; EC:2.1.1	Phosphoglycerate kir	IPR001576 (PRINTS): IPR015824 (G3	11,815	9,651	17,523	17,322	17,845									
Solyc09g008140	membrane magnesium transporter-like protein (AHRD V3.3 *** AT5G03345.1)		C:GO:0005769: C:G(	C:early endosome; C:Golgi apparatus; C:plasma membrane; F:i			IPR018937 (PFAM): PTHR21181:SF7	9,667	9,656	21,015	22,825	19,789									
Solyc09g008150	Transcription initiation factor TFIID subunit-like protein (AHRD V3.3 *** A0A072VQR3_MEDTR)		C:GO:0005669: F:G(	C:transcription factor TFIID complex; F:protein heterodimerizatic			IPR009072 (G3DSA:1.10.20.GENE3D	8,670	10,181	13,186	11,215	11,293									
Solyc09g008160	Cysteine proteinases superfamily protein, putative isoform 5 (AHRD V3.3 --* A0A061FZR3_THECC)							46,685	56,177	94,600	105,062	101,422									
Solyc09g008170	Small auxin up-regulated RNA69	SAUR69	P:GO:0009733	P:response to auxin			IPR003676 (PFAM): mobidb-lite (MOB	0,040	0,122	78,095	143,891	62,198					0,886	0,027			up
Solyc09g008175	SAUR-like auxin-responsive protein family (AHRD V3.3 *-* AT2G28085.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF1	0,103	0,114	23,858	30,949	14,689			-0,700	0,048				down	
Solyc09g008180	LOW QUALITY:Clathrin heavy chain (AHRD V3.3 --* I1INY7_BRADI)		C:GO:0005739	C:mitochondrion				0,000	0,018	1,031	1,392	0,398									
Solyc09g008190	Acylphosphatase (AHRD V3.3 *-* A0A0B0PI53_GOSAR)		F:GO:0003998	F:acylphosphatase	EC:3.6.1.7	Acylphosphatase	IPR020456 (PRINTS): G3DSA:3.30.70	12,559	14,527	66,998	65,629	61,397									
Solyc09g008200	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G03380.1)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	116,203	55,643	427,452	374,397	322,301	-1,034	0,005	-0,410	0,028			down	down	
Solyc09g008205	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)		C:GO:0016021: F:G(	C:integral component of membrane; F:transferase activity, trans			IPR029044 (G3DSA:3.90.550.GENE3	8,702	13,420	4,850	8,666	4,167									

Solyc09g008210	Omega-6 fatty acid desaturase, chloroplastic (AHRD V3.3 --* FAD6C_SOYBN)							0,000	0,018	0,000	0,048	0,071									
Solyc09g008220	Unknown protein (AHRD V3.3)							0,142	0,134	0,197	0,184	0,353									
Solyc09g008230	Zinc finger family protein (AHRD V3.3 *** A9P9T1_POPTR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR022755 (PFAM): G3DSA:3.30.160	93,961	82,061	123,013	103,723	112,586									
Solyc09g008240	ABC transporter B family protein (AHRD V3.3 *** G7L3V6_MEDTR)	ABCB14	F:GO:0005524: C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	91,261	60,653	17,371	15,200	17,317									
Solyc09g008250	blind-like1	R2R3MYB38	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,021	0,101	0,051	0,025	0,071									
Solyc09g008260	5'-AMP-activated kinase-like protein, putative (AHRD V3.3 *-* A0A072VJE8_MEDTR)		C:GO:0009507: P:G(	C:chloroplast; P:regulation of starch biosynthetic process			IPR013783 (G3DSA:2.60.40.GENE3D	4,591	5,780	2,738	2,579	3,402									
Solyc09g008270	translation initiation factor (AHRD V3.3 *** AT2G36885.1)		C:GO:0016020: P:G(	C:membrane; P:respiratory electron transport chain			IPR025067 (PFAM): PTHR36738 (PAN	4,098	4,997	1,282	1,385	1,465									
Solyc09g008280	S-adenosyl-L-methionine synthetase Z24743		F:GO:0004478: F:G(	F:methionine adeno	EC:2.5.1.6	Methionine adenosyl	IPR002133 (PIRSF): G3DSA:3.30.300	0,397	0,709	0,194	0,193	0,213									
Solyc09g008295	Thioredoxin, putative (AHRD V3.3 *** B9S0G2_RICCO)		P:GO:0006662: F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			G3DSA:3.40.30.10 (GENE3D): IPR01:	6,656	6,745	9,412	7,600	9,865									
Solyc09g008310	Phosphoadenosine phosphosulfate reductase family protein (AHRD V3.3 *** G7L3W8_MEDTR)		F:GO:0003824	F:catalytic activity			IPR001453 (PFAM): IPR036425 (G3D	17,654	15,289	28,738	31,844	26,359									
Solyc09g008320	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CQM0_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR000757 (PFAM): IPR010713 (PFA	50,037	46,756	3,228	2,768	4,450									
Solyc09g008330	RING/U-box superfamily protein (AHRD V3.3 --* AT1G51930.1)		F:GO:0004842: F:G(	F:ubiquitin-protein transferase activity; F:protein binding; C:nucl			IPR013083 (G3DSA:3.30.40.GENE3D	10,838	8,471	9,871	8,441	7,988									
Solyc09g008340	transmembrane protein (AHRD V3.3 *** AT5G03460.1)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): PTHR377	29,510	30,254	49,899	46,638	43,784									
Solyc09g008350	ACT domain-containing family protein (AHRD V3.3 *** B9GIE7_POPTR)						G3DSA:3.30.70.260 (GENE3D): IPR0(	32,449	38,878	17,083	10,333	14,322					-0,723	0,003			down
Solyc09g008370	LOW QUALITY:Major facilitator superfamily protein (AHRD V3.3 *** AT2G39210.1)		C:GO:0016021: P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	2,530	5,034	15,386	18,417	8,084			-0,929	0,004				down	
Solyc09g008380	Pectate lyase (AHRD V3.3 *** K4CQM6_SOLLC)		C:GO:0016021: F:G(	C:integral compone	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS): IPR012334 (G3	0,976	1,231	0,000	0,051	0,071									
Solyc09g008400	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9IFU5_POPTR)		C:GO:0000159: P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR002554 (PIRSF): IPR011989 (G3D	12,685	11,666	15,294	13,907	12,881									
Solyc09g008410	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4CQM9_SOLLC)		P:GO:0000413: F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR002130 (PF	22,075	24,028	29,863	33,504	30,410									
Solyc09g008430	CHY zinc finger family protein, expressed (AHRD V3.3 *** Q337P1_ORYSJ)		F:GO:0008270: C:G(	F:zinc ion binding; C:integral component of membrane; F:ligase			IPR039512 (PFAM): IPR013083 (G3D	11,766	10,931	13,745	16,801	16,492									
Solyc09g008440	Zinc finger family protein (AHRD V3.3 *** B9N876_POPTR)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM): C2H2	0,196	0,177	0,226	0,430	0,354									
Solyc09g008450	Ankyrin repeat family protein (AHRD V3.3 *** AT3G09890.1)		F:GO:0005515	F:protein binding			IPR002110 (PFAM): IPR036770 (G3D	2,592	2,700	1,987	1,672	1,626									
Solyc09g008460	Ras-related gtp-binding protein (AHRD V3.3 *** C1E029_MICCC)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	9,104	5,362	1,304	1,063	1,080									
Solyc09g008470	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT2G32600.1)		F:GO:0003676: C:G(	F:nucleic acid binding; C:nucleus; F:zinc ion binding			PF12874 (PFAM): IPR031781 (PFAM)	30,813	29,809	53,011	50,243	47,085									
Solyc09g008480	1-phosphatidylinositol-4-phosphate 5-kinase							0,021	0,043	0,091	0,045	0,047									
Solyc09g008485	Phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *** B9S0D1_RICCO)		F:GO:0005524: F:G(	F:ATP binding; F:1-(	EC:2.7.1.68	1-phosphatidylinositc	IPR017163 (PIRSF): IPR027484 (G3D	33,672	34,543	26,919	27,443	27,398									
Solyc09g008490	HEAT repeat-containing 7A (AHRD V3.3 *** A0A0B0Q1K1_GOSAR)		P:GO:0009660: C:G(	P:amyloplast organization; C:plant-type vacuole membrane; P:n			IPR032682 (PFAM): IPR011989 (G3D	59,747	50,129	56,968	65,672	62,421									
Solyc09g008505	Transmembrane protein 184C family (AHRD V3.3 *-* A0A151QYG0_CAJCA)		P:GO:0007033: C:G(	P:vacuole organization; C:plant-type vacuole membrane; C:inte			IPR005178 (PANTHER): PTHR23423:	0,021	0,018	0,075	0,075	0,024									
Solyc09g008520	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *** A0A072VVJ3_MEDTR)		F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR013083 (G3DSA:3.30.40.GENE3D	17,588	18,437	10,085	10,667	10,238									
Solyc09g008525	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 *-*		F:GO:0046872	F:metal ion binding			PTHR42672 (PANTHER): PTHR42672	10,622	10,751	6,130	5,927	6,140									
Solyc09g008530	F-box and Leucine Rich Repeat domains containing protein, putative isoform 1 (AHRD V3.3 *** A0A061ETN1_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,697	1,777	2,707	5,615	3,361					1,058	0,017			up
Solyc09g008550	Cytosine/purine uracil thiamine allantoin permease (AHRD V3.3 *** G7IA71_MEDTR)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmer			IPR001248 (PFAM): IPR038271 (G3D	5,427	4,735	11,873	17,214	16,081			0,435	0,041	0,539	0,005		up	up
Solyc09g008560	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G36690.2)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	13,102	20,274	1,527	1,798	1,708									
Solyc09g008600	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT5G22850.1)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032799 (PF	21,097	23,663	16,131	15,245	18,602									
Solyc09g008610	ER membrane protein complex subunit 1 (AHRD V3.3 *** A0A199VQY4_ANACO)		F:GO:0005515: C:G(	F:protein binding; C:ER membrane protein complex			IPR011678 (PFAM): IPR002372 (PFA	139,132	124,089	170,463	167,064	158,347									
Solyc09g008620	Polyadenylate-binding protein (AHRD V3.3 *** K4CQP8_SOLLC)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,381	0,575	0,237	0,246	0,258									
Solyc09g008625	Polyadenylate-binding protein (AHRD V3.3 *-* K4CQP8_SOLLC)		F:GO:0003723	F:RNA binding			G3DSA:1.10.1900.10 (GENE3D): IPR(	0,077	0,100	0,046	0,075	0,069									
Solyc09g008630	DNA replication complex GINS protein PSF1 (AHRD V3.3 *** B6THR1_MAIZE)		C:GO:0000811: P:G(	C:GINS complex; P:DNA replication			IPR021151 (PFAM): mobidb-lite (MOB	3,290	3,285	2,827	2,751	2,583									
Solyc09g008640	Kinase family protein (AHRD V3.3 *** A0A061EUG0_THECC)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	2,510	3,161	1,340	0,698	1,642									
Solyc09g008650	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 *** AT3G10060.1)		P:GO:0000413: F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer	G3DSA:3.10.50.40 (GENE3D): IPR00	3,812	7,730	1,056	1,734	2,412	1,047	0,007					up		
Solyc09g008660	LOW QUALITY:Protein CHUP1, chloroplastic (AHRD V3.3 *** A0A0B2P3P6_GLYSO)		C:GO:0009707: C:G(	C:chloroplast outer membrane; C:integral component of membra			IPR040265 (PANTHER): PTHR31342:	1,223	1,480	0,929	0,774	0,519									
Solyc09g008670	threonine deaminase	td	F:GO:0004794: P:G(	F:L-threonine amm	EC:4.3.1.19	Threonine ammonia-l	IPR005787 (TIGRFAM): G3DSA:3.40.	0,761	1,992	1,214	9,747	6,624			2,427	0,007	2,979	0,000		up	up
Solyc09g008680	FAD-binding protein (AHRD V3.3 *** AT3G49645.2)						PTHR35305 (PANTHER)	3,423	2,538	4,255	5,048	4,901									
Solyc09g008690	GDSL esterase/lipase (AHRD V3.3 *** W9R8E1_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	2,291	1,301	0,541	0,167	0,258									
Solyc09g008700	E3 ubiquitin-protein ligase (AHRD V3.3 *** A0A072U2X8_MEDTR)		F:GO:0004842	F:ubiquitin-protein transferase activity			G3DSA:3.30.2160.10 (GENE3D): G3D	31,938	22,363	37,975	37,799	35,699									
Solyc09g008720	Exostosin-like protein (AHRD V3.3 *** A0A103XZW6_CYNCS)		P:GO:0006486: F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR040911 (PFAM): PTHR11062:SF6	2,966	3,066	4,975	8,185	4,101					0,723	0,017			up
Solyc09g008730	GTP-binding protein (AHRD V3.3 *** A0A0B2PD78_GLYSO)		F:GO:0005525	F:GTP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	17,077	17,565	13,357	12,363	14,624									
Solyc09g008740	VQ motif-containing protein (AHRD V3.3 --* AT4G37710.2)						IPR008889 (PFAM): mobidb-lite (MOB	0,000	0,021	0,125	0,047	0,024									
Solyc09g008750	VQ motif-containing protein, putative (AHRD V3.3 *** A0A061DH87_THECC)						IPR008889 (PFAM): mobidb-lite (MOB	0,000	0,018	0,134	0,000	0,000									
Solyc09g008760	VQ motif-containing protein (AHRD V3.3 *-* AT4G37710.2)						IPR008889 (PFAM): mobidb-lite (MOB	0,000	0,057	0,075	0,022	0,023									
Solyc09g008770	Late embryogenesis abundant protein, putative (AHRD V3.3 *** G7I9D0_MEDTR)		C:GO:0005829	C:cytosol			IPR004238 (PFAM): G3DSA:1.20.120	8,457	11,218	5,867	14,624	1,208									
Solyc09g008780	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G36630.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM): PTHR14255:SF5	20,217	30,439	421,741	368,200	387,662									
Solyc09g008790	Kinase family protein (AHRD V3.3 *** B9MYL8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	33,090	22,240	17,041	17,190	19,091									
Solyc09g008800	60S ribosomal protein L24 (AHRD V3.3 *** RL24_PRUAV)		P:GO:0000027: F:G(	P:ribosomal large subunit assembly; F:RNA binding; F:structural			G3DSA:3.30.160.440 (GENE3D): IPR(	234,077	251,170	201,675	176,463	174,593									
Solyc09g008810	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072U315_MEDTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000047 (PRIN HD-ZIP	0,019	0,021	0,000	0,000	0,000									
Solyc09g008820	F-box protein PP2-A13 (AHRD V3.3 *** A0A072U2Z8_MEDTR)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): G3DSA:1.20.128(	20,112	18,361	18,280	16,664	17,842									
Solyc09g008830	Transcription factor, putative (AHRD V3.3 *** B9RIA5_RICCO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	33,784	32,933	43,660	18,091	32,617					-1,266	0,000			down
Solyc09g008840	Pyruvate kinase family protein (AHRD V3.3 *** AT3G52990.1)		F:GO:0000287: F:G(	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS): IPR040442 (G3	24,581	24,679	87,271	81,099	93,923									
Solyc09g008850	Uridylate kinase (AHRD V3.3 *** W9SIW1_9ROSA)		C:GO:0005737: P:G(	C:cytoplasm; P:pyri	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	IPR001057 (PRIN Trihelix	17,541	15,302	22,186	18,117	20,479									
Solyc09g008860	Ovary receptor kinase 14 (AHRD V3.3 *** S4WME3_SOLCH)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0:	1,790	2,497	0,718	0,846	0,821									
Solyc09g008920	Geranylgeranyl pyrophosphate synthase family protein (AHRD V3.3 *** B9HR16_P(	GGPS1	P:GO:0008299	P:isoprenoid biosynthetic process			IPR008949 (G3DSA:1.10.600.GENE3	58,110	81,523	104,659	93,699	113,670									
Solyc09g008930	Plant/T32M21-140 protein (AHRD V3.3 *** G7J6T8_MEDTR)						IPR021864 (PFAM): IPR007700 (PFA	44,434	27,890	56,359	44,154	48,561	-0,643	0,045					down		
Solyc09g008940	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7I9B1_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	10,659	10,126	9,514	9,327	9,621									
Solyc09g008970	LOW QUALITY:AT3g10020/T22K18_16 (AHRD V3.3 *** Q9SR67_ARATH)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): mobidb-lit	40,006	16,380	104,333	113,635	111,534	-1,261	0,002					down		
Solyc09g008980	plant/protein (AHRD V3.3 *** AT3G10020.1)		P:GO:0045892	P:negative regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): IPR0397	0,019	0,000	0,075	0,200	0,000									
Solyc09g009010	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)		C:GO:0016021: F:G(	C:integral component of membrane; F:transferase activity, trans			IPR029044 (G3DSA:3.90.550.GENE3	0,543	0,883	0,000	0,025	0,023									
Solyc09g009020	enolase	er28	C:GO:0000015: F:G(	C:phosphopyruvate	EC:4.2.1.11	Phosphopyruvate hy	IPR000941 (PRINTS): IPR036849 (G3	1363,294	1230,698	1047,980	847,896	977,215									
Solyc09g009030	Histone deacetylase HDT1 (AHRD V3.3 *** HDT1_SOLCH)		F:GO:0003676	F:nucleic acid binding			G3DSA:2.60.120.340 (GENE3D): IPR(	166,506	166,358	128,842	106,423	115,209									
Solyc09g009040	Sterol C-14 reductase (AHRD V3.3 *** A0A072VKE7_MEDTR)		C:GO:0016020	C:membrane			G3DSA:1.20.120.1630 (GENE3D): IPI	18,355	15,491	12,106	8,421	10,553									
Solyc09g009080	DNA demethylase1	DML1	F:GO:0003824: P:G(	F:catalytic activity; P:base-excision repair			IPR028925 (PFAM): IPR028924 (PFA	86,938	76,519	24,112	23,940	27,289									
Solyc09g009090	CTR1-like protein kinase-3	CTR3	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): PF14381 (PFAI	37,306	39,341	41,138	40,476	40,283									
Solyc09g009100	SolycHsfA3	HSF-24	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	220,070	188,534	54,693	49,077	57,225									
Solyc09g009120	Pre-mRNA cleavage complex 2 protein Pcf11 (AHRD V3.3 *** W9R453_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR006903 (PFAN C2H2	37,406	34,173	41,589	42,251	42,018									
Solyc09g009130	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)		C:GO:0005576: F:G(	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM): IPR009438 (PAN	3,796	5,823	1,998	1,470	1,527									
Solyc09g009140	Gamma-tubulin complex component (AHRD V3.3 *** K4CQU3_SOLLC)		C:GO:0000922: C:G(	C:spindle pole; C:microtubule organizing center; P:microtubule n			IPR040457 (PFAM): IPR041470 (PFA	8,351	7,083	3,400	2,923	3,526									
Solyc09g009150	Serine/threonine-protein kinase (AHRD V3.3 *** D8RWA6_SELML)		P:GO:0048544	P:recognition of pollen			IPR035446 (PIRSF): IPR000858 (PFA	0,061	0,332	0,000	0,075	0,071									
Solyc09g009160	Aminotransferase-like (AHRD V3.3 *-* Q5JJS3_ORYSJ)						IPR019557 (PFAM): mobidb-lite (MOB	0,908	0,646	0,099	0,251	0,023									
Solyc09g009170	ACI14	aci14	F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR004843 (PF	26,944	24,885	50,820	43,660	47,278									
Solyc09g009175	SAC3/GANP/Nin1/mts3/eIF-3 p25 family (AHRD V3.3 --* AT3G06290.4)							0,000	0,018	0,047	0,075	0,000									
Solyc09g009180	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XPY1_CYNCS)		P:GO:0031204	P:posttranslational protein targeting to membrane, translocation			IPR001623 (PRINTS): IPR004179 (PF	53,787	47,928	49,833	48,121	49,569									
Solyc09g009190	Starch branching enzyme (AHRD V3.3 *** Q9XIS5_PHAVU)	SBE1	F:GO:0003844: F:G(	F:1,4-alpha-glucan I	EC:2.4.1.18	1,4-alpha-glucan brai	IPR004193 (PFAM): IPR006047 (PFA	80,689	80,405	47,601	42,088	48,831									
Solyc09g009200	Growth-regulating factor (AHRD V3.3 *** G7L5Z0_MEDTR)		F:GO:0005524: C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten			IPR014978 (PFAM GRF	0,019	0,000	0,025	0,025	0,070									
Solyc09g009210	transcriptional activator (DUF662) (AHRD V3.3 *** AT2G36410.2)						IPR007033 (PFAM): mobidb-lite (MOB	33,130	24,089	38,341	39,661	30,706									
Solyc09g009220	histone-lysine N-methyltransferase SETD1B-like protein (AHRD V3.3 *-* AT5G03670.1)						IPR025486 (PFAM): PTHR33623:SF5	0,717	1,442	1,798	1,316	1,559									
Solyc09g009250	Trihelix transcription factor GT-2-like protein (AHRD V3.3 *** A0A0B0PED7_GOSAR)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			PF13837 (PFAM): Trihelix	0,478	0,386	0,072	0,073	0,047									
Solyc09g009260	fructose-1,6-bisphosphate aldolase		F:GO:0004332: P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	600,990	581,968	1122,878	1039,615	1009,186									
Solyc09g009270	Protein ELC (AHRD V3.3 *** W9RB65_9ROSA)		P:GO:0006464: P:G(	P:cellular protein modification process; P:protein transport			IPR017916 (PFAM): IPR016135 (G3D	11,778	12,939	12,597	12,347	10,437									
Solyc09g009280	LOW QUALITY:DUF868 family protein (AHRD V3.3 *** G7L506_MEDTR)						IPR008586 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc09g009290	Ankyrin repeat family protein (AHRD V3.3 *** AT5G40160.1)		F:GO:0005515	F:protein binding			IPR020683 (PFAM): IPR036770 (G3D	9,720	11,980	27,988	28,194	29,861									
Solyc09g009300	Protein BUD31 like 2 (AHRD V3.3 *** A0A0B2PXU2_GLYSO)		C:GO:0005634	C:nucleus			IPR001748 (PRINTS): IPR001748 (PF	10,476	9,804	14,015	16,262	15,277									
Solyc09g009310	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *-* A0A061F4Q5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,022	0,000	0,000									
Solyc09g009340	Double-strand break repair protein MRE11 (AHRD V3.3 *** MRE11_ARATH)		F:GO:0004519: P:G(	F:endonuclease activity; P:double-strand break repair; F:3'-5' e:			IPR007281 (PFAM): IPR004843 (PFA	13,575	10,942	7,898	7,696	8,055									
Solyc09g009350	calcium-dependent lipid-binding family protein (AHRD V3.3 *-* AT1G48090.6)		C:GO:0016021	C:integral component of membrane			IPR031642 (PFAM): IPR026854 (PFA	12,417	7,947	10,676	16,128	13,242									
Solyc09g009370	Calcium-dependent lipid-binding-like protein (AHRD V3.3 *** A0A072V2R4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR009543 (PFAM): IPR031642 (PFA	119,820	89,896	112,636	136,611	120,659									
Solyc09g009380	Protein kinase (AHRD V3.3 *-* A0A0K9NMI8_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): mobidb-lite (MOB	6,122	4,702	1,304	1,352	1,276									
Solyc09g009390	Monodehydroascorbate reductase (AHRD V3.3 *** MDAR_SOLLC)		F:GO:0016491: F:G(	F:oxidoreductase activity; F:flavin adenine dinucleotide binding;			PR00411 (PRINTS): PR00368 (PRINT	97,316	99,064	152,456	145,641	134,454									
Solyc09g009400	APO protein 3, mitochondrial, putative (AHRD V3.3 *** B9RX46_RICCO)		F:GO:0003723	F:RNA binding			IPR023342 (PFAM): PTHR10388:SF1	2,494	3,588	5,456	5,379	5,792									
Solyc09g009410	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G26060.1)		F:GO:0005515: P:G(	F:protein binding; P:iron-sulfur cluster assembly; C:CIA complex			IPR020472 (PRINTS): IPR015943 (G3	0,096	0,139	0,046	0,025	0,119									
Solyc09g009420	LOW QUALITY:AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT2G47240.4)		P:GO:0009785	P:blue light signaling pathway			mobidb-lite (MOBIDB_LITE): IPR0403	1,197	1,016	0,193	0,076	0,165									
Solyc09g009430	Cell division protein ftsZ, putative (AHRD V3.3 *** B9SRX2_RICCO)	FTsZ2	F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR003008 (PRINTS): IPR003008 (PF	60,089	66,150	107,545	95,662	107,530									
Solyc09g009440	Iron-sulfur cluster assembly protein IscA (AHRD V3.3 *** I3T186_MEDTR)		F:GO:0005198: F:G(	F:structural molecule activity; F:iron-sulfur cluster binding; P:iro			IPR035903 (G3DSA:2.60.300.GENE3	3,419	2,135	5,322	5,180	6,150									
Solyc09g009450	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *-* A0A072UVU8_MEDTR)		F:GO:0003677	F:DNA binding			IPR024752 (PFAM): PTHR31704:SF6	3,727	2,143	3,907	4,293	4,220									
Solyc09g009460	Iron-sulfur cluster assembly protein IscA (AHRD V3.3 *-* I3T186_MEDTR)		F:GO:0005198: F:G(	F:structural molecule activity; F:iron-sulfur cluster binding; P:iro			IPR016092 (TIGRFAM): IPR000361 (I	4,910	4,004	8,415	9,076	7,757									
Solyc09g009470	F-box family protein (AHRD V3.3 *** B9HQ03_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	6,864	8,167	9,739	10,984	9,120									
Solyc09g009480	LOW QUALITY:F-box protein (AHRD V3.3 *-* A0A0P0CKG2_CITMA)						IPR017451 (TIGRFAM): IPR013187 (I	0,019	0,060	0,000	0,000	0,000									
Solyc09g009490	Abscisic acid insensitive (AHRD V3.3 *** B3U2B5_CUCSA)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:respon			G3DSA:1.20.5.17(bZIP	0,382	0,699	0,121	0,769	0,165									
Solyc09g009500	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	11,446	11,826	13,237	12,665	12,599									
Solyc09g009510	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	14,543	15,587	23,356	22,763	21,743									
Solyc09g009520	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,288	0,311	0,191	0,314	0,401									
Solyc09g009530	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)		C:GO:0016021	C:integral component of membrane			IPR000073 (PFAM): IPR029058 (G3D	28,370	30,827	66,044	51,011	53,790									
Solyc09g009540	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,022	0,000									
Solyc09g009550	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)		C:GO:0016021	C:integral component of membrane			IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,025	0,000									
Solyc09g009570	Fatty acyl-CoA reductase (AHRD V3.3 *-* K4CQY6_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			IPR013120 (PFAM): G3DSA:3.40.50.7	0,000	0,000	0,241	0,121	0,023									
Solyc09g009590	A20/AN1 zinc finger protein		F:GO:0003677: F:G(	F:DNA binding; F:zinc ion binding			IPR000058 (PFAM): IPR035896 (G3D	19,952	9,394	86,058	101,107	67,352	-1,057	0,005	-0,356	0,049			down	down	
Solyc09g009600	Purple acid phosphatase (AHRD V3.3 *** K4CQY9_SOLLC)		F:GO:0003993: F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR004843 (PFAM): IPR015914 (PFA	0,286	0,605	0,241	1,294	0,213									
Solyc09g009610	Purple acid phosphatase (AHRD V3.3 *** K4CQZ0_SOLLC)		F:GO:0003993: F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR025733 (PFAM): IPR004843 (PFA	0,249	0,368	0,000	0,000	0,000									
Solyc09g009620	Protein LITTLE ZIPPER 4 (AHRD V3.3 *** A0A199VL62_ANACO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,036	0,000	0,000	0,000									
Solyc09g009630	CAAX prenyl protease 2 (AHRD V3.3 *** A0A0B2PVZ1_GLYSO)		F:GO:0004222: C:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR003675 (PFAM): IPR039731 (PAN	3,717	3,326	6,029	6,973	5,925									
Solyc09g009640	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT2G03870.2)		P:GO:0000398: P:G(	P:mRNA splicing, via spliceosome; P:nuclear-transcribed mRNA			IPR001163 (PFAM): PIRSF037188 (P	35,700	34,424	44,833	40,054	41,405									
Solyc09g009650	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G18110.1)							45,132	41,266	56,999	70,237	59,608									
Solyc09g009660	Solute carrier family 35 protein (AHRD V3.3 *** G7KWQ4_MEDTR)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR009262 (PFAM): PTHR14233:SF1	4,499	3,725	0,978	1,332	1,103									
Solyc09g009670	Solute carrier family 35 protein (AHRD V3.3 *** G7KWQ4_MEDTR)		C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport			IPR009262 (PFAM): PTHR14233:SF1	2,107	1,649	0,047	0,022	0,094									
Solyc09g009680	Transcription initiation factor TFIID subunit 12 (AHRD V3.3 *** A0A151RJE5_CAJCA)		C:GO:0000124: C:G(	C:SAGA complex; C:transcription factor TFIID complex; P:DNA-			IPR009072 (G3DSA:1.10.20.GENE3D	23,566	19,858	29,999	29,974	29,881									
Solyc09g009690	Inosine-uridine preferring nucleoside hydrolase, putative (AHRD V3.3 *** B9SRU5_RICCO)		C:GO:0005829: P:G(	C:cytosol; P:purine	EC:3.2.2.1	Purine nucleosidase	IPR036452 (G3DSA:3.90.245.GENE3	30,030	24,958	49,588	54,639	49,201									
Solyc09g009700	GDSL esterase/lipase (AHRD V3.3 *** V5K506_GOSHI)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	2,003	1,998	0,237	0,582	0,568									
Solyc09g009710	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G19485.2)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	17,643	13,936	3,927	4,066	4,791									
Solyc09g009720	ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** AT5G59300.1)		P:GO:0000209: F:G(	P:protein polyubiquitination; F:ATP binding; P:ubiquitin-depende			IPR016135 (G3DSA:3.10.110.GENE3	24,310	25,001	28,062	23,786	23,330									
Solyc09g009743	DWNN domain, a CCHC-type zinc finger (AHRD V3.3 --* AT5G47430.6)							0,019	0,019	0,000	0,000	0,000									
Solyc09g009747	DCD (Development and Cell Death) domain protein (AHRD V3.3 --* AT2G35140.6)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:myosin binding				0,040	0,036	0,093	0,098	0,046									
Solyc09g009760	LOW QUALITY:BZIP transcription factor family protein (AHRD V3.3 *-* B9MTQ4_POPTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			G3DSA:1.20.5.17(bZIP	0,451	0,509	2,640	2,746	4,206									
Solyc09g009770	Calmodulin binding protein, putative (AHRD V3.3 *** B9T5N0_RICCO)						mobidb-lite (MOBIDB_LITE): PTHR312	55,884	41,799	11,815	14,629	17,955			0,599	0,028				up	
Solyc09g009780	Glucosamine 6-phosphate N-acetyltransferase, putative (AHRD V3.3 *** B9SRX8_RICCO)		F:GO:0004343: P:G(	F:glucosamine 6-ph	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR000182 (PFAM): G3DSA:3.40.630	14,214	12,386	15,355	18,372	16,292									
Solyc09g009790	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IGL4_POPTR)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR011990 (G3D	2,652	3,643	2,900	2,723	2,650									
Solyc09g009800	B-block binding subunit of TFIIIC (AHRD V3.3 *** AT1G17450.2)		C:GO:0000127: F:G(	C:transcription factor TFIIIC complex; F:RNA polymerase III ger			IPR036388 (G3DSA:1.10.10.GENE3D	37,499	25,492	31,580	35,643	33,383									
Solyc09g009810	LOW QUALITY:TSA: Wollemia nobilis Ref_Wollemi_Transcript_15479_650 transcribed RNA sequence (AHRD V3.3 *** A0A0C9RS79_9SPER)						IPR025322 (PFAM): PTHR33148:SF2	0,178	0,340	0,231	0,025	0,143									
Solyc09g009820	Glutathione S-transferase domain-containing protein (AHRD V3.3 *** A0A0K9Q3C0_ZOSMR)		F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): IPR00	9,072	12,125	6,501	5,926	9,759			0,579	0,038				up	
Solyc09g009830	Carbonic anhydrase family protein (AHRD V3.3 *** D7LUA2_ARALL)		F:GO:0004089: F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR036398 (G3DSA:3.10.200.GENE3	31,805	26,258	3,510	1,609	2,928					-1,125	0,003			down
Solyc09g009840	LOW QUALITY:At2g36220/F2H17.17 (AHRD V3.3 *** Q9SJN3_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,966	31,140	18,853	18,664	17,261	0,989	0,000					up		
Solyc09g009850	Mediator-associated protein 2 (AHRD V3.3 *** MDA2_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	17,731	18,132	12,210	12,124	12,108									
Solyc09g009860	LOW QUALITY:Glutaredoxin family protein, putative (AHRD V3.3 *** A0A061ETX1_THECC)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			G3DSA:3.40.30.10 (GENE3D): IPR00:	0,192	0,354	0,000	0,000	0,000									
Solyc09g009880	F-box family protein (AHRD V3.3 *** B9IIU6_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128(	30,812	26,319	54,627	54,646	56,038									
Solyc09g009890	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT3G52660.3)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	47,140	57,430	50,381	47,271	45,682									

Solyc09g009900	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103YMS1_CYNCS)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D			G3DSA:2.40.50.140 (GENE3D): IPR0	1,227	1,340	0,513	0,120	0,283									
Solyc09g009910	ABC transporter family protein (AHRD V3.3 *** A0A097P9R7_HEVBR)	ABCB24	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	6,520	6,194	10,594	11,118	12,362									
Solyc09g009920	LOW QUALITY:F-box family protein (AHRD V3.3 *** D7MLR5_ARALL)		F:GO:0005515	F:protein binding			IPR006566 (PFAM): IPR032675 (G3D	6,736	5,255	6,266	6,328	6,230									
Solyc09g009940	Signal recognition particle 54 kDa protein (AHRD V3.3 *** W9R2A9_9ROSA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000897 (PFAM): G3DSA:3.40.50.3	51,177	93,470	51,008	70,191	102,498	0,896	0,000	1,004	0,000	0,464	0,015	up	up	up
Solyc09g009960	4'-phosphopantetheinyl transferase (AHRD V3.3 *** A0A151RRT2_CAJCA)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.8.7	Holo-[acyl-carrier-pro	IPR037143 (G3DSA:3.90.470.GENE3I	6,779	6,888	9,515	11,107	10,622									
Solyc09g009970	Rho GTPase-activating protein gacA (AHRD V3.3 *** A0A151TVS8_CAJCA)		P:GO:0007165	P:signal transduction			IPR000198 (PFAM): IPR008936 (G3D	4,611	4,564	0,676	0,662	0,850									
Solyc09g009985	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	2,281	3,649	1,057	1,885	3,428			1,694	0,004				up	
Solyc09g009990	GATA zinc finger domain-containing protein C1393.08 isoform 2 (AHRD V3.3 *** A0A061F1A4_THECC)						PTHR34375:SF1 (PANTHER): PTHR3	23,871	23,763	6,273	6,917	9,520			0,602	0,027				up	
Solyc09g010000	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	12,192	31,664	3,379	7,216	8,084	1,401	0,000	1,251	0,004	1,092	0,001	up	up	up
Solyc09g010010	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,000	0,000	0,025	0,023									
Solyc09g010030	50S ribosomal protein L7/L12, putative (AHRD V3.3 *** B9RB19_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR014719 (G3DSA:3.30.1390.GENE	13,274	14,145	14,564	13,265	13,597									
Solyc09g010040	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR026992 (PFA	0,078	0,055	0,000	0,025	0,047									
Solyc09g010050	cullin 1 (AHRD V3.3 *** AT4G02570.4)		P:GO:0006511; F:G(	P:ubiquitin-dependent protein catabolic process; F:ubiquitin prot			G3DSA:1.10.10.2620 (GENE3D): G3D	0,840	0,871	0,926	1,066	1,106									
Solyc09g010060	Kinesin-related protein (AHRD V3.3 *** A0A0B0NF68_GOSAR)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR036961 (G3	3,873	3,550	0,801	0,675	0,919									
Solyc09g010070	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061F1A8_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,674	1,081	0,804	0,611	0,474									
Solyc09g010080	beta-fructofuranosidase	IN5	F:GO:0004564; P:G(	F:beta-fructofurano:	EC:3.2.1.26	Beta-fructofuranosid:	IPR013189 (PFAM): IPR023296 (G3D	26,087	20,339	10,676	7,577	13,101									
Solyc09g010090	cell-wall invertase	IN7	F:GO:0004564; P:G(	F:beta-fructofurano:	EC:3.2.1.26	Beta-fructofuranosid:	G3DSA:2.60.120.560 (GENE3D): IPR(	3,240	3,102	0,429	0,465	0,447									
Solyc09g010095	plant/protein (AHRD V3.3 --* AT2G41150.1)							4,812	5,383	2,869	2,826	2,568									
Solyc09g010100	30S ribosomal protein S11 (AHRD V3.3 *** A0A0K9PVQ7_ZOSMR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001971 (PFAM): IPR001971 (PIRS	126,712	127,966	109,000	103,599	102,248									
Solyc09g010110	chaperone protein dnaJ-like protein (AHRD V3.3 *** AT5G06130.2)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			mobidb-lite (MOBIDB_LITE): PTHR158	21,002	32,948	123,347	129,407	130,227	0,677	0,005					up		
Solyc09g010120	Alpha-amylase (AHRD V3.3 *** A0A1D1XX21_9ARAE)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast stroma			PTHR36352 (PANTHER)	11,075	16,902	9,668	10,416	16,542	0,638	0,037	0,767	0,001			up	up	
Solyc09g010130	ribosomal protein S11 family protein		F:GO:0035091	F:phosphatidylinositol binding			IPR015404 (PFAM): IPR036871 (G3D	26,753	28,333	48,030	50,033	45,483									
Solyc09g010140	Senescence regulator (AHRD V3.3 *** A0A103Y6R7_CYNCS)						IPR007608 (PFAM): PTHR33083:SF1(	14,624	8,235	23,033	17,684	18,212	-0,802	0,018					down		
Solyc09g010150	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G04070.1)		C:GO:0016021	C:integral component of membrane			IPR002347 (PRINTS): IPR002347 (PF	5,641	4,894	6,569	7,473	6,813									
Solyc09g010170	Vacuolar protein sorting-associated protein 55 like (AHRD V3.3 *** A0A0B2QGA7_GLYSO)		C:GO:0005768; C:G(	C:endosome; C:vacuole; C:integral component of membrane; P:			IPR007262 (PFAM): IPR007262 (PAN	12,251	10,613	20,533	22,571	20,637									
Solyc09g010180	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G11540	spy	F:GO:0005515	F:protein binding			G3DSA:3.40.50.2000 (GENE3D): IPR(	139,409	118,265	151,366	154,514	151,277									
Solyc09g010190	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4CR47_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR002130 (PF	22,468	24,197	23,583	23,131	23,099									
Solyc09g010210	endo-1,4-beta-glucanase precursor (Cel2)	cel2	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001701 (PFAM): IPR012341 (G3D	2,317	3,687	529,556	683,311	340,181									
Solyc09g010220	Lysosomal pro-X carboxypeptidase, putative (AHRD V3.3 *** B9SX01_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity			IPR008758 (PFAM): G3DSA:1.20.120.	0,275	0,635	0,025	0,072	0,024									
Solyc09g010230	B3 domain-containing protein family (AHRD V3.3 *** A0A151U3H1_CAJCA)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM_B3	0,196	0,325	0,190	0,166	0,163									
Solyc09g010240	Embryo defective 2735 (AHRD V3.3 *-* U5U071_PHAVU)							0,339	0,592	0,171	0,237	0,188									
Solyc09g010250	importin alpha isoform 4 (AHRD V3.3 --* AT1G09270.3)							0,061	0,105	0,097	0,000	0,048									
Solyc09g010260	Trichome birefringence-like 8, putative (AHRD V3.3 *** A0A061EUN4_THECC)		C:GO:0016021	C:integral component of membrane			IPR025846 (PFAM): IPR026057 (PFA	0,633	0,592	1,596	1,631	2,073									
Solyc09g010280	LETM1-like protein (AHRD V3.3 *** AT3G11560.4)		C:GO:0016021	C:integral component of membrane			IPR011685 (PFAM): mobidb-lite (MOB	68,871	85,543	154,386	155,168	193,039									
Solyc09g010285	Intron maturase, type II family protein (AHRD V3.3 *** AT1G74350.1)		P:GO:0006397	P:mRNA processing			IPR000477 (PFAM): IPR024937 (PFA	18,037	16,552	24,791	30,347	26,053									
Solyc09g010300	mRNA-decapping enzyme-like protein (AHRD V3.3 *** A0A0B2REC5_GLYSO)		P:GO:0000290; F:G(	P:deadenylation-dependent decapping of nuclear-transcribed ml			IPR011993 (G3DSA:2.30.29.GENE3D	24,112	20,435	24,201	24,457	24,087									
Solyc09g010320	Mitochondrial fission protein ELM1 (AHRD V3.3 *** A0A199UV44_ANACO)						IPR009367 (PFAM): IPR009367 (PAN	9,978	7,667	11,404	10,906	10,170									
Solyc09g010330	Nascent polypeptide-associated complex subunit beta (AHRD V3.3 *** K4CR60_SOLLC)		P:GO:0009651	P:response to salt stress			IPR002715 (PFAM): IPR038187 (G3D	70,416	73,423	85,289	80,249	84,230									
Solyc09g010350	DNA-binding protein, putative (AHRD V3.3 *** A0A072VL98_MEDTR)						PTHR42672:SF11 (PANTHER): PTHR4	44,875	28,095	28,656	26,743	25,572	-0,647	0,014					down		
Solyc09g010360	WAT1-related protein (AHRD V3.3 *** K4CR63_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOB	14,185	8,956	4,922	4,467	4,847									
Solyc09g010370	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G59840.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	111,817	98,963	78,608	76,790	72,485									
Solyc09g010380	Soluble inorganic pyrophosphatase (AHRD V3.3 *** A0A0B0Q0H5_GOSAR)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.1	Inorganic diphosphat	IPR008162 (PFAM): IPR036649 (G3D	48,653	81,153	6,977	10,154	10,538	0,767	0,018	0,587	0,032			up	up	
Solyc09g010390	LOW QUALITY:AT3g53630/F4P12_330 (AHRD V3.3 *** Q8VXU5_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	13,236	14,136	20,117	18,505	16,934									
Solyc09g010400	Histone H2A (AHRD V3.3 *** K4CR67_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR007125 (PF	72,235	66,694	91,908	83,103	75,238									
Solyc09g010410	BRI1-KD interacting protein (AHRD V3.3 *** T2DLB0_PHAVU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	27,031	28,854	28,640	27,312	26,402									
Solyc09g010420	Arginine biosynthesis bifunctional protein ArgJ, chloroplastic (AHRD V3.3 *** K4CR69_SOLLC)		F:GO:0004358; P:G(	F:glutamate N-acety	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	G3DSA:3.30.2330.10 (GENE3D): IPR(	21,865	25,334	23,103	17,921	20,148									
Solyc09g010430	LOW QUALITY:Histone H3 K4-specific methyltransferase SET7/9 family protein (AHRD V3.3 --* AT1G21920.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,560	6,517	14,850	15,463	10,029									
Solyc09g010440	Actin depolymerizing factor, putative (AHRD V3.3 *** B9T4D2_RICCO)		F:GO:0003779; C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolyme			IPR002108 (PFAM): IPR029006 (G3D	358,072	357,350	510,648	419,412	408,323									
Solyc09g010450	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT3G53700.1)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	8,485	6,450	8,270	7,957	9,160									
Solyc09g010460	Eukaryotic translation initiation factor 3 subunit A (AHRD V3.3 *** K4CR73_SOLLC)		C:GO:0005852	C:eukaryotic translation initiation factor 3 complex			G3DSA:1.25.40.860 (GENE3D): IPR0(	283,284	292,841	236,471	216,725	225,540									
Solyc09g010470	Ion channel regulatory protein, UNC-93 (AHRD V3.3 *** A0A103YHZ3_CYNCS)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; P:pot			IPR010291 (PFAM): G3DSA:1.20.125	7,973	8,448	2,617	2,468	4,420									
Solyc09g010480	LOW QUALITY:forkhead box protein G1 (AHRD V3.3 *** AT2G37530.1)		C:GO:0016021	C:integral component of membrane			PTHR34658 (PANTHER)	0,303	0,123	0,072	0,000	0,071									
Solyc09g010500	DNA-directed RNA polymerase II family protein (AHRD V3.3 *** B9ID35_POPTR)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR012293 (G3DSA:3.90.940.GENE3I	103,794	99,687	102,458	92,584	97,706									
Solyc09g010510	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT2G37540.2)						G3DSA:3.40.50.720 (GENE3D): IPR0(	0,617	0,577	0,025	0,025	0,000									
Solyc09g010520	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *** A0A0K9Q1P3_ZOSMR)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (PF	456,878	387,350	386,791	337,370	329,554									
Solyc09g010530	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral			IPR038770 (G3DSA:1.20.1530.GENE	0,000	0,021	0,000	0,000	0,000									
Solyc09g010540	dentin sialophosphoprotein-like protein (AHRD V3.3 *-* AT5G02520.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	7,579	8,664	2,458	2,777	2,828									
Solyc09g010550	SANTA (SANT associated) protein (AHRD V3.3 *-* A0A072VWG5_MEDTR)						IPR015216 (PFAM): mobidb-lite (MOB	1,916	1,982	0,725	0,720	0,802									
Solyc09g010560	5-oxoprolinase (AHRD V3.3 *** OPLA_ARATH)		F:GO:0016787	F:hydrolase activity			IPR003692 (PFAM): IPR002821 (PFA	81,691	88,525	100,308	92,581	99,972									
Solyc09g010562	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit (AHRD V3.3 *-* AT3G09455.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity			IPR018943 (PFAM): PTHR28677 (PAN	34,780	36,466	46,016	43,040	38,771									
Solyc09g010564	P-hydroxybenzoic acid efflux pump subunit aaeB (AHRD V3.3 *-* A0A061GW63_THECC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:trar			PTHR30509:SF7 (PANTHER): PTHR3(	0,122	0,133	0,096	0,101	0,023									
Solyc09g010566	Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein (AHRD V3.3 *-* A0A103)		F:GO:0005515; C:G(	F:protein binding; C:plasma membrane; C:integral component of			PTHR30509 (PANTHER): PTHR30509	0,687	0,430	0,265	0,385	0,354									
Solyc09g010568	PLATZ transcription factor family protein (AHRD V3.3 --* AT1G21000.2)							0,314	0,152	0,072	0,097	0,095									
Solyc09g010580	histidine biosynthesis bifunctional protein (HISIE) (AHRD V3.3 --* AT1G31860.3)							0,543	0,376	0,383	0,298	0,306									
Solyc09g010590	LOW QUALITY:Photosystem II CP47 reaction center protein (AHRD V3.3 --* PSBB_ANGEV)		F:GO:0016787	F:hydrolase activity			PTHR12320:SF14 (PANTHER): IPR03	0,021	0,019	0,000	0,074	0,000									
Solyc09g010595	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		F:GO:0008270; P:G(	F:zinc ion binding; P:protein ubiquitination; F:ligase activity; F:m			IPR001841 (PFAM): IPR013083 (G3D	0,973	0,822	0,815	0,873	0,873									
Solyc09g010610	RING/U-box superfamily protein (AHRD V3.3 --* AT5G02750.1)		F:GO:0008270; F:G(	F:zinc ion binding; F:metal ion binding			SSF57850 (SUPERFAMILY)	0,264	0,302	0,143	0,144	0,140									
Solyc09g010630	HSC2-like	hsc2	F:GO:0005524; C:G(	F:ATP binding; C:cy	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS): G3DSA:3.30.42	6790,012	6093,196	2156,222	2172,502	2185,212									
Solyc09g010640	LOW QUALITY:HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT2G37570.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	77,010	103,049	79,281	91,727	94,227									
Solyc09g010650	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G37580.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	1,140	0,979	6,837	6,297	5,085									
Solyc09g010660	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061ER80_T		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297 (PAN	5,987	5,005	6,259	5,345	6,373									
Solyc09g010670	Transcription factor DP (AHRD V3.3 *** AT5G02470.3)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:transcription facto			IPR036388 (G3DS_E2F/DP	3,468	3,968	2,079	2,178	2,289									
Solyc09g010680	Dof zinc finger protein (AHRD V3.3 *** W9S882_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM_Dof	5,535	4,816	3,999	5,390	4,456									
Solyc09g010690	Ankyrin repeat family protein (AHRD V3.3 *** B9GJP4_POPTR)		F:GO:0005515	F:protein binding			IPR020683 (PFAM): IPR036770 (G3D	156,590	104,017	56,273	30,238	41,555					-0,893	0,000			down
Solyc09g010700	ATP synthase subunit epsilon (AHRD V3.3 *** W9SG58_9ROSA)						mobidb-lite (MOBIDB_LITE): PTHR335	1,377	1,224	0,022	0,051	0,000									
Solyc09g010710	peptide transporter family protein (AHRD V3.3 *** AT3G09430.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,872	1,948	0,589	0,551	1,103									
Solyc09g010720	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7L3F0_MEDTR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	0,019	0,041	0,000	0,000	0,000									
Solyc09g010740	Cysteine proteinase inhibitor (AHRD V3.3 --* A0A0L9UVV9_PHAAN)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			G3DSA:3.10.450.10 (GENE3D): IPR0(	34,441	27,357	34,503	29,877	25,952									
Solyc09g010770	Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase (AHRD V3.3 *** W9SG54_9ROSA)		F:GO:0004583; C:G(	F:dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransfera:			IPR016900 (PFAM): IPR016900 (PIRS	10,529	11,902	11,213	12,313	12,672									
Solyc09g010780	Protein phosphatase 2C family protein (AHRD V3.3 *** G7L4F6_MEDTR)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): mobidb-lite (MOB	3,394	7,508	1,421	2,831	2,046	1,171	0,020			1,008	0,022	up		up
Solyc09g010800	metallothionein II-like protein		F:GO:0046872	F:metal ion binding			IPR000347 (PFAM): IPR000347 (PAN	2972,382	3155,649	5064,937	4403,478	5229,329									
Solyc09g010810	Kinesin-like protein (AHRD V3.3 *** K4CRA7_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	1,155	1,550	0,255	0,213	0,306									
Solyc09g010820	MYB family protein (AHRD V3.3 *** A0A067KKV6_JATCU)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(_MYB	11,503	11,951	16,422	16,191	14,597									
Solyc09g010830	E3 ubiquitin-protein ligase (AHRD V3.3 *** W9SG42_9ROSA)		F:GO:0008270; F:G(	F:zinc ion binding; F:ubiquitin protein ligase activity; P:ubiquitin-(			IPR003126 (PFAM): G3DSA:2.10.110.	83,281	61,156	132,807	150,731	135,656									
Solyc09g010840	phantastica	R2R3MYB9/PHAN	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:transcription, DNA-templated; P:lea			PF13921 (PFAM):_MYB	85,854	97,197	45,517	48,152	51,714									
Solyc09g010850	Protein kinase (AHRD V3.3 *** A3RI54_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	12,154	38,989	7,911	10,170	17,352	1,701	0,011	1,128	0,000			up	up	
Solyc09g010860	expansin precursor 4	EXPA4	C:GO:0005576; P:G(	C:extracellular region; P:plant-type cell wall organization			IPR002963 (PRINTS): IPR007118 (PF	28,654	40,011	1,977	2,549	2,586									
Solyc09g010870	Ribonuclease II (AHRD V3.3 *** A0A072UIX7_MEDTR)		F:GO:0003723; F:G(	F:RNA binding; F:ribonuclease activity			IPR001900 (PFAM): PTHR23355:SF5:	36,390	32,898	55,742	57,200	60,745									
Solyc09g010880	Rhomboid-like protein (AHRD V3.3 *** K4CRB4_SOLLC)		F:GO:0004252; P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM): IPR035952 (G3D	20,815	18,057	40,983	42,385	38,504									
Solyc09g010910	LOW QUALITY:Phosphatidylinositol 4-kinase alpha (AHRD V3.3 --* M8A4X8_TRIUA)							1,978	0,907	1,027	1,166	0,942									
Solyc09g010913	transcription regulator (AHRD V3.3 --* AT5G13240.2)							2,068	1,473	1,268	1,210	1,489									
Solyc09g010915	Protein phosphatase 2C-like protein (AHRD V3.3 --* G7JLG9_MEDTR)							1,054	0,829	0,561	0,437	0,543									
Solyc09g010917	F-box family protein (AHRD V3.3 --* A0A061G9M7_THECC)							2,097	1,896	1,864	1,705	1,320									
Solyc09g010920	GRAS family transcription factor (AHRD V3.3 *** A0A072U0I2_MEDTR)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM_GRAS	8,291	10,334	7,600	7,500	8,749									
Solyc09g010930	NAD(P)-binding rossmann-fold protein (AHRD V3.3 *** I3TAJ6_MEDTR)						IPR016040 (PFAM): G3DSA:3.40.50.7	60,985	119,963	260,312	253,339	326,181	1,003	0,000					up		
Solyc09g010940	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** I3S857_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR006439 (TIGRFAM): IPR010237 (T	41,012	36,122	99,713	112,236	109,967									
Solyc09g010950	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** A0A0K9PCT4_ZOSMR)		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR005936 (TIGRFAM): IPR041569 (F	39,266	36,945	62,511	61,013	59,506									
Solyc09g010960	WRKY transcription factor 49	WRKY49	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036576 (G3DS_WRKY	0,000	0,122	0,000	0,025	0,000									
Solyc09g010970	Carbonic anhydrase (AHRD V3.3 *** K4CRC3_SOLLC)		F:GO:0004089; F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001765 (PFAM): IPR036874 (G3D	15,000	16,683	13,673	17,000	14,268									
Solyc09g010980	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 -** AT5G02220.1)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): IPR0403	9,720	25,162	1,990	2,081	2,485									
Solyc09g010993	Laccase (AHRD V3.3 *-* M1AHJ4_SOLTU)		F:GO:0005507; P:G(	F:copper ion binding; P:oxidation-reduction process			IPR011707 (PFAM): IPR001117 (PFA	0,019	0,059	0,000	0,025	0,000									
Solyc09g011010	Photosystem II 22 kDa protein, chloroplastic (AHRD V3.3 --* PSBS_SPIOL)		C:GO:0009535	C:chloroplast thylakoid membrane			PTHR14154 (PANTHER): PTHR14154	0,019	0,082	0,172	0,025	0,117									
Solyc09g011020	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G02130.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	13,746	9,972	17,195	16,148	14,208									
Solyc09g011023	AGAMOUS-like 14 (AHRD V3.3 --* AT4G11880.4)							0,000	0,021	0,044	0,097	0,000									
Solyc09g011027	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072TZL3_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS): IPR001938 (PF	0,000	0,018	0,000	0,000	0,000									
Solyc09g011030	Hsp70-binding protein 1 (AHRD V3.3 *** W9RWP5_9ROSA)		F:GO:0000774; C:G(	F:adenyl-nucleotide exchange factor activity; C:endoplasmic ret			IPR011989 (G3DSA:1.25.10.GENE3D	93,973	102,782	297,970	282,999	232,773									
Solyc09g011040	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061EYX5_THECC)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032799 (PF	19,368	8,592	19,439	18,526	13,255	-1,141	0,045					down		
Solyc09g011045	Laccase (AHRD V3.3 *** M1AHJ4_SOLTU)		F:GO:0005507; P:G(	F:copper ion binding; P:oxidation-reduction process			IPR008972 (G3DSA:2.60.40.GENE3D	0,040	0,080	0,000	0,000	0,000									
Solyc09g011060	Clade IV lectin receptor kinase (AHRD V3.3 *** K4CRD2_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001220 (PFAM): IPR011709 (PFA	2,061	5,231	0,355	0,481	0,516	1,361	0,004					up		
Solyc09g011070	clade XI lectin receptor kinase		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	2,690	2,162	0,634	0,432	0,420									
Solyc09g011080	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *** V9IMY5_NICAT)		F:GO:0005524	F:ATP binding			G3DSA:1.10.8.1070 (GENE3D): G3DS	62,961	97,107	24,956	19,913	54,903			1,132	0,000				up	
Solyc09g011100	Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT3G16970.1)						IPR010264 (PFAM): PTHR31232:SF5	0,084	0,155	0,000	0,000	0,000									
Solyc09g011107	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *-* AT4G16195.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM): PTHR31232:SF5	0,040	0,039	0,000	0,000	0,000									
Solyc09g011110	LOW QUALITY:Zinc finger, C2H2 (AHRD V3.3 *** A0A118K1X3_CYNCS)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.60 (GENE3D): PTHF	0,235	0,249	1,213	2,140	1,508									
Solyc09g011120	LOW QUALITY:Zinc finger, C2H2 (AHRD V3.3 *** A0A103Y6E0_CYNCS)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM):_C2H2	0,021	0,021	0,000	0,025	0,000									
Solyc09g011140	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	35,648	35,359	0,755	0,554	0,702									
Solyc09g011150	LOW QUALITY:Ycf68 protein (AHRD V3.3 *-* A0A0K0Q5V3_9CARY)		C:GO:0009507	C:chloroplast				0,040	0,000	0,051	0,073	0,000									
Solyc09g011160	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT3G53830.3)						IPR000408 (PRINTS): IPR009091 (G3	2,323	1,116	3,045	3,365	2,945									
Solyc09g011170	Prf interactor 30137		F:GO:0046983	F:protein dimerization activity			IPR025610 (PFAM): mobidb-lite (MOB	1,705	1,867	0,976	1,096	1,129									
Solyc09g011190	LOW QUALITY:Legume-specific protein (AHRD V3.3 *-* K9N5V5_9FABA)						PTHR34670 (PANTHER): PTHR34670	6,576	4,470	1,201	1,227	1,202									
Solyc09g011210	RNA binding protein (AHRD V3.3 *** B6U487_MAIZE)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	8,757	9,219	13,051	14,175	16,759									
Solyc09g011220	Mannose-1-phosphate guanyltransferase, putative (AHRD V3.3 *** B9SE08_RICCO)		P:GO:0009058; F:G(	P:biosynthetic process; F:nucleotidyltransferase activity			G3DSA:2.160.10.10 (GENE3D): IPR0(	25,270	22,407	58,374	49,179	46,628									
Solyc09g011230	CASP-like protein (AHRD V3.3 *** K4CRE9_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021 (PAN	2,320	2,102	1,839	1,677	2,002									
Solyc09g011240	aldo-keto reductase 4B-like		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR020471 (PII	23,737	28,263	11,812	9,377	12,959									
Solyc09g011250	Mitochondrial glycoprotein family protein (AHRD V3.3 *** AT3G55605.1)		C:GO:0005759	C:mitochondrial matrix			IPR003428 (PFAM): IPR036561 (G3D	3,487	3,710	5,941	6,577	6,990									
Solyc09g011260	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G37820.1)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation; P:intracellular signal transc			IPR004146 (PFAM): PTHR13871 (PAN	0,000	0,191	0,000	0,025	0,000									
Solyc09g011270	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G37820.1)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			G3DSA:3.30.60.90 (GENE3D): IPR00	0,000	0,371	0,025	0,000	0,072									
Solyc09g011280	LOW QUALITY:Invertase/pectin methylesterase inhibitor family protein (AHRD V3.3 -** B9N451_POPTR)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM): IPR006501 (TIGF	0,040	0,039	0,000	0,000	0,000									
Solyc09g011290	LOW QUALITY:cell wall / vacuolar inhibitor of fructosidase 2 (AHRD V3.3 *** AT5G64620.1)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM): IPR006501 (TIGF	0,019	0,019	0,000	0,000	0,000									
Solyc09g011295	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 --* AT5G500		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM): IPR035513 (G3D	0,037	0,000	0,000	0,000	0,000									
Solyc09g011300	Uracil phosphoribosyltransferase (AHRD V3.3 *** M1HEU7_SOLTU)		F:GO:0004845; P:G(	F:uracil phosphoribc	EC:2.4.2.9	Uracil phosphoribosy	G3DSA:3.40.50.2020 (GENE3D): PF1	30,120	41,960	30,786	25,858	33,282	0,505	0,049					up		
Solyc09g011305	Plant invertase/pectin methylesterase inhibitor superfamily (AHRD V3.3 --* AT4G02300.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,243	2,443	3,421	3,623	3,432									
Solyc09g011310	PRA1 family protein (AHRD V3.3 *** K4CRF7_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR12859:SF0	32,874	34,086	62,324	65,310	55,801									
Solyc09g011320	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0K0XR56_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	28,654	29,336	37,689	38,899	34,585									
Solyc09g011330	Serine/threonine-protein kinase (AHRD V3.3 *** M1C8X1_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR001480 (PFAM): IPR000719 (PFA	0,374	0,556	0,350	0,569	0,448									
Solyc09g011340	reticulata-like protein, putative (DUF3411) (AHRD V3.3 *** AT2G37860.4)		C:GO:0016021	C:integral component of membrane			IPR021825 (PFAM): mobidb-lite (MOB	39,194	41,563	35,753	26,106	31,914									
Solyc09g011350	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT2G37880.1)						IPR006460 (TIGRFAM): IPR006460 (F	0,059	0,103	0,022	0,000	0,093									
Solyc09g011360	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT3G53940.1)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpc			IPR002067 (PRINTS): IPR018108 (PF	8,497	10,591	9,999	9,534	8,240									
Solyc09g011370	F-box family protein (AHRD V3.3 *** B9IJF9_POPTR)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	17,062	18,523	31,519	29,218	28,053									
Solyc09g011380	BEL1-like homeodomain protein (AHRD V3.3 *** G7L5K2_MEDTR)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			G3DSA:1.10.10.6(_TALE	12,698	12,007	8,084	8,323	8,272									
Solyc09g011390	Major facilitator superfamily protein (AHRD V3.3 *** AT3G53960.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,981	1,407	0,409	0,905	0,689									

Solyc09g011410	Plastid RNA-binding protein 1 (AHRD V3.3 *** D9J062_NICBE)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	12,395	12,950	37,344	36,353	37,943									
Solyc09g011420	Ribosomal protein l7ae (AHRD V3.3 *** A0A0A0LF58_CUCSA)		F:GO:0003723; C:G(	F:RNA binding; C:nucleolus			IPR018492 (PRINTS): IPR002415 (PF	37,381	43,545	37,716	30,709	32,283									
Solyc09g011450	Proteasome inhibitor-related (AHRD V3.3 *** A0A061ERS7_THECC)		C:GO:0000502; P:G(	C:proteasome complex; P:ubiquitin-dependent protein catabolic			IPR021625 (PFAM): G3DSA:3.40.100	41,982	43,802	66,358	58,405	58,023									
Solyc09g011470	Plant/T7H20-70 protein (AHRD V3.3 *** G7L5L0_MEDTR)		P:GO:0009651	P:response to salt stress			mobidb-lite (MOBIDB_LITE): mobidb-lit	7,004	7,564	58,646	73,072	61,260									
Solyc09g011480	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9T764_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.2010 (GENE3D): G3D	31,333	21,592	87,785	101,312	90,089									
Solyc09g011490	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GSTU29	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:1.20.105	0,827	1,547	0,099	0,524	0,753									
Solyc09g011500	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GSTU30	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	0,140	0,265	0,097	0,196	0,117									
Solyc09g011510	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GSTU31	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:1.20.105	0,000	0,036	0,000	0,025	0,000									
Solyc09g011520	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GSTU32	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:3.40.30.1	0,057	2,369	0,217	1,406	1,408									
Solyc09g011540	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GSTU34	F:GO:0005515	F:protein binding			IPR004046 (PFAM): IPR004045 (PFA	0,098	0,096	0,047	0,048	0,000									
Solyc09g011550	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GSTU35	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): G3DS/	1,136	1,269	4,002	3,444	2,150			-0,898	0,016				down	
Solyc09g011560	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GSTU36	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): IPR00	0,346	0,902	0,412	0,296	0,375									
Solyc09g011570	Glutathione S-transferase-like protein (AHRD V3.3 *** A8DUB0_SOLLC)	GSTU37	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:1.20.105	0,165	0,137	0,025	0,022	0,047									
Solyc09g011580	Glutathione S-transferase-like protein (AHRD V3.3 *** F8UX80_SOLHA)	GSTU38	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	4,148	8,341	5,736	8,686	5,579									
Solyc09g011590	Glutathione S-transferase-like protein (AHRD V3.3 *-* A8DUB0_SOLLC)	GSTU39	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): G3DS/	0,144	1,623	1,024	3,309	6,467			2,642	0,003	1,698	0,002		up	up
Solyc09g011600	glutathione S-transferase	GSTU40	F:GO:0005515	F:protein binding			IPR004046 (PFAM): G3DSA:1.20.105	0,353	0,254	0,197	0,101	0,070									
Solyc09g011610	Glutathione S-transferase (AHRD V3.3 *-* C0LF68_CAPAN)	GSTU41	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:1.20.105	0,063	0,093	0,091	0,075	0,071									
Solyc09g011620	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GSTU42	F:GO:0005515	F:protein binding			IPR004045 (PFAM): IPR004046 (PFA	0,000	0,036	0,589	0,269	0,072									
Solyc09g011630	putative glutathione S-transferase T2	GSTU43	F:GO:0005515	F:protein binding			IPR004046 (PFAM): IPR004045 (PFA	0,000	0,000	0,000	0,000	0,024									
Solyc09g011640	Putative glutathione S-transferase T2	GSTU44	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): IPR00	0,019	0,000	0,000	0,025	0,023									
Solyc09g011650	Glutathione S-transferase (AHRD V3.3 *** A0A0N9HTE9_HELAN)	GSTU45	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	4,870	4,092	3,052	4,134	2,650									
Solyc09g011660	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G53990.1)						IPR006015 (PRINTS): IPR014729 (G3	38,001	61,490	8,900	11,760	13,683	0,719	0,036	0,615	0,026			up	up	
Solyc09g011670	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G53990.1)						IPR006015 (PRINTS): IPR014729 (G3	20,917	25,449	2,506	2,338	3,778									
Solyc09g011675	Copper transporter, putative (AHRD V3.3 *** A0A061ERR1_THECC)		F:GO:0005375; C:G(	F:copper ion transmembrane transporter activity; C:integral com			IPR007274 (PFAM): PTHR12483:SF2	1,080	1,232	0,220	0,439	0,210									
Solyc09g011690	WAS/WASL-interacting protein family member 2, putative isoform 1 (AHRD V3.3 *** A0A061FLH8_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	186,307	107,893	27,880	56,782	64,012	-0,763	0,005	1,195	0,000	1,027	0,000	down	up	up
Solyc09g011700	Copper transporter, putative (AHRD V3.3 *** A0A061ERR1_THECC)		F:GO:0005375; C:G(	F:copper ion transmembrane transporter activity; C:integral com			IPR007274 (PFAM): PTHR12483:SF2	0,000	0,021	0,000	0,000	0,000									
Solyc09g011710	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	Hsp24.5	P:GO:0006457; P:G(	P:protein folding; P:response to heat; P:response to salt stress;			IPR008978 (G3DSA:2.60.40.GENE3D	108,742	102,032	85,312	97,858	96,139									
Solyc09g011715	DNA replication licensing factor MCM3 homolog 3 (AHRD V3.3 --* MCM33_MAIZE)						mobidb-lite (MOBIDB_LITE)	0,000	0,018	0,000	0,000	0,000									
Solyc09g011720	DUF3527 domain protein (AHRD V3.3 *-* A0A072UIS7_MEDTR)						IPR021916 (PFAM): mobidb-lite (MOB	0,143	0,078	0,097	0,069	0,047									
Solyc09g011730	F-box protein SKIP8 (AHRD V3.3 *** W9RGT7_9ROSA)		F:GO:0005515	F:protein binding			IPR037401 (PFAM): IPR001943 (PFA	3,269	3,311	4,587	3,963	4,673									
Solyc09g011740	Phosphatidylinositol:ceramide inositolphosphotransferase (AHRD V3.3 *** IPCS_ORYSI)		C:GO:0005802; C:G(	C:trans-Golgi netwc	EC:2.7.8.3; EC:2.7.8	Ceramide cholinepho	IPR025749 (PFAM): PTHR21290:SF4	55,363	60,100	43,834	53,587	54,659									
Solyc09g011750	Kinase family protein (AHRD V3.3 *** B9IG10_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			G3DSA:3.30.200.20 (GENE3D): G3DS	0,833	1,757	0,216	0,192	0,117									
Solyc09g011760	Mitochondrial import inner membrane translocase subunit TIM10 (AHRD V3.3 *** A0A199VR11_ANACO)		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion comple			IPR035427 (G3DSA:1.10.287.GENE3	3,597	3,379	5,715	8,529	4,910									
Solyc09g011770	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EYJ3_THECC)		F:GO:0008270	F:zinc ion binding			IPR011016 (PFAM): IPR013083 (G3D	10,085	10,432	5,534	4,333	4,443									
Solyc09g011780	R2R3MYB transcription factor 1	R2R3MYB1	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	8,765	6,757	7,041	7,238	7,039									
Solyc09g011800	PAR1 protein (AHRD V3.3 *** A0A061EYI9_THECC)						IPR009489 (PFAM): mobidb-lite (MOB	0,000	0,021	0,025	0,000	0,023									
Solyc09g011810	Fructose-1,6-bisphosphatase (AHRD V3.3 *** Q9XF82_SOLTU)		P:GO:0005975; F:G(	P:carbohydrate met	EC:3.1.3.23; EC:3.1.	Sugar-phosphatase;	IPR028343 (PRINTS): IPR000146 (PII	3,220	10,162	3,080	6,075	12,892	1,682	0,000	2,053	0,000	0,978	0,002	up	up	up
Solyc09g011820	DNA double-strand break repair rad50 ATPase, putative isoform 1 (AHRD V3.3 *** A0A061EYI5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,749	0,722	0,137	0,047	0,143									
Solyc09g011830	Transcription antitermination nusg (AHRD V3.3 *** A0A0B0P8C3_GOSAR)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR014722 (G3DSA:2.30.30.GENE3D	31,228	37,449	38,854	38,316	48,513									
Solyc09g011840	LOW QUALITY:Lectin protein kinase family protein (AHRD V3.3 *** A0A0K9NN93_ZOSMR)		F:GO:0030246	F:carbohydrate binding			IPR001220 (PFAM): G3DSA:2.60.120	31,535	22,340	60,127	53,126	46,591									
Solyc09g011850	Fructokinase, putative (AHRD V3.3 *** B9SPF8_RICCO)		C:GO:0005634; F:G(	C:nucleus; F:fructok	EC:2.7.1.4; EC:2.7.1	Fructokinase; Hexoki	IPR011611 (PFAM): IPR029056 (G3D	9,397	15,055	33,312	31,994	35,229	0,709	0,023					up		
Solyc09g011860	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G54100.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF): G3DSA:3.40.50.	56,937	70,360	19,564	14,774	31,146									
Solyc09g011870	Arogenate dehydrogenase 2 (AHRD V3.3 *** F1BPV6_SOLPN)	ADH(2)	F:GO:0004665; P:G(	F:prephenate dehyc	EC:1.3.1.12; EC:1.3.	Prephenate dehydroc	G3DSA:3.40.50.720 (GENE3D): IPR0(	0,382	1,146	0,365	0,269	0,375									
Solyc09g011880	chaperone protein dnaJ-like protein (AHRD V3.3 *** AT2G38000.1)						PTHR15852:SF20 (PANTHER): PTHR	158,777	227,341	118,353	133,574	138,978									
Solyc09g011910	DUF674 family protein (AHRD V3.3 *** G7JS94_MEDTR)						IPR007750 (PFAM): IPR007750 (PAN	2,630	4,554	1,992	1,788	2,143									
Solyc09g011920	uncoupling protein AF472619		P:GO:0006839; F:G(	P:mitochondrial transport; F:transmembrane transporter activity			IPR002030 (PRINTS): IPR018108 (PF	28,218	40,562	93,662	100,581	89,008	0,550	0,041					up		
Solyc09g011930	mRNA capping enzyme family protein (AHRD V3.3 *** AT3G09100.2)		F:GO:0003910; F:G(	F:DNA ligase (ATP)	EC:2.7.7.5; EC:3.1.3	mRNA guanylyltransf	IPR013846 (PFAM): G3DSA:3.30.470	95,613	79,933	97,840	98,259	99,884									
Solyc09g011933	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 --* AT4G17680.1)							0,079	0,061	0,193	0,047	0,190									
Solyc09g011960	Laccase (AHRD V3.3 *** A0A067L6R3_JATCU)		F:GO:0005507; P:G(	F:copper ion bindinc	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR008972 (G3DSA:2.60.40.GENE3D	0,409	0,436	0,025	0,051	0,047									
Solyc09g011970	Laccase (AHRD V3.3 *** B9HBT3_POPTR)		F:GO:0005507; P:G(	F:copper ion bindinc	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR017761 (TIGRFAM): IPR008972 ((	0,174	0,081	0,025	0,048	0,023									
Solyc09g011980	receptor lectin kinase (AHRD V3.3 *-* AT2G37710.1)		P:GO:0002229; F:G(	P:defense response	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): PTHF	0,935	0,827	0,000	0,047	0,118									
Solyc09g011990	Clade IV lectin receptor kinase (AHRD V3.3 *** K4CRM4_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,650	0,781	0,047	0,096	0,023									
Solyc09g012000	Clade IV lectin receptor kinase (AHRD V3.3 *** K4CRM5_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001220 (PFAM): IPR000719 (PFA	5,544	8,287	2,421	1,600	3,053									
Solyc09g012020	LOW QUALITY:F-box protein (AHRD V3.3 *** W9SM54_9ROSA)						IPR013187 (PFAM): IPR017451 (TIGF	0,019	0,000	0,000	0,000	0,000									
Solyc09g012040	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT5G48655.6)							0,173	0,220	0,242	0,168	0,118									
Solyc09g013070	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *-* AT2G38050.1)		F:GO:0003865; C:G(	F:3-oxo-5-alpha-ste	EC:1.3.99.5	3-oxo-5-alpha-steroic	PTHR10556:SF37 (PANTHER): IPR03	21,497	12,485	25,841	19,896	21,396	-0,756	0,011					down		
Solyc09g013080	Alpha-carboxyltransferase subunit (AHRD V3.3 *** C9EI97_JATCU)		F:GO:0003989; P:G(	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	IPR001095 (PRINTS): IPR001095 (PF	180,552	198,833	419,094	491,556	462,997									
Solyc09g013090	OTU domain-containing protein (AHRD V3.3 *** A0A1D1YE81_9ARAE)		F:GO:0004843; P:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.80 (GENE3D): IPR00	7,222	8,218	8,451	8,645	9,527									
Solyc09g013100	histone-lysine N-methyltransferase ATXR3-like protein (AHRD V3.3 *** AT5G01590.1)		F:GO:0008565; C:G(	F:protein transporter activity; C:chloroplast inner membrane; P:t			IPR025640 (PFAM): mobidb-lite (MOB	19,664	23,159	38,683	35,919	41,832									
Solyc09g013110	Reticulon-like protein (AHRD V3.3 *** K4CRN7_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994:SF6	3,905	2,780	4,688	4,549	5,298									
Solyc09g013120	E3 ubiquitin-protein ligase Hakai (AHRD V3.3 *** A0A0B0MJ11_GOSAR)		F:GO:0003676; P:G(	F:nucleic acid binding; P:protein ubiquitination; F:ubiquitin protei			IPR013083 (G3DSA:3.30.40.GENE3D	7,380	7,522	7,319	7,227	6,920									
Solyc09g013130	Defective in exine formation protein (AHRD V3.3 *** G7JLW6_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	66,289	64,703	86,266	85,279	84,740									
Solyc09g013140	Transmembrane protein (AHRD V3.3 *** B7FGN5_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR009305 (PFAM): PTHR34205:SF2	4,980	5,099	9,222	12,557	8,215									
Solyc09g013150	Phosphate transporter (AHRD V3.3 *** A0A0B5WYW1_MANES)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): G3D	32,496	20,517	56,010	104,719	58,366					0,906	0,000			up
Solyc09g013160	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G09080.3)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	0,722	0,581	0,000	0,022	0,097									
Solyc09g014160	UPF0503 protein, chloroplastic (AHRD V3.3 *** A0A199UN58_ANACO)		C:GO:0005886	C:plasma membrane			IPR008004 (PFAM): mobidb-lite (MOB	3,352	2,450	1,037	0,887	0,543									
Solyc09g014170	AT-rich interactive domain protein (AHRD V3.3 *-* Q2HUC6_MEDTR)						IPR000949 (PFAM): mobidb-lite (MOB	15,087	15,081	10,757	9,906	10,358									
Solyc09g014210	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IG54_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	3,272	3,216	1,961	2,318	2,641									
Solyc09g014215	8-amino-7-oxononanoate synthase (AHRD V3.3 *** AT3G09050.1)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR357	1,357	1,400	1,288	1,146	1,976									
Solyc09g014220	Peptide transporter, putative (AHRD V3.3 *** B9T6M4_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): PTHR11654:SF7	0,138	0,057	0,000	0,050	0,000									
Solyc09g014230	Peptide transporter, putative (AHRD V3.3 *** B9T6M4_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): IPR000109 (PAN	0,208	0,402	0,000	0,100	0,047									
Solyc09g014240	Laccase (AHRD V3.3 *** P93366_TOBAC)		F:GO:0005507; P:G(	F:copper ion bindinc	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR017761 (TIGRFAM): IPR001117 (F	2,215	2,184	0,022	0,022	0,048									
Solyc09g014250	MYB transcription factor (AHRD V3.3 *** Q66RN1_HEVBR)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	4,599	4,581	4,548	3,872	3,905									
Solyc09g014280	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G01210.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	39,252	136,774	70,601	81,703	53,848	1,827	0,000					up		
Solyc09g014300	sulfoquinovosyldiacylglycerol 2 (AHRD V3.3 *** AT5G01220.1)		P:GO:0009247; C:G(	P:glycolipid biosynthetic process; C:chloroplast envelope; P:sul			G3DSA:3.40.50.2000 (GENE3D): IPR(	22,978	20,140	67,615	69,806	56,509									
Solyc09g014310	Desiccation-related PCC13-62 (AHRD V3.3 *** A0A0B0N4G5_GOSAR),Pfam:PF13668		C:GO:0016021	C:integral component of membrane			PF13668 (PFAM): PTHR31694:SF4 (F	3,357	1,812	0,776	1,749	1,379					1,169	0,027			up
Solyc09g014320	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G01230.1)		P:GO:0008033; F:G(	P:tRNA processing; F:tRNA methyltransferase activity; P:methy			G3DSA:3.40.50.150 (GENE3D): IPR0(	11,005	12,606	16,695	17,449	16,768									
Solyc09g014325	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT5G01230.1)		P:GO:0008033; F:G(	P:tRNA processing; F:tRNA methyltransferase activity			IPR028590 (PTHR10920:PANTHER):	2,093	1,639	3,384	3,795	3,416									
Solyc09g014340	Ulp1 protease family protein (AHRD V3.3 --* AT5G28810.1)						IPR015410 (PFAM): mobidb-lite (MOB	0,037	0,000	0,000	0,000	0,000									
Solyc09g014350	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7L6J6_MEDTR)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (PFAM): IPR023214 (G3D	157,954	96,418	0,193	0,367	0,305									
Solyc09g014380	SILAX1		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): PTHR22950 (PAN	4,694	3,431	3,021	4,588	3,692									
Solyc09g014400	starch-binding domain-containing protein		F:GO:2001070	F:starch binding			IPR002044 (PFAM): IPR013783 (G3D	29,866	24,092	12,832	11,180	14,353									
Solyc09g014410	Serinc-domain containing serine and sphingolipid biosynthesis protein (AHRD V3.3 --* AT2G33205.6)							10,847	10,384	9,819	11,118	11,196									
Solyc09g014440	RNA polymerase II C-terminal domain phosphatase-like 2 (AHRD V3.3 *** A0A0B0MDD0_GOSAR)		F:GO:0008420; P:G(	F:RNA polymerase	EC:3.1.3.16	Protein-serine/threor	G3DSA:3.30.160.20 (GENE3D): IPR0(	46,865	43,609	55,108	51,389	56,535									
Solyc09g014450	Clathrin light chain protein (AHRD V3.3 *** AT2G40060.1)		F:GO:0005198; P:G(	F:structural molecule activity; P:intracellular protein transport; P			mobidb-lite (MOBIDB_LITE): mobidb-lit	43,346	35,854	92,382	84,491	75,915									
Solyc09g014460	Kinase family protein (AHRD V3.3 *** B9IG83_POPTR)		F:GO:0004672; P:G(	F:protein kinase activity; P:protein phosphorylation			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,000	0,018	0,000	0,000	0,000									
Solyc09g014470	Kinase family protein (AHRD V3.3 *** B9IG83_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,019	0,000	0,000	0,000	0,000									
Solyc09g014475	Histone-lysine N-methyltransferase ATX2 (AHRD V3.3 --* M8ACK8_TRIUA)							0,103	0,079	0,244	0,122	0,236									
Solyc09g014480	Polygalacturonase inhibitor protein (AHRD V3.3 *** Q40160_SOLLC)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR001611 (PFA	1,287	4,553	0,143	0,047	0,047	1,836	0,000					up		
Solyc09g014490	ATP binding protein, putative (AHRD V3.3 *** B9SLM8_RICCO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	3,345	2,815	0,336	0,098	0,213									
Solyc09g014500	Protein yippee-like (AHRD V3.3 *** K4CRS7_SOLLC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	7,980	7,830	13,352	11,586	11,403									
Solyc09g014510	Mitochondrial inner membrane protease subunit, putative (AHRD V3.3 *** B9SQ38_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity; C:membrane			IPR000223 (PRINTS): G3DSA:2.10.1(	6,326	6,475	10,062	10,503	8,742									
Solyc09g014520	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4CRS9_SOLLC)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	258,853	566,775	168,365	203,671	377,241	1,159	0,006	1,161	0,000			up	up	
Solyc09g014530	MLP (AHRD V3.3 *** G8DRV9_GOSBA)		P:GO:0006952	P:defense response			IPR000916 (PFAM): IPR023393 (G3D	0,250	0,393	0,000	0,000	0,000									
Solyc09g014540	MLP-like protein (AHRD V3.3 *** G8DRW0_GOSBA)		P:GO:0006952	P:defense response			IPR023393 (G3DSA:3.30.530.GENE3	0,000	0,000	0,000	0,025	0,000									
Solyc09g014550	MLP (AHRD V3.3 *** G8DRV9_GOSBA)		P:GO:0006952	P:defense response			IPR023393 (G3DSA:3.30.530.GENE3	0,331	0,200	0,068	0,213	0,095									
Solyc09g014610	S-type anion channel (AHRD V3.3 *** A0A098GMQ9_9ROSI)		P:GO:0006873; F:G(	P:cellular ion homeostasis; F:voltage-gated anion channel activ			IPR004695 (PFAM): IPR038665 (G3D	1,087	1,771	0,211	0,370	0,891									
Solyc09g014620	High mobility group protein (AHRD V3.3 *** O49948_SOLTU)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR036910 (G3DSA:1.10.30.GENE3D	141,389	140,155	181,383	156,296	162,018									
Solyc09g014628	Zinc finger CCCH domain-containing protein (AHRD V3.3 *-* A0A0K9Q4D8_ZOSMR)		F:GO:0046872	F:metal ion binding			PTHR14493 (PANTHER): PTHR14493	0,000	0,146	0,025	0,000	0,000									
Solyc09g014640	Zinc finger CCCH domain-containing protein (AHRD V3.3 *-* A0A0K9PNZ2_ZOSMR)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): PTHR144	0,000	0,039	0,000	0,000	0,000									
Solyc09g014710	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:1.10.510.10 (GENE3D): G3DS	1,310	2,103	1,187	1,497	1,978									
Solyc09g014720	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:2.10.25.10 (GENE3D): G3DS/	0,000	0,160	0,071	0,000	0,023									
Solyc09g014730	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR001881 (PFAM): G3DSA:3.30.200	0,000	0,019	0,000	0,000	0,000									
Solyc09g014740	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR001881 (PFAM): G3DSA:3.30.200	5,741	4,422	1,163	1,437	1,640									
Solyc09g014760	Chlorophyll synthase (AHRD V3.3 *** C3W4Q2_TOBAC)	CHLG	P:GO:0015995; C:G(	P:chlorophyll biosyr	EC:2.5.1.62	Chlorophyll synthase	IPR000537 (PFAM): G3DSA:1.10.357	42,971	55,595	63,406	57,772	75,610									
Solyc09g014770	AMP deaminase (AHRD V3.3 *** W9RW60_9ROSA)		F:GO:0003876; P:G(	F:AMP deaminase ;	EC:3.5.4.17; EC:3.5.	Adenosine-phosphate	IPR006329 (TIGRFAM): G3DSA:2.30.	114,484	106,158	92,509	83,930	92,021									
Solyc09g014780	Regulatory-associated protein of TOR 1 (AHRD V3.3 *** AT3G08850.1)		F:GO:0005515; P:G(	F:protein binding; P:TOR signaling; C:TORC1 complex			PR01547 (PRINTS): IPR015943 (G3D	131,445	116,975	156,074	166,116	154,829									
Solyc09g014790	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G38150.3)							105,488	94,036	116,887	130,846	125,251									
Solyc09g014860	LURP-one-like protein (AHRD V3.3 *** G7KW19_MEDTR)						IPR007612 (PFAM): IPR038595 (G3D	0,118	0,360	0,150	0,317	0,916									
Solyc09g014890	zincin-like metalloproteases family protein		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR024080 (G3DSA:1.20.1050.GENE	10,926	9,477	6,645	6,952	7,454									
Solyc09g014900	Cytochrome P450, putative (AHRD V3.3 *** B9RMP3_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	30,299	26,182	25,757	24,599	30,982									
Solyc09g014910	LURP-one-like protein (AHRD V3.3 *** G7KW21_MEDTR)						IPR007612 (PFAM): IPR038595 (G3D	0,021	0,021	0,047	0,171	0,046									
Solyc09g014930	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061EQ92_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,021	0,984	1,961	1,492	1,488									
Solyc09g014940	Wound-induced protein 1 (AHRD V3.3 *** A0A0B2R5F9_GLYSO)						G3DSA:3.10.450.50 (GENE3D): IPR0(	0,080	0,085	0,087	0,025	0,000									
Solyc09g014950	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 --* AT2G20110.3)						mobidb-lite (MOBIDB_LITE)	0,021	0,124	0,025	0,051	0,000									
Solyc09g014970	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)		P:GO:0009694; P:G(	P:jasmonic acid me	EC:3.1.1.1	Carboxylesterase	IPR000073 (PFAM): IPR029058 (G3D	0,000	0,000	0,000	0,022	0,000									
Solyc09g014977	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *** A0A061FD65_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR025525 (PFAM): IPR008906 (PFA	0,000	0,036	0,000	0,000	0,000									
Solyc09g014980	Protein SCAR2, putative (AHRD V3.3 *-* B9SL38_RICCO)		F:GO:0003779; C:G(	F:actin binding; C:cytoskeleton; P:actin cytoskeleton organizatic			G3DSA:1.20.58.1570 (GENE3D): G3D	89,090	87,800	71,271	72,223	77,261									
Solyc09g014990	WRKY transcription factor 33	WRKY33	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036576 (G3DS WRKY	22,425	26,915	2,635	3,567	7,798			1,560	0,001				up	
Solyc09g015000	Heat-shock protein, putative (AHRD V3.3 *** B9S3B2_RICCO)	Hsp15.2					IPR008978 (G3DSA:2.60.40.GENE3D	72,497	61,651	306,566	277,148	372,906									
Solyc09g015020	Heat-shock protein, putative (AHRD V3.3 *** B9S3B2_RICCO)	Hsp17.7B					IPR008978 (G3DSA:2.60.40.GENE3D	24,371	13,694	83,094	70,012	97,142	-0,803	0,009					down		
Solyc09g015030	LOW QUALITY:cation/H+ exchanger 18 (AHRD V3.3 --* AT5G41610.3)							0,038	0,039	0,000	0,000	0,024									
Solyc09g015035	Pinene synthase, chloroplastic (AHRD V3.3 --* TPSD3_ABIGR)							0,000	0,018	0,000	0,000	0,000									
Solyc09g015040	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamilyprotein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	77,310	41,506	59,070	114,547	85,439	-0,873	0,005	0,529	0,006	0,957	0,000	down	up	up
Solyc09g015060	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT5G38220.3)						IPR036691 (G3DSA:3.60.10.GENE3D	0,019	0,019	0,000	0,025	0,072									
Solyc09g015070	Aldo/keto reductase (AHRD V3.3 *** A0A103XQA6_CYNCS)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR023210 (PF	1,623	2,914	1,087	3,223	0,325									
Solyc09g015080	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G72160_TBP						IPR011074 (PFAM): IPR001251 (PFA	12,478	13,161	0,950	1,020	1,382									
Solyc09g015100	Endoribonuclease Dicer homolog 2 (AHRD V3.3 --* DCL2_ARATH)							0,019	0,134	0,000	0,159	0,023									
Solyc09g015110	Homeobox-leucine zipper family protein (AHRD V3.3 *-* U5GMZ5_POPTR)		F:GO:0003677	F:DNA binding			IPR001356 (PFAM HB-other	0,196	0,426	0,000	0,000	0,000									
Solyc09g015120	Kelch repeat-containing family protein (AHRD V3.3 *** B9IGK0_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:	EC:6.3.2.4	D-alanine--D-alanine	IPR011095 (PFAM): IPR015915 (G3D	19,554	18,031	19,687	14,913	15,031									
Solyc09g015130	D-alanine-D-alanine ligase family (AHRD V3.3 *-* AT3G08840.7)		F:GO:0008716	F:D-alanine-D-alani	EC:6.3.2.4	D-alanine--D-alanine	IPR011095 (PFAM): G3DSA:3.30.470	0,000	0,019	0,000	0,000	0,000									
Solyc09g015140	Replication protein A 70 kDa DNA-binding subunit B (AHRD V3.3 --* RFA1B_ARATH)						IPR013955 (PFAM): G3DSA:2.40.50.1	1,149	0,932	1,025	1,424	0,753									
Solyc09g015150	LOW QUALITY:Shattering 4 (AHRD V3.3 --* D1FPB3_ORYRU)						PTHR33492:SF3 (PANTHER): PTHR3	0,019	0,000	0,000	0,000	0,000									
Solyc09g015155	PRA1 family protein (AHRD V3.3 *** M1B0H1_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR19317:SF3	27,759	29,915	26,411	24,488	21,837									
Solyc09g015160	RING/U-box superfamily protein (AHRD V3.3 --* AT3G29270.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,081	0,021	0,047	0,050	0,000									
Solyc09g015170	Receptor-like kinase (AHRD V3.3 *** C0SW26_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			PR00019 (PRINTS): G3DSA:1.10.510	1,267	1,450	0,347	0,244	0,259									
Solyc09g015180	BRCA1-A complex subunit Abraxas (AHRD V3.3 *** A0A0B0PBG0_GOSAR)						IPR023238 (PRINTS): IPR023241 (PF	24,328	20,998	83,072	83,791	69,660									
Solyc09g015190	Dehydration responsive element binding transcription factor (AHRD V3.3 *-* W6FJ00_9ROSA)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR036955 (G3DSA:3.30.730.GENE3	0,679	0,646	1,727	1,862	1,647									
Solyc09g015270	30S ribosomal protein S4, chloroplastic (AHRD V3.3 *** RR4_SOLBU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR002942 (PFAM): IPR036986 (G3D	0,000	0,021	0,022	0,000	0,000									
Solyc09g015280	Photosystem I assembly protein Ycf3 (AHRD V3.3 *** YCF3_SOLLC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,062	0,000	0,000	0,023									
Solyc09g015290	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_GOSHI)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,000	0,000	0,000	0,023									

Solyc09g015300	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_GOSHI)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me	IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,000	0,050	0,100	0,071									
Solyc09g015310	30S ribosomal protein S4, chloroplastic (AHRD V3.3 *** RR4_NICSY)		F:GO:0003723	F:RNA binding	IPR036986 (G3DSA:3.10.290.GENE3I	0,000	0,043	0,025	0,050	0,048									
Solyc09g015320	Photosystem I assembly protein Ycf3 (AHRD V3.3 *** YCF3_SOLLC)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,057	0,083	0,075	0,075	0,024									
Solyc09g015330	30S ribosomal protein S4, chloroplastic (AHRD V3.3 *** RR4_SOLBU)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos	IPR036986 (G3DSA:3.10.290.GENE3I	0,000	0,165	0,050	0,123	0,046									
Solyc09g015340	Photosystem I assembly protein Ycf3 (AHRD V3.3 *** YCF3_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:plastid; C:thylakoid; C:membrane; P:photos	PTHR26312 (PANTHER): PTHR26312	0,000	0,021	0,050	0,025	0,023									
Solyc09g015350	TRICHOME BIREFRINGENCE-LIKE 34 (AHRD V3.3 *** AT2G38320.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; P:xylan	IPR026057 (PFAM): IPR029971 (PTH	0,082	0,182	0,025	0,000	0,000									
Solyc09g015360	Chaperone protein DnaJ (AHRD V3.3 *** W9S2E5_9ROSA)				IPR001623 (PRINTS): IPR036869 (G3	11,546	14,599	13,210	16,929	15,400									
Solyc09g015375	FMN-linked oxidoreductases superfamily protein (AHRD V3.3 --* AT1G09400.1)				mobidb-lite (MOBIDB_LITE)	0,038	0,064	0,000	0,000	0,000									
Solyc09g015380	Abscisic acid receptor (AHRD V3.3 *** G7KT83_MEDTR)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR019587 (PFAM): IPR023393 (G3D	1,599	0,456	0,483	0,370	0,072	-1,737	0,046					down		
Solyc09g015390	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SHP6_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAI	0,019	0,000	0,000	0,000	0,000									
Solyc09g015430	Negative regulator of sporulation MDS3 (AHRD V3.3 --* A0A0B0N6H6_GOSAR)				PTHR33181 (PANTHER): PTHR33181	0,080	0,133	0,000	0,000	0,000									
Solyc09g015440	GDT1-like protein (AHRD V3.3 *** A2Q167_MEDTR)		C:GO:0016020	C:membrane	IPR001727 (PFAM): PTHR12608:SF4	6,062	7,152	4,226	3,556	4,266									
Solyc09g015450	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_BARVE)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,117	0,098	0,116	0,167	0,116									
Solyc09g015457	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G50140.5)					2,051	1,994	2,249	2,131	2,075									
Solyc09g015460	Glycine cleavage T-protein aminomethyltransferase (AHRD V3.3 *-* G7L8V3_MEDTR)		F:GO:0005515	F:protein binding	IPR027266 (G3DSA:3.30.1360.GENE	0,100	0,021	0,072	0,124	0,046									
Solyc09g015470	Protein TIC 56, chloroplastic (AHRD V3.3 *-* A0A199W2K9_ANACO)		F:GO:0008565; C:G(	F:protein transporter activity; C:chloroplast inner membrane; P:1	IPR037471 (PANTHER)	1,774	1,967	1,777	1,583	1,673									
Solyc09g015473	histone-lysine N-methyltransferase ATXR3-like protein (AHRD V3.3 *-* AT5G01590.1)		F:GO:0008565; C:G(	F:protein transporter activity; C:chloroplast inner membrane; P:1	IPR025640 (PFAM): IPR037471 (PAN	2,111	1,970	2,162	1,436	1,738									
Solyc09g015475	SPOC domain / Transcription elongation factor S-II protein (AHRD V3.3 --* AT5G25520.7)		F:GO:0008565; C:G(	F:protein transporter activity; C:chloroplast inner membrane; P:1	mobidb-lite (MOBIDB_LITE): IPR0374	0,894	1,296	1,208	0,992	1,130									
Solyc09g015490	Phosphoenolpyruvate carboxylase (AHRD V3.3 *-* C7DY59_BRANA)		P:GO:0006099; F:G(	P:tricarboxylic acid_EC:4.1.1.31; EC:4.1._Phosphoenolpyruvate	IPR021135 (PFAM): PTHR30523:SF6	11,501	11,300	6,762	7,682	7,803									
Solyc09g015495	Phosphoenolpyruvate carboxylase protein (AHRD V3.3 *-* J9XVK0_CUCSA)		P:GO:0006099; F:G(	P:tricarboxylic acid_EC:4.1.1.31; EC:4.1._Phosphoenolpyruvate	IPR021135 (PRINTS): IPR021135 (PF	0,124	0,080	0,000	0,025	0,000									
Solyc09g015505	Ankyrin repeat domain-containing protein 2 (AHRD V3.3 *-* A0A0B2RKA1_GLYSO)		F:GO:0030941; C:G(	F:chloroplast targeting sequence binding; C:integral component of chloroplast outer membrane; P:protei		0,000	0,000	0,147	0,025	0,072									
Solyc09g015520	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** A0A061EHU9_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS): G3DSA:1.10.510	7,305	4,377	3,008	7,549	5,070					1,321	0,000			up
Solyc09g015530	transmembrane protein (AHRD V3.3 *** AT3G51580.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	4,635	4,851	6,993	9,113	7,200									
Solyc09g015590	LOW QUALITY:DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT1G08260.2)				PTHR36005 (PANTHER)	0,124	0,021	0,174	0,025	0,000									
Solyc09g015613	Glycerol-3-phosphate transporter family protein (AHRD V3.3 *** B9MUJ6_POPTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:transmembrane transporter activity; P:transmembra		0,019	0,468	0,000	0,000	0,164									
Solyc09g015617	Chlorophyllide a oxygenase (AHRD V3.3 *-* W9SD87_9ROSA)	CAO	F:GO:0005506; F:G(	F:iron ion binding; F:chlorophyllide a oxygenase [overall] activity; F:oxidoreductase activity; F:2 iron, 2		0,019	0,083	0,025	0,000	0,023									
Solyc09g015630	Chlorophyllide a oxygenase (AHRD V3.3 *-* W9SD87_9ROSA)	CAO	F:GO:0005506; F:G(	F:iron ion binding; F:chlorophyllide a oxygenase [overall] activity	PTHR21266 (PANTHER): PTHR21266	0,000	0,232	0,000	0,000	0,094									
Solyc09g015650	Non-green plastid inner envelope membrane protein (AHRD V3.3 *** G7KY60_MEDTR)		C:GO:0016020	C:membrane	IPR005349 (PFAM): mobidb-lite (MOB	64,618	72,132	106,127	112,767	102,338									
Solyc09g015660	Transcription factor GTE1 (AHRD V3.3 *** A0A0B2PDN7_GLYSO)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t	IPR001487 (PRINTS): IPR027353 (PF	13,301	13,473	18,062	16,345	16,361									
Solyc09g015670	Vacuolar sorting receptor family protein (AHRD V3.3 *** B9HDJ2_POPTR)		F:GO:0005509; C:G(	F:calcium ion binding; C:endosome; C:trans-Golgi network; P:ub	G3DSA:3.50.30.30 (GENE3D): G3DSA	205,664	166,522	359,032	300,992	341,166									
Solyc09g015680	LOW QUALITY:Aquaporin TIP3-2 (AHRD V3.3 --* TIP32_MAIZE)					0,915	1,047	1,242	1,065	1,017									
Solyc09g015700	Replication factor C subunit 3 (AHRD V3.3 --* RFC3_ORYSJ)					1,425	1,670	0,878	1,188	1,319									
Solyc09g015770	WRKY transcription factor 81	WRKY81	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR036576 (G3DS_WRKY	103,665	117,264	21,908	104,808	50,928			1,212	0,000	2,258	0,000		up	up
Solyc09g015820	Thioredoxin h-like protein (AHRD V3.3 *** Q8H6X3_TOBAC)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu	PR00421 (PRINTS): G3DSA:3.40.30.1	33,765	38,606	43,260	43,894	40,957									
Solyc09g015830	Kinase, putative (AHRD V3.3 *** B9SRU2_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): G3DSA:3.30.200	224,222	195,605	365,169	457,978	425,441									
Solyc09g015840	Receptor-like kinase (AHRD V3.3 *-* C6ZRN8_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; C:plasma membrane; C	G3DSA:2.60.120.430 (GENE3D): IPR(	17,505	12,599	24,533	39,866	31,693					0,701	0,000			up
Solyc09g015850	Ribosomal protein S3 (AHRD V3.3 *** A0A075VXF7_CAPAN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001351 (PFAM): IPR036419 (G3D	0,349	0,603	0,550	1,311	0,397									
Solyc09g015870	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* J7MFY4_MALDO)		F:GO:0004129; F:G(	F:cytochrome-c oxi_EC:1.9.3.1 Cytochrome-c oxidas	PR01166 (PRINTS): IPR036257 (G3D	0,096	0,339	0,274	0,697	0,233									
Solyc09g015880	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* A0A0C5B2A3_HYONI)		F:GO:0004129; F:G(	F:cytochrome-c oxi_EC:1.9.3.1 Cytochrome-c oxidas	PR01166 (PRINTS): IPR011759 (PFA	0,138	0,520	0,714	1,092	0,540									
Solyc09g015900	LOW QUALITY:Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 --* AT3G13800.4)					0,019	0,064	0,000	0,000	0,000									
Solyc09g015930	RNA helicase DEAD28	DEAD28	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): G3DS	45,283	50,310	71,744	69,308	71,943									
Solyc09g016930	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_COFAR)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl	IPR000932 (PFAM): IPR000932 (PAN	0,000	0,021	0,046	0,000	0,000									
Solyc09g016935	SH2 domain protein B (AHRD V3.3 --* AT1G78540.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	3,413	3,087	4,140	4,872	4,054									
Solyc09g016940	Mitochondrial ATP synthase D chain-related protein, putative (AHRD V3.3 *** A0A061EHB1_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	21,935	20,032	21,328	25,237	21,502									
Solyc09g016950	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT2G43700.5)					20,068	17,032	15,628	15,646	16,144									
Solyc09g018000	LOW QUALITY:Translocase inner membrane subunit 44-2 isoform 1 (AHRD V3.3 --* A0A061DP09_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,022	0,000									
Solyc09g018010	Non-specific lipid-transfer protein (AHRD V3.3 *** M0ZNZ5_SOLTU)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding	IPR000528 (PRINTS): G3DSA:1.10.11	1,948	3,674	0,025	0,000	0,023									
Solyc09g018030	MACPF domain protein (AHRD V3.3 *** G7ILM1_MEDTR)		C:GO:0005886; P:G(	C:plasma membrane; P:plant-type hypersensitive response	IPR020864 (PFAM): PTHR33199:SF5	8,224	11,222	4,191	3,308	5,136									
Solyc09g018040	LOW QUALITY:BTB/POZ domain-containing protein (AHRD V3.3 --* AT1G55760.1)					3,148	3,447	3,948	3,705	4,226									
Solyc09g018050	LOW QUALITY:Calcium-dependent phosphotriesterase superfamily protein (AHRD V3.3 --* AT5G22020.3)					0,061	0,054	0,000	0,022	0,047									
Solyc09g018060	MAP kinase kinase kinase 69	MAPKKK69	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): IPR0(	8,247	8,542	9,499	9,339	10,119									
Solyc09g018070	Protein DETOXIFICATION (AHRD V3.3 *** K4CS74_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (TIGRFAM): IPR002528 (F	0,773	0,273	2,657	2,666	2,822									
Solyc09g018080	cytochrome P450%2C family 705%2C subfamily A%2C polypeptide 28 (AHRD V3.3 --* AT3G20935.1)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo	mobidb-lite (MOBIDB_LITE)	0,117	0,116	0,716	0,275	0,475									
Solyc09g018160	Nucleotidyltransferase domain containing protein, expressed (AHRD V3.3 *** A0A0K9PDV3_ZOSMR)		F:GO:0003729	F:mRNA binding	G3DSA:1.10.1410.10 (GENE3D): G3D	14,131	14,234	21,565	20,686	20,971									
Solyc09g018170	MAP kinase kinase kinase 70	MAPKKK70	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): G3DS	1,356	1,718	2,573	4,196	4,104									
Solyc09g018180	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G38500.1)		C:GO:0016021	C:integral component of membrane	PTHR34945 (PANTHER): PTHR34945	0,000	0,000	0,000	0,048	0,023									
Solyc09g018200	LOW QUALITY:ovate family protein 17	OFP17	F:GO:0003677; P:G(	F:DNA binding; P:negative regulation of transcription, DNA-temp	IPR006458 (TIGRFAM): IPR006458 (F	0,098	0,019	0,136	0,097	0,118									
Solyc09g018220	Tobacco mosaic virus resistance-2		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR032675 (G3D	2,891	2,420	0,620	0,893	0,821									
Solyc09g018230	U-box domain-containing protein 16 (AHRD V3.3 *** W9QXE8_9ROSA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR013083 (G3DSA:3.30.40.GENE3D	10,707	6,515	4,875	7,981	6,582					0,715	0,020			up
Solyc09g018250	LOW QUALITY:RNA polymerase II degradation factor-like protein (DUF1296) (AHRD V3.3 *-* AT1G29370.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,306	0,072	0,051	0,141									
Solyc09g018280	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CS94_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR004041 (PFAM): PIRSF000654 (P	89,334	114,864	99,577	172,704	124,787					0,797	0,000			up
Solyc09g018310	Reticulocyte-binding protein 2 like a (AHRD V3.3 *** A0A0B2S7G0_GLYSO)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	51,883	46,179	63,601	61,304	59,882									
Solyc09g018370	ARM repeat superfamily protein (AHRD V3.3 *** AT5G27970.1)				IPR032817 (PFAM): IPR015403 (PFA	65,051	55,427	61,501	64,460	66,220									
Solyc09g018430	Gamma-interferon-inducible lysosomal thiol reductase (AHRD V3.3 *-* A0A151RU75_CAJCA)				IPR004911 (PFAM): PTHR13234:SF4	0,421	0,367	0,025	0,000	0,071									
Solyc09g018440	Gamma-interferon-inducible lysosomal thiol reductase, putative (AHRD V3.3 *-* B9SKZ5_RICCO)				IPR004911 (PANTHER): PTHR13234:	0,331	0,356	0,025	0,022	0,000									
Solyc09g018450	Ubiquitin activating enzyme E1 (AHRD V3.3 *** P93393_TOBAC)		P:GO:0006464; F:G(	P:cellular protein modification process; F:ubiquitin-like modifier a	IPR000011 (PRINTS): G3DSA:2.40.30	148,573	163,279	138,316	129,618	141,733									
Solyc09g018460	LOW QUALITY:GRAS5	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM_GRAS	1,004	1,019	3,752	4,385	2,829									
Solyc09g018490	Serine/threonine-protein kinase (AHRD V3.3 *-* G4XXY5_NICAT)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph	IPR035446 (PIRSF): IPR036426 (G3D	1,991	2,664	0,356	0,551	0,702									
Solyc09g018500	Transcription factor bHLH61-like protein (AHRD V3.3 *** A0A0B0MKH5_GOSAR)		F:GO:0046983	F:protein dimerization activity	PTHR31945 (PANTHER): PTHR31945	0,040	0,037	0,000	0,000	0,000									
Solyc09g018510	Phytol kinase (AHRD V3.3 *** F1BPW2_SOLPN)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph	IPR039606 (PANTHER): PTHR32523:	30,024	29,095	22,088	21,146	22,246									
Solyc09g018550	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT5G46870.2)					2,603	1,224	1,315	2,320	1,343									
Solyc09g018610	LOW QUALITY:Mitochondrial ATP synthase subunit G protein (AHRD V3.3 --* AT4G26210.2)					2,343	2,582	0,656	0,509	1,383									
Solyc09g018630	Bis(5'-adenosyl)-triphosphatase (AHRD V3.3 *-* A0A151R882_CAJCA)		F:GO:0003824	F:catalytic activity	IPR001310 (PFAM): IPR036265 (G3D	15,331	20,257	21,812	20,271	23,238									
Solyc09g018640	LOW QUALITY:phosphatidylinositol-glycan biosynthesis class X-like protein (AHRD V3.3 --* AT5G46850.3)					0,421	0,517	0,464	0,438	0,471									
Solyc09g018650	Bis(5'-adenosyl)-triphosphatase (AHRD V3.3 *-* A0A1D1ZLP4_9ARAE)		F:GO:0003824	F:catalytic activity	IPR036265 (G3DSA:3.30.428.GENE3I	4,079	4,449	5,482	5,700	5,502									
Solyc09g018670	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRD V3.3 *** AT4G10360.3)		C:GO:0016021	C:integral component of membrane	IPR006634 (PFAM): PTHR13439 (PAI	9,368	7,931	16,503	19,327	16,699									
Solyc09g018690	ATP-dependent DNA helicase RecQ (AHRD V3.3 *** A0A072UZI8_MEDTR)		F:GO:0000166; F:G(	F:nucleotide bindinc_EC:3.6.1.3; EC:3.6.1_Adenosinetriphospha	IPR036388 (G3DSA:1.10.10.GENE3D	18,748	15,298	14,925	14,313	13,502									
Solyc09g018695	Reverse transcriptase (AHRD V3.3 *-* D5LVJ7_ELEAC)		F:GO:0016787; P:G(	F:hydrolase activity; P:nucleic acid metabolic process	IPR041577 (PFAM): G3DSA:3.30.70.2	0,462	0,316	0,190	0,390	0,307									
Solyc09g018720	Phosphoglycerate mutase-like family protein (AHRD V3.3 --* AT3G01310.3)					5,628	4,897	5,255	5,230	5,152									
Solyc09g018730	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** M1BT38_SOLTU)		F:GO:0004843; C:G(	F:thiol-dependent ul_EC:3.4.19.12 Ubiquitinyl hydrolase	IPR001578 (PRINTS): G3DSA:1.20.58	32,610	34,291	36,625	35,479	34,790									
Solyc09g018740	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT1G31420.3)					0,080	0,018	0,025	0,025	0,000									
Solyc09g018750	CBS domain-containing protein (AHRD V3.3 *** A0T1V6_PLESU)				G3DSA:3.10.580.10 (GENE3D): IPR0(	123,394	113,405	80,196	78,153	96,787									
Solyc09g018780	Oligoribonuclease (AHRD V3.3 *** A0A1D1Z113_9ARAE)		F:GO:0000175; F:G(	F:3'-5'-exoribonucle_EC:3.1.13; EC:3.1.1! Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3I	2,045	3,012	2,648	2,151	3,770									
Solyc09g018785	RNI-like superfamily protein isoform 2 (AHRD V3.3 --* A0A061EXQ9_THECC)					0,353	0,307	0,393	0,595	0,281									
Solyc09g018790	Succinic semialdehyde reductase isofom1	SSR1	F:GO:0016491; F:G(	F:oxidoreductase activity; F:NADP binding; F:NAD binding; P:ox	IPR006115 (PFAM): IPR013328 (G3D	69,947	81,992	94,731	79,959	82,809									
Solyc09g018800	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_JASNU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me	IPR001280 (PFAM): IPR036408 (G3D	0,000	0,000	0,000	0,000	0,023									
Solyc09g018807	embryo sac development arrest 7 (AHRD V3.3 --* AT3G56990.1)		C:GO:0005886; P:G(	C:plasma membrane; P:carbohydrate transport; F:protein-N(PI)-	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,060	0,000	0,022	0,023									
Solyc09g018810	Unknown protein (AHRD V3.3)					0,000	0,000	0,068	0,025	0,071									
Solyc09g018840	MLO-like protein (AHRD V3.3 *** M1BT43_SOLTU)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane	IPR004326 (PFAM): PTHR31942 (PAI	3,625	3,997	6,296	8,444	5,932									
Solyc09g018845	MLO-like protein (AHRD V3.3 *-* M1BT43_SOLTU)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane	IPR004326 (PFAM): PTHR31942 (PAI	0,079	0,178	0,075	0,075	0,093									
Solyc09g018850	A/G-specific adenine DNA glycosylase (AHRD V3.3 *** W9QVM6_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:base-excision repair; F:DNA N-glycosylase ac	IPR005760 (TIGRFAM): G3DSA:1.10.1	1,338	1,282	0,875	1,043	0,564									
Solyc09g018890	DUF2996 family protein (AHRD V3.3 *** A0A072TND8_MEDTR)		C:GO:0044424	C:intracellular part	IPR021374 (PFAM): PTHR36341:SF2	0,078	0,159	0,000	0,050	0,070									
Solyc09g018900	SCP1-like small phosphatase 4 (AHRD V3.3 --* AT5G46410.3)					0,079	0,220	0,000	0,076	0,023									
Solyc09g018920	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151S244_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAI	0,000	0,000	0,025	0,095	0,023									
Solyc09g018955	DnaJ domain protein (AHRD V3.3 *-* G8A1N6_MEDTR)		C:GO:0005829; C:G(	C:cytosol; C:plasma membrane; C:cell plate; F:clathrin binding;	IPR036869 (G3DSA:1.10.287.GENE3I	62,973	71,718	63,082	61,557	60,076									
Solyc09g018960	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *-* AT4G12770.2)		C:GO:0005737; F:G(	C:cytoplasm; F:clathrin binding; C:vesicle; C:intracellular membr	mobidb-lite (MOBIDB_LITE): PTHR231	15,578	15,919	15,922	15,450	14,557									
Solyc09g019970	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** B9SWA7_RICCO)		F:GO:0004843; P:G(	F:thiol-dependent ul_EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:3.10.20.90 (GENE3D): G3DSA	63,183	45,323	64,004	67,069	68,717									
Solyc09g019980	Cytochrome b561/ferric reductase transmembrane with DOMON related domain, putative (AHRD V3.3 *** A(		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce	G3DSA:1.20.120.1770 (GENE3D): IPI	3,055	5,546	1,927	2,477	2,328									
Solyc09g020000	histone H2A deubiquitinase (DUF3755) (AHRD V3.3 *** AT3G07565.1)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 (GENE3D): IPR02	9,878	9,276	15,009	15,068	12,946									
Solyc09g020010	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *-* AT5G19480.4)				mobidb-lite (MOBIDB_LITE): mobidb-lit	11,493	10,245	13,731	16,191	14,446									
Solyc09g020060	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A0B2SU38_GLYSO)		F:GO:0003677	F:DNA binding	G3DSA:2.40.50.140 (GENE3D)	0,000	0,000	0,000	0,000	0,046									
Solyc09g020065	ARM repeat superfamily protein (AHRD V3.3 --* AT5G06120.9)					0,275	0,000	0,388	0,265	0,047									
Solyc09g020073	Sodium/sulfate cotransporter 2 (AHRD V3.3 --* SLT2_CHLRE)					0,120	0,117	0,025	0,000	0,000									
Solyc09g020110	T2-type RNase		F:GO:0003723; F:G(	F:RNA binding; F:rit_EC:3.1.31; EC:3.1.2' Acting on ester bonds	IPR036430 (G3DSA:3.90.730.GENE3I	51,864	47,050	108,713	105,793	101,465									
Solyc09g020130	60S ribosomal protein L5 (AHRD V3.3 *** RL5_CUCSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR005485 (PRINTS): G3DSA:3.30.42	117,152	125,974	119,297	107,515	108,920									
Solyc09g020140	GPN-loop GTPase-like protein (AHRD V3.3 *** A0A0K9Q4T7_ZOSMR)		F:GO:0005525; F:G(	F:GTP binding; F:hydrolase activity	G3DSA:3.40.50.300 (GENE3D): IPR0(	47,628	57,874	59,720	55,299	56,905									
Solyc09g020150	Glycine--tRNA ligase beta subunit (AHRD V3.3 *** A0A1D1YWE6_9ARAE)				PTHR37766 (PANTHER)	6,584	7,780	5,908	4,595	5,201									
Solyc09g020190	non-specific phospholipase C1-like		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR017849 (G3DSA:3.40.720.GENE3I	71,506	48,176	111,780	102,392	98,635	-0,543	0,036					down		
Solyc09g025200	60S ribosomal protein L18 (AHRD V3.3 *-* RL18_CICAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR021131 (PFAM): G3DSA:3.100.10	0,021	0,059	0,025	0,000	0,046									
Solyc09g025210	alcohol dehydrogenase-2	adh2	F:GO:0045735	F:nutrient reservoir activity	IPR006044 (PRINTS): IPR014710 (G3	3357,503	3091,917	122,812	256,380	18,206									
Solyc09g025220	Legumin 11S-globulin (AHRD V3.3 *** Q39770_GINBI)		F:GO:0045735	F:nutrient reservoir activity	IPR006044 (PRINTS): IPR014710 (G3	0,175	0,037	0,000	0,000	0,000									
Solyc09g025230	Phosphatidylinositol transfer protein (AHRD V3.3 *** A0A0K9NNU5_ZOSMR)				IPR001251 (PFAM): IPR036865 (G3D	0,000	0,000	0,025	0,000	0,000									
Solyc09g025240	ENTH/VHS/ANTH family protein		C:GO:0005622; P:G(	C:intracellular; P:intracellular protein transport	IPR008942 (G3DSA:1.25.40.GENE3D	10,496	9,247	16,363	12,800	13,242									
Solyc09g025245	DnaJ subfamily C member 13 (AHRD V3.3 --* A0A1D1Y1K4_9ARAE)					0,284	0,233	0,254	0,047	0,285									
Solyc09g025250	S26 Type I signal peptidase family protein				G3DSA:2.10.109.10 (GENE3D): PTHF	25,436	32,636	57,951	56,449	55,368									
Solyc09g025260	SAP-like protein BP-73 (AHRD V3.3 *** W9QWA9_9ROSA)		P:GO:0006353	P:DNA-templated transcription, termination	IPR011112 (PFAM): mobidb-lite (MOB	8,095	14,330	23,055	21,315	23,991	0,851	0,006					up		
Solyc09g025270	U-box domain-containing protein 3 (AHRD V3.3 *** W9RQV1_9ROSA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot	IPR000225 (PFAM): IPR011989 (G3D	41,413	35,379	28,369	26,568	30,405									
Solyc09g025310	NAC domain protein, (AHRD V3.3 *** A0A061DNM9_THECC)	NAC082	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM_NAC	0,332	0,266	0,096	0,613	0,632									
Solyc09g030360	LOW QUALITY:Thiamine biosynthetic bifunctional enzyme TH1, chloroplastic (AHRD V3.3 --* TPS1L_ARATH)				mobidb-lite (MOBIDB_LITE)	6,652	6,626	4,984	5,567	6,027									
Solyc09g030370	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SPC5_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	1,399	2,426	0,169	0,198	0,210									
Solyc09g030385	mitogen-activated protein kinase homolog 2 (AHRD V3.3 --* AT1G59580.2)					1,991	1,950	2,382	2,437	2,518									
Solyc09g030390	Serine/arginine repetitive matrix protein 1 (AHRD V3.3 *** A0A151RS01_CAJCA)		P:GO:0006397	P:mRNA processing	IPR002483 (PFAM): G3DSA:1.20.139	99,396	87,882	92,587	91,090	88,899									
Solyc09g030420	auxin response factor, putative (DUF688) (AHRD V3.3 --* AT3G61840.1)					0,516	0,735	0,340	0,486	0,493									
Solyc09g030450	Receptor-like kinase (AHRD V3.3 *** G7K0V8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR032675 (G3DSA:3.80.10.GENE3D	13,615	11,086	2,793	3,279	2,980									
Solyc09g030470	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G46450.3)					0,021	0,000	0,000	0,000	0,000									
Solyc09g031520	LOW QUALITY:Phosphoglycerate mutase family protein (AHRD V3.3 --* AT5G62840.2)					0,224	0,254	0,124	0,314	0,094									
Solyc09g031522	Early-responsive to dehydration stress protein (ERD4) (AHRD V3.3 --* AT3G54510.5)					0,042	0,096	0,025	0,022	0,094									
Solyc09g031523	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G72660.4)					0,442	0,354	0,311	0,269	0,306									
Solyc09g031528	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *-* A0A0V0IG10_SOLCH)		F:GO:0008716	F:D-alanine-D-alani_EC:6.3.2.4 D-alanine--D-alanine	IPR011095 (PFAM): G3DSA:3.30.470	1,798	2,032	0,436	0,562	0,755									
Solyc09g031540	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT1G64430.3)					0,000	0,018	0,000	0,000	0,000									
Solyc09g031570	LOW QUALITY:Cellulose synthase family protein (AHRD V3.3 --* AT5G05170.1)		C:GO:0016020; F:G(	C:membrane; F:cell_EC:2.4.1.12 Cellulose synthase (U	IPR005150 (PFAM)	0,019	0,039	0,000	0,000	0,000									
Solyc09g031580	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *-* G7K198_MEDTR)		F:GO:0046872	F:metal ion binding	G3DSA:3.40.630.30 (GENE3D): IPR0	54,118	44,715	44,379	45,813	42,890									
Solyc09g031590	sorting nexin 2B (AHRD V3.3 *** AT5G07120.2)		F:GO:0035091	F:phosphatidylinositol binding	IPR027267 (G3DSA:1.20.1270.GENE	26,838	24,426	39,531	40,887	39,099									
Solyc09g031610	DAMAGED DNA BINDING PROTEIN1		F:GO:0003684; F:G(	F:damaged DNA binding; F:protein binding; C:nucleus; P:DNA re	IPR001680 (PFAM): IPR015943 (G3D	17,395	19,353	24,297	23,430	25,674									
Solyc09g031650	RING/U-box superfamily protein (AHRD V3.3 --* AT3G58030.4)		F:GO:0003677; F:G(	F:DNA binding; F:he_EC:3.6.1.15 Nucleoside-triphosph	IPR013083 (G3DSA:3.30.40.GENE3D	141,876	123,068	138,616	139,401	138,899									
Solyc09g031680	Mitochondrial uncoupling protein (AHRD V3.3 *** A0A0K9PNF7_ZOSMR)		P:GO:0006839; F:G(	P:mitochondrial transport; F:transmembrane transporter activity	IPR002030 (PRINTS): IPR023395 (G3	9,617	8,988	13,930	13,978	12,709									
Solyc09g031685	Reverse transcriptase (AHRD V3.3 *-* O82684_GINBI)		F:GO:0003676; P:G(	F:nucleic acid binding; P:DNA integration	G3DSA:3.30.70.270 (GENE3D): G3DS	0,158	0,122	0,074	0,050	0,023									
Solyc09g031700	Phosphate transporter (AHRD V3.3 *** A0A0A1G3W1_MANES)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM): G3DSA:1.20.125	10,062	9,229	16,560	16,947	16,447									
Solyc09g031705	Phosphate transporter (AHRD V3.3 *-* A0A0A1G3W1_MANES)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	PTHR11662 (PANTHER): PTHR11662	0,516	0,684	0,797	1,244	0,800									
Solyc09g031730	LOW QUALITY:Photosystem II D2 protein (AHRD V3.3 *-* PSBD_PHAVU)		P:GO:0009772; F:G(	P:photosynthetic electron transport in photosystem II; F:electro	IPR000484 (PFAM): PTHR33149:SF8	0,000	0,000	0,025	0,000	0,000									
Solyc09g031750	Phosphate transporter (AHRD V3.3 *** G7L4P4_MEDTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D): IPR(	30,419	27,726	37,736	36,502	41,488									

Solyc09g031760	Ribosomal protein L19 (AHRD V3.3 *** V4MK59_EUTSA)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; P:translatio		G3DSA:1.10.1200.240 (GENE3D); IPF	0,514	0,919	0,386	0,294	0,425									
Solyc09g031770	JOSEPHIN-like protein (AHRD V3.3 *** AT2G29640.1)		F:GO:0004843; P:GO	F:thiol-dependent ul	EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:1.10.287.10 (GENE3D); IPR0	3,316	2,336	3,658	4,333	3,845									
Solyc09g031780	Chloroplast inner envelope family protein (AHRD V3.3 *** B9INP5_POPTR)		C:GO:0009507	C:chloroplast		IPR031610 (PFAM); IPR031610 (PAN	110,618	140,404	151,353	140,861	152,427									
Solyc09g031785	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 *-* AT3G24255.7)					IPR026960 (PFAM)	0,019	0,000	0,072	0,025	0,047									
Solyc09g031790	Structure-specific endonuclease subunit SLX1 homolog (AHRD V3.3 *** K4CSN5_SOLLC)		F:GO:0004520; C:GO	F:endodeoxyribonuclease activity; C:nucleus; P:DNA metabolic		IPR035901 (G3DSA:3.40.1440.GENE	2,660	3,300	1,865	1,878	1,648									
Solyc09g031800	Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast		IPR008543 (PFAM); IPR008543 (PAN	0,000	0,039	0,050	0,100	0,047									
Solyc09g031810	Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast		IPR008543 (PFAM); IPR008543 (PAN	0,019	0,078	0,025	0,100	0,093									
Solyc09g031820	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast		IPR008543 (PFAM); IPR008543 (PAN	0,019	0,019	0,000	0,097	0,000									
Solyc09g031830	Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast		IPR008543 (PFAM); IPR008543 (PAN	0,021	0,021	0,025	0,050	0,024									
Solyc09g031840	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast		IPR008543 (PFAM); IPR008543 (PAN	0,000	0,000	0,000	0,025	0,023									
Solyc09g031870	ADP-ribosylation factor family protein (AHRD V3.3 *** AT2G18390.1)		F:GO:0005525	F:GTP binding		IPR006689 (PRINTS); G3DSA:3.40.50	0,155	0,227	0,196	0,097	0,141									
Solyc09g031875	Cytochrome P450 (AHRD V3.3 *-* C5NM78_TOBAC)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR036396 (G3DSA:1.10.630.GENE3	0,098	0,085	0,075	0,047	0,000									
Solyc09g031880	galacturonic acid kinase (AHRD V3.3 *** AT3G10700.3)		F:GO:0004335; C:GO	F:galactokinase act	EC:2.7.1.6 Galactokinase	PR00959 (PRINTS); IPR036554 (G3D	0,021	0,021	0,025	0,000	0,046									
Solyc09g031890	galacturonic acid kinase (AHRD V3.3 --* AT3G10700.2)		F:GO:0004335; F:GO	F:galactokinase act	EC:2.7.1.6 Galactokinase		0,000	0,021	0,000	0,000	0,000									
Solyc09g031910	iron regulated 1 (AHRD V3.3 --* AT2G38460.8)					PS51257 (PROSITE_PROFILES)	0,155	0,082	0,050	0,050	0,070									
Solyc09g031920	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *** Q9M386_AR		C:GO:0009506; C:GO	C:plasmodesma; C:integral component of membrane; C:anchore		IPR004864 (PFAM); PTHR31852:SF4	23,377	24,638	22,866	34,456	25,962					0,591	0,041			up
Solyc09g031930	KH domain-containing family protein (AHRD V3.3 *** B9MTT7_POPTR)		F:GO:0003723	F:RNA binding		IPR032377 (PFAM); IPR004088 (PFA	61,478	62,645	71,657	72,756	67,335									
Solyc09g031940	Protein RETICULATA-RELATED 3, chloroplastic (AHRD V3.3 *** RER3_ARATH)		C:GO:0016021	C:integral component of membrane		IPR021825 (PFAM); mobidb-lite (MOB	17,386	15,003	17,970	14,758	15,612									
Solyc09g031960	LOW QUALITY:Cyclin family protein (AHRD V3.3 --* AT5G45190.3)					PTHR33499:SF7 (PANTHER); PTHR3	0,058	0,019	0,000	0,048	0,000									
Solyc09g031970	Alpha-1,4 glucan phosphorylase (AHRD V3.3 *** K4CSQ2_SOLLC)		P:GO:0005975; F:GO	P:carbohydrate met	EC:2.4.1.1 Glycogen phosphoryl	IPR000811 (PIRSF); IPR011833 (TIG	103,208	127,914	69,715	59,426	78,073									
Solyc09g031975	60S acidic ribosomal protein family (AHRD V3.3 --* AT4G00810.2)						0,325	0,158	0,122	0,195	0,212									
Solyc09g037010	LOW QUALITY:Serine/threonine-protein kinase TOR (AHRD V3.3 *-* TOR_ARATH)		F:GO:0005488; F:GO	F:binding; F:transferase activity			0,021	0,037	0,072	0,025	0,024									
Solyc09g037025	Alcohol dehydrogenase (AHRD V3.3 --* Q59IN5_WISFL)						0,000	0,037	0,000	0,000	0,000									
Solyc09g037030	LOW QUALITY:Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7LHE4_ARALL)						0,834	0,657	0,504	0,415	0,704									
Solyc09g037050	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7LHE4_ARALL)						0,098	0,041	0,050	0,069	0,024									
Solyc09g037080	Alcohol dehydrogenase (AHRD V3.3 --* Q4LAW8_CAPCH)						0,180	0,079	0,022	0,099	0,096									
Solyc09g037083	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G36570.1)						0,038	0,000	0,022	0,000	0,046									
Solyc09g037120	Alcohol dehydrogenase (AHRD V3.3 --* D4I621_9SOLA)						0,000	0,000	0,025	0,000	0,000									
Solyc09g037125	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7LHE4_ARALL)						0,278	0,224	0,068	0,048	0,095									
Solyc09g037130	Alcohol dehydrogenase (AHRD V3.3 --* Q4LAW8_CAPCH)						0,137	0,076	0,072	0,047	0,046									
Solyc09g037133	LOW QUALITY:cystathionine beta-lyase (AHRD V3.3 --* AT3G57050.3)		F:GO:0003676; F:GO	F:nucleic acid binding; F:catalytic activity; F:zinc ion binding; F:i		IPR000277 (PFAM); G3DSA:4.10.60.1	0,061	0,000	0,000	0,000	0,023									
Solyc09g042230	LOW QUALITY:AIG2-like (avirulence induced gene) family protein (AHRD V3.3 --* AT2G24390.2)					mobidb-lite (MOBIDB_LITE)	0,019	0,145	2,690	1,731	1,731									
Solyc09g042250	LOW QUALITY:Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061EQ47_THECC		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	2,863	3,342	4,398	3,854	4,337									
Solyc09g042260	Protein kinase atsik, putative (AHRD V3.3 *** B9SRS3_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:1.10.510.10 (GENE3D); IPR0	26,111	29,131	46,087	41,992	38,080									
Solyc09g042263	PIF1-like helicase (AHRD V3.3 *** G7K719_MEDTR)		P:GO:0000723; F:GO	P:telomere mainten	EC:3.6.1.15 Nucleoside-triphosph	IPR010285 (PFAM); G3DSA:3.40.50.3	0,000	0,018	0,000	0,000	0,000									
Solyc09g042270	PIF1-like helicase (AHRD V3.3 *** G7JQP0_MEDTR)		P:GO:0000723; F:GO	P:telomere mainten	EC:3.6.1.15 Nucleoside-triphosph	IPR003840 (PFAM); G3DSA:3.40.50.3	0,019	0,000	0,000	0,000	0,000									
Solyc09g042290	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JXR5_CYNCS)		F:GO:0005515	F:protein binding		IPR002885 (PFAM); IPR033443 (PFA	0,142	0,146	0,075	0,145	0,307									
Solyc09g042300	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *-* W0TSU1_ACAMN)		F:GO:0005524; C:GO	F:ATP binding; C:pl	EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	PTHR19241 (PANTHER); PTHR19241	0,040	0,000	0,000	0,000	0,000									
Solyc09g042480	LOW QUALITY:E3 ubiquitin-protein ligase SHPRH (AHRD V3.3 *-* W9RI37_9ROSA)		F:GO:0005524; F:GO	F:ATP binding; F:ligase activity; F:metal ion binding		mobidb-lite (MOBIDB_LITE)	0,000	0,019	0,000	0,000	0,000									
Solyc09g042660	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1B3J2_SOLTU)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		G3DSA:1.10.510.10 (GENE3D); PIRSI	2,132	2,050	0,960	0,792	0,754									
Solyc09g042670	Methyltransferase MT-A70 family protein isoform 1 (AHRD V3.3 --* A0A061FJR2_THECC)						1,223	0,877	1,306	1,319	1,439									
Solyc09g042690	LOW QUALITY:Fructose-1,6-bisphosphatase, chloroplastic (AHRD V3.3 --* F16P1_ORYSJ)						0,176	0,259	0,051	0,144	0,071									
Solyc09g042695	Myb family transcription factor family protein (AHRD V3.3 *-* B9H5N1_POPTR)		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.60 (GENE3D); PTHR4	0,000	0,018	0,000	0,000	0,000									
Solyc09g042700	Saposin B domain-containing family protein (AHRD V3.3 *** B9HDA3_POPTR)		C:GO:0005764; P:GO	C:lysosome; P:sphingolipid metabolic process		IPR008373 (PRINTS); IPR008138 (PF	8,418	7,209	5,660	6,685	7,046									
Solyc09g042710	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT2G38370.2)		C:GO:0005829; P:GO	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac		IPR008545 (PFAM); mobidb-lite (MOB	6,236	4,721	2,004	2,427	2,449									
Solyc09g042728	trichome birefringence-like protein (DUF828) (AHRD V3.3 --* AT3G12060.1)						0,000	0,039	0,025	0,025	0,024									
Solyc09g042740	Formin-like protein (AHRD V3.3 *** K4CSX6_SOLLC)		C:GO:0016021	C:integral component of membrane		IPR015425 (PFAM); G3DSA:1.20.58.2	0,019	0,018	0,047	0,045	0,023									
Solyc09g042750	Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9T2I4_RICCO)					G3DSA:3.10.129.10 (GENE3D); G3DS	25,605	28,459	62,792	70,520	66,021									
Solyc09g042760	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G48390.1)		F:GO:0005515; P:GO	F:protein binding; P:meiotic cell cycle		IPR011990 (G3DSA:1.25.40.GENE3D	0,461	0,394	0,246	0,226	0,187									
Solyc09g042770	Rhodanese-like (AHRD V3.3 *** A2Q5X2_MEDTR)					IPR036873 (G3DSA:3.40.250.GENE3	14,871	14,167	32,312	28,580	30,626									
Solyc09g042785	DNA gyrase subunit A, chloroplastic/mitochondrial (AHRD V3.3 --* GYRA_ARATH)						6,116	5,128	6,070	5,031	5,560									
Solyc09g047840	Autophagy-related protein 10 (AHRD V3.3 *** A0A0K0XR68_TOBAC)		P:GO:0006914	P:autophagy		G3DSA:3.30.1460.50 (GENE3D); IPR	3,361	2,264	4,086	3,954	3,486									
Solyc09g047855	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* A0A072UBR2_MEDTR)					IPR025558 (PFAM); PTHR34427 (PAN	0,059	0,078	0,025	0,098	0,048									
Solyc09g047860	HAT transposon superfamily (AHRD V3.3 *-* A0A061G5I4_THECC)		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM); PTHR32166 (PAN	0,117	0,076	0,000	0,050	0,023									
Solyc09g047870	Hemolysin A (AHRD V3.3 *** A0A118JWD6_CYNCS)		F:GO:0003723; F:GO	F:RNA binding; F:methyltransferase activity; P:methylation		G3DSA:3.40.50.150 (GENE3D); G3DS	6,144	6,193	3,532	2,561	4,292									
Solyc09g047900	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G12830.1)		C:GO:0009507; F:GO	C:chloroplast; F:hydrolase activity		IPR000073 (PRINTS); IPR000073 (PF	8,987	8,134	11,634	13,196	13,894									
Solyc09g047910	lysine ketoglutarate reductase trans-splicing-like protein, putative (DUF707) (AHRD V3.3 *** AT4G18530.1)		C:GO:0016021	C:integral component of membrane		IPR007877 (PFAM); mobidb-lite (MOB	0,400	0,464	0,669	0,504	0,797									
Solyc09g047930	maternal effect embryo arrest protein (AHRD V3.3 *** AT3G07510.3)		C:GO:0016021	C:integral component of membrane		PTHR33430:SF4 (PANTHER); PTHR3	3,918	4,367	2,230	1,607	1,824									
Solyc09g048970	DNA-directed RNA polymerase II subunit RPB7 (AHRD V3.3 *-* A0A0B0PUV3_GOSAR)		F:GO:0003899; P:GO	F:DNA-directed 5'-3' RNA polymerase activity; P:transcription, D		G3DSA:2.40.50.140 (GENE3D); PTHF	2,765	2,346	2,054	1,480	2,266									
Solyc09g048980	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** G7KY72_MEDTR)		F:GO:0005515	F:protein binding		IPR000210 (PFAM); IPR027356 (PFA	0,000	0,019	0,000	0,000	0,000									
Solyc09g050020	cytochrome b (AHRD V3.3 *-* AT2G07727.1)		F:GO:0009055; C:GO	F:electron transfer activity; C:membrane; P:respiratory electron		G3DSA:1.10.287.980 (GENE3D); IPR	0,097	0,246	0,150	0,622	0,237									
Solyc09g050030	30S ribosomal protein S14, putative (AHRD V3.3 *** B9T2M2_RICCO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		G3DSA:4.10.830.10 (GENE3D); IPR0	0,021	0,101	0,050	0,123	0,000									
Solyc09g050040	Ribosomal protein L5 (AHRD V3.3 *** Q70G83_SOLCO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		IPR002132 (PANTHER); PTHR11994:	0,058	0,081	0,119	0,075	0,069									
Solyc09g050050	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* A0A151UEH4_CAJCA)		P:GO:0008152	P:metabolic process		mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,121	0,096	0,174	0,141									
Solyc09g055180	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *-* AT5G01950.8)		F:GO:0004674; F:GO	F:protein serine/thr	EC:2.7.11 Transferring phospho	IPR032675 (G3DSA:3.80.10.GENE3D	3,457	2,812	4,040	6,654	5,258									
Solyc09g055183	Protein kinase-like (AHRD V3.3 *** Q5QMM2_ORYSJ)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		IPR001245 (PFAM); PIRSF000615 (P	8,755	10,310	14,068	16,443	16,001									
Solyc09g055230	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHR		F:GO:0005524; P:GO	F:ATP binding; P:protein metabolic process		IPR001270 (PRINTS); IPR003959 (PF	59,252	46,223	46,826	47,343	49,553									
Solyc09g055260	E3 ubiquitin-protein ligase listerin-like protein (AHRD V3.3 *** A0A072UEK1_MEDTR)		F:GO:0061630; C:GO	F:ubiquitin protein ligase activity; C:RQC complex; P:ribosome-a		IPR013083 (G3DSA:3.30.40.GENE3D	53,198	43,963	80,967	95,280	83,244									
Solyc09g055310	Ethylene-overproduction protein 1 (AHRD V3.3 *** ETO1_ARATH)		F:GO:0005515	F:protein binding		IPR011990 (G3DSA:1.25.40.GENE3D	45,024	44,985	74,920	76,882	67,554									
Solyc09g055320	LOW QUALITY:Oxygen-evolving enhancer protein 2, chloroplastic (AHRD V3.3 --* PSBP_HELAN)						0,599	0,759	1,677	1,298	1,772									
Solyc09g055340	MAU2 chromatid cohesion factor like (AHRD V3.3 *-* A0A0B2S9M1_GLYSO)		C:GO:0000785; F:GO	C:chromatin; F:double-stranded DNA binding; C:SMC loading complex; P:maintenance of mitotic sister c			17,709	15,761	15,619	14,193	15,358									
Solyc09g055343	MAU2 chromatid cohesion factor like (AHRD V3.3 *-* A0A0B2S4C3_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion		IPR019440 (PANTHER)	19,559	17,558	16,543	16,696	16,411									
Solyc09g055345	MAU2 chromatid cohesion factor like (AHRD V3.3 *-* A0A0B2S9M1_GLYSO)		P:GO:0007064	P:mitotic sister chromatid cohesion		IPR019440 (PFAM); IPR019440 (PAN	21,804	19,028	17,692	16,692	17,900									
Solyc09g055350	ABC transporter family protein (AHRD V3.3 *** A0A097P9Q8_HEVBR)	ABCB25	F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0	34,836	35,318	47,966	50,595	47,684									
Solyc09g055420	Nucleoside diphosphate kinase (AHRD V3.3 *** NDK_CAPAN)		F:GO:0000166; F:GO	F:nucleotide binding	EC:2.7.4.6 Nucleoside-diphosph	IPR034907 (PFAM); IPR036850 (G3D	0,418	0,624	0,240	0,167	0,327									
Solyc09g055425	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT2G33170.2)		F:GO:0005515	F:protein binding		IPR001611 (PFAM); IPR032675 (G3D	0,019	0,064	0,000	0,000	0,023									
Solyc09g055460	50S ribosomal protein L20 (AHRD V3.3 *-* A0A0V0GV30_SOLCH)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation;		IPR035566 (G3DSA:1.10.1900.GENE	0,514	0,360	0,515	0,511	0,376									
Solyc09g055470	multiprotein bridging factor 1a		F:GO:0043565	F:sequence-specific DNA binding		G3DSA:1.10.260.40 (GENE3D); IPR0	18,582	18,441	27,382	26,069	27,546									
Solyc09g055500	Sulfotransferase (AHRD V3.3 *** K4CT47_SOLLC)		F:GO:0008146	F:sulfotransferase activity		IPR000863 (PFAM); G3DSA:3.40.50.3	0,534	0,302	0,000	0,000	0,000									
Solyc09g055540	AP2/ERF and B3 domain-containing protein Os01g0693400 (AHRD V3.3 --* Y1934_ORYSJ)						0,000	0,019	0,000	0,000	0,000									
Solyc09g055550	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT1G50440.5)						3,065	2,140	2,972	3,003	2,953									
Solyc09g055570	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT1G06840.1)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro		G3DSA:1.10.510.10 (GENE3D); IPR0	97,955	81,238	76,011	84,843	84,632									
Solyc09g055590	heat-inducible transcription repressor (AHRD V3.3 *** AT5G01970.1)					mobidb-lite (MOBIDB_LITE); mobidb-lit	29,430	26,901	23,440	22,251	23,513									
Solyc09g055650	R2R3MYB transcription factor 100	R2R3MYB100	F:GO:0003677	F:DNA binding		PF13921 (PFAM); MYB	0,040	0,021	0,000	0,000	0,000									
Solyc09g055660	Bromodomain (AHRD V3.3 *-* A4PP03_MEDTR)		F:GO:0005515	F:protein binding		IPR001487 (PFAM); IPR036427 (G3D	0,000	0,000	0,025	0,000	0,023									
Solyc09g055700	Protein FLX-like 1 (AHRD V3.3 *** A0A199W6G6_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds		IPR006912 (PFAM); IPR040353 (PAN	24,621	23,337	32,946	33,006	30,159									
Solyc09g055710	lysophosphatidyl acyltransferase 5 (AHRD V3.3 --* AT3G18850.6)						2,074	2,048	2,696	2,746	2,707									
Solyc09g055715	aluminum induced protein with YGL and LRDR motifs (AHRD V3.3 --* AT5G19140.3)		F:GO:0003677; F:GO	F:DNA binding; F:catalytic activity; F:DNA-directed DNA polyme		mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,018	0,025	0,123	0,141									
Solyc09g055760	myosin heavy chain-like protein (AHRD V3.3 *** AT5G59210.2)					PTHR45393 (PANTHER)	40,965	44,462	38,853	37,736	41,562									
Solyc09g055765	Transcription factor, putative (AHRD V3.3 *** B9TBR8_RICCO)		F:GO:0046983	F:protein dimerization activity		PTHR33124:SF31 (PANTHER); PTHR	3,405	3,228	1,610	3,044	2,089									
Solyc09g055810	LOW QUALITY:Protein transport protein sec23, putative (AHRD V3.3 *-* B9RN42_RICCO)		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:cytosol; P:intracellular pr		IPR037364 (PANTHER); PTHR11141:	0,000	0,021	0,000	0,000	0,000									
Solyc09g055830	cation/hydrogen exchanger family protein (AHRD V3.3 --* AT2G28180.1)						0,042	0,119	0,000	0,100	0,024									
Solyc09g055840	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_SILLA)		C:GO:0005739; C:GO	C:mitochondrion; C:	EC:1.6.99.5; EC:1.6 Acting on NADH or NADPH; NADH dehydrogenase; NADH:ub		0,078	0,103	0,025	0,096	0,071									
Solyc09g055850	Proline-rich protein PRCC (AHRD V3.3 *-* A0A0B2QCD0_GLYSO)					IPR018800 (PFAM); mobidb-lite (MOB	3,570	3,028	6,049	5,722	5,590									
Solyc09g055860	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 --* AT2G31432.2)						0,212	0,238	0,242	0,540	0,329									
Solyc09g055870	Proline-rich protein PRCC (AHRD V3.3 *** A0A0B2QCD0_GLYSO)					mobidb-lite (MOBIDB_LITE); mobidb-lit	25,883	22,924	46,038	43,945	43,379									
Solyc09g055890	Lipoxygenase (AHRD V3.3 *-* V4UAR3_9ROSI)		F:GO:0005515; F:GO	F:protein binding; F:	EC:1.13.11 Acting on single donc	IPR001246 (PRINTS); IPR013819 (PF	6,596	5,983	4,859	5,761	5,426									
Solyc09g055900	Lipoxygenase (AHRD V3.3 *** K4CT85_SOLLC)		F:GO:0016702; F:GO	F:oxidoreductase a	EC:1.13.11 Acting on single donc	IPR013819 (PRINTS); IPR001246 (PF	3,215	3,523	3,315	2,826	3,554									
Solyc09g055910	FAD-dependent oxidoreductase family protein (AHRD V3.3 *** AT5G48440.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process		IPR006076 (PFAM); IPR036188 (G3D	31,191	34,432	24,738	22,016	23,769									
Solyc09g055920	Poly(A)-specific ribonuclease PARN-like protein (AHRD V3.3 *** W9QZE5_9ROSA)		F:GO:0003676	F:nucleic acid binding		IPR036397 (G3DSA:3.30.420.GENE3	9,257	9,521	7,859	7,568	8,318									
Solyc09g055930	Monocopper oxidase-like protein SKU5 (AHRD V3.3 *** A0A151SII9_CAJCA)		F:GO:0005507; F:GO	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red		IPR001117 (PFAM); IPR011707 (PFA	24,762	19,983	13,975	12,820	15,107									
Solyc09g055940	Sodium Bile acid symporter family (AHRD V3.3 *** AT3G25410.1)		C:GO:0016020	C:membrane		IPR002657 (PFAM); IPR038770 (G3D	26,847	29,314	35,138	31,099	37,887									
Solyc09g055950	Photosystem II D2 protein (AHRD V3.3 *-* PSBD_MANES)		P:GO:0009772; F:GO	P:photosynthetic electron transport in photosystem II; F:electro		IPR000484 (PFAM); IPR036854 (G3D	0,140	0,534	0,300	0,640	0,521									
Solyc09g055990	ADP-ribosylation factor (AHRD V3.3 *-* ARF_VIGUN)		F:GO:0005525	F:GTP binding		G3DSA:3.40.50.300 (GENE3D); IPR0	0,040	0,124	0,025	0,143	0,000									
Solyc09g056010	LOW QUALITY:ACT-like protein tyrosine kinase family protein (AHRD V3.3 --* AT2G17700.1)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination; F:transferase activity			0,966	0,950	0,371	0,783	0,591									
Solyc09g056030	Ubiquitin family protein (AHRD V3.3 --* AT4G02890.2)		C:GO:0005737; P:GO	C:cytoplasm; P:protein ubiquitination; F:ubiquitin protein ligase activity			0,201	0,118	0,044	0,048	0,024									
Solyc09g056035	E3 ubiquitin-protein ligase UPL5-like protein (AHRD V3.3 --* G7JKJ3_MEDTR)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination			0,205	0,178	0,094	0,000	0,070									
Solyc09g056040	E3 ubiquitin-protein ligase UPL5-like protein (AHRD V3.3 *** G7IM29_MEDTR)		F:GO:0004842	F:ubiquitin-protein transferase activity		IPR000569 (PFAM); G3DSA:3.90.175	1,118	1,944	0,411	0,220	0,889									
Solyc09g056070	LOW QUALITY:Maturase (AHRD V3.3 *** O79414_SOLTU)		P:GO:0006397	P:mRNA processing		IPR024937 (PFAM); mobidb-lite (MOB	0,038	0,518	0,000	0,050	0,211									
Solyc09g056080	LOW QUALITY:Maturase (AHRD V3.3 *-* O79414_SOLTU)		C:GO:0005739; P:GO	C:mitochondrion; P:mRNA processing		PTHR33642 (PANTHER); PTHR33642	0,019	0,143	0,000	0,000	0,047									
Solyc09g056090	LOW QUALITY:Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic (AHRD V3.3 --* RCA		C:GO:0005739	C:mitochondrion			0,019	0,307	0,000	0,000	0,070									
Solyc09g056100	LOW QUALITY:DDT domain superfamily (AHRD V3.3 --* AT1G18950.3)		F:GO:0003676	F:nucleic acid binding		PTHR38146 (PANTHER)	0,000	0,502	0,000	0,000	0,166									
Solyc09g056110	Mitovirus RNA-dependent RNA polymerase (AHRD V3.3 --* ATMG01110.1)		C:GO:0005739; C:GO	C:mitochondrion; C:membrane; C:integral component of membra		IPR008686 (PANTHER); PTHR34456:	0,000	0,060	0,000	0,000	0,000									
Solyc09g056130	Cellular retinaldehyde-binding/triple function, C-terminal (AHRD V3.3 *-* Q2HW59_MEDTR)					IPR001251 (PFAM); IPR036865 (G3D	0,118	0,116	0,025	0,047	0,000									
Solyc09g056135	Ribosomal protein L15 (AHRD V3.3 *** K4CTA8_SOLLC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		IPR000439 (PFAM); IPR024794 (G3D	5,123	3,749	1,487	1,254	1,692									
Solyc09g056160	Chaperone surA (AHRD V3.3 *** A0A1D1YVG1_9ARAE)		P:GO:0006355; C:GO	P:regulation of transcription, DNA-templated; C:chloroplast nucle		mobidb-lite (MOBIDB_LITE); IPR0389	63,463	71,649	106,924	89,847	99,334									
Solyc09g056170	Fimbrin, putative (AHRD V3.3 *** B9SMN8_RICCO)		F:GO:0051015; P:GO	F:actin filament binding; P:actin filament bundle assembly		IPR036872 (G3DSA:1.10.418.GENE3	2,908	2,856	0,683	0,438	0,704									
Solyc09g056180	Dehydroascorbate reductase (AHRD V3.3 *-* Q1G0W3_SOLLC),Pfam:PF13410	DHAR4	P:GO:0010731; F:GO	P:protein glutathion	EC:1.8.5.1 Glutathione dehydroc	G3DSA:1.20.1050.10 (GENE3D); PTH	0,859	1,303	1,226	3,265	3,639			1,558	0,000	1,403	0,004		up	up
Solyc09g056200	F-box/RNI-like/FBD-like domains-containing protein (AHRD V3.3 --* AT5G56380.2)						5,583	6,694	10,431	10,150	9,699									
Solyc09g056220	LOW QUALITY:Cellulase (glycosyl hydrolase family 5) protein (AHRD V3.3 --* AT3G26140.2)						0,084	0,000	0,100	0,095	0,000									
Solyc09g056260	tRNA pseudouridine synthase (AHRD V3.3 *** K4CTC1_SOLLC)		P:GO:0001522; F:GO	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn		IPR020095 (G3DSA:3.30.70.GENE3D	10,366	11,828	12,643	13,668	13,629									
Solyc09g056270	Chlorophyllide a oxygenase, chloroplastic (AHRD V3.3 --* CAO_ARATH)	CAO	F:GO:0005488; F:GO	F:binding; F:oxidoreductase activity			5,420	4,490	4,929	5,354	4,809									
Solyc09g056310	LOW QUALITY:Maturase (AHRD V3.3 *-* O79414_SOLTU)		C:GO:0005739; P:GO	C:mitochondrion; P:mRNA processing		PTHR33642 (PANTHER); PTHR33642	0,000	0,000	0,025	0,000	0,000									
Solyc09g056340	Ras family (AHRD V3.3 *** A0A191UMR0_SOLDE)		F:GO:0003924; F:GO	F:GTPase activity;	EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS); G3DSA:3.40.50.3	35,353	39,146	88,083	122,075	99,418					0,473	0,023			up
Solyc09g056350	lipase class 3 family protein (AHRD V3.3 *** AT3G07400.1)		P:GO:0006629	P:lipid metabolic process		G3DSA:3.40.50.300 (GENE3D); IPR0	46,733	68,013	55,174	55,890	55,073									
Solyc09g056360	Auxin induced-like protein (AHRD V3.3 *** E0Z5V6_PICSI)		C:GO:0016021; P:GO	C:integral component of membrane; P:oxidation-reduction proce		IPR006593 (PFAM); IPR005018 (PFA	21,050	18,205	18,971	25,709	24,871									
Solyc09g056370	LOW QUALITY:Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 --* A		C:GO:0009507	C:chloroplast			3,761	6,280	2,643	7,350	7,383			1,480	0,011	1,480	0,019		up	up
Solyc09g056380	60S ribosomal protein L18a (AHRD V3.3 *** Q3HRW8_SOLTU)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		G3DSA:3.10.20.10 (GENE3D); IPR02	1,647	1,961	1,135	1,105	0,994									
Solyc09g056385	auxin-induced in root cultures-like protein (AHRD V3.3 *** AT3G07390.1)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane		IPR005018 (PFAM); IPR017214 (PIRS	4,904	8,335	2,165	1,385	1,734									
Solyc09g056395	Dynein heavy chain 2 (AHRD V3.3 --* A8J063_CHLRE)					mobidb-lite (MOBIDB_LITE)	0,137	0,146	0,000	0,000	0,024									
Solyc09g056430	Kinase family protein (AHRD V3.3 *** B9GQP3_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati		PIRSF000654 (PIRSF); IPR000719 (F	2,812	1,996	1,718	1,317	1,806									
Solyc09g056450	U-box domain-containing protein 9 (AHRD V3.3 *** W9RDX3_9ROSA)		F:GO:0004842; F:GO	F:ubiquitin-protein transferase activity; F:protein binding; P:prote		IPR011989 (G3DSA:1.25.10.GENE3D	164,494	61,181	82,475	237,636	133,726	-1,402	0,000	0,694	0,006	1,528	0,000	down	up	up
Solyc09g057500	LOW QUALITY:monofunctional riboflavin biosynthesis protein RIBA 3 (AHRD V3.3 --* AT5G59750.2)						0,061	0,000	0,000	0,000	0,000									
Solyc09g057510	LOW QUALITY:Homeobox leucine zipper protein (AHRD V3.3 *-* A0A072UAM9_MEDTR)		F:GO:0003677; C:GO	F:DNA binding; C:nucleus; F:lipid binding		PTHR24326 (PANTHER); PTHR24326	0,000	0,019	0,000	0,000	0,000									
Solyc09g057515	Zinc finger CCCH domain-containing protein 53 (AHRD V3.3 --* C3H53_ORYSJ)		F:GO:0046872	F:metal ion binding		mobidb-lite (MOBIDB_LITE); mobidb-lit	0,038	0,000	0,000	0,000	0,000									
Solyc09g057522	Cyclic nucleotide-regulated ion channel family protein (AHRD V3.3 --* AT5G15410.2)						0,113	0,060	0,000	0,025	0,000									
Solyc09g057580	UV-B-induced protein, chloroplastic (AHRD V3.3 *** A0A199VW76_ANACO)					IPR008479 (PFAM); PTHR31808:SF2	10,419	9,664	12,410	13,949	14,827									
Solyc09g057587	Cytochrome P450, putative (AHRD V3.3 *-* B9S4U5_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR036396 (G3DSA:1.10.630.GENE3	0,182	0,099	0,270	0,480	0,281									
Solyc09g057630	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** A0A072TYH8_MEDTR)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb		IPR000490 (PFAM); G3DSA:3.20.20.8	14,591	15,905	3,804	3,798	2,925									
Solyc09g057640	Cellulose synthase-like protein (AHRD V3.3 *** L0AUR7_POPTO)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity		PF13641 (PFAM); IPR029044 (G3DSA	29,660	27,441	21,321	22,424	21,628									
Solyc09g057650	40S ribosomal protein S8 (AHRD V3.3 *** K4CTF6_SOLLC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation		G3DSA:1.10.168.20 (GENE3D); IPR0	38,189	41,048	29,253	25,370	27,666									

Solyc09g057660	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NXQ5_ZOSMR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	75,876	62,539	44,666	41,909	44,705									
Solyc09g057670	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NV42_ZOSMR)		P:GO:0000413; F:GO	P:protein peptidyl-p EC:5.2.1.8 Peptidylprolyl isomer	IPR001179 (PFAM); G3DSA:3.10.50.4	101,413	91,511	102,644	96,275	89,790									
Solyc09g057680	Receptor-like kinase (AHRD V3.3 *** C0SW32_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	G3DSA:1.10.510.10 (GENE3D); IPR0	2,973	1,151	0,608	0,658	0,400									
Solyc09g057710	bHLH transcription factor 057	bHLH057	P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR036638 (G3DS bHLH	33,019	20,256	15,008	17,494	16,185	-0,678	0,009					down		
Solyc09g057760	LOW QUALITY:DUF506 family protein (AHRD V3.3 *-* G7LF52_MEDTR)				IPR006502 (TIGRFAM); IPR006502 (F	0,482	0,621	0,896	1,146	1,050									
Solyc09g057790	DNA-directed RNA polymerase subunit (AHRD V3.3 --* A0A1C7D1W4_9FABA)		P:GO:0000724; F:GO	P:double-strand break repair via homologous recombination; F:[	IPR037489 (PANTHER); PTHR34050:	4,294	4,830	6,277	5,392	6,164									
Solyc09g057830	LOW QUALITY:Maturase (AHRD V3.3 *-* Q4W4J1_9SOLA)		C:GO:0005739; P:GO	C:mitochondrion; P:mRNA processing	PTHR33642 (PANTHER); PTHR33642	0,000	0,000	0,000	0,022	0,000									
Solyc09g057870	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 *-* AT3G07500.1)		P:GO:0006355	P:regulation of transcription, DNA-templated	PTHR31669:SF46 FAR1	1,129	1,030	1,421	1,148	1,342									
Solyc09g057875	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 *-* AT3G07500.1)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR004330 (PFAM); mobidb-lite (MOB	4,851	4,580	4,130	4,687	4,139									
Solyc09g057880	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 *** AT2G43280.1)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR004330 (PFAM FAR1	4,632	3,728	5,666	6,649	6,200									
Solyc09g057887	ABC transporter G family member 34 (AHRD V3.3 --* AB34G_ORYSJ)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,120	0,036	0,025	0,000	0,000									
Solyc09g057900	evolutionarily conserved C-terminal region 4 (AHRD V3.3 --* AT1G55500.6)					0,019	0,133	0,047	0,067	0,023									
Solyc09g057903	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *-* A0A0K9NH83_ZOSMR)		F:GO:0016787; P:GO	F:hydrolase activity; P:phosphatidylinositol dephosphorylation		0,142	0,076	0,071	0,022	0,047									
Solyc09g057910	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G58450.2)		F:GO:0005515	F:protein binding	IPR019183 (PFAM); IPR011990 (G3D	9,652	8,688	10,439	11,464	10,347									
Solyc09g057920	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G58450.2)		F:GO:0016740	F:transferase activity	IPR019183 (PFAM); IPR019183 (PTH	11,582	11,570	12,015	10,699	12,267									
Solyc09g057940	Ribosomal protein L15 (AHRD V3.3 *** K4CTI3_SOLLC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR024794 (G3DSA:3.40.1120.GENE	0,000	0,021	0,050	0,000	0,000									
Solyc09g057950	Asparaginyl-tRNA synthetase family protein (AHRD V3.3 *** B9GQQ2_POPTR)		F:GO:0004816; F:GO	F:asparagine-tRNA EC:6.1.1.22 Asparagine--tRNA lig	IPR004364 (PFAM); IPR004522 (TIGF	0,244	0,354	0,094	0,092	0,094									
Solyc09g057960	Cysteine-rich RLK (Receptor-like kinase) protein (AHRD V3.3 *** G7KY09_MEDTR)				IPR038408 (G3DSA:3.30.430.GENE3I	0,000	0,000	0,025	0,000	0,000									
Solyc09g058960	LOW QUALITY:Uracil phosphoribosyltransferase, chloroplastic (AHRD V3.3 --* UPP_ARATH)					0,021	0,000	0,000	0,000	0,000									
Solyc09g058980	long-chain acyl-CoA synthetase 7 (AHRD V3.3 --* AT5G27600.1)					0,335	0,568	0,489	0,564	0,379									
Solyc09g058990	translocon at the outer envelope membrane of chloroplasts 159 (AHRD V3.3 --* AT4G02510.4)				mobidb-lite (MOBIDB_LITE); mobidb-lit	16,886	16,244	31,249	32,105	30,498									
Solyc09g058998	Quinone oxidoreductase (AHRD V3.3 --* H6VQ90_CAMSI)					0,103	0,000	0,000	0,000	0,000									
Solyc09g059020	Quinone-oxidoreductase QR1 (AHRD V3.3 *** Q9AYU1_TRIVS)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	G3DSA:3.90.180.10 (GENE3D); G3DS	0,293	0,243	0,075	0,000	0,048									
Solyc09g059030	Oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 *** A0A061DLX9_THECC)		P:GO:0055114	P:oxidation-reduction process	G3DSA:3.40.50.720 (GENE3D); G3DS	101,467	85,864	129,312	126,191	123,804									
Solyc09g059040	fructose 1,6-bisphosphate aldolase		P:GO:0055114	P:oxidation-reduction process	G3DSA:3.40.50.720 (GENE3D); G3DS	99,010	118,445	181,791	173,457	194,150									
Solyc09g059085	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_LEMMI)					0,021	0,220	0,000	0,119	0,259									
Solyc09g059125	CW14 protein (DUF1336) (AHRD V3.3 --* AT1G59650.1)					0,197	0,055	0,219	0,266	0,047									
Solyc09g059130	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		F:GO:0008270; F:GO	F:zinc ion binding; F:ligase activity; F:metal ion binding	IPR001841 (PFAM); IPR013083 (G3D	0,019	0,000	0,000	0,022	0,000									
Solyc09g059170	Glycosyltransferase (AHRD V3.3 *** M1C989_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); G3D	15,209	17,329	115,329	133,779	160,964			0,478	0,046				up	
Solyc09g059210	Class I heat shock protein (AHRD V3.3 *-* F4YBC5_SOLNI)	Hsp7.8	P:GO:0006457; P:GO	P:protein folding; P:response to heat; P:response to salt stress;	IPR002068 (PFAM); IPR008978 (G3D	1,154	0,714	1,239	0,782	0,984									
Solyc09g059220	LOW QUALITY:neuronal acetylcholine receptor subunit alpha-5 (AHRD V3.3 *** AT2G31490.1)		C:GO:0005747; P:GO	C:mitochondrial respiratory chain complex I; P:photorespiration;	PTHR35479 (PANTHER); PTHR35479	1,110	1,716	0,441	0,478	0,612									
Solyc09g059240	Cytochrome P450, putative (AHRD V3.3 *** B9SYM4_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS); IPR001128 (PF	0,562	0,203	0,098	0,099	0,187									
Solyc09g059250	global transcription factor group E4 (AHRD V3.3 --* AT1G06230.4)		F:GO:0016301; P:GO	F:kinase activity; P:phosphorylation	mobidb-lite (MOBIDB_LITE)	5,304	4,486	2,580	1,974	2,587									
Solyc09g059260	CBL-interacting protein kinase 3 (AHRD V3.3 --* AT2G26980.5)					13,495	9,755	6,388	5,795	6,181									
Solyc09g059270	ER lumen retaining receptor family-like protein (AHRD V3.3 *** Q38JH5_SOLTU)		P:GO:0006621; C:GO	P:protein retention in ER lumen; C:integral component of membr	IPR000133 (PRINTS); IPR000133 (PF	47,833	36,989	66,088	71,109	59,233									
Solyc09g059280	Histone H3 (AHRD V3.3 *** A0A078CWM8_BRANA)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS); IPR009072 (G3	4,950	3,819	3,006	3,306	3,223									
Solyc09g059285	methyl esterase 17 (AHRD V3.3 --* AT3G10870.1)					0,416	0,331	0,401	0,293	0,259									
Solyc09g059290	Chloroplast envelope membrane protein (AHRD V3.3 --* CEMA_JASNU)					0,395	0,215	0,176	0,094	0,165									
Solyc09g059300	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G19210.3)					2,135	1,303	1,620	1,955	1,365									
Solyc09g059310	Nuclear transport factor 2 family protein with RNA binding domain, putative isoform 2 (AHRD V3.3 *** A0A06		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM); G3DSA:3.10.450	62,284	63,907	62,141	57,555	60,864									
Solyc09g059340	serine/threonine protein kinase 2 (AHRD V3.3 --* AT3G08720.4)					0,466	0,352	0,487	0,529	0,351									
Solyc09g059345	Zinc finger, CW-type (AHRD V3.3 --* A0A103YNR4_CYNCS)		F:GO:0008270	F:zinc ion binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,202	0,116	0,072	0,261	0,117									
Solyc09g059380	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G34310.9)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,381	0,210	0,193	0,147	0,330									
Solyc09g059390	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT5G43930.3)				PTHR33233 (PANTHER)	0,615	0,331	0,314	0,383	0,589									
Solyc09g059400	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein (AHRD V3.3 --* AT5G12440		F:GO:0008270	F:zinc ion binding		0,925	2,842	2,270	3,109	3,584	1,629	0,001					up		
Solyc09g059430	RPM1-interacting protein 4 (AHRD V3.3 *** B9GQK9_POPTR)		C:GO:0005886; P:GO	C:plasma membrane; P:defense response signaling pathway, re	IPR008700 (PFAM); mobidb-lite (MOB	12,452	28,098	5,253	5,432	9,179	1,198	0,017	0,800	0,035			up	up	
Solyc09g059440	LOW QUALITY:Cell division control protein 45-like protein (AHRD V3.3 *** W9RYN1_9ROSA)		P:GO:0006270	P:DNA replication initiation	IPR003874 (PFAM); mobidb-lite (MOB	2,673	2,084	0,340	0,334	0,257									
Solyc09g059450	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DV39_THECC)		F:GO:0016874	F:ligase activity	mobidb-lite (MOBIDB_LITE); mobidb-lit	28,481	35,652	35,290	34,081	33,480									
Solyc09g059460	Vacuolar iron transporter (VIT) family protein (AHRD V3.3 *-* A0A061G9Q5_THECC)		C:GO:0016021	C:integral component of membrane	PTHR38937 (PANTHER); cd01059 (CI	1,052	1,747	0,143	0,146	0,374									
Solyc09g059470	Trypsin-like cysteine/serine peptidase domain-containing protein (AHRD V3.3 *** A0A103YNC2_CYNCS)				mobidb-lite (MOBIDB_LITE); mobidb-lit	7,802	2,252	1,260	2,483	4,224	-1,761	0,000	1,724	0,000			down	up	
Solyc09g059473	S-norcoclaurine synthase 1 (AHRD V3.3 *** A0A061FEF4_THECC)		P:GO:0006952	P:defense response	IPR023393 (G3DSA:3.30.530.GENE3I	5,438	3,071	1,460	1,982	2,505									
Solyc09g059500	Forkhead-associated (FHA) domain-containing protein (AHRD V3.3 *** A0A103Y779_CYNCS)		F:GO:0005515	F:protein binding	IPR000253 (PFAM); G3DSA:2.60.200	30,962	31,778	39,289	35,341	34,405									
Solyc09g059510	Ethylene-responsive transcription factor-like protein (AHRD V3.3 *** W9RYM6_9ROSA)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR036955 (G3DS ERF	8,683	10,805	6,428	7,039	6,982									
Solyc09g059520	SolycHsfA8	HSF-16	F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	42,909	63,529	26,629	27,620	29,512									
Solyc09g059550	acidic leucine-rich nuclear phosphoprotein 32 family B protein (AHRD V3.3 *** AT3G25130.1)		C:GO:0016021	C:integral component of membrane	PTHR36760 (PANTHER)	0,297	0,372	0,261	0,119	0,141									
Solyc09g059570	B-cell receptor-associated protein 31-like (AHRD V3.3 *** A0A061DME9_THECC)		C:GO:0005783; P:GO	C:endoplasmic reticulum; P:intracellular protein transport; C:inte	PTHR12701:SF13 (PANTHER); IPR00	7,088	7,507	6,687	5,134	4,922									
Solyc09g059580	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GQK7_POPTR)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,811	1,848	1,395	1,204	1,602									
Solyc09g059583	GPI transamidase component PIG-S-like protein (AHRD V3.3 *-* AT3G07180.2)		P:GO:0016255; C:GO	P:attachment of GPI anchor to protein; C:GPI-anchor transamid	IPR019540 (PFAM); IPR025558 (PFA	21,501	19,814	26,681	25,567	23,795									
Solyc09g059600	GPI transamidase component PIG-S (AHRD V3.3 *** A0A0B2PTJ3_GLYSO)		P:GO:0016255; C:GO	P:attachment of GPI anchor to protein; C:GPI-anchor transamid	IPR019540 (PFAM); IPR019540 (PAN	12,092	12,015	15,952	17,675	16,381									
Solyc09g059610	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* L7TPF9_9POAL)		F:GO:0003899; P:GO	F:DNA-directed 5'-3' RNA polymerase activity; P:RNA biosynthe	IPR010800 (PFAM); mobidb-lite (MOB	8,187	6,229	0,046	0,111	0,743									
Solyc09g059620	Sterile alpha motif domain-containing protein (AHRD V3.3 *-* A0A118K250_CYNCS)		F:GO:0005515	F:protein binding	IPR001660 (PFAM); G3DSA:1.10.150	6,012	7,189	6,073	6,115	5,861									
Solyc09g059625	Sterile alpha motif domain-containing protein (AHRD V3.3 *** A0A118K250_CYNCS)		F:GO:0004620	F:phospholipase activity	mobidb-lite (MOBIDB_LITE); mobidb-lit	23,313	25,648	22,945	22,298	22,023									
Solyc09g059630	Ubiquitin-associated domain-containing family protein (AHRD V3.3 *** B9GQK2_POPTR)		F:GO:0005515	F:protein binding	IPR018997 (PFAM); IPR015940 (PFA	1,231	1,260	0,510	0,193	0,471									
Solyc09g059640	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLLC)		C:GO:0009522; P:GO	C:photosystem I; P:photosynthesis; C:integral component of me	IPR001280 (PRINTS); IPR001280 (PF	0,042	0,190	0,125	0,347	0,117									
Solyc09g059650	Vacuolar iron transporter family protein (AHRD V3.3 --* A0A061DZC1_THECC)					6,759	5,627	6,661	7,519	6,112									
Solyc09g059670	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT5G14210.2)					2,555	2,277	1,283	1,579	1,417									
Solyc09g059675	alpha/beta hydrolase family protein (AHRD V3.3 *** AT1G15060.2)		F:GO:0016298; P:GO	F:lipase activity; P:cellular lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	8,201	6,903	5,168	4,515	5,485									
Solyc09g059710	Ribose-5-phosphate isomerase, putative (AHRD V3.3 *-* B9REQ4_RICCO)		F:GO:0004751; P:GO	F:ribose-5-phospha EC:5.3.1.6 Ribose-5-phosphate	G3DSA:3.40.50.1360 (GENE3D); G3D	0,080	0,181	0,025	0,096	0,118									
Solyc09g059720	Ribose 5-phosphate isomerase-related family protein (AHRD V3.3 *-* U5GAQ0_POPTR)		F:GO:0004751; P:GO	F:ribose-5-phospha EC:5.3.1.6 Ribose-5-phosphate	G3DSA:3.40.50.1360 (GENE3D); PTH	0,000	0,103	0,000	0,022	0,094									
Solyc09g059738	Reverse transcriptase (AHRD V3.3 *-* Q56GG4_CYCRE)		F:GO:0003676; C:GO	F:nucleic acid binding; C:nucleus; P:DNA integration	G3DSA:3.10.10.10 (GENE3D); IPR04	0,000	0,018	0,000	0,000	0,000									
Solyc09g059740	LOW QUALITY:Protein OBERON 1-like protein (AHRD V3.3 *-* A0A0B0NZZ1_GOSAR)				IPR032881 (PFAM); PTHR33345:SF2	0,000	0,039	0,000	0,000	0,000									
Solyc09g059830	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)		F:GO:0005515; F:GO	F:protein binding; F:ADP binding	PR00364 (PRINTS); IPR002182 (PFA	0,000	0,000	0,000	0,000	0,023									
Solyc09g059910	LOW QUALITY:Protein OBERON 1-like protein (AHRD V3.3 *-* A0A0B0NZZ1_GOSAR)				IPR032881 (PFAM); PTHR33345:SF2	0,000	0,021	0,000	0,000	0,000									
Solyc09g059950	Amino acid--[acyl-carrier-protein] ligase (AHRD V3.3 *** A0A0B0MIR3_GOSAR)				PTHR39104 (PANTHER)	0,679	0,676	3,389	2,636	2,053									
Solyc09g059960	GPI transamidase component Gpi16 subunit family protein (AHRD V3.3 *** AT3G07140.1)		P:GO:0016255; C:GO	P:attachment of GPI anchor to protein; C:GPI-anchor transamid	IPR007245 (PFAM); IPR007245 (PAN	3,233	2,862	4,439	4,185	4,068									
Solyc09g059970	Small ubiquitin-related modifier (AHRD V3.3 *** Q9SMD1_SOLLC)		F:GO:0005515; P:GO	F:protein binding; P:protein sumoylation	G3DSA:3.10.20.90 (GENE3D); IPR02	36,072	31,285	27,020	21,261	22,323									
Solyc09g059990	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** AT3G25030.4)		F:GO:0016874	F:ligase activity	PF13920 (PFAM); IPR013083 (G3DSA	3,168	2,678	0,486	0,693	0,985									
Solyc09g060000	Histone-lysine N-methyltransferase (AHRD V3.3 *-* A0A0K9P7Y1_ZOSMR)		F:GO:0005515	F:protein binding	G3DSA:2.170.270.10 (GENE3D); IPR(	0,000	0,021	0,000	0,000	0,000									
Solyc09g060040	LOW QUALITY:PIF1-like helicase (AHRD V3.3 *-* G7KNG1_MEDTR)		P:GO:0000723; F:GO	P:telomere mainten EC:3.6.1.15 Nucleoside-triphosph	PTHR44114 (PANTHER); PTHR44114	0,019	0,037	0,000	0,000	0,047									
Solyc09g060050	LOW QUALITY:Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (AHRD V3.3 --* AT1(		P:GO:0006259; F:GO	P:DNA metabolic process; F:hydrolase activity	PTHR10492:SF21 (PANTHER); PTHR	0,139	0,021	0,144	0,075	0,069									
Solyc09g060070	RAP release 2, galactose-binding-like domain protein, putative (DUF1997) (AHRD V3.3 --* AT5G04440.2)					0,115	0,064	0,022	0,119	0,046									
Solyc09g060080	Helicase/SANT-associated, DNA binding protein (AHRD V3.3 *** AT3G24880.3)				IPR014012 (PFAM); mobidb-lite (MOB	50,187	43,122	51,480	53,549	55,325									
Solyc09g060090	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** A0A061DNB3_THECC)				PR00180 (PRINTS); G3DSA:1.10.8.20	24,310	19,548	12,343	10,348	10,965									
Solyc09g060100	transmembrane protein (AHRD V3.3 *** AT4G13150.1)		C:GO:0016021	C:integral component of membrane	IPR032816 (PFAM); PTHR30353:SF0	1,260	1,601	1,092	1,726	1,718									
Solyc09g060110	Kinase, putative (AHRD V3.3 *** B9S521_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D); IPR0(	0,144	0,021	0,025	0,025	0,023									
Solyc09g060120	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* A0A061E701_THECC)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3I	0,019	0,000	0,000	0,000	0,024									
Solyc09g060150	Homeobox leucine zipper protein (AHRD V3.3 *-* A0A072UAM9_MEDTR)		F:GO:0008289	F:lipid binding	IPR002913 (PFAM); mobidb-lite (MOB	0,000	0,000	0,000	0,000	0,024									
Solyc09g060160	Homeobox leucine zipper protein (AHRD V3.3 *-* G7IKH9_MEDTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(HB-other	0,000	0,000	0,000	0,000	0,023									
Solyc09g060180	Zinc finger CCCH domain-containing protein (AHRD V3.3 --* A0A0K9NPI2_ZOSMR)		F:GO:0046872	F:metal ion binding	IPR000571 (PFAM)	0,040	0,000	0,000	0,025	0,000									
Solyc09g060187	LOW QUALITY:BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THE		F:GO:0003677	F:DNA binding	IPR025525 (PFAM); PTHR23272 (PAI	1,712	1,630	0,775	0,912	1,175									
Solyc09g061230	Cytochrome b5 (AHRD V3.3 *** CYB5_TOBAC)		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:integral component of me	IPR001199 (PRINTS); IPR001199 (PF	24,627	26,325	23,533	20,132	22,110									
Solyc09g061250	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** A0A061DNC1_THECC)		F:GO:0005515	F:protein binding	G3DSA:3.30.710.10 (GENE3D); IPR0(	0,763	0,584	0,075	0,075	0,281									
Solyc09g061260	LOW QUALITY:Protein OBERON 1-like protein (AHRD V3.3 *** A0A0B0NZZ1_GOSAR)				IPR032881 (PFAM); PTHR33345 (PAI	1,856	1,661	2,580	0,521	1,827					-2,253	0,000			down
Solyc09g061270	BSD domain-containing protein (AHRD V3.3 *** AT3G24820.1)				IPR005607 (PFAM); PTHR31923:SF3	8,241	8,342	9,565	11,452	10,151									
Solyc09g061280	p27KIP1-related-protein 2	krp2	F:GO:0004861; C:GO	F:cyclin-dependent protein serine/threonine kinase inhibitor acti	IPR003175 (PFAM); G3DSA:4.10.365	2,170	6,114	4,557	6,070	7,920	1,515	0,008	0,793	0,035			up	up	
Solyc09g061290	Transcriptional corepressor LEUNIG (AHRD V3.3 *** W9S398_9ROSA)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3I	115,355	106,514	135,614	117,326	120,956									
Solyc09g061310	PPPDE putative thiol peptidase family protein (AHRD V3.3 *** AT3G07090.2)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm	G3DSA:3.90.1720.30 (GENE3D); IPR(	47,917	47,834	92,097	105,939	86,329									
Solyc09g061320	Solute carrier family 35 protein (AHRD V3.3 *** G7L198_MEDTR)		C:GO:0016021; F:GO	C:integral component of membrane; F:transmembrane transport	IPR009262 (PFAM); PTHR23051 (PAI	20,705	17,086	10,738	14,610	17,063			0,665	0,003				up	
Solyc09g061330	Kinase family protein (AHRD V3.3 *** D7L628_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); G3DSA:1.10.510	0,080	0,078	0,000	0,050	0,047									
Solyc09g061340	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199VVG3_ANACO)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR002885 (F	10,643	10,322	10,234	9,135	10,011									
Solyc09g061380	NHL repeat-containing protein 2 (AHRD V3.3 *** W9S395_9ROSA)		F:GO:0005515	F:protein binding	IPR001258 (PFAM); IPR011042 (G3D	19,416	20,100	23,493	22,404	22,032									
Solyc09g061390	LOW QUALITY:Maturase K (AHRD V3.3 *-* MATK_SOLLC)		P:GO:0006397; C:GO	P:mRNA processing; C:chloroplast	IPR024942 (PFAM); IPR002866 (PAN	0,040	0,149	0,025	0,126	0,094									
Solyc09g061410	LOW QUALITY:CLAVATA3/ESR (CLE)-related protein TDIF (AHRD V3.3 *** TDIF_ZINVI)		P:GO:0010089; F:GO	P:xylem development; F:receptor serine/threonine kinase bindin	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,228	2,118	1,213	1,949	1,368									
Solyc09g061420	phosphoglycolate phosphatase (AHRD V3.3 *** AT5G48830.1)				IPR022552 (PFAM); PTHR36807 (PAI	9,783	9,770	8,809	9,713	10,643									
Solyc09g061430	nuclear GTPase DQ304482		F:GO:0005525	F:GTP binding	IPR006073 (PRINTS); IPR006073 (PF	0,078	0,041	0,025	0,163	0,119									
Solyc09g061440	Ubiquitin-conjugating enzyme E2 I (AHRD V3.3 --* B6U359_MAIZE)		C:GO:0009535; C:GO	C:chloroplast thylakoid membrane; C:plastoglobule	mobidb-lite (MOBIDB_LITE); mobidb-lit	7,011	9,298	16,372	15,998	16,307									
Solyc09g061450	LOW QUALITY:30S ribosomal protein S7, chloroplastic (AHRD V3.3 *-* RR7_TOBAC)		P:GO:0006412	P:translation	IPR000235 (PIRSF); IPR023798 (PFA	2,208	3,602	1,816	2,610	2,286									
Solyc09g061460	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *** A0A0X8IHH4_9GENT)		C:GO:0005886; F:GO	C:plasma membran EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001750 (PFAM); PTHR45564 (PAI	0,120	0,466	0,315	0,393	0,377									
Solyc09g061620	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9S543_RICCO)		C:GO:0016021; P:GO	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS); G3DSA:1.20.5.	125,149	130,550	90,920	108,753	95,169									
Solyc09g061650	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151R878_CAJCA)				IPR019557 (PFAM); PTHR16007:SF4	0,021	0,057	0,225	0,000	0,023									
Solyc09g061660	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151TBK9_CAJCA)				IPR019557 (PFAM); PTHR44194 (PAI	0,021	0,076	0,025	0,000	0,000									
Solyc09g061680	Pantoate--beta-alanine ligase (AHRD V3.3 *** A0A0B0PQU6_GOSAR)		F:GO:0004592; P:GO	F:pantoate-beta-ala EC:6.3.2.1 Pantoate--beta-alanii	G3DSA:3.30.1300.10 (GENE3D); IPR(	34,185	31,100	32,672	28,209	30,484									
Solyc09g061690	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151S601_CAJCA)		F:GO:0004721; F:GO	F:phosphoprotein phosphatase activity; F:protein serine/threoni	IPR019557 (PFAM); mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc09g061700	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G48850.1)		F:GO:0005515	F:protein binding	IPR019734 (PFAM); IPR011990 (G3D	1,072	0,470	0,563	0,365	0,474									
Solyc09g061710	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT3G07030.5)		F:GO:0003676	F:nucleic acid binding	IPR036882 (G3DSA:3.30.110.GENE3I	33,397	33,971	42,408	36,221	37,374									
Solyc09g061730	Late embryogenesis abundant protein 1 (AHRD V3.3 --* LEA1_ORYSI)				PTHR36038 (PANTHER)	0,233	0,121	0,044	0,045	0,023									
Solyc09g061750	Cellulose synthase 2 (AHRD V3.3 *** A0A0B0N012_GOSAR)				IPR012866 (PFAM); mobidb-lite (MOB	34,726	35,436	56,083	55,085	53,735									
Solyc09g061760	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061DKY9_THECC)		F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR011990 (G3D	1,339	1,646	1,684	2,078	1,910									
Solyc09g061790	LOW QUALITY:Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* A0A061DKY9_THECC		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,099	1,325	1,088	0,802	0,752									
Solyc09g061793	Cytochrome P450 (AHRD V3.3 *-* A0A103Y530_CYNCS)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS); IPR001128 (PF	3,181	3,025	10,261	11,260	11,236									
Solyc09g061820	Beta-galactosidase (AHRD V3.3 *-* K4B416_SOLLC)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PANTHER); PTHR23421:	0,000	0,000	0,000	0,022	0,000									
Solyc09g061825	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT2G35130.3)					0,986	0,532	0,596	1,010	0,944									
Solyc09g061827	F-box associated interaction domain-containing protein (AHRD V3.3 *-* A0A103XHT5_CYNCS)					0,448	0,193	0,246	0,211	0,189									
Solyc09g061830	LOW QUALITY:Short chain dehydrogenase/reductase family protein (AHRD V3.3 --* C1E7Z3_MICCC)					0,139	0,059	0,000	0,100	0,141									
Solyc09g061840	3-ketoacyl-CoA thiolase (AHRD V3.3 *** P93112_9ROSI)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc	IPR020616 (PFAM); IPR002155 (TIGF	42,384	125,277	25,386	21,356	32,286	1,586	0,001					up		
Solyc09g061860	UDP-glucose:sterol 3-O-glucosyltransferase (AHRD V3.3 *** Q8H9B4_PANGI)		P:GO:0005975; F:GO	P:carbohydrate metabolic process; F:transferase activity, trans	IPR004276 (PFAM); IPR002213 (PFA	16,363	13,542	13,442	10,250	12,038									
Solyc09g061880	LOW QUALITY:Wall-associated kinase family protein (AHRD V3.3 --* AT1G69730.1)					0,175	0,161	0,050	0,405	0,165									
Solyc09g061890	Pectate lyase (AHRD V3.3 *** M1BAL5_SOLTU)		F:GO:0030570; P:GO	F:pectate lyase act EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS); IPR002022 (PF	16,126	26,360	2,977	1,507	2,607									
Solyc09g061910	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 --* AT1G20080.5)				PTHR38365 (PANTHER); SSF49562 (	0,000	0,019	0,000	0,000	0,000									
Solyc09g061930	Ovary receptor kinase 7 (AHRD V3.3 *** S4WHD2_SOLCH)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001245 (PFAM); IPR001611 (PFA	14,415	14,332	5,168	9,996	7,252					0,955	0,000			up
Solyc09g061940	Receptor protein kinase (AHRD V3.3 *** Q9FEU2_PINSY)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS); IPR032675 (G3D	0,038	0,128	0,000	0,000	0,000									
Solyc09g061950	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *-* AT4G36590.1)		F:GO:0003677; F:GO	F:DNA binding; F:protein dimerization activity	IPR002100 (PRIN M-type_MADS	0,000	0,043	0,000	0,000	0,000									
Solyc09g061960	Late embryogenesis abundant protein family protein, putative (AHRD V3.3 *** A0A061EZ48_THECC)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,037	0,000	0,000	0,000	0,000									
Solyc09g062970	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT3G53100.1)					0,171	0,253	0,000	0,000	0,023									
Solyc09g063010	bHLH transcription factor 058	PIF1a	P:GO:0006355	P:regulation of transcription, DNA-templated	mobidb-lite (MOBII bHLH	5,292	3,416	7,668	8,102	9,041									
Solyc09g063015	Transcription factor PIF1-like protein (AHRD V3.3 *-* A0A0B0P1J2_GOSAR)		C:GO:0005634; P:GO	C:nucleus; P:regulation of transcription, DNA-templated; F:prote	mobidb-lite (MOBIDB_LITE); mobidb-lit	9,525	6,809	12,858	14,111	13,324									
Solyc09g063020	Integral membrane HRF1 family protein (AHRD V3.3 *** AT1G30890.2)		C:GO:0005789; C:GO	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G	IPR005578 (PFAM); IPR005578 (PAN	8,434	8,147	9,902	9,974	9,307									
Solyc09g063025	nucleolar pre-ribosomal-associated protein (AHRD V3.3 --* AT1G72270.1)					0,079	0,043	0,000	0,150	0,095									
Solyc09g063030	CLIP-associating family protein (AHRD V3.3 *** B9GR98_POPTR)		F:GO:0005515	F:protein binding	IPR011989 (G3DSA:1.25.10.GENE3D	156,794	116,025	105,715	106,747	107,475									
Solyc09g063060	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RSX5_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	5,326	3,828	0,025	0,000	0,000									
Solyc09g063070	Tetraspanin family protein, putative (AHRD V3.3 *** A0A061DNH5_THECC)		C:GO:0016021	C:integral component of membrane	IPR018499 (PFAM); PTHR19282:SF2	23,155	20,533	10,553	7,981	9,352									

Solyc09g063130	Photosystem I reaction center subunit IV (AHRD V3.3 *** A0A0K9P6J8_ZOSMR)		C:GO:0009538: P:G(	C:photosystem I reaction center; P:photosynthesis			G3DSA:2.30.30.50 (GENE3D): IPR00	30,741	85,293	10,914	20,101	39,469	1,499	0,000	1,847	0,000	0,882	0,000	up	up	up
Solyc09g063140	Protein LOW PSII ACCUMULATION 1, chloroplastic (AHRD V3.3 *** A0A199UH97_ANACO)		C:GO:0016021	C:integral component of membrane			IPR021883 (PFAM): PTHR35498 (PAI	0,019	0,039	0,000	0,025	0,024									
Solyc09g063150	Glutathione s-transferase, putative (AHRD V3.3 *** B9SH83_RICCO)	GSTU46	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	5,839	8,791	3,746	4,061	5,166									
Solyc09g064160	Flavin-containing monooxygenase (AHRD V3.3 *** K4CU47_SOLLC)		F:GO:0004499: F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.'	Flavin-containing mo	PR00469 (PRINTS): PR00368 (PRINT	0,101	0,142	0,000	0,025	0,024									
Solyc09g064200	Myosin (AHRD V3.3 *** W5ZTD6_MAIZE)		F:GO:0003774: F:G(	F:motor activity; F:(	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): IPR004009 (PF	137,654	236,416	137,118	136,982	129,257	0,805	0,023					up		
Solyc09g064230	C2 domain-containing family protein (AHRD V3.3 *** B9GRA8_POPTR)		C:GO:0016021	C:integral component of membrane			IPR035892 (G3DSA:2.60.40.GENE3D	0,131	0,176	0,022	0,000	0,024									
Solyc09g064240	pfkB-like carbohydrate kinase family protein (AHRD V3.3 *** AT4G28706.3)		F:GO:0016301	F:kinase activity			IPR002139 (PRINTS): IPR011611 (PF	26,286	31,680	26,221	22,856	27,882									
Solyc09g064270	Kinase family protein (AHRD V3.3 *** B9IBD6_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	24,088	28,691	12,905	9,968	14,031									
Solyc09g064277	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** A0A072UYX1_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,058	0,039	0,000	0,000	0,024									
Solyc09g064310	WD-repeat protein, putative (AHRD V3.3 *** B9T5V7_RICCO)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	4,069	4,084	3,742	3,473	2,939									
Solyc09g064320	Transducin/WD40 repeat protein (AHRD V3.3 *** A0A072VM11_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	3,507	3,160	3,253	2,695	3,466									
Solyc09g064330	RmlC-like cupins superfamily protein (AHRD V3.3 *** A0A061DW96_THECC)						IPR014710 (G3DSA:2.60.120.GENE3I	0,058	0,043	0,072	0,123	0,095									
Solyc09g064370	Alcohol dehydrogenase (AHRD V3.3 *** ADH_FRAAN)	GSNOR	P:GO:0006069: F:G(	P:ethanol oxidation;	EC:1.1.1.284	S-(hydroxymethyl)glu	G3DSA:3.40.50.720 (GENE3D): G3DS	506,532	460,658	667,164	526,243	653,803									
Solyc09g064380	Tetratricopeptide repeat-containing family protein (AHRD V3.3 *** B9GRB6_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	23,442	13,949	32,048	29,170	30,700	-0,721	0,007					down		
Solyc09g064410	50S ribosomal protein L33, chloroplastic (AHRD V3.3 *** RK33_SOLTU)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001705 (TIGRFAM): IPR038584 ((	0,163	0,292	0,050	0,272	0,165									
Solyc09g064420	28 kDa ribonucleoprotein, chloroplastic (AHRD V3.3 *-* M7YFE5_TRIUA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,498	13,491	23,618	21,248	22,953									
Solyc09g064430	Tyrosine decarboxylase family protein (AHRD V3.3 *** B9GRB9_POPTR)		P:GO:0006520: F:G(	P:cellular amino acid metabolic process; F:carboxy-lyase activit			IPR010977 (PRINTS): G3DSA:1.20.13	18,974	19,521	29,634	31,121	31,083									
Solyc09g064440	ABC transporter family protein (AHRD V3.3 *** A0A097P9R4_HEVBR)	ABCC8	F:GO:0005524: C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	59,755	52,326	61,832	58,476	57,099									
Solyc09g064450	NAD(P)-binding Rossmann-fold superfamily protein		F:GO:0003954: C:G(	F:NADH dehydroge	EC:1.6.99.3	NADH dehydrogenas	G3DSA:3.40.50.720 (GENE3D): IPR0	112,415	102,809	173,738	177,034	166,432									
Solyc09g064470	Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *** W9QX13_9ROSA)		P:GO:0006486: F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): mobidb-lite (MOB	62,856	64,936	13,916	7,523	14,575									
Solyc09g064480	Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *-* A0A0B2SXE6_GLYSO)		P:GO:0006486: F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): mobidb-lite (MOB	29,212	30,517	6,674	2,859	5,607					-1,221	0,002			down
Solyc09g064490	Subtilisin-like protease SDD1 (AHRD V3.3 *** W9RB94_9ROSA)		F:GO:0004252: P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bo	IPR015500 (PRINTS): IPR041469 (PF	0,292	0,235	0,022	0,000	0,023									
Solyc09g064500	Photosystem II reaction center Psb28 protein (AHRD V3.3 *** K4CU78_SOLLC)		C:GO:0009654: P:G(	C:photosystem II oxygen evolving complex; P:photosynthesis			IPR038676 (G3DSA:2.40.30.GENE3D	12,370	28,069	8,995	13,134	26,948	1,209	0,000	1,577	0,000			up	up	
Solyc09g064510	heme oxygenase-like, multi-helical (AHRD V3.3 *** AT5G32470.1)		C:GO:0005829: F:G(	C:cytosol; F:hydrolase activity			IPR023214 (G3DSA:3.40.50.GENE3D	25,168	28,293	7,505	15,227	14,946			0,988	0,001	1,018	0,001		up	up
Solyc09g064520	Receptor protein kinase CLAVATA1, putative (AHRD V3.3 *** B9TAC6_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	8,273	5,128	3,348	4,602	5,592			0,732	0,031				up	
Solyc09g064530	auxin-regulated IAA12	IAA12	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	21,633	21,652	12,013	9,847	12,051									
Solyc09g064540	vacuolar sorting-associated protein (DUF946) (AHRD V3.3 *** AT1G04090.1)						IPR009291 (PFAM): PTHR42656:SF3	18,253	15,571	18,073	18,944	19,624									
Solyc09g064580	photosystem II reaction center protein M (AHRD V3.3 *** ATCG00220.1)		C:GO:0009523: C:G(	C:photosystem II; C:integral component of membrane; P:photos			IPR007826 (PFAM): IPR007826 (TIGF	0,040	0,085	0,075	0,047	0,023									
Solyc09g064590	Pre-mRNA-processing factor 39 (AHRD V3.3 *** A0A0B2P4C7_GLYSO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	116,565	100,283	113,301	116,614	115,169									
Solyc09g064600	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** A0A072TFP7_MEDTR)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	4,369	3,777	3,561	3,823	3,845									
Solyc09g064610	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFAI	12,229	12,197	10,931	10,769	10,667									
Solyc09g064620	sigma factor E (AHRD V3.3 --* AT5G24120.3)							0,040	0,000	0,025	0,000	0,000									
Solyc09g064630	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT4G17940.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	26,562	35,826	7,552	5,782	10,058									
Solyc09g064640	LOW QUALITY:Cold acclimation protein WCOR518, related (AHRD V3.3 *-* Q6L3L4_SOLDE)		C:GO:0005576: C:G(	C:extracellular region; C:vesicle; P:regulation of double fertilizat			IPR008502 (PFAM): mobidb-lite (MOB	0,000	0,000	0,000	0,000	0,023									
Solyc09g064660	Small nuclear ribonucleoprotein Sm D1 (AHRD V3.3 *** A0A1D1XRZ8_9ARAE)		P:GO:0000387	P:spliceosomal snRNP assembly			IPR001163 (PFAM): G3DSA:2.30.30.1	66,915	66,261	40,997	38,596	41,065									
Solyc09g064720	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9SFP3_RICCO)		F:GO:0016787	F:hydrolase activity			IPR002925 (PFAM): IPR029058 (G3D	69,423	69,681	243,693	292,111	239,707									
Solyc09g064730	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT3G06130.1)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	0,000	0,000	11,865	13,628	6,969									
Solyc09g064740	RNA exonuclease-like protein (AHRD V3.3 *** B7FI33_MEDTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.60 (GENE3D): IPR03	1,189	1,598	1,668	2,003	2,119									
Solyc09g064750	root hair specific 16 (AHRD V3.3 --* AT4G29180.3)						PTHR37908 (PANTHER)	0,019	0,000	0,000	0,000	0,000									
Solyc09g064770	LOW QUALITY:WD40 repeat-like protein (AHRD V3.3 *-* I0YVP9_COCSC)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	0,000	0,000	0,025	0,025	0,000									
Solyc09g064775	LOW QUALITY:BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THE		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): mobidb-lite (MOB	0,042	0,021	0,000	0,025	0,047									
Solyc09g064780	Mediator of RNA polymerase II transcription subunit 33A (AHRD V3.3 *** G7IKE7_MEDTR)		C:GO:0016592: P:G(	C:mediator complex; P:regulation of phenylpropanoid metabolic			PTHR33739:SF7 (PANTHER): IPR039	28,146	69,016	23,494	26,533	29,698	1,317	0,006					up		
Solyc09g064790	pale cress protein (PAC) (AHRD V3.3 *** AT2G48120.1)		C:GO:0009536: P:G(	C:plastid; P:chloroplast organization; P:chloroplast mRNA proce			IPR034563 (PANTHER)	25,868	24,891	27,919	28,025	31,829									
Solyc09g064800	Isoamylase isoform 2 (AHRD V3.3 *** Q84YG6_SOLTU)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR004193 (PFAM): IPR013780 (G3D	20,011	18,238	29,079	26,118	26,027									
Solyc09g064810	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G02900.4)		C:GO:0016020	C:membrane			IPR003864 (PFAM): IPR032880 (PFAI	0,851	0,828	0,044	0,193	0,117									
Solyc09g064820	EID1-like F-box protein 2 (AHRD V3.3 *** A0A0B2NUB4_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,487	2,255	1,394	1,876	1,791									
Solyc09g064840	Tudor/PWWP/MBT domain-containing protein (AHRD V3.3 *-* AT3G63070.1)						IPR008942 (G3DSA:1.25.40.GENE3D	63,122	62,195	56,439	55,299	55,607									
Solyc09g064850	Glutathione peroxidase (AHRD V3.3 *** K4CUB2_SOLLC)	GPX	F:GO:0004602: P:G(	F:glutathione peroxi	EC:1.11.1.9; EC:1.1	Glutathione peroxida	IPR000889 (PRINTS): IPR000889 (PF	12,632	11,819	14,237	14,398	11,994									
Solyc09g064860	ELKS/Rab6-interacting/CAST family protein (AHRD V3.3 *-* AT4G02880.2)		F:GO:0005515	F:protein binding			mobidb-lite (MOBIDB_LITE): PTHR162	122,763	97,953	136,205	125,017	125,565									
Solyc09g064870	DUF21 domain-containing-like protein (AHRD V3.3 *** A0A0B0P4N8_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM): mobidb-lite (MOB	3,838	6,119	0,707	1,033	0,982									
Solyc09g064880	LOW QUALITY:Protein argonaute (AHRD V3.3 *-* A0A151T3S6_CAJCA)		F:GO:0003676: P:G(	F:nucleic acid binding; P:gene silencing by RNA			G3DSA:3.40.50.2300 (GENE3D): PTH	0,000	0,000	0,000	0,000	0,023									
Solyc09g064890	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT3G63095.1)						mobidb-lite (MOBIDB_LITE): PTHR343	13,506	11,426	12,788	12,006	11,289									
Solyc09g064910	Adenylate isopentenyltransferase (AHRD V3.3 *** I0IUP8_SOLLC)		P:GO:0008033	P:tRNA processing			G3DSA:3.40.50.300 (GENE3D): G3DS	0,081	0,057	0,211	0,000	0,024									
Solyc09g064920	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G03040.2)		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	9,575	10,147	9,043	9,012	7,948									
Solyc09g064930	R3H domain protein (AHRD V3.3 *** AT1G03250.1)		F:GO:0003676	F:nucleic acid binding			IPR025952 (PFAM): IPR036867 (G3D	44,436	41,416	74,823	73,678	72,336									
Solyc09g064940	Phenazine biosynthesis PhzC/PhzF family protein (AHRD V3.3 *** B9HYD6_POPTR)		F:GO:0003824: P:G(	F:catalytic activity; P:biosynthetic process			G3DSA:3.10.310.10 (GENE3D): G3DS	74,652	106,002	344,886	321,004	287,849									
Solyc09g065000	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061DRU5_THECC)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bo	IPR032861 (PFAM): IPR021109 (G3D	3,909	6,000	8,290	11,120	9,327									
Solyc09g065010	mRNA capping enzyme family protein (AHRD V3.3 *-* AT3G09100.2)		F:GO:0004484: P:G(	F:mRNA guanylyltra	EC:2.7.7.5	mRNA guanylyltransf	G3DSA:2.40.50.140 (GENE3D): IPR0(	8,822	9,969	13,278	13,969	13,964									
Solyc09g065015	mRNA capping enzyme family protein (AHRD V3.3 *-* AT3G09100.1)		F:GO:0004484: F:G(	F:mRNA guanylyltra	EC:2.7.7.5; EC:3.1.3	mRNA guanylyltransf	IPR029021 (G3DSA:3.90.190.GENE3I	5,149	4,659	6,180	8,044	7,023									
Solyc09g065020	F-box family protein (AHRD V3.3 *** A0A061DRU1_THECC)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): PTH	5,615	4,611	18,840	18,506	16,174									
Solyc09g065030	TRICHOME BIREFRINGENCE-LIKE 11 (AHRD V3.3 *** AT5G19160.1)		C:GO:0005794: C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFAI	6,344	5,135	6,517	6,050	7,976									
Solyc09g065070	Aluminum activated malate transporter family protein, putative (AHRD V3.3 *** A0A061DXR0_THECC)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): PTHR31086:SF1	0,328	0,185	0,414	0,000	0,117									
Solyc09g065080	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT2G18510.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,096	0,039	0,000	0,000	0,000									
Solyc09g065090	Cleavage stimulation factor subunit 2 (AHRD V3.3 *-* A0A1D1XLU8_9ARAE)		P:GO:0031124	P:mRNA 3'-end processing			IPR038192 (G3DSA:1.10.20.GENE3D	0,040	0,144	0,000	0,025	0,000									
Solyc09g065100	bHLH transcription factor 150		F:GO:0046983	F:protein dimerization activity			IPR025610 (PFAN bHLH	2,684	4,508	0,380	1,187	1,951			2,308	0,000				up	
Solyc09g065110	non-structural protein (AHRD V3.3 *** AT1G03180.5)						G3DSA:3.30.900.20 (GENE3D): PTHF	4,457	3,947	5,090	4,160	3,790									
Solyc09g065120	Preprotein translocase subunit SecY (AHRD V3.3 *** A0A072U218_MEDTR)		P:GO:0015031: C:G(	P:protein transport; C:membrane			PR00303 (PRINTS): IPR023201 (G3D	45,152	45,873	52,181	61,272	62,528									
Solyc09g065130	Mitochondrial Rho GTPase (AHRD V3.3 *** K4CUE0_SOLLC)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFAI	104,643	78,275	91,286	85,847	83,402									
Solyc09g065155	FZO-like (AHRD V3.3 *-* A0A061DQU9_THECC)		F:GO:0003824	F:catalytic activity			IPR013785 (G3DSA:3.20.20.GENE3D	12,463	12,566	9,481	10,486	14,238			0,583	0,010				up	
Solyc09g065160	FZO-like protein (AHRD V3.3 *-* G7IED3_MEDTR)		F:GO:0003824: F:G(	F:catalytic activity; F:GTP binding; C:integral component of men			PTHR43681 (PANTHER)	11,159	11,717	8,386	9,340	13,827			0,715	0,001				up	
Solyc09g065170	30S ribosomal protein S7, chloroplastic (AHRD V3.3 --* A0A088CKE9_9CHLO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,096	0,118	0,025	0,000	0,046									
Solyc09g065180	binding protein precursor AF106660		F:GO:0003824: F:G(	F:catalytic activity; F:coenzyme binding			IPR001509 (PFAM): G3DSA:3.40.50.7	19,874	46,147	11,317	9,898	26,803	1,242	0,000	1,238	0,000			up	up	
Solyc09g065190	RAN GTPase activating protein 2 (AHRD V3.3 *** A0A061ELQ9_THECC)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	30,282	28,534	19,061	18,271	20,110									
Solyc09g065200	cyclinU3_1	CycU3_1	P:GO:0000079: F:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			IPR013922 (PFAM): G3DSA:1.10.472	25,192	25,959	12,533	11,173	11,657									
Solyc09g065210	ARM repeat protein interacting with ABF2 (AHRD V3.3 *** AT5G19330.1)		F:GO:0005515	F:protein binding			IPR011989 (G3DSA:1.25.10.GENE3D	70,819	63,092	72,070	62,980	66,131									
Solyc09g065240	Patatin (AHRD V3.3 *** K4CUF1_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM): G3DSA:3.40.109(	59,711	41,962	8,747	7,793	7,547									
Solyc09g065250	Early nodulin-like protein (AHRD V3.3 *** A0A0K9P6C2_ZOSMR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc09g065260	Early nodulin-like protein (AHRD V3.3 *** A0A0K9P6C2_ZOSMR)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	14,756	15,881	0,000	0,047	0,000									
Solyc09g065270	Ribosome recycling factor family protein (AHRD V3.3 *** B9GSN2_POPTR)		P:GO:0006412	P:translation			IPR002661 (TIGRFAM): G3DSA:1.10.1	16,094	26,571	18,584	23,112	32,471	0,751	0,016	0,801	0,000			up	up	
Solyc09g065280	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT4G02730.1)		F:GO:0005515: C:G(	F:protein binding; C:spliceosomal complex; P:RNA splicing			IPR020472 (PRINTS): G3DSA:1.20.94	142,823	116,929	150,612	129,140	133,185									
Solyc09g065290	Terpenoid cyclases/Protein prenyltransferases superfamily protein (AHRD V3.3 --* AT1G31950.3)							2,448	2,067	2,734	2,740	2,671									
Solyc09g065300	spindle pole body-associated protein (AHRD V3.3 *** AT4G02725.1)		C:GO:0009507: C:G(	C:chloroplast; C:integral component of membrane			PTHR36046 (PANTHER)	4,277	6,146	5,932	6,873	8,292									
Solyc09g065305	Mitochondrial outer membrane protein porin of 34 kDa (AHRD V3.3 --* VDAC1_SOLTU)							0,021	0,041	0,050	0,025	0,000									
Solyc09g065320	Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)						PTHR33985:SF10 (PANTHER): PTHR3	0,202	0,157	0,000	0,000	0,023									
Solyc09g065330	40S ribosomal protein S24 (AHRD V3.3 *** K4CAS8_SOLLC)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.70.3370 (GENE3D): IPR(	95,534	109,709	88,826	77,363	76,683									
Solyc09g065340	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 *-* AT5G36740.5)		F:GO:0003677: F:G(	F:DNA binding; F:metal ion binding			IPR032308 (PFAM): IPR013083 (G3D	46,849	41,647	30,801	28,049	28,802									
Solyc09g065350	LOW QUALITY:ovate family protein 18	OFP18	P:GO:0045892	P:negative regulation of transcription, DNA-templated			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,000	0,000	0,000									
Solyc09g065360	Seed maturation protein/ Late embryogenesis abundant protein (AHRD V3.3 *** A0A0K9PC32_ZOSMR)		C:GO:0005730: C:G(	C:nucleolus; C:cytosol; P:cellular ion homeostasis; P:response			IPR007011 (PFAM): PTHR31174:SF7	0,241	0,402	0,172	0,388	0,140									
Solyc09g065370	Heat shock 22 kDa protein (AHRD V3.3 *** A0A072VPF4_MEDTR)						PTHR33879 (PANTHER): PTHR33879	35,547	35,314	19,016	21,042	23,380									
Solyc09g065380	flocculation FLO11-like protein (AHRD V3.3 *** AT4G02715.2)						PF15365 (PFAM): mobidb-lite (MOBID	115,201	92,542	114,819	114,387	100,867									
Solyc09g065383	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 --* ATPA_JASNU)							33,443	27,122	35,058	36,418	28,150									
Solyc09g065390	LOW QUALITY:Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 *-* A0A061GBF7_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	8,887	4,300	9,886	8,737	7,494	-1,013	0,012					down		
Solyc09g065400	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9GSL6_POPTR)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3I	8,650	8,163	10,870	10,158	11,653									
Solyc09g065405	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --* AT2G33490.3)							1,007	0,977	1,009	1,123	1,063									
Solyc09g065420	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,021	0,000	0,000	0,000	0,047									
Solyc09g065430	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)		P:GO:0006869: F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): G3DSA:1.10.11	0,059	0,019	0,428	0,095	0,279									
Solyc09g065440	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *-* B9NBN8_POPTR)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,122	0,212	0,269	0,468									
Solyc09g065457	Cytochrome P450, putative (AHRD V3.3 *-* B9SA84_RICCO)		C:GO:0016020: F:G(	C:membrane; F:oxi(	EC:1.14.13	Acting on paired donors, with incorporation or reduction of m		0,000	0,000	0,000	0,000	0,023									
Solyc09g065470	7S globulin (AHRD V3.3 *** Q9AUD0_SESIN)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (PFAM): IPR014710 (G3D	65,101	75,898	9,956	28,145	2,202									
Solyc09g065480	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** A0A151RLD8_CAJCA)		F:GO:0004439: F:G(	F:phosphatidylinosit	EC:3.1.3.36	Phosphoinositide 5-p	IPR036691 (G3DSA:3.60.10.GENE3D	1,927	1,999	0,229	0,389	0,513									
Solyc09g065490	Protein kinase superfamily protein (AHRD V3.3 --* AT5G26110.3)							0,894	0,609	0,093	0,169	0,234									
Solyc09g065493	Homeobox-leucine zipper protein HDG9 (AHRD V3.3 --* HDG9_ARATH)							0,000	0,018	0,000	0,000	0,023									
Solyc09g065510	UPF0690 protein C1orf52 (AHRD V3.3 *** A0A1D1Z6A3_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,110	5,010	4,412	4,431	4,429									
Solyc09g065520	Homocysteine S-methyltransferase-like protein (AHRD V3.3 *** A0A072UD84_MEDTR)		F:GO:0008270: P:G(	F:zinc ion binding; F	EC:2.1.1.5	Betaine--homocystei	IPR003726 (PFAM): IPR036589 (G3D	57,359	57,292	130,125	139,897	120,412									
Solyc09g065530	LOW QUALITY:RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT3G02890.4)							0,000	0,021	0,000	0,000	0,000									
Solyc09g065540	biotin-binding protein		F:GO:0005524: F:G(	F:ATP binding; F:metal ion binding			IPR005482 (PFAM): IPR005479 (PFAI	64,549	57,849	104,101	115,855	107,168									
Solyc09g065550	Kinase interacting (KIP1-like) family protein, putative (AHRD V3.3 *** A0A061DQM7_THECC)		F:GO:0003779	F:actin binding			IPR011684 (PFAM): PTHR32258 (PAI	22,005	16,365	21,655	20,370	20,662									
Solyc09g065560	Sulfate transporter (AHRD V3.3 *** D7LTZ8_ARALL)		F:GO:0008271: P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR002645 (PFAM): IPR001902 (TIGF	3,228	8,026	55,230	69,993	71,829									
Solyc09g065570	Kinase family protein (AHRD V3.3 *** B9GSJ9_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,828	0,568	0,065	0,047	0,093									
Solyc09g065580	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G63290.1)		C:GO:0009506: P:G(	C:plasmodesma; P:pollen development; F:dioxygenase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	5,408	4,668	5,487	5,838	4,976									
Solyc09g065590	auxin canalization protein (DUF828) (AHRD V3.3 *** AT3G22810.1)		P:GO:0009734: P:G(	P:auxin-activated signaling pathway; P:phloem or xylem histoge			IPR013666 (PFAM): IPR008546 (PFAI	1,656	1,767	0,169	0,119	0,047									
Solyc09g065595	GDP-mannose transporter, putative (AHRD V3.3 *** B9STN8_RICCO)		F:GO:0005457: C:G(	F:GDP-fucose transmembrane transporter activity; C:Golgi app			IPR004853 (PFAM): mobidb-lite (MOB	2,743	2,068	2,002	1,901	1,534									
Solyc09g065600	GDP-mannose transporter, putative (AHRD V3.3 *-* B9STN8_RICCO)		F:GO:0005457: C:G(	F:GDP-fucose transmembrane transporter activity; C:Golgi app			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,726	0,545	0,433	0,605	0,493									
Solyc09g065610	Bax inhibitor (AHRD V3.3 *-* A0A0K1ETI6_TECGR)		C:GO:0016021	C:integral component of membrane			IPR006214 (PFAM): IPR006214 (PAN	44,229	51,227	25,702	38,893	30,125					0,596	0,035			up
Solyc09g065620	Chlorophyllase (AHRD V3.3 *** W6EIP8_WHEAT)	CLH2	P:GO:0015996: C:G(	P:chlorophyll catabo	EC:3.1.1.14; EC:3.1.	Chlorophyllase; Carb	IPR041127 (PFAM): IPR029058 (G3D	0,040	0,096	0,000	0,000	0,000									
Solyc09g065630	BIG SEEDS 2 (AHRD V3.3 *** K4CUI9_SOLLC)		C:GO:0005634: P:G(	C:nucleus; P:response to wounding; C:membrane; P:regulation (			IPR010399 (PFAM): mobidb-lite (MOB	11,661	11,384	9,484	9,673	10,329									
Solyc09g065640	ethylene overproducer-like 1	eol1	F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	54,571	50,672	48,863	54,598	49,043									
Solyc09g065645	Plant protein 1589 of unknown function (AHRD V3.3 --* AT3G55240.1)						mobidb-lite (MOBIDB_LITE)	0,000	0,019	0,025	0,000	0,000									
Solyc09g065650	kinase superfamily protein (AHRD V3.3 *** AT3G63340.5)		F:GO:0004672: F:G(	F:protein kinase ac	EC:3.1.3.16	Protein-serine/threor	G3DSA:1.10.510.10 (GENE3D): IPR0(	23,709	20,819	47,988	51,172	48,992									
Solyc09g065655	kinase superfamily protein (AHRD V3.3 *-* AT3G63340.12)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	PTHR13832:SF266 (PANTHER): IPR0	1,756	0,942	2,373	3,834	3,535									
Solyc09g065660	SolycHsfA7	HSF-06	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	8,965	4,473	32,384	32,346	31,826	-0,973	0,013					down		
Solyc09g065670	Zinc finger family protein (AHRD V3.3 *** B9H8D5_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	22,809	22,246	12,677	6,530	6,680			-0,927	0,000	-0,955	0,000		down	down
Solyc09g065680	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 --* AT2G27385.3)							0,021	0,000	0,025	0,000	0,000									
Solyc09g065690	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G19840.1)		F:GO:0016706: P:G(	F:2-oxoglutarate-de	EC:1.14.11	Acting on paired don	IPR041667 (PFAM): G3DSA:2.60.120	8,512	8,138	8,754	8,286	8,413									
Solyc09g065700	BEACH-DOMAIN HOMOLOG A1 (AHRD V3.3 *** AT1G03060.2)		F:GO:0005515	F:protein binding			IPR011989 (G3DSA:1.25.10.GENE3D	111,726	82,518	101,308	102,139	107,655									
Solyc09g065710	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S4P3_RICCO)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (TIGF	1,173	1,164	1,525	1,472	1,362									
Solyc09g065720	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0B2NZG8_GLYSO)		P:GO:0000413: F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR029000 (G3	55,523	49,852	78,255	70,708	72,881									
Solyc09g065730	2-methyl-6-phytyl-1,4-benzoquinone methyltransferase 1 (AHRD V3.3 *** F1BPV9_S	VTE3a	F:GO:0008168: P:G(	F:methyltransferase activity; P:methylation			IPR013216 (PFAM): G3DSA:3.40.50.1	33,988	30,690	33,900	28,168	29,970									
Solyc09g065740	Ammonium transporter (AHRD V3.3 *** K4CUK0_SOLLC)		F:GO:0008519: C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR002229 (PRINTS): IPR001905 (TI(	0,200	0,413	0,189	0,097	0,119									
Solyc09g065755	Histone H2A (AHRD V3.3 *** A0A0V0HFX8_SOLCH)		C:GO:0000786: F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimer			IPR002119 (PRINTS): IPR032454 (PF	149,011	156,546	134,638	127,847	127,870									
Solyc09g065760	DUF506 family protein (AHRD V3.3 *** G7ICN8_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (F	33,319	25,002	14,564	18,871	17,065									
Solyc09g065770	LOW QUALITY:Ubiquitin-conjugating enzyme/RWD-like protein, putative (AHRD V3.3 *** A0A061DQB8_THE		P:GO:0006464: P:G(	P:cellular protein modification process; P:protein transport			IPR016135 (G3DSA:3.10.110.GENE3I	0,019	0,000	0,000	0,025	0,024									
Solyc09g065780	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4CUK4_SOLLC)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR016039 (G3DSA:3.40.47.GENE3D	4,987	5,272	1,939	2,408	1,934									
Solyc09g065790	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4CUK5_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo	EC:3.4.21	Acting on peptide bo	IPR001907 (PRINTS): IPR023562 (PF	0,414	0,898	0,503	1,102	0,541									
Solyc09g065800	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4CUK6_SOLLC)		P:GO:0006633: C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR012392 (PIRS	0,019	0,000	0,000	0,000	0,000									
Solyc09g065810	Guanylate-binding family protein (AHRD V3.3 *** AT2G38840.1)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR015894 (PFAM): G3DSA:3.40.50.3	26,702	25,992	12,390	11,739	11,849									
Solyc09g065820	bHLH transcription factor 059		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAN bHLH	26,025	34,220	22,423	21,895	22,704									
Solyc09g065830	NADH-ubiquinone oxidoreductase 24 kDa subunit (AHRD V3.3 *** AT4G02580.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			G3DSA:1.10.10.1590 (GENE3D): IPR(	84,901	87,558	116,646	104,336	110,870									
Solyc09g065840	single-stranded DNA binding protein-like protein		F:GO:0003697: P:G(	F:single-stranded DNA binding; P:DNA replication			IPR011344 (TIGRFAM): G3DSA:2.40.5	2,589	3,628	2,511	1,869	2,401									
Solyc09g065850	auxin-regulated IAA3	IAA3	F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			IPR033389 (PFAM): G3DSA:3.10.20.9	0,061	0,083	0,143	0,121	0,095									
Solyc09g065860	Phosphoribulokinase/uridine kinase family protein (AHRD V3.3 *** U5GGU8_POPTR)		F:GO:0005524: F:G(	F:ATP binding; F:kinase activity			IPR006083 (PFAM): G3DSA:3.40.50.3	22,322	20,451	30,076	27,555	28,750									

Solyc09g065870	E3 ubiquitin-protein ligase RGLG2-like protein (AHRD V3.3 *** A0A072V0P7_MEDTR)		F:GO:0016874	F:ligase activity	IPR010734 (PFAM): mobidb-lite (MOB	26,350	21,944	29,389	32,502	31,966									
Solyc09g065880	F-box family protein (AHRD V3.3 *** B9GS69_POPTR)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	25,025	25,630	4,911	2,609	4,603									
Solyc09g065890	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061DP20_THECC)		P:GO:0006629	P:lipid metabolic process	IPR002921 (PFAM): G3DSA:3.40.50.1	4,166	6,318	0,464	0,807	0,912									
Solyc09g065900	glutathione reductase, chloroplastic	GR	F:GO:0004362: P:G(	F:glutathione-disulfi EC:1.8.1.7 Glutathione-disulfide	PR00368 (PRINTS): PR00411 (PRINT	46,551	43,669	101,145	109,697	105,996									
Solyc09g065910	photosystem II reaction center W (AHRD V3.3 *** AT2G30570.1)		C:GO:0009507: C:G(	C:chloroplast; C:photosystem II; P:photosynthesis	IPR009806 (PFAM): IPR009806 (PAN	151,431	264,574	90,937	104,060	172,389	0,834	0,005	0,919	0,000			up	up	
Solyc09g065920	Magnesium transporter MRS2-like protein (AHRD V3.3 *** A0A072UDJ3_MEDTR)		C:GO:0016020: P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane	IPR002523 (PFAM): G3DSA:2.40.128	16,732	14,785	23,222	26,226	20,598									
Solyc09g065930	transmembrane protein (AHRD V3.3 *** AT2G41945.1)		C:GO:0016021	C:integral component of membrane	PTHR34459 (PANTHER): PTHR34459	5,235	4,661	8,410	7,998	7,007									
Solyc09g065940	U6 snRNA-associated Sm-like protein LSm4 (AHRD V3.3 *** B6UB12_MAIZE)		P:GO:0000398: P:G(	P:mRNA splicing, via spliceosome; P:nuclear-transcribed mRNA	G3DSA:2.30.30.100 (GENE3D): mobic	1,390	1,149	1,231	0,989	0,919									
Solyc09g065950	F-actin capping protein alpha subunit (AHRD V3.3 *** B9I7I3_POPTR)		C:GO:0008290: P:G(	C:F-actin capping protein complex; P:barbed-end actin filament	IPR002189 (PRINTS): G3DSA:2.40.16	28,978	31,765	36,318	38,251	34,166									
Solyc09g065955	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G51000.1)					2,710	2,884	3,029	4,250	2,658									
Solyc09g065990	E3 ubiquitin protein ligase DRIP2 (AHRD V3.3 *** W9RBR4_9ROSA)		F:GO:0016874	F:ligase activity	PF13923 (PFAM): IPR013083 (G3DS/	23,339	25,234	23,870	24,314	23,754									
Solyc09g066010	WRKY transcription factor 24	WRKY24	F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR018872 (PFAM WRKY	6,117	4,191	4,691	3,726	3,911									
Solyc09g066030	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072UAM9_MEDTR)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding	IPR001356 (PFAM HD-ZIP	0,040	0,058	0,000	0,415	0,000									
Solyc09g066045	Homeobox-leucine zipper protein (AHRD V3.3 *-* A0A059UE00_9POAL)		F:GO:0003677	F:DNA binding	IPR001356 (PFAM): G3DSA:1.10.10.6	0,097	0,000	0,075	0,000	0,024									
Solyc09g066050	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072UAM9_MEDTR)		F:GO:0008289	F:lipid binding	IPR023393 (G3DSA:3.30.530.GENE3I	0,178	0,099	0,172	0,069	0,024									
Solyc09g066060	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9N3B2_POPTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(HB-other	0,021	0,093	1,583	1,787	2,479									
Solyc09g066070	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072UAM9_MEDTR)		F:GO:0008289	F:lipid binding	IPR023393 (G3DSA:3.30.530.GENE3I	0,042	0,130	2,418	2,444	3,756									
Solyc09g066080	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein (AHRD V3.3 *-* W9R323_9ROSA)		P:GO:0006281	P:DNA repair	IPR001357 (PFAM): IPR036420 (G3D	7,152	5,662	12,410	14,187	12,087									
Solyc09g066100	Histone H1 (AHRD V3.3 *** H1_SOLLC)		C:GO:0000786: F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem	IPR005819 (PRINTS): IPR036388 (G3	52,064	70,848	86,574	87,390	85,081									
Solyc09g066120	Poly(RC)-binding protein, putative (AHRD V3.3 *** B9S7H6_RICCO)		F:GO:0003723	F:RNA binding	G3DSA:3.30.310.210 (GENE3D): IPR(	7,970	6,960	7,918	7,392	7,061									
Solyc09g066130	PfkB-like carbohydrate kinase family protein (AHRD V3.3 *** A0A061DQ42_THECC)		C:GO:0005634: C:G(	C:nucleus; C:cytoplasm; F:kinase activity; P:phosphorylation	IPR011611 (PFAM): IPR029056 (G3D	25,613	22,396	47,167	49,024	48,470									
Solyc09g066140	myosin-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *-* AT1G08800.4)		F:GO:0017022	F:myosin binding	IPR007656 (PFAM): mobidb-lite (MOB	15,791	12,130	11,834	14,557	11,856									
Solyc09g066145	Glucose-6-phosphate isomerase (AHRD V3.3 --* F6H116_VITVI)					0,138	0,043	0,169	0,101	0,048									
Solyc09g066150	Cytochrome P450, putative (AHRD V3.3 *** B9S4U5_RICCO)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS): IPR002401 (PF	27,733	39,138	718,615	966,394	425,306			-0,759	0,027				down	
Solyc09g066155	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SE46_CAJCA)				IPR019557 (PFAM): PTHR44194 (PAN	0,021	0,000	0,025	0,000	0,046									
Solyc09g066210	F-box/kelch-repeat protein (AHRD V3.3 *** W9S979_9ROSA)		F:GO:0005515	F:protein binding	IPR015915 (G3DSA:2.120.10.GENE3I	5,531	4,830	4,563	4,074	3,845									
Solyc09g066280	basic helix loop helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT1G06150.1)		F:GO:0046983	F:protein dimerization activity	IPR025610 (PFAM): mobidb-lite (MOB	57,275	57,954	43,160	35,891	41,235									
Solyc09g066290	Kinesin light chain, putative (AHRD V3.3 *** B9T299_RICCO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	10,677	10,926	15,618	14,272	13,155									
Solyc09g066340	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R427_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,000	0,018	0,000	0,000	0,000									
Solyc09g066350	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R427_9ROSA)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,000	0,158	0,000	0,000	0,000									
Solyc09g066360	Ethylene Response Factor C.3		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	1,733	4,955	2,920	1,409	0,760	1,532	0,027	-1,931	0,000	-1,038	0,032	up	down	down
Solyc09g066370	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS): IPR002401 (PF	0,000	0,039	0,022	0,025	0,000									
Solyc09g066400	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS): IPR002401 (PF	0,000	0,018	0,112	0,000	0,023									
Solyc09g066410	Phosphate transporter (AHRD V3.3 *** A0A0B5GK48_SOLLC)		F:GO:0005315: P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph	IPR005828 (PFAM): IPR004738 (TIGF	0,038	0,179	0,146	0,480	0,331									
Solyc09g066420	TBC1 domain family protein		F:GO:0005096: C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp	G3DSA:1.10.8.270 (GENE3D): IPR0(	11,596	11,080	10,700	9,145	11,943									
Solyc09g066430	60S ribosomal protein L14, putative (AHRD V3.3 *** B9SV21_RICCO)		F:GO:0003723: F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR014722 (G3DSA:2.30.30.GENE3D	199,272	192,435	125,636	105,710	114,556									
Solyc09g066440	Casein kinase, putative (AHRD V3.3 *** B9SS69_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	39,806	43,145	35,778	33,383	34,681									
Solyc09g066460	Protein kinase family protein (AHRD V3.3 *** AT1G03920.3)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): mobidb-lite (MOB	28,275	21,658	14,965	14,588	14,265									
Solyc09g066470	ABC transporter family protein (AHRD V3.3 *** F5A834_CAMSI)	ABCI8	F:GO:0005524: F:G(	F:ATP binding; F:AT EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003439 (PFAM): mobidb-lite (MOB	37,995	42,961	27,386	28,688	32,425									
Solyc09g066500	chromatin remodeling 8 (AHRD V3.3 *** AT2G18760.7)		F:GO:0005524	F:ATP binding	IPR001650 (PFAM): IPR038718 (G3D	51,386	59,831	35,117	31,859	36,625									
Solyc09g072560	Legumin 11S-globulin (AHRD V3.3 *** Q39770_GINBI)		F:GO:0045735	F:nutrient reservoir activity	IPR006044 (PRINTS): IPR014710 (G3	2080,194	1979,026	104,440	191,593	12,558									
Solyc09g072570	Pre-mRNA-splicing factor SLU7 (AHRD V3.3 *** SLU7_ORYSI)		F:GO:0000386: P:G(	F:second spliceosomal transesterification activity; P:mRNA spli	IPR021715 (PFAM): mobidb-lite (MOB	76,924	66,973	99,621	89,195	89,961									
Solyc09g072580	histone acetyltransferase subunit NuA4-domain protein (AHRD V3.3 *** AT4G14385.1)		C:GO:0000123: P:G(	C:histone acetyltransferase complex; P:histone acetylation	IPR015418 (PFAM): mobidb-lite (MOB	5,631	5,654	8,222	7,899	8,629									
Solyc09g072583	Tubulin beta chain (AHRD V3.3 *-* TBB_HORVU)		F:GO:0005200: F:G(	F:structural constituent of cytoskeleton; F:GTP binding; C:micro	IPR000217 (PRINTS): IPR036525 (G3	2,124	1,946	1,162	0,803	1,131									
Solyc09g072587	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 --*		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane		0,121	0,039	0,025	0,025	0,024									
Solyc09g072590	Actin-depolymerizing factor (AHRD V3.3 *** ADF_VITVI)		F:GO:0003779: C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymei	IPR029006 (G3DSA:3.40.20.GENE3D	26,951	25,019	63,717	68,982	56,570									
Solyc09g072600	Actin-depolymerizing factor (AHRD V3.3 *-* ADF_VITVI)		F:GO:0003779: C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymei	IPR029006 (G3DSA:3.40.20.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc09g072610	Long-chain-alcohol oxidase (AHRD V3.3 *** K4CUT7_SOLLC)		F:GO:0046577: F:G(	F:long-chain-alcoho EC:1.1.3.2 Long-chain-alcohol o	IPR012400 (PIRSF): IPR007867 (PFA	0,550	0,366	0,936	1,074	0,730									
Solyc09g072620	Phytochelatin synthase (AHRD V3.3 *** Q84JR4_SOLTU)		P:GO:0010038: F:G(	P:response to meta EC:2.3.2.15 Glutathione gamma-c	IPR038156 (G3DSA:3.90.70.GENE3D	19,955	17,370	6,605	7,403	6,907									
Solyc09g072640	ROP-interactive CRIB motif protein (AHRD V3.3 *-* A0A072U2K9_MEDTR)				IPR000095 (PFAM): mobidb-lite (MOB	0,452	0,536	0,025	0,073	0,024									
Solyc09g072650	Tetratricopeptide repeat 7A (AHRD V3.3 *** A0A0B0PQU8_GOSAR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	23,664	18,860	24,192	22,981	22,424									
Solyc09g072660	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061G813_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI	G3DSA:3.40.462.20 (GENE3D): G3DS	1,001	1,155	2,433	3,326	2,480									
Solyc09g072670	Rho GDP-dissociation inhibitor 1 (AHRD V3.3 *** A0A0B2NZI9_GLYSO)		F:GO:0005094: C:G(	F:Rho GDP-dissociation inhibitor activity; C:cytoplasm	IPR000406 (PRINTS): IPR024792 (G3	14,609	15,399	19,312	18,425	16,437									
Solyc09g072680	F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XV28_CYNCS)		F:GO:0005515	F:protein binding	IPR017451 (TIGRFAM): IPR001810 (I	4,857	5,343	4,203	4,368	4,170									
Solyc09g072690	Cation calcium exchanger (AHRD V3.3 *** A0A072U799_MEDTR)		C:GO:0016021: P:G(	C:integral component of membrane; P:transmembrane transport	IPR004837 (PFAM): PTHR12266:SF2	0,058	0,039	0,025	0,022	0,070									
Solyc09g072700	Peroxidase (AHRD V3.3 *** K4CUU6_SOLLC)		F:GO:0004601: P:G(	F:peroxidase activit EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,040	0,455	0,025	0,000	0,023									
Solyc09g072710	Phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** A0A151T5V3_CAJCA)		P:GO:0006629: F:G(	P:lipid metabolic process; F:O-acyltransferase activity	IPR003386 (PFAM): PTHR11440:SF7	14,839	15,528	15,386	13,814	15,157									
Solyc09g072720	Exocyst complex component 8 (AHRD V3.3 *** A0A0B0PVF9_GOSAR)		C:GO:0000145: P:G(	C:exocyst; P:exocytosis	PTHR21426:SF13 (PANTHER): IPR03	0,021	0,000	0,000	0,000	0,000									
Solyc09g072750	LOW QUALITY:Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 --* AT1G29380.3)		C:GO:0016020	C:membrane		0,019	0,019	0,000	0,000	0,000									
Solyc09g072770	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *-* AT2G41400.1)		P:GO:0008150: C:G(	P:biological_process; C:membrane; C:integral component of me	PTHR34458:SF5 (PANTHER): IPR040	0,019	0,000	0,022	0,000	0,000									
Solyc09g072790	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G55550.6)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	3,817	4,842	4,432	4,818	4,861									
Solyc09g072800	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, putative isoform 3 (AHRD V3.3 *-* A0A061DK4		P:GO:0007142	P:male meiosis II	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,065	1,064	0,125	0,025	0,046									
Solyc09g072820	Cellulose synthase (AHRD V3.3 *** M5VVD4_PRUPE)		C:GO:0016020: F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (U	IPR005150 (PFAM): IPR013083 (G3D	9,223	5,220	0,577	0,094	0,686									
Solyc09g072830	Myb-like transcription factor family protein (AHRD V3.3 *** G7KXD8_MEDTR)		F:GO:0003677	F:DNA binding	IPR025756 (PFAM G2-like	29,077	36,238	59,518	68,076	60,890									
Solyc09g072840	Heavy metal-associated domain containing protein, expressed (AHRD V3.3 --* H2KVZ0_ORYSJ)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding	PTHR22814:SF115 (PANTHER): PTHF	0,021	0,000	0,000	0,025	0,023									
Solyc09g072860	fanconi anemia group F protein (FANCF) (AHRD V3.3 *** AT5G44010.4)		P:GO:0036297: C:G(	P:interstrand cross-link repair; C:Fanconi anaemia nuclear com	IPR035428 (PFAM): mobidb-lite (MOB	5,788	6,882	4,680	5,148	5,562									
Solyc09g072870	50S ribosomal protein L14 (AHRD V3.3 *** A0A0K9PMD0_ZOSMR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000218 (PFAM): IPR036853 (G3D	200,096	224,298	190,166	172,068	169,971									
Solyc09g072873	LOW QUALITY:UDP-N-acetylglucosamine 1-carboxyvinyltransferase (AHRD V3.3 *-* W9S9V0_9ROSA)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth	IPR036968 (G3DSA:3.65.10.GENE3D	0,000	0,000	0,147	0,167	0,094									
Solyc09g072877	aluminum activated malate transporter family protein (AHRD V3.3 --* AT5G46610.2)					0,000	0,000	0,072	0,025	0,094									
Solyc09g072880	Fluorescent in blue light, chloroplastic-like protein (AHRD V3.3 *** A0A0B0PKQ3_GOSAR)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	6,157	5,466	4,979	4,879	4,899									
Solyc09g072885	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT4G21130.1)					0,795	0,393	0,311	0,291	0,331									
Solyc09g072890	Histone-lysine N-methyltransferase (AHRD V3.3 *-* W9QWZ0_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C EC:2.1.1.43 Histone-lysine N-met	IPR007728 (PFAM): IPR018848 (PFA	18,010	16,694	14,288	13,178	13,816									
Solyc09g072900	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9SFP3_RICCO)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	30,781	33,068	18,443	16,140	21,796									
Solyc09g072920	LOW QUALITY:F-box/RNI-like superfamily protein (AHRD V3.3 --* AT5G03100.2)		F:GO:0003677: F:G(	F:DNA binding; F:protein binding	G3DSA:1.10.10.60 (GENE3D): IPR0(	0,000	0,000	0,025	0,025	0,000									
Solyc09g072930	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYN(		F:GO:0005515	F:protein binding	IPR001810 (PFAM): IPR017451 (TIGF	0,538	0,669	0,572	0,530	0,421									
Solyc09g072950	Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** A0A072U6T5_MEDTR)		P:GO:0043086: F:G(	P:negative regulation of catalytic activity; F:pectinesterase inhil	IPR006501 (TIGRFAM): IPR035513 ((	0,080	1,031	0,093	0,099	0,212									
Solyc09g072960	F-box/RNI-like superfamily protein (AHRD V3.3 *** AT1G13570.2)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc09g072970	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT1G03330.1)		P:GO:0006397	P:mRNA processing	IPR016654 (PIRSF): IPR001163 (PFA	22,140	23,221	30,773	27,835	29,739									
Solyc09g072980	BTB/POZ/MATH-domain protein (AHRD V3.3 *** G7I2K6_MEDTR)		F:GO:0005515	F:protein binding	G3DSA:1.25.40.420 (GENE3D): IPR0(	24,734	20,355	17,477	18,164	16,894									
Solyc09g072990	mRNA, clone: RTFL01-07-P23 (AHRD V3.3 *** E4MWC7_EUTHA)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	43,356	43,514	36,455	39,484	40,032									
Solyc09g073000	Elongation factor Tu (AHRD V3.3 *** K4CUX6_SOLLC)		F:GO:0003746: F:G(	F:translation elonga EC:3.6.1.15 Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.40.5(	84,645	90,491	143,953	135,765	132,234									
Solyc09g073020	LOW QUALITY:16.9 kDa class I heat shock protein 2 (AHRD V3.3 --* HS16B_WHEAT)					0,000	0,039	0,000	0,000	0,000									
Solyc09g073030	carbamoyl phosphate synthetase A (AHRD V3.3 --* AT3G27740.2)				mobidb-lite (MOBIDB_LITE)	3,497	2,839	2,368	5,420	3,915					1,190	0,000			up
Solyc09g073040	amino-terminal region of chorein (AHRD V3.3 --* AT3G20720.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,060	0,064	0,119	0,393	0,494									
Solyc09g074040	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 --* AT5G25970.3)					3,274	3,283	1,931	2,054	2,196									
Solyc09g074050	2OG-Fe(II) oxygenase family oxidoreductase (AHRD V3.3 *** A0A072VPE6_MEDTR)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR037151 (G3DSA:2.60.120.GENE3I	33,972	34,795	23,346	20,077	25,417									
Solyc09g074060	LOW QUALITY:BSD domain-containing protein (AHRD V3.3 *-* AT1G03350.1)				IPR005607 (PFAM): IPR035925 (G3D	129,982	104,502	123,625	115,015	113,666									
Solyc09g074090	Exosome complex component RRP4 homolog (AHRD V3.3 *** RRP4_ARATH)		C:GO:0000178: F:G(	C:exosome (RNase complex); F:RNA binding	G3DSA:2.40.50.100 (GENE3D): IPR0(	8,771	8,889	9,057	7,973	7,414									
Solyc09g074095	tRNA-specific 2-thiouridylase mnmA (AHRD V3.3 *-* W9RR02_9ROSA),Pfam:PF03054		P:GO:0008033: F:G(	P:tRNA processing; F:sulfurtransferase activity	PF03054 (PFAM): G3DSA:2.40.30.10	5,062	3,913	4,393	3,712	3,906									
Solyc09g074100	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (AHRD V3.3 *** AT1G51310.1)		P:GO:0008033: F:G(	P:tRNA processing; F:sulfurtransferase activity	IPR014729 (G3DSA:3.40.50.GENE3D	7,202	6,148	5,736	6,253	6,433									
Solyc09g074110	piezo-type mechanosensitive ion channel component (AHRD V3.3 *-* AT2G48060.2)		F:GO:0008381: C:G(	F:mechanosensitive ion channel activity; C:integral component	PTHR13167:SF45 (PANTHER): IPR02	4,162	2,436	4,580	5,712	4,927									
Solyc09g074113	piezo-type mechanosensitive ion channel component (AHRD V3.3 *** AT2G48060.2)		F:GO:0008381: C:G(	F:mechanosensitive ion channel activity; C:integral component	IPR031334 (PFAM): mobidb-lite (MOB	54,053	42,583	61,701	63,219	62,838									
Solyc09g074120	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G03000.2)		F:GO:0016874	F:ligase activity	PF13920 (PFAM): IPR013083 (G3DS/	0,058	0,039	0,000	0,000	0,000									
Solyc09g074130	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03000.2)		F:GO:0016874	F:ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	0,019	0,097	0,000	0,000	0,000									
Solyc09g074140	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G03000.2)		F:GO:0016874	F:ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	0,059	0,192	0,000	0,000	0,000									
Solyc09g074170	RING/U-box superfamily protein, putative (AHRD V3.3 *-* A0A061DXX2_THECC)		F:GO:0016874	F:ligase activity	PTHR10044:SF164 (PANTHER): PTHI	0,019	0,000	0,000	0,000	0,000									
Solyc09g074175	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G03000.6)		F:GO:0016874	F:ligase activity	PTHR10044 (PANTHER): PTHR10044	0,042	0,021	0,000	0,000	0,000									
Solyc09g074180	phytochrome interacting factor 3-like 5 (AHRD V3.3 --* AT2G20180.7)				mobidb-lite (MOBIDB_LITE)	0,582	0,524	0,425	0,365	0,564									
Solyc09g074185	LOW QUALITY:BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061FVD3_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity	IPR025525 (PFAM): IPR008906 (PFA	0,208	0,000	0,331	0,000	0,000									
Solyc09g074190	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DXX2_THECC)		F:GO:0016874	F:ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	0,140	0,138	0,000	0,000	0,000									
Solyc09g074200	RING/U-box superfamily protein (AHRD V3.3 *** AT4G03000.2)		F:GO:0016874	F:ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	0,115	0,182	0,000	0,000	0,000									
Solyc09g074210	Endonuclease/exonuclease/phosphatase family protein (AHRD V3.3 *** A0A072VYY9_MEDTR)		P:GO:0006506	P:GPI anchor biosynthetic process	IPR036691 (G3DSA:3.60.10.GENE3D	14,165	18,807	18,119	15,788	18,267									
Solyc09g074230	SlSFP7	SFP7	C:GO:0016021: F:G(	C:integral component of membrane; F:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D): IPR(	15,391	16,328	14,562	15,849	22,382									
Solyc09g074235	BEACH-DOMAIN HOMOLOG A1 (AHRD V3.3 --* AT1G03060.4)					0,040	0,021	0,000	0,025	0,024									
Solyc09g074240	Kinase, putative (AHRD V3.3 *** B9SFK9_RICCO)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	22,426	15,803	10,227	17,512	14,692					0,776	0,000			up
Solyc09g074250	Protein kinase family protein (AHRD V3.3 *** AT5G35960.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): PIRS	5,028	4,948	2,215	3,190	3,559									
Solyc09g074260	LOW QUALITY:Leucine-rich repeat receptor-like kinase (AHRD V3.3 *** A0A0K9PKL2_ZOSMR)		F:GO:0005515	F:protein binding	IPR013210 (PFAM): IPR001611 (PFA	0,171	0,218	0,197	0,144	0,094									
Solyc09g074270	Gid1-like gibberellin receptor (AHRD V3.3 *** M9N8R2_NICAT)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM): IPR029058 (G3D	13,591	11,104	36,439	73,281	56,152			0,620	0,000	1,009	0,000		up	up
Solyc09g074280	LOW QUALITY:Ankyrin repeat-containing protein (AHRD V3.3 *** A0A118K274_CYNCS)		F:GO:0005515	F:protein binding	IPR002110 (PRINTS): IPR036770 (G3	3,033	6,748	1,159	2,127	2,957			1,342	0,010				up	
Solyc09g074290	LOW QUALITY:Ankyrin repeat-containing protein (AHRD V3.3 *** A0A118K274_CYNCS)		F:GO:0005515	F:protein binding	IPR002110 (PRINTS): IPR020683 (PF	0,000	0,000	0,022	0,000	0,000									
Solyc09g074300	Histone H2A (AHRD V3.3 *** K4CV07_SOLLC)		C:GO:0000786: F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimei	IPR002119 (PRINTS): IPR032454 (PF	2,557	3,200	0,597	0,410	0,353									
Solyc09g074310	Oxidoreductase, aldo/keto reductase family protein, expressed (AHRD V3.3 *** Q2R0H4_ORYSJ)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR023210 (PFAM): IPR036812 (G3D	6,557	6,780	4,694	3,720	4,064									
Solyc09g074320	Serine/threonine-protein phosphatase (AHRD V3.3 *** K4CV09_SOLLC)		F:GO:0004721: F:G(	F:phosphoprotein pl EC:3.1.3.16 Protein-serine/threor	IPR006186 (PRINTS): IPR015915 (G3	34,295	27,303	42,397	37,960	37,325									
Solyc09g074330	sequence-specific DNA binding transcription factor ATNDX (AHRD V3.3 *** AT4G03090.5)		F:GO:0003697: P:G(	F:single-stranded DNA binding; P:flower development	mobidb-lite (MOBIDB_LITE): mobidb-lit	22,846	18,764	17,758	17,556	17,994									
Solyc09g074340	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9PZI3_ZOSMR)		P:GO:0007165	P:signal transduction	IPR008936 (G3DSA:1.10.555.GENE3I	3,240	5,677	1,398	1,123	1,669									
Solyc09g074350	LOW QUALITY:chromatin remodeling factor17 (AHRD V3.3 --* AT5G18620.2)		F:GO:0003746: P:G(	F:translation elongation factor activity; P:translational elongatio	PTHR35726 (PANTHER): PTHR35726	0,249	0,318	0,193	0,094	0,071									
Solyc09g074360	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G03457.2)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	13,775	17,473	14,236	15,591	16,187									
Solyc09g074365	RNA binding protein, putative (AHRD V3.3 *-* B9S3Y1_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	3,868	3,688	2,975	3,619	3,080									
Solyc09g074370	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT4G03115.1)		F:GO:0022857	F:transmembrane transporter activity	IPR018108 (PFAM): IPR023395 (G3D	2,468	2,902	5,582	6,952	5,377									
Solyc09g074380	DCD (Development and Cell Death) domain protein (AHRD V3.3 *-* AT2G32910.1)				IPR013989 (PFAM): mobidb-lite (MOB	3,366	2,643	2,143	2,347	2,224									
Solyc09g074390	LOW QUALITY:F-box protein family (AHRD V3.3 *** A0A151RL68_CAJCA)		F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D): IPR(	0,059	0,107	0,143	0,072	0,047									
Solyc09g074400	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G26060.1)		F:GO:0005515: P:G(	F:protein binding; P:iron-sulfur cluster assembly; C:CIA complex	IPR020472 (PRINTS): IPR001680 (PF	73,043	71,923	89,284	91,941	88,662									
Solyc09g074410	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G03140.1),Pfam:PF13561		C:GO:0016021: F:G(	C:integral component of membrane; F:oxidoreductase activity; I	IPR002347 (PRINTS): IPR002347 (PF	9,592	8,906	4,479	3,924	5,987									
Solyc09g074420	Protease Do-like 2, chloroplastic (AHRD V3.3 *** DEGP2_ARATH)		F:GO:0004252: F:G(	F:serine-type endor EC:3.4.21 Acting on peptide bor	IPR001940 (PRINTS): PF13365 (PFAI	33,973	39,525	25,615	21,769	32,348									
Solyc09g074430	Sl Monooxygenase		F:GO:0004499: F:G(	F:N,N-dimethylanilir EC:1.14.13.8; EC:1. Flavin-containing mo	PR00469 (PRINTS): PR00368 (PRINT	5,685	5,659	0,050	0,127	0,211									
Solyc09g074440	Defensin protein (AHRD V3.3 *** B1N678_SOLLC)		C:GO:0005576: P:G(	C:extracellular region; P:defense response; P:killing of cells of c	IPR036574 (G3DSA:3.30.30.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc09g074450	LOW QUALITY:Hydroxyproline-rich glycoprotein (AHRD V3.3 *** B9I9X0_POPTR)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR357	11,276	10,243	12,838	17,660	15,095									
Solyc09g074460	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G01980.1)		F:GO:0061630	F:ubiquitin protein ligase activity	IPR039525 (PFAM): IPR013083 (G3D	237,420	178,779	190,447	161,671	169,655									
Solyc09g074470	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** G7KQY6_MEDTR)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): mobidb-lite (MOB	0,610	1,196	0,118	0,100	0,000									
Solyc09g074500	Unknown protein (AHRD V3.3)					0,000	0,000	1,609	0,662	4,099									
Solyc09g074505	50S ribosomal protein L16, chloroplastic (AHRD V3.3 --* RK16_JASNU)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,165	0,176	0,216	0,093									
Solyc09g074510	Tubby-like F-box protein (AHRD V3.3 *** M0RYY8_MUSAM)		F:GO:0005515	F:protein binding	IPR000007 (PRINTS): IPR001810 (PF	0,991	1,461	3,737	3,041	2,831									
Solyc09g074520	Transport inhibitor response 1 (AHRD V3.3 *** C7E4R3_TOBAC)		F:GO:0005515	F:protein binding	IPR041101 (PFAM): IPR032675 (G3D	64,725	52,226	22,980	20,976	23,102									
Solyc09g074530	Nodulin MtN3 family protein		C:GO:0016021	C:integral component of membrane	IPR004316 (PFAM): G3DSA:1.20.128	47,473	25,562	1,694	2,502	1,599									
Solyc09g074540	Cytochrome b6-f complex subunit 6 (AHRD V3.3 *** K4CV31_SOLLC)		F:GO:0009055: C:G(	F:electron transfer activity; C:cytochrome b6f complex	IPR007802 (PFAM): IPR007802 (PAN	0,000	0,000	0,000	0,000	0,023									
Solyc09g074550	CASP-like protein (AHRD V3.3 *** M1ASY5_SOLTU)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane	IPR006702 (PFAM): IPR006459 (TIGF	0,042	0,078	0,208	0,047	0,046									
Solyc09g074560	CONSTANS-like zinc finger protein (AHRD V3.3 *** A0A0H3YNS5_9ROSI)	BBX11	F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding	IPR010402 (PFAM CO-like	29,629	27,251	23,163	19,795	24,300									
Solyc09g074570	Glutaredoxin (AHRD V3.3 *** B3F8F2_SOLTU)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR002109 (PFAM): G3DSA:3.40.30.1	0,243	0,337	0,100	0,121	0,071									
Solyc09g074590	Glutaredoxin (AHRD V3.3 *** A0A103Y7J3_CYNCS)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): IPR011905 (TI(	0,021	0,285	0,025	0,050	0,071									
Solyc09g074600	Glutaredoxin (AHRD V3.3 *** A0A103Y7J3_CYNCS)		F:GO:0009055: F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR014025 (PRINTS): G3DSA:3.40.3(	0,000	0,019	0,025	0,000	0,000									
Solyc09g074610	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *** A0A061EBG7_THECC)		C:GO:0016021	C:integral component of membrane	IPR001623 (PRINTS): IPR001623 (PF	0,102	0,099	0,022	0,050	0,000									

Solyc09g074620	Zinc metalloproteinase aureolysin (AHRD V3.3 *** A0A0B0PSB0_GOSAR)				PTHR37235 (PANTHER)	0,488	0,218	0,545	0,336	0,330									
Solyc09g074630	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT1G03010.2)		F:GO:0005515	F:protein binding	IPR027356 (PFAM): G3DSA:3.30.710	38,868	31,193	8,890	5,950	8,989									
Solyc09g074640	Zinc finger transcription factor 54	C3H54	F:GO:0046872	F:metal ion binding	IPR000571 (PFAM C3H	24,600	24,504	20,263	18,451	20,441									
Solyc09g074650	Peptide chain release factor 1 (AHRD V3.3 *** AT3G62910.1)		P:GO:0006415: F:G(	P:translational termination: F:translation release factor activity.	IPR005139 (PFAM): G3DSA:3.30.160	12,656	14,839	34,798	33,748	37,759									
Solyc09g074660	Spermatogenesis-associated 20 (AHRD V3.3 *** A0A0B0PFF5_GOSAR)		F:GO:0003824	F:catalytic activity	IPR012341 (G3DSA:1.50.10.GENE3D	36,078	24,049	69,746	69,709	67,189	-0,558	0,027					down		
Solyc09g074670	Zinc finger, CW-type (AHRD V3.3 *** A0A103YNR4_CYNCS)		F:GO:0008270	F:zinc ion binding	G3DSA:3.30.40.100 (GENE3D): IPR0	77,446	77,935	74,673	66,535	76,986									
Solyc09g074680	cullin 1 (AHRD V3.3 *** AT4G02570.4)		P:GO:0006511: F:G(	P:ubiquitin-dependent protein catabolic process: F:ubiquitin prot	IPR001373 (PFAM): IPR019559 (PFA	49,606	48,781	91,939	96,655	87,200									
Solyc09g074690	Homeobox LUMINIDEPENDENS-like protein (AHRD V3.3 *-* A0A0B0NNT5_GOSAR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(HB-other	7,751	6,630	8,201	8,628	8,288									
Solyc09g074700	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *-* A0A0B2R2D8_GLYSO)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus	mobidb-lite (MOBIDB_LITE): mobidb-lit	3,270	2,597	3,236	2,882	3,085									
Solyc09g074710	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *-* A0A151TWD1_CAJCA)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus	mobidb-lite (MOBIDB_LITE): PTHR334	7,439	6,270	7,820	7,658	7,091									
Solyc09g074730	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *** A0A0B2S9W0_GLYSO)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus	mobidb-lite (MOBIDB_LITE): mobidb-lit	23,692	19,845	25,959	26,223	25,548									
Solyc09g074740	Metal tolerance-like protein (AHRD V3.3 *** A0A072VN24_MEDTR)		P:GO:0006812: F:G(	P:cation transport: F:cation transmembrane transporter activity:	IPR027469 (G3DSA:1.20.1510.GENE	6,526	4,568	8,489	8,148	6,989									
Solyc09g074750	Metal tolerance-like protein (AHRD V3.3 *** A0A072VNM6_MEDTR)		P:GO:0006812: F:G(	P:cation transport: F:cation transmembrane transporter activity:	IPR036837 (G3DSA:3.30.70.GENE3D	7,673	7,109	9,905	9,225	9,409									
Solyc09g074760	Nuclear transcription factor Y protein (AHRD V3.3 *** A0A072TR10_MEDTR)		F:GO:0046982	F:protein heterodimerization activity	PR00615 (PRINTS NF-YB	0,000	0,018	0,000	0,000	0,047									
Solyc09g074780	Zinc finger protein (AHRD V3.3 *** E9NZV2_PHAVU)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.6 C2H2	0,492	0,545	0,818	0,757	0,728									
Solyc09g074800	Potassium transporter (AHRD V3.3 *** M1AT44_SOLTU)		F:GO:0015079: C:G(	F:potassium ion transmembrane transporter activity: C:membrai	IPR003855 (TIGRFAM): IPR003855 (F	0,000	0,018	0,025	0,022	0,023									
Solyc09g074810	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT5G51790.2)		F:GO:0003677: P:G(	F:DNA binding: P:regulation of transcription by RNA polymerase	IPR036638 (G3DS bHLH	0,000	0,000	0,022	0,000	0,000									
Solyc09g074820	Potassium transporter (AHRD V3.3 *** M1AT44_SOLTU)		F:GO:0015079: C:G(	F:potassium ion transmembrane transporter activity: C:membrai	IPR003855 (PFAM): IPR003855 (TIGF	0,000	0,315	0,000	0,025	0,000									
Solyc09g074830	Protein kinase WEE1 (AHRD V3.3 *** Q2P9R8_SOLLC)	wee1	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati	IPR000719 (PFAM): G3DSA:3.30.200	1,485	1,154	0,352	0,389	0,350									
Solyc09g074840	kinetochore protein (AHRD V3.3 *** AT1G02960.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	35,502	24,575	23,661	24,905	24,109									
Solyc09g074850	Glutathione S-transferase (AHRD V3.3 *** Q42933_NICPL)	GSTF4	F:GO:0005515	F:protein binding	IPR004045 (PFAM): G3DSA:1.20.105	15,096	12,724	11,980	10,710	10,179									
Solyc09g074855	Cytochrome b-c1 complex subunit 6 (AHRD V3.3 *** A0A0V0GP56_SOLCH)		P:GO:0006122: F:G(	P:mitochondrial ele(EC:1.1.2: EC:1.1.2.2 Acting on diphenols a	IPR036811 (G3DSA:1.10.287.GENE3	0,038	0,019	0,046	0,022	0,117									
Solyc09g074860	DNA-directed RNA polymerase subunit beta N-terminal section (AHRD V3.3 --* RPOB1_PLETE)					0,222	0,206	0,194	0,244	0,189									
Solyc09g074870	Cytochrome b-c1 complex subunit 6 (AHRD V3.3 *** QCR6_SOLTU)		P:GO:0005975: P:G(	P:carbohydrate met EC:1.1.2: EC:1.1.2.2 Acting on diphenols a	IPR023184 (PFAM): IPR014718 (G3D	73,639	78,340	96,570	104,740	102,178									
Solyc09g074880	Photosystem I assembly protein ycf3 (AHRD V3.3 *** A0A1D1YLR6_9ARAE)		F:GO:0005515	F:protein binding	IPR021883 (PFAM): IPR011990 (G3D	11,006	17,303	10,042	9,923	17,349	0,681	0,023	0,786	0,000			up	up	
Solyc09g074890	Rapid alkalinization factor (AHRD V3.3 *** RALF_TOBAC)		C:GO:0009506: P:G(	C:plasmodesma; P:calcium-mediated signaling	IPR008801 (PFAM): PTHR33136 (PAN	2,612	4,339	8,907	6,722	5,570									
Solyc09g074900	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase (AHRD V3.3 *** ALG3_ARATH)		F:GO:0000030: C:G(	F:mannosyltransferase activity: C:integral component of endopl	IPR007873 (PFAM): IPR007873 (PAN	10,849	11,245	18,356	20,135	17,910									
Solyc09g074910	TSPO(Outer membrane tryptophan-rich sensory protein)-related (AHRD V3.3 *** A0A061DQD9_THECC)		C:GO:0016021	C:integral component of membrane	IPR004307 (PFAM): IPR004307 (PIRS	4,132	2,959	1,706	2,335	1,495									
Solyc09g074920	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G31600.4)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR037151 (G3DSA:2.60.120.GENE3	4,017	3,406	4,968	4,101	3,768									
Solyc09g074930	Rubber elongation factor (AHRD V3.3 *** C9E7B4_MORAL)		C:GO:0005811: C:G(	C:lipid droplet: C:membrane: P:lipid droplet organization: P:posit	IPR008802 (PFAM): mobidb-lite (MOB	133,854	87,588	44,431	45,501	40,750									
Solyc09g074940	(DB240) meloidogyne-induced giant cell protein		F:GO:0005525: F:G(	F:GTP binding; F:hydrolase activity, acting on acid anhydrides	IPR024283 (PFAM): IPR005690 (TIGF	83,964	92,090	89,472	84,657	98,105									
Solyc09g074950	ATPase family AAA domain-containing protein 1 (AHRD V3.3 *** A0A0B0NTB1_GOSAR)		F:GO:0005515: F:G(	F:protein binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): G3DS	136,680	93,729	136,890	136,664	130,431									
Solyc09g074960	Yellow stripe 1A transporter (AHRD V3.3 *** A0A0K9P9K5_ZOSMR)		P:GO:0055085	P:transmembrane transport	IPR004813 (TIGRFAM): IPR004813 (F	0,000	0,113	0,000	0,000	0,023									
Solyc09g074970	Thiamin pyrophosphokinase 1 (AHRD V3.3 *** A0A0B0NKA2_GOSAR)		F:GO:0004788: F:G(	F:thiamine diphospt EC:2.7.6.2 Thiamine diphosphok	IPR006282 (TIGRFAM): IPR036759 ((	0,319	0,619	0,093	0,095	0,191									
Solyc09g074990	DNA mismatch repair protein (AHRD V3.3 *** AT4G02460.1)		F:GO:0004788: F:G(	F:thiamine diphospt EC:2.7.6.2: EC:3.6.1 Thiamine diphosphok	G3DSA:2.30.42.20 (GENE3D): IPR00	5,546	3,956	2,818	2,986	3,281									
Solyc09g075000	Transducin/WD40 repeat protein (AHRD V3.3 *** G7LCS5_MEDTR)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	29,559	28,040	31,207	25,564	28,182									
Solyc09g075010	HSP20-like chaperones superfamily protein (AHRD V3.3 *-* AT4G02450.2)		C:GO:0005634: C:G(	C:nucleus: C:cytosol: C:plasma membrane: P:response to heat:	IPR007052 (PFAM): IPR008978 (G3D	151,964	184,368	235,925	226,646	213,114									
Solyc09g075020	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *** G7IF78_ABCC9		F:GO:0005524: C:G(	F:ATP binding: C:int EC:3.6.1.3: EC:3.6.1 Adenosinetriphospha	IPR011527 (PFAM): G3DSA:3.40.50.3	32,850	85,576	83,801	128,478	196,619	1,408	0,000	1,225	0,000			up	up	
Solyc09g075030	Nucleolar 16 (AHRD V3.3 *** A0A0B0MNY1_GOSAR)		C:GO:0005730: P:G(	C:nucleolus; P:ribosomal large subunit biogenesis	IPR019002 (PFAM): mobidb-lite (MOB	45,439	39,451	41,217	37,273	37,361									
Solyc09g075040	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4CV81_SOLLC)		F:GO:0016874: F:G(	F:ligase activity; F:metal ion binding	PF13920 (PFAM): IPR013083 (G3DS/	2,456	2,300	1,750	1,924	2,076									
Solyc09g075050	Mannose-binding lectin superfamily protein (AHRD V3.3 --* AT3G16460.2)					0,000	0,000	0,000	0,025	0,000									
Solyc09g075060	Beta-glucosidase, putative (AHRD V3.3 *** B9SAQ6_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb	IPR001360 (PRINTS): IPR001360 (PF	4,144	4,259	2,708	2,527	3,455									
Solyc09g075070	Beta-glucosidase, putative (AHRD V3.3 *** B9SAQ6_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb	IPR001360 (PRINTS): G3DSA:3.20.20	0,486	0,643	0,701	0,381	0,399									
Solyc09g075080	Phytochrome A-associated F-box protein, putative (AHRD V3.3 *** B9SAQ8_RICCO)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): IPR040267 (PAN	12,097	16,215	11,923	10,196	10,380									
Solyc09g075090	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G02840.2)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	60,709	54,801	55,057	50,301	51,560									
Solyc09g075100	Complex 1 family protein (AHRD V3.3 *** B9I9R9_POPTR)				IPR008011 (PFAM): PTHR13166:SF2	14,479	13,780	14,779	12,940	12,968									
Solyc09g075120	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 *** A0A0B0MR69_GOSAR)		C:GO:0016021: F:G(	C:integral compone EC:4.1.1.35 UDP-glucuronate dec	G3DSA:3.40.50.720 (GENE3D): IPR0	66,889	105,688	85,720	76,342	73,363	0,687	0,030					up		
Solyc09g075130	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT3G62840.1)		P:GO:0008380: C:G(	P:RNA splicing; C:small nuclear ribonucleoprotein complex	IPR001163 (PFAM): G3DSA:2.30.30.1	147,365	155,909	157,302	132,703	142,032									
Solyc09g075140	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G62860.1)		C:GO:0016020	C:membrane	IPR000073 (PRINTS): IPR022742 (PF	3,101	4,649	5,190	11,595	7,029					1,154	0,000			up
Solyc09g075150	60S ribosomal protein L22-2 (AHRD V3.3 *** RL222_ARATH)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR002671 (PFAM): IPR038526 (G3D	58,081	53,200	67,949	64,247	64,499									
Solyc09g075160	60S ribosomal protein L22-2 (AHRD V3.3 *** RL222_ARATH)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038526 (G3DSA:3.30.1360.GENE	10,164	11,944	6,106	6,866	6,086									
Solyc09g075180	cryptochrome DASH family protein				IPR006050 (PFAM): IPR014729 (G3D	54,117	80,126	188,742	195,349	186,822	0,594	0,022					up		
Solyc09g075190	Gamma-tubulin complex component (AHRD V3.3 *** K4CV96_SOLLC)		C:GO:0000922: C:G(	C:spindle pole: C:microtubule organizing center: P:microtubule n	IPR040457 (PFAM): IPR041470 (PFA	11,079	10,597	11,677	10,779	10,623									
Solyc09g075200	U1 small nuclear ribonucleoprotein (AHRD V3.3 *** A0A072UPG1_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	33,612	30,785	34,387	30,246	32,910									
Solyc09g075210	Late embryogenesis abundant protein Lea5 (AHRD V3.3 *** F2VPP8_SOLNI)		C:GO:0005739	C:mitochondrion	IPR004926 (PFAM): PTHR33509:SF5	30919,118	22049,430	10000,674	7370,853	9134,371					-0,438	0,022			down
Solyc09g075220	LOW QUALITY:pectinesterase (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT1G02816.1)				IPR036758 (G3DSA:2.30.240.GENE3	13,518	12,051	15,645	16,818	14,287									
Solyc09g075230	pectinesterase (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT1G02816.1)				IPR036758 (G3DSA:2.30.240.GENE3	6,229	5,292	9,989	9,315	9,583									
Solyc09g075260	pectinesterase (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G02816.1)				IPR036758 (G3DSA:2.30.240.GENE3	7,457	5,935	7,306	6,545	7,415									
Solyc09g075270	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G02360.1)				IPR007493 (PFAM): IPR036758 (G3D	0,529	0,743	1,211	2,465	1,552					1,005	0,025			up
Solyc09g075280	exocyst complex component sec15B (AHRD V3.3 *** AT4G02350.2)		C:GO:0000145: P:G(	C:exocyst; P:vesicle docking involved in exocytosis	IPR007225 (PIRSF): IPR007225 (PFA	35,960	38,183	37,376	37,897	43,319									
Solyc09g075290	60S ribosomal protein L18, putative (AHRD V3.3 *** B9SAT7_RICCO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR021131 (PFAM): G3DSA:3.100.10	111,494	135,475	82,028	77,863	79,293									
Solyc09g075300	Epoxide hydrolase, putative (AHRD V3.3 *** B9SAT9_RICCO)		F:GO:0003824	F:catalytic activity	IPR000639 (PRINTS): IPR000073 (PF	22,087	24,931	12,714	9,602	11,206									
Solyc09g075320	RING/U-box superfamily protein (AHRD V3.3 *** AT4G15975.1)		C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40.GENE3D	6,962	5,558	1,735	2,026	2,489									
Solyc09g075330	Pectinesterase (AHRD V3.3 *** K4CVB0_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a EC:3.1.1.11: EC:3.1. Pectinesterase: Cart	IPR006501 (TIGRFAM): IPR035513 ((	0,145	0,478	0,219	0,073	0,236									
Solyc09g075350	Pectinesterase (AHRD V3.3 *** K4CVB2_SOLLC)		F:GO:0004857: F:G(	F:enzyme inhibitor a EC:3.1.1.11: EC:3.1. Pectinesterase: Cart	IPR012334 (G3DSA:2.160.20.GENE3	0,059	0,462	0,072	0,025	0,000									
Solyc09g075360	endo-1,4-beta-glucanase precursor	U20590	F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb	IPR001701 (PFAM): IPR012341 (G3D	4,603	3,929	0,401	0,319	0,705									
Solyc09g075370	39S ribosomal protein L46, mitochondrial (AHRD V3.3 *** A0A0B2RLR6_GLYSO)		F:GO:0003735	F:structural constituent of ribosome	G3DSA:3.90.79.10 (GENE3D): IPR04	9,244	10,037	10,064	9,526	10,388									
Solyc09g075380	LOW QUALITY:CRS1 / YhbY (CRM) domain-containing protein (AHRD V3.3 --* AT4G29750.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE)	0,063	0,021	0,047	0,147	0,096									
Solyc09g075390	Rela-spot homolog family protein (AHRD V3.3 *** B9I9P5_POPTR)		P:GO:0015969	P:guanosine tetraphosphate metabolic process	IPR004095 (PFAM): G3DSA:1.10.321	53,772	66,598	82,407	80,327	88,738									
Solyc09g075400	cytidinediphosphate diacylglycerol synthase 4 (AHRD V3.3 --* AT2G45150.3)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane		0,314	0,291	0,050	0,000	0,024									
Solyc09g075410	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** B9GSD1_POPTR)				PF01190 (PFAM): PTHR33470 (PANT	0,019	0,000	0,000	0,000	0,000									
Solyc09g075420	ethylene response factor E.1	ERF.E1	F:GO:0003677: F:G(	F:DNA binding: F:DI EC:3.1.4.3: EC:3.1.4 Phospholipase C: Ph	IPR001471 (PRIN ERF	134,495	127,113	116,217	118,417	138,223									
Solyc09g075430	Ribosomal protein L19 (AHRD V3.3 *** K4CVC0_SOLLC)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: P:translatio	IPR000196 (PFAM): IPR015972 (G3D	389,959	435,199	362,504	304,130	326,338									
Solyc09g075440	Never ripe-2	ETR3	F:GO:0000155: F:G(	F:phosphorelay ser EC:2.7.13.3 Histidine kinase	IPR004358 (PRINTS): IPR003594 (PF	42,661	55,299	544,252	689,823	517,241									
Solyc09g075445	zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 --* AT1G57800.2)					3,045	3,414	34,879	57,809	38,193					0,730	0,000			up
Solyc09g075450	Fumarate hydratase (AHRD V3.3 *** G7IEJ2_MEDTR)		F:GO:0004333: P:G(	F:fumarate hydrata: EC:4.2.1.2 Fumarate hydratase	IPR000362 (PRINTS): IPR005677 (TI(	48,115	61,296	112,547	123,448	110,392									
Solyc09g075460	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G16850.1)	PG48-2	F:GO:0004650: P:G(	F:polygalacturonase EC:3.2.1.15 Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	64,397	41,849	33,193	51,905	45,150					0,647	0,002			up
Solyc09g075470	LOW QUALITY:DnaJ-like protein (AHRD V3.3 *** Q8H2B1_SOYBN)				IPR001623 (PRINTS): IPR001623 (PF	0,157	0,100	0,338	0,345	0,402									
Solyc09g075480	Kinesin-like protein (AHRD V3.3 *** F8UN41_TOBAC)		F:GO:0003777: F:G(	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	14,727	11,966	4,613	6,725	5,651									
Solyc09g075490	Mitochondrial substrate carrier family protein (AHRD V3.3 *** B9GSE1_POPTR)		F:GO:0022857: P:G(	F:transmembrane transporter activity: P:transmembrane transpo	IPR002067 (PRINTS): IPR023395 (G3	27,863	30,625	60,256	59,324	59,245									
Solyc09g075500	DUF789 family protein (AHRD V3.3 *** A0A072UTC8_MEDTR)				IPR008507 (PFAM): mobidb-lite (MOB	6,987	7,747	7,165	7,072	7,257									
Solyc09g075510	Dehydration-induced 19-like protein (AHRD V3.3 *** E3T7S4_GOSHI)				IPR027935 (PFAM): IPR008598 (PFA	8,378	14,941	10,119	11,210	11,580									
Solyc09g075530	Syntaxin (AHRD V3.3 *** A0A0A0YT45_ALBBR)		C:GO:0016020: P:G(	C:membrane; P:vesicle-mediated transport	G3DSA:1.20.58.70 (GENE3D): G3DS/	6,637	5,924	7,075	6,961	7,275									
Solyc09g075540	Protein COBRA, putative (AHRD V3.3 *** B9RZK6_RICCO)		P:GO:0010215: P:G(	P:cellulose microfibril organization: P:cell growth: C:anchored c(	IPR006918 (PFAM): PTHR31052 (PAN	0,098	0,041	0,143	0,075	0,118									
Solyc09g075550	Cellulose synthase (AHRD V3.3 *** A0A103XPU9_CYNCS)		C:GO:0016020: F:G(	C:membrane: F:cell EC:2.4.1.12 Cellulose synthase (U	IPR005150 (PFAM): IPR029044 (G3D	0,684	1,109	0,025	0,073	0,024									
Solyc09g075560	Hexosyltransferase (AHRD V3.3 *** K4CVD3_SOLLC)		F:GO:0016757	F:transferase activity, transferring glycosyl groups	IPR029044 (G3DSA:3.90.550.GENE3	15,027	8,092	2,790	3,927	3,765	-0,864	0,025					down		
Solyc09g075570	LOW QUALITY:Flagellar biosynthesis protein flhA (AHRD V3.3 *** A0A1D1Z6Y1_9ARAE)				PTHR33702:SF5 (PANTHER): PTHR3	9,898	8,343	6,212	7,441	5,885									
Solyc09g075580	LOW QUALITY:CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)		C:GO:0016021	C:integral component of membrane	PR01217 (PRINTS): mobidb-lite (MOB	0,422	0,396	0,269	0,245	0,118									
Solyc09g075590	LOW QUALITY:BnaA01g17710D protein (AHRD V3.3 *** A0A078H5Y0_BRANA)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,025	0,000	0,047									
Solyc09g075600	GATA transcription factor-like protein (AHRD V3.3 *** AT1G02700.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	22,290	17,849	16,156	16,164	21,054									
Solyc09g075610	GATA transcription factor, putative (AHRD V3.3 *** B9RNI7_RICCO)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans	IPR000679 (PFAM GATA	1,382	1,588	1,152	1,095	1,082									
Solyc09g075620	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A061DYZ4_THI		F:GO:0005525: C:G(	F:GTP binding; C:integral component of membrane	PTHR14241:SF18 (PANTHER): PTHR	0,019	0,000	0,000	0,025	0,000									
Solyc09g075640	Protein FAR1-RELATED SEQUENCE 11 (AHRD V3.3 *** A0A0B2PUA0_GLYSO)		P:GO:0006355: F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding	IPR004330 (PFAM FAR1	14,724	12,911	13,531	13,255	14,340									
Solyc09g075650	DUF3511 domain protein (AHRD V3.3 *** G7IEH6_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR021899 (PFAM): PTHR33193:SF1	0,019	0,021	0,000	0,025	0,000									
Solyc09g075670	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity	IPR029058 (G3DSA:3.40.50.GENE3D	0,481	1,852	1,341	0,673	0,968	1,924	0,014					up		
Solyc09g075700	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM): IPR029058 (G3D	0,000	0,000	0,025	0,000	0,000									
Solyc09g075710	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)		F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM): IPR029058 (G3D	0,038	0,059	0,000	0,000	0,046									
Solyc09g075720	Kinase family protein (AHRD V3.3 *** B9HLI5_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): G3DS	1,815	1,707	7,538	10,259	5,141									
Solyc09g075730	Leucine-rich repeat family protein / protein kinase family protein (AHRD V3.3 *** A0A0K9PIB6_ZOSMR)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	9,414	6,636	23,367	34,017	24,017					0,547	0,032			up
Solyc09g075750	membrane-associated kinase regulator (AHRD V3.3 *** AT5G26230.1)		C:GO:0005886: F:G(	C:plasma membrane; F:kinase inhibitor activity	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,120	0,380	0,000	0,124	0,188									
Solyc09g075760	cyclinT1_3	CycT1_3	F:GO:0003824	F:catalytic activity	IPR000873 (PFAM): G3DSA:1.10.472	74,457	72,212	113,169	130,389	117,226									
Solyc09g075770	Ethylene-responsive transcription factor, putative (AHRD V3.3 --* B9RBA8_RICCO)					0,000	0,018	0,000	0,000	0,000									
Solyc09g075780	Long-chain acyl-CoA synthetase 1 (AHRD V3.3 --* A0A088MTP0_9ERIC)		F:GO:0003824	F:catalytic activity		0,919	0,790	0,071	0,047	0,095									
Solyc09g075790	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0R5QM74_SALMI)		F:GO:0003824	F:catalytic activity	G3DSA:3.40.50.12780 (GENE3D): IPF	5,370	4,569	0,566	0,630	0,588									
Solyc09g075795	LOW QUALITY:NADH dehydrogenase subunit 7 (AHRD V3.3 *-* ATMG00510.1)		F:GO:0016651: F:G(	F:oxidoreductase activity, acting on NAD(P)H: F:quinone bindin(	IPR038290 (G3DSA:1.10.645.GENE3	0,298	0,329	0,459	0,405	0,286									
Solyc09g075800	Chloride channel protein (AHRD V3.3 *-* K4CVF7_SOLLC)		F:GO:0005247: P:G(	F:voltage-gated chloride channel activity: P:chloride transport: (	IPR002251 (PRINTS): IPR001807 (PF	32,484	24,949	37,201	40,321	37,466									
Solyc09g075810	Early nodulin-like protein (AHRD V3.3 *** A0A0K9P6C2_ZOSMR)		F:GO:0009055	F:electron transfer activity	IPR003245 (PFAM): IPR008972 (G3D	5,878	6,353	0,075	0,050	0,071									
Solyc09g075820	Sugar transporter protein 2	STP2	C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport	IPR003663 (PRINTS): G3DSA:1.20.12	1,602	17,747	4,563	5,159	7,873	3,489	0,000					up		
Solyc09g075830	Protein TIME FOR COFFEE-like protein (AHRD V3.3 *** A0A0B0MVU7_GOSAR)		P:GO:0042752	P:regulation of circadian rhythm	mobidb-lite (MOBIDB_LITE): mobidb-lit	285,705	228,839	339,866	376,405	349,717									
Solyc09g075850	Vacuole membrane 1 (AHRD V3.3 *** A0A0B0NWV3_GOSAR)		C:GO:0005783: C:G(	C:endoplasmic reticulum; C:integral component of membrane	IPR032816 (PFAM): PTHR10281 (PAN	17,004	15,915	22,170	26,597	23,554									
Solyc09g075860	Lipoxygenase (AHRD V3.3 *** A0A0V0IV70_SOLCH)	LOX6	F:GO:0005515: F:G(	F:protein binding: F: EC:1.13.11 Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	105,287	101,653	15,357	15,730	21,377									
Solyc09g075880	CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)					0,040	0,155	0,000	0,000	0,000									
Solyc09g075890	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** B7FKK9_MEDTR)		F:GO:0016787	F:hydrolase activity	G3DSA:1.10.150.450 (GENE3D): IPR(	60,728	51,947	13,114	16,485	17,262									
Solyc09g075900	Spermidine synthase (AHRD V3.3 *** F8WLB6_CITUN)		F:GO:0003824	F:catalytic activity	G3DSA:3.40.50.150 (GENE3D): PF01	1,734	2,397	0,000	0,000	0,023									
Solyc09g075910	Serine/threonine-protein kinase (AHRD V3.3 *** K4CVG8_SOLLC)		F:GO:0004674: F:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	IPR036426 (G3DSA:2.90.10.GENE3D	7,947	24,576	1,591	2,697	4,840			1,596	0,000				up	
Solyc09g075920	Serine/threonine-protein kinase (AHRD V3.3 *** K4CVG9_SOLLC)		F:GO:0004674: F:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	G3DSA:3.30.200.20 (GENE3D): IPR0	4,843	11,427	1,440	1,523	2,447									
Solyc09g075930	Amine oxidase (AHRD V3.3 *** K4CVH0_SOLLC)		F:GO:0005507: F:G(	F:copper ion bindin(EC:1.4.3.21 Primary-amine oxida:	IPR015798 (PFAM): IPR015802 (PFA	0,251	0,811	0,047	0,050	0,094									
Solyc09g075940	Amine oxidase (AHRD V3.3 *** K4CVH1_SOLLC)		F:GO:0005507: F:G(	F:copper ion bindin(EC:1.4.3.21 Primary-amine oxida:	IPR015802 (PFAM): IPR015800 (PFA	0,513	0,347	0,025	0,075	0,048									
Solyc09g075950	Heat shock protein 70 (AHRD V3.3 *** B9HJX1_POPTR)		F:GO:0005524: C:G(	F:ATP binding: C:cy EC:3.6.1.3: EC:3.6.1 Adenosinetriphospha	IPR013126 (PRINTS): IPR013126 (PF	38,068	17,539	287,246	246,556	244,076	-1,092	0,002					down		
Solyc09g075960	Plant/T24G3-80 protein (AHRD V3.3 *** G7I6W7_MEDTR)				IPR008586 (PFAM): PTHR31972:SF4	1,065	0,909	0,159	0,123	0,212									
Solyc09g075970	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G05370.1)				IPR036865 (G3DSA:3.40.525.GENE3	2,021	2,529	2,844	4,291	3,233									
Solyc09g075980	BnaA05g17230D protein (AHRD V3.3 *** A0A078FCG1_BRANA)				PTHR33181 (PANTHER): PTHR33181	0,874	1,513	0,856	0,728	0,450									
Solyc09g075990	5'-nucleotidase surE (AHRD V3.3 *** W9QLZ8_9ROSA)		F:GO:0008252	F:nucleotidase acti EC:3.1.3.31 Nucleotidase	IPR036523 (G3DSA:3.40.1210.GENE	5,295	4,657	7,596	7,392	6,706									
Solyc09g076000	MAP kinase kinase kinase 71	MAPKKK71	F:GO:0004674: F:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	IPR000719 (PFAM): G3DSA:1.10.510	19,681	13,703	22,094	22,235	29,404			0,408	0,025				up	
Solyc09g076010	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein, putative (AHRD V3.3 *** A0A061I		F:GO:0046872	F:metal ion binding	IPR032308 (PFAM): IPR013083 (G3D	51,451	47,534	59,828	64,046	60,815									
Solyc09g076020	Imidazoleglycerol-phosphate dehydratase (AHRD V3.3 *** K4CVH9_SOLLC)		P:GO:0000105: F:G(	P:histidine biosynth EC:4.2.1.19 Imidazoleglycerol-pho	IPR000807 (PFAM): IPR038494 (G3D	22,438	26,599	49,573	46,995	48,504									
Solyc09g076030	Photosystem II protein (AHRD V3.3 *-* A0A1D1ZBF0_9ARAE)		P:GO:0010207	P:photosystem II assembly	IPR038450 (G3DSA:1.20.58.GENE3D	4,673	7,845	3,835	4,892	5,734									
Solyc09g076040	Protein SUPPRESSOR OF GENE SILENCING 3 (AHRD V3.3 *** A0A1D1YP94_9ARAE)		P:GO:0031047	P:gene silencing by RNA	IPR038588 (G3DSA:3.30.70.GENE3D	134,411	115,665	163,549	150,499	158,621									
Solyc09g076050	FRIGIDA-like protein (AHRD V3.3 *** AT3G22440.1)		P:GO:0009908: P:G(	P:flower development; P:cell differentiation	IPR012474 (PFAM): mobidb-lite (MOB	191,526	169,058	183,263	172,915	188,779									
Solyc09g082050	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1 (AHRD V3.3 *** SUVH1_TOBAC)		F:GO:0005515: C:G(	F:protein binding: C EC:2.1.1.43 Histone-lysine N-met	IPR007728 (PFAM): IPR036987 (G3D	31,720	31,405	39,521	37,855	36,134									
Solyc09g082060	Cysteine synthase (AHRD V3.3 *** CYSK_SOLTU)		F:GO:0004124: P:G(	F:cysteine synthase EC:2.5.1.47 Cysteine synthase	G3DSA:3.40.50.1100 (GENE3D): IPR(	162,779	183,413	51,111	36,243	48,814									
Solyc09g082065	Preprotein translocase subunit SECE1 (AHRD V3.3 *** SECE1_ARATH)		P:GO:0009306: C:G(	P:protein secretion: C:chloroplast thylakoid membrane: F:P-P-b(	IPR038379 (G3DSA:1.20.5.GENE3D):	3,747	5,364	3,947	3,498	3,608									
Solyc09g082080	LOW QUALITY:ovate family protein 19	OFP19	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (TIGRFAM): IPR006458 (F	0,000	0,043	0,000	0,000	0,000									
Solyc09g082100	Seed maturation protein/ Late embryogenesis abundant protein (AHRD V3.3 *** A0A0K9PC32_ZOSMR)		C:GO:0005730: C:G(	C:nucleolus: C:cytosol: P:cellular ion homeostasis: P:response	IPR007011 (PFAM): PTHR31174 (PAN	0,715	1,107	1,155	3,802	0,372									
Solyc09g082110	Seed maturation protein/ Late embryogenesis abundant protein (AHRD V3.3 *** A0A0K9PC32_ZOSMR)				IPR007011 (PFAM): mobidb-lite (MOB	0,318	0,685	1,016	2,430	0,468									
Solyc09g082120	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT2G32090.1)		F:GO:0016829	F:lyase activity	IPR029068 (G3DSA:3.10.180.GENE3	24,844	28,791	22,667	22,813	26,890									
Solyc09g082130	spindle assembly abnormal protein (AHRD V3.3 *** AT3G22520.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	11,356	11,012	36,436	33,990	34,141									
Solyc09g082140	Protein OBERON 1-like protein (AHRD V3.3 *** A0A0B0NZZ1_GOSAR)				IPR032881 (PFAM): PTHR33345:SF2	15,054	15,204	13,780	11,784	12,102									
Solyc09g082150	LOW QUALITY:17.4 kDa class I heat shock protein (AHRD V3.3 --* HS174_ORYSJ)		C:GO:0016020	C:membrane	PTHR33879 (PANTHER): PTHR33879	0,968	1,076	1,710	1,252	1,439									
Solyc09g082160	Thioredoxin superfamily protein (AHRD V3.3 --* AT3G26060.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	9,267	9,661	19,892	18,699	19,247									
Solyc09g082170	Pentatricopeptide repeat-containing-like protein (AHRD V3.3 *** A0A0B0NLW2_GOSAR)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding	IPR002885 (PFAM): IPR002885 (PFA	0,717	1,039	2,609	3,084	2,883									

Solyc09g082190	LOW QUALITY:DUF1677 family protein (AHRD V3.3 *** G7K3P0_MEDTR)						IPR012876 (PFAM): mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc09g082200	Major facilitator superfamily protein (AHRD V3.3 *** AT2G32040.1)		C:GO:0016021	C:integral component of membrane			IPR039309 (PFAM): IPR004324 (TIGF	17,020	16,928	34,386	35,798	40,869									
Solyc09g082210	Senescence-associated family protein (AHRD V3.3 *** B9HUU5_POPTR)		P:GO:0009744; P:G(	P:response to sucrose; P:response to glucose; P:response to s			IPR007650 (PFAM): mobidb-lite (MOB	23,835	21,423	17,242	18,336	15,402									
Solyc09g082220	LOW QUALITY:Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** A0A072U473_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): G3DSA:3.40.630	1,468	2,050	0,165	0,050	0,000									
Solyc09g082230	LOW QUALITY:N-acetyltransferase, putative (AHRD V3.3 *** B9RTP4_RICCO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): G3DSA:3.40.630	5,386	19,218	1,153	1,330	1,692	1,859	0,000					up		
Solyc09g082240	Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** A0A072U473_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): G3DSA:3.40.630	3,265	10,708	0,748	0,979	0,897	1,734	0,000					up		
Solyc09g082250	Acetyltransferase (GNAT) domain protein (AHRD V3.3 *-* A0A072UXR7_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			G3DSA:3.40.630.30 (GENE3D): IPR0(	2,760	3,682	0,427	0,528	0,425									
Solyc09g082260	LOW QUALITY:Acetyltransferase (GNAT) domain protein (AHRD V3.3 *** A0A072UXR7_MEDTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR000182 (PFAM): G3DSA:3.40.630	0,322	0,458	0,025	0,000	0,000									
Solyc09g082270	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): G3DSA:1.10.11	0,159	0,436	0,140	0,334	0,376									
Solyc09g082280	Lipid transfer protein (AHRD V3.3 *** Q5MJA5_CAPAN)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding; C:integral component of membra			IPR016140 (PFAM): G3DSA:1.10.110	0,000	0,000	0,000	0,000	0,023									
Solyc09g082290	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9NBN8_POPTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph			G3DSA:1.10.110.10 (GENE3D): IPR0	0,000	0,018	0,022	0,025	0,000									
Solyc09g082330	SM80.1 Vicilin (AHRD V3.3 *** A0A158RFR1_SOLME)		F:GO:0045735	F:nutrient reservoir activity			IPR014710 (G3DSA:2.60.120.GENE3	0,309	0,575	0,071	0,353	0,046									
Solyc09g082340	vicilin	vicilin	F:GO:0045735	F:nutrient reservoir activity			IPR014710 (G3DSA:2.60.120.GENE3	1292,268	1695,856	149,558	468,620	27,884									
Solyc09g082350	Vicilin-like protein (AHRD V3.3 *-* Q9SEW4_9ROSI)		F:GO:0045735	F:nutrient reservoir activity			IPR014710 (G3DSA:2.60.120.GENE3	2,262	3,122	0,196	0,704	0,047									
Solyc09g082360	Globulin-1 (AHRD V3.3 *** A0A0F6Q0Q8_MAIZE)		F:GO:0045735	F:nutrient reservoir activity			IPR006045 (PFAM): IPR014710 (G3D	1,206	1,317	0,049	0,451	0,023									
Solyc09g082370	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** W9RZ96_9ROSA)		F:GO:0004439; F:G(	F:phosphatidylinosi	EC:3.1.3.36	Phosphoinositide 5-p	IPR036691 (G3DSA:3.60.10.GENE3D	2,832	3,108	1,120	1,499	1,877									
Solyc09g082380	ATP-dependent RNA helicase (AHRD V3.3 *** AT4G14790.2)		F:GO:0016817	F:hydrolase activity, acting on acid anhydrides			G3DSA:1.20.58.1080 (GENE3D): IPR(	2,319	2,400	3,635	4,079	3,457									
Solyc09g082390	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061ELP3_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	0,162	0,443	0,196	0,147	0,211									
Solyc09g082400	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SPW3_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,998	2,521	1,786	1,745	1,678									
Solyc09g082410	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT1G56690.1)							0,338	0,176	0,269	0,312	0,210									
Solyc09g082420	RNA-directed DNA methylation protein (AHRD V3.3 *** G7K3Q7_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:regulation of DNA methylation			IPR036319 (G3DSA:1.20.120.GENE3	0,058	0,000	0,025	0,072	0,071									
Solyc09g082430	RNA-directed DNA methylation protein (AHRD V3.3 *** G7K3Q7_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:regulation of DNA methylation			IPR015270 (PFAM): IPR036319 (G3D	0,000	0,000	0,025	0,000	0,000									
Solyc09g082440	RNA-directed DNA methylation protein (AHRD V3.3 *-* G7K3Q7_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:regulation of DNA methylation			IPR015270 (PFAM): IPR036319 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc09g082450	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HUS7_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,121	2,974	5,027	4,578	4,015									
Solyc09g082460	Homocysteine S-methyltransferase (AHRD V3.3 *** M1P405_PRUPE)		F:GO:0008270; P:G(	F:zinc ion binding; F	EC:2.1.1.5	Betaine--homocystei	IPR036589 (G3DSA:3.20.20.GENE3D	3,274	3,010	157,111	300,675	130,226					0,941	0,001			up
Solyc09g082470	Protein kinase family protein (AHRD V3.3 *** X5I191_IPONI)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): IPR001245 (PF	3,416	4,620	14,321	25,542	17,590					0,840	0,000			up
Solyc09g082490	Protein XRI1-like protein (AHRD V3.3 *** A0A0B0NEL0_GOSAR)		P:GO:0007140; P:G(	P:male meiotic nuclear division; P:female meiotic nuclear divisic			mobidb-lite (MOBIDB_LITE): IPR0399	7,146	7,109	9,294	9,515	8,995									
Solyc09g082500	Tesmin/TSO1-like CXC domain protein (AHRD V3.3 *** G7K3P9_MEDTR)						mobidb-lite (MOBIL_CPP	5,294	4,010	3,905	4,705	5,856									
Solyc09g082505	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 *-* AT3G22780.1)						IPR005172 (PFAM): mobidb-lite (MOB	4,496	3,888	3,201	4,095	3,944									
Solyc09g082510	Kinase interacting (KIP1-like) family protein, putative (AHRD V3.3 *** A0A061DQM7_THECC)		F:GO:0003779	F:actin binding			IPR011684 (PFAM): mobidb-lite (MOB	137,015	123,965	32,185	24,558	33,562									
Solyc09g082520	40S ribosomal protein S3a (AHRD V3.3 *** K4CVM9_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001593 (PFAM): mobidb-lite (MOB	223,933	205,018	202,962	182,784	185,845									
Solyc09g082530	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PTR8_ZOSMR)						IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc09g082540	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G04190.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	27,080	26,414	28,579	26,304	25,502									
Solyc09g082550	Sulfate transporter (AHRD V3.3 *** D7LTZ8_ARALL)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR001902 (TIGRFAM): IPR036513 ((	0,613	0,798	0,187	0,126	0,280									
Solyc09g082560	SUN-like protein 26	SUN26	F:GO:0005515	F:protein binding			IPR000048 (PFAM): IPR025064 (PFA	0,780	0,877	0,647	0,917	0,588									
Solyc09g082570	Neurogenic locus notch-like protein (AHRD V3.3 *** A0A072VSF9_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33881:SF5 (PANTHER): PTHR3	5,341	2,462	6,769	7,513	6,281	-1,084	0,015					down		
Solyc09g082580	auxin canalization protein (DUF828) (AHRD V3.3 *** AT3G22810.1)		P:GO:0009734; P:G(	P:auxin-activated signaling pathway; P:phloem or xylem histoge			IPR013666 (PFAM): IPR008546 (PFA	9,141	7,944	0,119	0,098	0,141									
Solyc09g082590	Bax inhibitor (AHRD V3.3 *** A0A0K1ETI6_TECGR)		C:GO:0016021	C:integral component of membrane			IPR006214 (PFAM): mobidb-lite (MOB	0,000	0,000	0,146	0,215	0,190									
Solyc09g082600	Chlorophyllase (AHRD V3.3 *** F1BPW6_SOLPN)	CLH3	P:GO:0015996; F:G(	P:chlorophyll catab	EC:3.1.1.14; EC:3.1.	Chlorophyllase; Carb	IPR017395 (PFAM): IPR029058 (G3D	1,691	0,318	0,000	0,000	0,000									
Solyc09g082620	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *-* AT4G14723.1)		P:GO:0010374	P:stomatal complex development			PF17181 (PFAM): IPR039455 (PANTH	0,078	0,112	0,000	0,025	0,000									
Solyc09g082630	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (AHRD V3.3 *** A0A0H2UIA1_SOLLC)		F:GO:0010309; P:G(	F:acireductone dio:	EC:1.13.11; EC:1.13	Acting on single donc	IPR004313 (PFAM): IPR014710 (G3D	48,345	42,311	45,311	37,282	43,844									
Solyc09g082650	acireductone dioxygenase		F:GO:0010309; P:G(	F:acireductone dio:	EC:1.13.11; EC:1.13	Acting on single donc	IPR004313 (PFAM): IPR014710 (G3D	418,380	395,330	1039,789	891,892	957,279									
Solyc09g082660	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** Q2YHM9_PLAMJ)		F:GO:0008171	F:O-methyltransferase activity			IPR002935 (PFAM): G3DSA:3.40.50.1	0,076	0,345	0,000	0,000	0,072									
Solyc09g082670	SolycHsfA6a	HSF-13	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN_HSF	0,500	0,453	0,633	0,190	0,423									
Solyc09g082680	Dymeclin (AHRD V3.3 *** A0A124SCE4_CYNCS),Pfam:PF09742		C:GO:0005794; P:G(	C:Golgi apparatus; P:Golgi organization			PF09742 (PFAM): IPR019142 (PANTH	10,346	7,268	8,357	10,464	7,754									
Solyc09g082690	superoxide dismutase	sod	C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			IPR022796 (PFAM): mobidb-lite (MOB	3,319	4,613	158,634	136,497	206,145									
Solyc09g082710	Histone H2A (AHRD V3.3 *** K4CVP7_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimei			IPR002119 (PRINTS): IPR032454 (PF	40,996	42,786	35,790	29,579	27,992									
Solyc09g082720	Aldo_keto reductase family protein_IPR001395_Aldo_keto reductase						IPR036812 (G3DSA:3.20.20.GENE3D	105,275	96,112	224,413	229,551	224,352									
Solyc09g082730	Aldo_keto reductase family protein_IPR001395_Aldo_keto reductase						IPR036812 (G3DSA:3.20.20.GENE3D	101,520	93,718	182,737	162,223	167,253									
Solyc09g082760	Aspartic proteinase (AHRD V3.3 *** A0A0B2PY44_GLYSO)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR008138 (PF	2,112	4,536	0,608	1,556	0,912	1,130	0,036					up		
Solyc09g082770	Transmembrane emp24 domain-containing protein p24beta3 (AHRD V3.3 *** P24B3_ARATH)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:endoplasmic reticulum-Golgi interme			IPR009038 (PFAM): PTHR22811:SF3	46,380	51,117	72,400	70,641	65,640									
Solyc09g082780	Stem-specific protein TSJT1 (AHRD V3.3 *** A0A0B0PHH6_GOSAR)						IPR029055 (G3DSA:3.60.20.GENE3D	69,110	65,663	41,639	39,607	48,225									
Solyc09g082790	Disrupted meiotic cDNA 1 protein (AHRD V3.3 *** B9VR62_WHEAT)		F:GO:0000150; F:G(	F:recombinase acti	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:1.10.150.20 (GENE3D): IPR0	3,683	2,577	5,509	2,874	4,332					-0,933	0,002			down
Solyc09g082800	LRR-RLK (AHRD V3.3 *** A0A127AUM6_VERFO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PF14381 (PFAM): G3DSA:1.10.510.1(	37,703	37,043	31,881	33,657	31,703									
Solyc09g082810	Glycine-rich protein (AHRD V3.3 *-* D2K2U0_TOBAC)						IPR010800 (PFAM): mobidb-lite (MOB	67,774	90,074	24,793	25,575	32,762									
Solyc09g082820	cytochrome P450, family 71, subfamily A, polypeptide 19 (AHRD V3.3 --* AT4G13290.1)							0,304	0,243	0,025	0,025	0,024									
Solyc09g082830	Argonaute 10a	AGO10a	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding			IPR014811 (PFAM): IPR032474 (PFA	19,623	12,001	12,576	13,426	11,159									
Solyc09g082840	Plant self-incompatibility protein S1 family (AHRD V3.3 -** AT4G16195.1)						IPR010264 (PFAM)	0,042	0,039	0,000	0,000	0,000									
Solyc09g082845	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 -** AT1G56385.1)						IPR010264 (PFAM)	0,038	0,332	0,000	0,000	0,000									
Solyc09g082850	LOW QUALITY:Calcium-dependent phosphotriesterase superfamily protein (AHRD V3.3 --* AT3G59530.3)							0,059	0,193	0,000	0,000	0,000									
Solyc09g082860	ATP-sulfurylase (AHRD V3.3 *** Q1W2K0_CAMSI)		P:GO:0000103; F:G(	P:sulfate assimilatic	EC:2.7.7.4	Sulfate adenylyltrans	IPR025980 (PFAM): G3DSA:3.10.400	5,450	10,517	15,706	39,261	33,335			1,085	0,000	1,326	0,000		up	up
Solyc09g082870	Calcium-transporting ATPase (AHRD V3.3 *** M1DTS0_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR001757 (TIGF	4,196	2,473	0,961	3,577	2,993			1,598	0,000	1,862	0,000		up	up
Solyc09g082880	LOW QUALITY:Calcium-transporting ATPase (AHRD V3.3 *-* M1DTS0_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR006068 (PFAM): G3DSA:1.20.11(	0,042	0,018	0,000	0,000	0,000									
Solyc09g082890	LOW QUALITY:Calcium-transporting ATPase (AHRD V3.3 *-* M1DHY7_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR001757 (TIGRFAM): PF00122 (PF	3,756	6,866	2,752	2,392	2,461									
Solyc09g082900	4-hydroxy-3-methylbut-2-enyl diphosphate synthase (AHRD V3.3 --* AT5G60600.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,102	0,101	0,000	0,025	0,046									
Solyc09g082920	LOW QUALITY:histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3-like protein (AHRD V3.3 --* AT1G17770.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,862	0,574	1,388	0,931	1,205									
Solyc09g082930	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT5G57565.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,135	0,158	0,025	0,075	0,000									
Solyc09g082940	G-protein gamma subunit 2 (AHRD V3.3 *** A0A061EU75_THECC)		P:GO:0007186	P:G protein-coupled receptor signaling pathway			IPR015898 (PFAM): PTHR32378 (PAN	5,650	5,355	7,706	6,015	7,428									
Solyc09g082950	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G07310.1)						IPR000008 (PFAM): IPR035892 (G3D	58,598	62,619	72,655	62,775	65,506									
Solyc09g082960	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT2G40640.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,041	0,025	0,000	0,000									
Solyc09g082970	Pyruvate kinase (AHRD V3.3 *** K4CVS3_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS): IPR015806 (G3	443,995	293,313	366,291	362,243	379,495	-0,571	0,045					down		
Solyc09g082975	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_PHYPA)							0,138	0,137	0,025	0,050	0,071									
Solyc09g082980	DUF506 family protein (AHRD V3.3 *** A0A072VMZ8_MEDTR)						IPR006502 (TIGRFAM): IPR006502 (F	101,092	134,425	112,955	71,535	93,589					-0,657	0,000			down
Solyc09g082990	GDP-mannose 3',5'-epimerase (AHRD V3.3 *** C6K2L0_SOLLC)	GME2	F:GO:0047918; F:G(	F:GDP-mannose 3,	EC:5.1.3.18	GDP-mannose 3,5-e	G3DSA:3.40.50.720 (GENE3D): G3DS	105,026	112,518	58,424	54,935	68,653									
Solyc09g083000	Armadillo repeat-containing protein LFR (AHRD V3.3 *** LFR_ARATH)		F:GO:0005515; P:G(	F:protein binding; P:chromatin remodeling; C:SWI/SNF superfar			IPR011989 (G3DSA:1.25.10.GENE3D	26,616	22,751	30,978	29,950	28,187									
Solyc09g083010	Endonuclease III homolog (AHRD V3.3 *** M1A6B0_SOLTU)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-(apurinic or apyrimidinic site) endonuclea			IPR003265 (PFAM): IPR023170 (G3D	6,892	10,262	5,822	5,276	6,871									
Solyc09g083020	Mannose-binding lectin superfamily protein (AHRD V3.3 *** AT1G05760.1)		F:GO:0030246	F:carbohydrate binding			IPR036404 (G3DSA:2.100.10.GENE3	47,895	73,424	23,649	22,523	28,659	0,643	0,017					up		
Solyc09g083030	LOW QUALITY:Mannose-binding lectin superfamily protein (AHRD V3.3 *** AT1G05760.1)		F:GO:0030246	F:carbohydrate binding			IPR036404 (G3DSA:2.100.10.GENE3	21,374	19,523	5,084	4,763	4,260									
Solyc09g083040	LOW QUALITY:Mannose-binding lectin superfamily protein (AHRD V3.3 *** AT1G05760.1)		F:GO:0030246	F:carbohydrate binding			IPR001229 (PFAM): IPR036404 (G3D	0,042	0,043	0,093	0,048	0,024									
Solyc09g083050	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1A6B6_SOLTU)		P:GO:0006633; C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR013601 (PFAM): IPR012392 (PIRS	0,665	0,733	0,094	0,391	0,185									
Solyc09g083060	U-box domain-containing protein 44 (AHRD V3.3 *** A0A151R6I4_CAJCA)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:cell			IPR003613 (PFAM): IPR011989 (G3D	21,820	86,657	15,499	33,307	36,853	2,012	0,000	1,245	0,000	1,104	0,000	up	up	up
Solyc09g083070	sporulation-specific protein (AHRD V3.3 *** AT4G14615.1)		C:GO:0005739; P:G(	C:mitochondrion; P:mitochondrial respiratory chain complex IV a			IPR018625 (PFAM): mobidb-lite (MOB	10,418	11,827	21,350	19,456	18,000									
Solyc09g083080	MAR-binding protein		F:GO:0030515; C:G(	F:snoRNA binding; C:box C/D snoRNP complex; C:small-subunit			G3DSA:1.10.150.460 (GENE3D): IPR(	86,788	95,655	77,092	65,632	66,280									
Solyc09g083090	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CVT6_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	55,298	44,357	13,912	9,074	12,909									
Solyc09g083100	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CVT6_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:3.30.3	63,577	43,443	68,263	70,867	72,384									
Solyc09g083105	Acylamino-acid-releasing enzyme (AHRD V3.3 *-* B6U4F7_MAIZE)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	PTHR42776:SF14 (PANTHER): PTHR	0,659	0,481	0,742	0,503	0,238									
Solyc09g083110	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XDL5_CYNCS)		F:GO:0005515; P:G(	F:protein binding; P:intracellular protein transport; P:vesicle-mec			IPR002885 (TIGRFAM): IPR011990 ((	8,168	8,917	12,429	11,408	11,514									
Solyc09g083120	Acylamino-acid-releasing enzyme, putative (AHRD V3.3 *** B9RTG2_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity			IPR001375 (PFAM): IPR029058 (G3D	3,581	5,487	2,771	3,350	2,735									
Solyc09g083130	Acylamino-acid-releasing enzyme (AHRD V3.3 *** A0A151R6E1_CAJCA)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity			IPR029058 (G3DSA:3.40.50.GENE3D	20,294	41,510	9,120	16,119	24,145	1,059	0,001	1,403	0,000	0,827	0,001	up	up	up
Solyc09g083150	NADH dehydrogenase-like complex N (AHRD V3.3 *** A0A0F7GZG2_9ROSI)		C:GO:0016020; F:G(	C:membrane; F:oxidoreductase activity, acting on NAD(P)H, qui			IPR020874 (PFAM): IPR020874 (PAN	9,916	15,947	7,595	8,497	16,761			1,135	0,000				up	
Solyc09g083160	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 -** G7K1L2_MEDTR)							0,019	0,000	0,000	0,000	0,000									
Solyc09g083170	Nodule Cysteine-Rich (NCR) secreted peptide (AHRD V3.3 -** G7K1L2_MEDTR)							0,310	1,830	0,000	0,000	0,000									
Solyc09g083190	NAD(P)H dehydrogenase 18 (AHRD V3.3 *** A0A061ELZ4_THECC)		P:GO:0006979; C:G(	P:response to oxidative stress; C:chloroplast			IPR034569 (PANTHER)	9,683	27,613	1,798	2,625	9,450	1,539	0,000	2,368	0,000			up	up	
Solyc09g083200	Receptor-like protein kinase (AHRD V3.3 *** W0TR82_ACAMN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	2,359	3,654	1,432	2,236	2,641									
Solyc09g083210	Receptor-like protein kinase (AHRD V3.3 *** W0TR82_ACAMN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	29,081	68,276	12,405	15,196	19,076	1,256	0,000	0,615	0,006			up	up	
Solyc09g083220	bHLH transcription factor 060		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS_bHLH	36,419	31,599	53,817	50,341	54,817									
Solyc09g083230	F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYNCS)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	5,625	4,353	6,866	7,702	6,287									
Solyc09g083240	F-Box protein, putative (AHRD V3.3 *-* Q6L3W3_SOLDE)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				3,324	2,429	4,281	4,328	3,978									
Solyc09g083260	Ion channel pollux-like protein (AHRD V3.3 *** A0A072VLS8_MEDTR)		P:GO:0006813; C:G(	P:potassium ion transport; C:integral component of membrane			G3DSA:3.40.50.720 (GENE3D): IPR0	2,493	1,966	0,917	0,989	1,250									
Solyc09g083270	rRNA-processing protein efg1 (AHRD V3.3 *** A0A199W0S6_ANACO)		P:GO:0006364	P:rRNA processing			IPR019310 (PFAM): mobidb-lite (MOB	11,315	12,078	10,613	11,654	11,431									
Solyc09g083280	auxin-regulated IAA1	IAA1	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			G3DSA:3.10.20.90 (GENE3D): IPR03	2,573	12,242	0,562	0,267	0,678	2,276	0,000					up		
Solyc09g083290	auxin-regulated IAA14	IAA14	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-			IPR033389 (PFAM): G3DSA:3.10.20.9	0,197	0,440	0,000	0,000	0,000									
Solyc09g083300	E3 ubiquitin protein ligase DRIP2 (AHRD V3.3 *-* DRIP2_ARATH)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,039	0,000	0,000	0,000									
Solyc09g083310	E3 ubiquitin ligase DRIP2-like protein (AHRD V3.3 *-* A0A0B0N1B0_GOSAR)		F:GO:0016874	F:ligase activity			IPR039642 (PANTHER): PTHR10825	1,778	1,170	0,000	0,025	0,000									
Solyc09g083320	PRA1 family protein (AHRD V3.3 *** K4CVV8_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane; P			IPR004895 (PFAM): PTHR19317:SF3	8,321	9,614	14,396	15,259	13,335									
Solyc09g083330	Phosphatidate cytidylyltransferase (AHRD V3.3 *** K4CVV9_SOLLC)		F:GO:0004605; C:G(	F:phosphatidate cyt	EC:2.7.7.41	Phosphatidate cytidy	IPR016720 (PIRSF): PF01148 (PFAM	1,351	1,064	1,070	1,106	0,989									
Solyc09g083340	DNA-directed RNA polymerase II subunit (AHRD V3.3 *** W9QJA8_9ROSA)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA pc	IPR036898 (G3DSA:3.30.1490.GENE	5,909	5,575	8,573	9,725	7,621									
Solyc09g083350	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic (AHRD V3.3 *** A0A0B0N0F1_GOSAR)		P:GO:0000373; F:G(	P:Group II intron splicing; F:RNA binding			IPR001890 (PFAM): IPR035920 (G3D	18,963	21,019	42,698	43,104	42,473									
Solyc09g083360	Basic helix-loop-helix (BHLH) family transcription factor (AHRD V3.3 --* A0A0K9PZ13_ZOSMR)		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM_bHLH	0,266	2,384	0,222	0,142	0,333									
Solyc09g083370	Ribosomal protein S19 family protein (AHRD V3.3 *** AT5G09510.1)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR002222 (PRINTS): IPR005713 (TI(	8,147	8,765	6,809	5,201	5,852									
Solyc09g083380	Histone H1 (AHRD V3.3 *-* H1_MAIZE)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome asser			IPR005819 (PRINTS): IPR005818 (PF	20,904	19,566	16,514	18,757	16,161									
Solyc09g083390	zinc knuckle (CCHC-type) family protein (AHRD V3.3 *-* AT5G43630.4)		F:GO:0003677; P:G(	F:DNA binding; P:transcription elongation from RNA polymerase			IPR004343 (PFAM): G3DSA:4.10.60.1	0,424	0,686	2,296	1,909	2,936									
Solyc09g083400	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT3G23090.4)						IPR027329 (PFAM): mobidb-lite (MOB	4,754	4,990	2,246	1,738	2,192									
Solyc09g083410	N-carbamyl-L-amino acid amidohydrolase (AHRD V3.3 *** G7I3Z0_MEDTR)		F:GO:0016813	F:hydrolase activity, acting on carbon-nitrogen (but not peptide)			G3DSA:3.40.630.10 (GENE3D): IPR0	78,382	74,072	113,757	105,387	104,517									
Solyc09g083420	CWF19-like protein 2 (AHRD V3.3 *** A0A151U7T1_CAJCA)						IPR006768 (PFAM): IPR006767 (PFA	67,792	49,918	54,503	49,430	50,359									
Solyc09g083440	PIN-I protein (AHRD V3.3 *** Q4FE22_SOLTU)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): IPR000864 (PF	0,423	1,642	0,051	0,444	0,071									
Solyc09g083445	Proteinase inhibitor 1 (AHRD V3.3 *** ICI1_SOLTU)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): G3DSA:3.30.10	34,795	92,444	1,044	2,297	3,412	1,439	0,000	1,691	0,019			up	up	
Solyc09g084450	proteinase inhibitor I		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): IPR000864 (PF	0,894	2,288	0,075	0,270	0,070									
Solyc09g084460	Proteinase inhibitor I (AHRD V3.3 *** Q43648_SOLTU)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): G3DSA:3.30.10	0,059	0,304	0,000	0,050	0,000									
Solyc09g084470	Wound-induced proteinase inhibitor 1 (AHRD V3.3 *** ICI1_SOLLC)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): IPR000864 (PF	0,019	0,099	0,000	0,000	0,000									
Solyc09g089530	PIN-I protein (AHRD V3.3 *** Q4FE22_SOLTU)		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc			IPR000864 (PRINTS): IPR000864 (PF	0,000	0,036	0,000	0,000	0,023									
Solyc09g089550	Zinc finger family protein (AHRD V3.3 *-* B9HF11_POPTR)		F:GO:0003677	F:DNA binding			IPR006456 (TIGRI_ZF-HD	11,787	10,928	18,249	23,221	18,021									
Solyc09g089560	MATH domain-containing protein (AHRD V3.3 *** W9QVS1_9ROSA)		F:GO:0005515	F:protein binding			IPR002083 (PFAM): IPR008974 (G3D	35,416	34,750	42,071	40,136	39,622									
Solyc09g089570	Agenet domain protein (AHRD V3.3 *** G7JN46_MEDTR)						IPR008395 (PFAM): PTHR31917 (PAN	0,428	0,310	0,739	0,318	0,541									
Solyc09g089580	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V	E8	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR005123 (PFA	254,032	370,193	14660,140	19354,425	12794,263					0,404	0,043			up
Solyc09g089590	LOW QUALITY:Zinc finger, C2H2 (AHRD V3.3 *** A0A103XIR7_CYNCS)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM):_C2H2	0,021	0,000	0,000	0,000	0,023									
Solyc09g089610	ethylene receptor-like protein (ETR6)	ETR6	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR014525 (PIRSF): IPR003661 (PFA	7,291	9,220	58,660	78,321	54,041									
Solyc09g089620	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A0K9PN07_ZOSMR)		F:GO:0003680	F:AT DNA binding			IPR014476 (PIRSF): IPR005175 (PFA	0,094	0,037	0,965	1,006	0,547									
Solyc09g089630	Bet1-like SNARE protein 1-1 (AHRD V3.3 *** I3S539_MEDTR)		P:GO:0015031; C:G(	P:protein transport; C:integral component of Golgi membrane			G3DSA:1.20.5.110 (GENE3D): IPR03	5,333	4,077	2,949	3,915	2,904									
Solyc09g089640	LOW QUALITY:Plant/T32M21-140 protein (AHRD V3.3 *** A0A072VGG8_MEDTR)						IPR021864 (PFAM): IPR007700 (PFA	4,052	3,108	4,719	8,634	4,843					0,867	0,001			up
Solyc09g089650	UMP-CMP kinase (AHRD V3.3 --* A0A0D2U7F1_GOSRA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,336	7,664	7,915	7,836	8,109									
Solyc09g089660	Actin-related protein (AHRD V3.3 *** A0A103XII1_CYNCS)		P:GO:0006338; C:G(	P:chromatin remodeling; C:Ino80 complex			G3DSA:3.90.640.10 (GENE3D): G3DS	28,697	27,793	40,440	39,727	38,871									
Solyc09g089670	HR-like lesion-inducing protein-like protein (AHRD V3.3 *** AT4G14420.1)		C:GO:0016021	C:integral component of membrane			IPR008637 (PFAM): PTHR31474 (PAN	20,062	24,320	16,330	19,834	15,675									
Solyc09g089680	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G04350.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,629	1,141	0,958	2,357	1,762					1,278	0,045			up
Solyc09g089690	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	24,953	20,358	7,000	7,603	13,213			0,908	0,000				up	
Solyc09g089700	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR027443 (G3DSA:2.60.120.GENE3	0,019	0,021	0,000	0,000	0,000									
Solyc09g089710	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,021	0,037	0,000	0,000	0,047									
Solyc09g089720	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,057	0,025	0,025	0,023									
Solyc09g089730	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	7,413	12,251	33,264	59,941	60,822			0,868	0,000	0,853	0,000		up	up
Solyc09g089740	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	1,321	1,859	5,213	5,840	5,189									
Solyc09g089750	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06650.2)		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			PTHR10209:SF122 (PANTHER): PTHI	0,199	0,295	0,660	0,791	0,777									

Solyc09g089770	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc09g089780	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,021	0,142	0,022	0,022	0,140									
Solyc09g089790	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,021	0,107	0,000	0,025	0,141									
Solyc09g089810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	0,000	0,000	0,000	0,025	0,000									
Solyc09g089820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	0,253	0,507	0,074	0,402	0,000									
Solyc09g089840	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT5G43450.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,000	0,000	0,025	0,025	0,000									
Solyc09g089850	CASP-like protein (AHRD V3.3 *** K4CW11_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021 (PAI	4,385	3,184	6,932	7,828	5,798									
Solyc09g089860	WAT1-related protein (AHRD V3.3 *** K4CW12_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM): mobidb-lite (MOBI	0,094	0,081	0,125	0,200	0,141									
Solyc09g089865	DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein (AHRD V3.3 --* AT1G31880.2)							0,221	0,215	0,238	0,338	0,258									
Solyc09g089870	bHLH transcription factor 061		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	20,240	16,045	23,316	20,856	19,474									
Solyc09g089880	Electron transfer flavoprotein beta-subunit, putative (AHRD V3.3 *** B9STH5_RICCO)		F:GO:0009055	F:electron transfer activity			IPR014730 (PFAM): IPR012255 (PIRS	30,141	35,096	46,252	46,534	45,540									
Solyc09g089890	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EMD3_THECC)		C:GO:0016021	C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	0,263	0,374	0,022	0,000	0,023									
Solyc09g089910	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R427_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,206	0,022	0,022	0,000									
Solyc09g089920	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R427_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,021	0,000	0,000	0,000									
Solyc09g089930	ethylene responsive factor E.2	ERF_E_2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,514	3,693	2,434	0,744	0,475	2,845	0,045			-1,687	0,001	up		down
Solyc09g089940	plant/protein (AHRD V3.3 *** AT5G43400.1)						IPR011205 (PIRSF): IPR011205 (PFA	148,007	190,068	129,207	111,464	114,073									
Solyc09g089950	LOW QUALITY:BEL1-like homeodomain 10 (AHRD V3.3 --* AT1G19700.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,931	7,402	0,000	0,000	0,000									
Solyc09g089970	LOW QUALITY:ABC-2 type transporter family protein (AHRD V3.3 --* AT3G55100.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc09g089980	transcription factor bHLH143 (AHRD V3.3 --* AT5G09460.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,892	6,147	0,000	0,000	0,000									
Solyc09g089990	Germin-like protein 1 (AHRD V3.3 *** B9NCV4_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR014710 (G3	0,040	0,018	0,000	0,000	0,000									
Solyc09g090020	Germin-like protein 1 (AHRD V3.3 *** A8QK89_VITVI)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR006045 (PF	4,570	4,154	2,014	1,441	1,997									
Solyc09g090030	Histone-lysine N-methyltransferase (AHRD V3.3 *** G7K6V9_MEDTR)		F:GO:0005515	F:protein binding			IPR001214 (PFAM): G3DSA:2.170.27(	6,863	7,254	5,882	5,187	5,089									
Solyc09g090040	Germin-like protein 1 (AHRD V3.3 *** B9NCV4_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR014710 (G3	36,966	40,408	13,396	10,814	15,137									
Solyc09g090050	Activating signal cointegrator 1 (AHRD V3.3 *** A0A0B0NUV2_GOSAR)		F:GO:0003713; C:G(	F:transcription coactivator activity; C:nucleus; P:positive regula			IPR007374 (PFAM): G3DSA:2.30.130	30,891	23,593	8,721	10,259	10,940									
Solyc09g090060	Serine/threonine-protein phosphatase (AHRD V3.3 *** O81955_CATRO)		F:GO:0016787	F:hydrolase activity			IPR006186 (PRINTS): IPR004843 (PF	26,645	23,664	27,418	26,592	23,586									
Solyc09g090070	phosphate transporter 1	pt1	F:GO:0005315; P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph			IPR004738 (TIGRFAM): IPR005828 (F	18,495	47,932	49,853	74,952	90,633									
Solyc09g090080	Phosphate transporter (AHRD V3.3 *** K0FGD5_9ERIC)		F:GO:0005315; P:G(	F:inorganic phosphate transmembrane transporter activity; P:ph			IPR005828 (PFAM): IPR004738 (TIGF	7,374	15,825	6,427	7,851	11,842			0,871	0,004				up	
Solyc09g090090	Phosphoenolpyruvate carboxylase kinase 2 (AHRD V3.3 *** Q84JP7_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRSI	1,742	0,651	0,453	0,409	0,356									
Solyc09g090100	cryptochrome 2	crypt2	P:GO:0009785; F:G(	P:blue light signaling pathway; F:blue light photoreceptor activity			IPR002081 (PRINTS): IPR014134 (TI(	73,491	57,807	82,935	84,037	77,945									
Solyc09g090105	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (AHRD V3.3 --* FHIT_ARATH)							2,601	2,952	2,338	2,608	2,562									
Solyc09g090110	Actin-depolymerizing factor (AHRD V3.3 *** A0A0B0PMX7_GOSAR)		F:GO:0003779; C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymei			IPR029006 (G3DSA:3.40.20.GENE3D	44,567	45,352	35,386	30,351	34,485									
Solyc09g090120	histone acetyltransferase subunit NuA4-domain protein (AHRD V3.3 *** AT4G14385.1)		C:GO:0000123; P:G(	C:histone acetyltransferase complex; P:histone acetylation			IPR015418 (PFAM): mobidb-lite (MOBI	8,721	8,141	6,593	5,425	5,909									
Solyc09g090130	R2R3MYB transcription factor 15	R2R3MYB15	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	4,798	4,521	2,841	2,310	1,979									
Solyc09g090140	ferredoxin 1	fer1	P:GO:0005975; P:G(	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	G3DSA:3.40.50.720 (GENE3D): IPR0(	681,604	718,142	672,977	557,701	634,866									
Solyc09g090150	11S storage globulin (AHRD V3.3 *** O82437_COFAR)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS): IPR014710 (G3	1471,999	1469,046	86,492	193,190	15,905									
Solyc09g090160	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A103XIQ5_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (PFAM): PF13637 (PFAM)	130,674	157,577	96,404	93,196	96,779									
Solyc09g090180	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT1G07090.1)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus; F			IPR006936 (PFAM): mobidb-lite (MOBI	7,276	4,417	2,229	1,236	0,846			-1,392	0,036				down	
Solyc09g090190	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G04430.3)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0(	115,862	167,947	47,985	47,335	52,344									
Solyc09g090200	Kinase family protein (AHRD V3.3 *** B9HKH3_POPTR)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR000719 (PFAM): IPR017892 (PFA	104,164	119,398	142,205	147,941	148,747									
Solyc09g090220	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7L3A6_ARALL)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	2,949	2,731	2,361	2,342	2,586									
Solyc09g090230	casein kinase I (AHRD V3.3 *-* AT4G14340.1)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): PTHF	1,631	1,470	1,238	1,194	1,250									
Solyc09g090240	casein kinase I (AHRD V3.3 *-* AT4G14340.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	1,609	1,793	1,229	1,282	1,252									
Solyc09g090250	Casein kinase, putative (AHRD V3.3 *** B9SS69_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	29,002	34,113	24,181	20,351	24,038									
Solyc09g090260	LOW QUALITY:C2H2 and C2HC zinc fingers superfamily protein (AHRD V3.3 --* AT3G01030.1)						mobidb-lite (MOBII C2H2	0,000	0,019	0,000	0,000	0,000									
Solyc09g090270	COP1-interacting-like protein (AHRD V3.3 *** G7I4V2_MEDTR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	118,676	93,829	80,547	78,976	84,064									
Solyc09g090280	Protein phosphatase 2c, putative (AHRD V3.3 *** B9SS62_RICCO)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR036457 (G3DSA:3.60.40.GENE3D	0,931	0,972	1,851	2,144	1,389									
Solyc09g090290	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT3G23370.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	9,782	9,173	9,885	6,889	7,415									
Solyc09g090300	DCTP pyrophosphatase 1 (AHRD V3.3 *** A0A061ENZ8_THECC)		P:GO:0009143; F:G(	P:nucleoside tripho:	EC:3.6.1.19	Acting on acid anhyd	G3DSA:1.10.287.1080 (GENE3D): IPF	0,452	0,580	0,775	0,678	0,662									
Solyc09g090310	Glycolipid transfer protein domain-containing protein (AHRD V3.3 *** A0A103Y7C8_CYNCS)		C:GO:0005737; P:G(	C:cytoplasm; P:intermembrane lipid transfer; F:intermembrane li			IPR014830 (PFAM): IPR036497 (G3D	0,000	0,041	0,000	0,000	0,000									
Solyc09g090320	Kinesin, motor domain-containing protein (AHRD V3.3 *** A0A103XI34_CYNCS)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	0,135	0,296	0,162	0,172	0,141									
Solyc09g090330	harpin binding protein 1	hrbp1					IPR006843 (PFAM): PTHR31906:SF1	14,693	24,250	47,821	42,777	51,001	0,749	0,002					up		
Solyc09g090340	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G14310.1)		C:GO:0005618	C:cell wall			mobidb-lite (MOBIDB_LITE): mobidb-lit	10,567	12,710	4,677	4,088	4,544									
Solyc09g090350	Long-chain-alcohol oxidase (AHRD V3.3 *** K4CW61_SOLLC)		F:GO:0046577; F:G(	F:long-chain-alcoho	EC:1.1.3.2	Long-chain-alcohol o	IPR000172 (PFAM): IPR012400 (PIRS	0,476	0,367	0,116	0,120	0,373									
Solyc09g090360	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0PBG6_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR004342 (PFAM): IPR004331 (PFA	6,475	5,825	4,034	4,355	5,139									
Solyc09g090370	Transcription factor GTE1 (AHRD V3.3 *** A0A0B2PDN7_GLYSO)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			IPR001487 (PRINTS): IPR001487 (PF	13,226	11,664	21,530	22,291	18,350									
Solyc09g090380	Embryo sac development arrest 6, putative (AHRD V3.3 *** A0A061EM44_THECC)		P:GO:0009561; P:G(	P:megagametogenesis; P:embryo development ending in seed (			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,415	8,570	10,468	9,301	9,563									
Solyc09g090390	2-oxoglutarate-dependent dioxygenase AOP2 (AHRD V3.3 --* AOP2V_ARATH)						PTHR39110 (PANTHER)	2,595	2,519	0,087	0,025	0,000									
Solyc09g090400	Translation initiation factor eIF-2B protein (AHRD V3.3 *** G7JWC0_MEDTR)		P:GO:0044237	P:cellular metabolic process			G3DSA:3.40.50.10470 (GENE3D): IPF	6,923	7,126	4,480	1,726	3,294					-1,367	0,001			down
Solyc09g090410	50S ribosomal protein L28, chloroplastic (AHRD V3.3 *** RK28_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001383 (TIGRFAM): IPR037147 ((	9,829	18,832	12,969	14,747	20,822	0,965	0,001	0,682	0,000			up	up	
Solyc09g090420	Splicing factor u2af large subunit, putative (AHRD V3.3 *** B9SS44_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	51,995	50,359	59,303	56,848	57,244									
Solyc09g090430	Cyanate hydratase (AHRD V3.3 *** M1BFS5_SOLTU)		F:GO:0003677; F:G(	F:DNA binding; F:cy	EC:4.2.1.14	Cyanase	IPR008076 (PRINTS): IPR003712 (PF	13,137	18,900	15,509	22,123	23,166			0,574	0,003	0,513	0,006		up	up
Solyc09g090440	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y2G7_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,281	2,655	2,189	2,768	2,865									
Solyc09g090445	Mannose-binding lectin (AHRD V3.3 *-* A0A103XWY0_CYNCS)		F:GO:0030246	F:carbohydrate binding			IPR036404 (G3DSA:2.100.10.GENE3I	0,744	0,749	0,418	0,464	0,280									
Solyc09g090460	Nucleolar GTP-binding protein 1 (AHRD V3.3 *** W9R5G2_9ROSA)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): IPR030389 (PF	16,481	21,257	22,629	25,817	27,150									
Solyc09g090470	Peptide transporter (AHRD V3.3 *** G7I4R9_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	2,624	2,704	1,612	2,511	2,236									
Solyc09g090500	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *** AT3G23510.1)		P:GO:0008610	P:lipid biosynthetic process			G3DSA:3.40.50.150 (GENE3D): IPR0(	0,019	0,039	0,025	0,025	0,094									
Solyc09g090510	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *** AT3G23510.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00419 (PRINTS): PF02353 (PFAM)	8,926	35,181	0,455	0,481	1,059	2,005	0,000					up		
Solyc09g090515	PDI-like 5-4 (AHRD V3.3 --* AT4G27080.2)							10,820	10,990	12,207	10,090	9,235									
Solyc09g090520	RNA-binding protein-like (AHRD V3.3 *-* Q8L779_ARATH)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	253,903	234,819	246,656	221,419	217,527									
Solyc09g090530	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G15570.3)		P:GO:0007142	P:male meiosis II			mobidb-lite (MOBIDB_LITE): IPR0393(	0,019	0,148	0,000	0,072	0,000									
Solyc09g090540	Low affinity potassium transport system protein (AHRD V3.3 --* AT1G22790.2)		P:GO:0009642	P:response to light intensity			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,785	1,456	1,951	2,229	1,652									
Solyc09g090550	Actin-related protein 2/3 complex subunit 2 (AHRD V3.3 *** A0A061EMV9_THECC)		C:GO:0005885; P:G(	C:Arp2/3 protein complex; P:Arp2/3 complex-mediated actin nuc			IPR034666 (G3DSA:3.30.1460.GENE	0,315	0,314	0,196	0,123	0,094									
Solyc09g090553	plant viral-response family protein (DUF716) (AHRD V3.3 --* AT5G13890.3)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR006904 (PFAM): IPR006904 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc09g090570	proton gradient regulation 5 (AHRD V3.3 *** AT2G05620.2)		P:GO:0009644; P:G(	P:response to high light intensity; P:photosynthetic electron trar			IPR037497 (PANTHER)	16,811	22,528	9,529	13,384	15,582			0,701	0,003				up	
Solyc09g090580	translation initiation factor iso4E	eifiso4e	F:GO:0003743; C:G(	F:translation initiation factor activity; C:cytoplasm; P:translation			IPR023398 (G3DSA:3.30.760.GENE3I	227,471	227,238	156,633	144,805	144,188									
Solyc09g090600	Acid phosphatase 1 (AHRD V3.3 *** A0A0B2QYK4_GLYSO)		F:GO:0003993	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR010028 (TIGRFAM): IPR005519 (F	0,363	0,786	0,000	0,045	0,000									
Solyc09g090610	50S ribosomal protein L14 (AHRD V3.3 *** A0A0K9PMD0_ZOSMR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000218 (PFAM): IPR036853 (G3D	41,170	47,315	36,519	26,093	30,944					-0,483	0,004			down
Solyc09g090620	Disease resistance family protein (AHRD V3.3 *-* B9NHG2_POPTR)		F:GO:0043531	F:ADP binding			IPR041118 (PFAM): PTHR43886:SF8	2,384	3,745	0,698	0,633	0,589									
Solyc09g090630	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9RT47_9ROSA)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR001214 (PFAM): IPR007728 (PFA	0,980	2,039	0,118	0,292	0,236									
Solyc09g090640	DUF3527 domain protein (AHRD V3.3 *** A0A072VKV6_MEDTR)						IPR021916 (PFAM): PTHR31390:SF2	80,721	50,044	98,205	155,087	139,028	-0,665	0,020	0,499	0,006	0,661	0,000	down	up	up
Solyc09g090650	CCT motif protein (AHRD V3.3 *** A0A072VLD7_MEDTR)		F:GO:0005515	F:protein binding			IPR010402 (PFAM): PTHR31717 (PAI	0,628	0,543	0,244	0,216	0,234									
Solyc09g090660	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* A0A0K9PSA6_ZOSMR)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:Prp19 complex; F:protein			IPR003613 (PFAM): IPR001680 (PFA	13,421	12,373	11,492	11,395	10,134									
Solyc09g090670	Oxidation resistance 1 (AHRD V3.3 *** A0A0B0PUF7_GOSAR)						IPR006571 (PFAM): mobidb-lite (MOBI	4,428	4,277	0,898	1,233	1,157									
Solyc09g090680	Cysteine-rich repeat secretory protein (AHRD V3.3 *** A0A0K9P487_ZOSMR)		C:GO:0009506; P:G(	C:plasmodesma; P:plasmodesmata-mediated intercellular transı			IPR002902 (PFAM): IPR038408 (G3D	1,262	1,600	0,855	0,756	0,965									
Solyc09g090690	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, putative (AHRD V3.3 *** A0A06		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			G3DSA:3.40.50.150 (GENE3D): PTHF	6,702	6,470	13,528	13,755	11,005									
Solyc09g090700	Aldehyde dehydrogenase (AHRD V3.3 *** A0A0V0ICD2_SOLCH)		F:GO:0009013; P:G(	F:succinate-semialc	EC:1.2.1.16	Succinate-semialdeh	IPR016162 (G3DSA:3.40.605.GENE3I	78,793	79,624	125,251	121,416	122,078									
Solyc09g090710	pfkB-like carbohydrate kinase family protein (AHRD V3.3 --* AT5G43910.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,179	5,954	12,640	15,585	11,899									
Solyc09g090720	26S proteasome regulatory subunit family protein (AHRD V3.3 *** B9MU88_POPTR)		F:GO:0005198; C:G(	F:structural molecule activity; C:nucleus; C:cytosol; P:ubiquitin-(			IPR000717 (PFAM): G3DSA:1.25.40.5	4,680	4,199	5,422	4,435	3,879									
Solyc09g090730	AMT1	amt1	F:GO:0008519; C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR024041 (PFAM): IPR001905 (TIGF	0,792	8,536	0,999	1,514	3,291	3,440	0,000	1,712	0,003			up	up	
Solyc09g090740	RNA helicase DEAD29	DEAD29	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	26,815	26,942	24,241	25,594	23,681									
Solyc09g090750	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7I2P1_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR006439 (TIGRFAM): G3DSA:1.10.:	0,281	0,243	0,578	0,576	0,332									
Solyc09g090760	FBT8 (AHRD V3.3 *** A0A161CAZ7_POPTO)		C:GO:0016021; F:G(	C:integral component of membrane; F:hydrolase activity			IPR006439 (TIGRFAM): PF13242 (PF	13,640	6,416	17,772	21,571	18,761	-1,056	0,009					down		
Solyc09g090770	calcium uniporter (DUF607) (AHRD V3.3 --* AT1G57610.4)		C:GO:0016021	C:integral component of membrane				0,731	0,499	0,327	0,259	0,212									
Solyc09g090775	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061F1A8_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (TIGF	1,186	1,211	2,124	1,966	1,388									
Solyc09g090790	R2R3MYB transcription factor 79	R2R3MYB79	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,178	0,378	2,839	7,120	2,564					1,322	0,001			up
Solyc09g090800	AWPM-19-like membrane family protein (AHRD V3.3 *** B9HSV5_POPTR)		C:GO:0016021	C:integral component of membrane			IPR008390 (PFAM): mobidb-lite (MOBI	0,844	3,305	2,225	5,528	0,441									
Solyc09g090810	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9P7F6_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR007728 (PFAM): IPR003105 (PFA	32,662	20,959	23,893	18,002	23,391									
Solyc09g090820	phospholipase D alpha 2 (AHRD V3.3 --* AT1G52570.3)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,647	7,771	8,656	7,472	7,788									
Solyc09g090830	BolA-like protein, expressed (AHRD V3.3 *** Q10PW0_ORYSJ)						G3DSA:3.30.300.9 GRAS	6,593	7,200	4,169	4,588	4,495									
Solyc09g090835	GRAS family transcription factor, putative (AHRD V3.3 *-* A0A061DR51_THECC)						IPR005202 (PFAM): PTHR31636 (PAI	0,317	0,543	0,605	0,675	0,594									
Solyc09g090840	Glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial (AHRD V3.3 *** K4CWB0_SOLL		F:GO:0016884	F:carbon-nitrogen ligase activity, with glutamine as amido-N-dor			IPR018027 (PFAM): IPR006075 (PFA	17,713	20,571	37,406	37,773	44,846									
Solyc09g090850	Adenine nucleotide alpha hydrolases-like superfamily protein, putative (AHRD V3.3 *** A0A061EN15_THECC		F:GO:0016787	F:hydrolase activity			IPR006016 (PFAM): mobidb-lite (MOBI	0,262	0,307	0,216	0,317	0,235									
Solyc09g090860	Protein transport sec20 (AHRD V3.3 *** A0A0B0MVD3_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR005606 (PFAM): IPR005606 (PAN	3,289	3,355	3,614	3,751	2,848									
Solyc09g090870	DNA mismatch repair protein 1	msh1	F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	18,563	19,236	14,350	13,906	15,059									
Solyc09g090873	PETER PAN-like protein (AHRD V3.3 --* AT5G61770.3)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process				0,061	0,021	0,050	0,095	0,024									
Solyc09g090880	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --*		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process				0,000	0,000	0,025	0,051	0,000									
Solyc09g090890	DNA mismatch repair protein (AHRD V3.3 *-* Q1XBQ6_SOLLC)		F:GO:0003684; F:G(	F:damaged DNA bir	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR11361:SF82 (PANTHER): PTHR	0,329	0,447	0,524	0,609	0,543									
Solyc09g090900	Aconitate hydratase (AHRD V3.3 *** A0A059LL79_9CHLO)		F:GO:0003861; P:G(	F:3-isopropylmalate	EC:4.2.1.33	3-isopropylmalate de	IPR001030 (PRINTS): IPR015931 (G3	28,637	46,526	11,239	13,804	25,812	0,727	0,011	1,195	0,000			up	up	
Solyc09g090910	auxin-regulated IAA13	IAA13	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			IPR033389 (PFAM): G3DSA:3.10.20.9	17,314	14,685	0,929	0,761	0,944									
Solyc09g090920	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** G7I6R0_MEDTR)						IPR000008 (PFAM): IPR035892 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc09g090930	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT1G04530.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	6,658	6,404	7,892	6,260	7,741									
Solyc09g090940	Nuclear transport factor 2 (AHRD V3.3 *** A0A103Y0S2_CYNCS)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR002075 (PFA	38,164	41,766	34,173	32,408	33,131									
Solyc09g090950	Far-red impaired responsive (FAR1) family protein (AHRD V3.3 -** AT3G59470.3)							4,105	4,543	3,695	3,672	3,765									
Solyc09g090960	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G60000.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	20,575	39,016	32,811	33,088	50,605	0,951	0,000	0,623	0,000			up	up	
Solyc09g090970	Major allergen Pru ar 1 (AHRD V3.3 *** A0A0B2QY84_GLYSO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (PF	0,386	1,673	0,959	5,351	0,819	2,116	0,033					up		
Solyc09g090980	Major allergen Mal d 1 (AHRD V3.3 *** Q84LA7_MALDO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (PF	66,094	48,527	34,767	33,718	57,954			0,732	0,001				up	
Solyc09g090990	PR10 protein (AHRD V3.3 *** K4CWC5_SOLLC)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR023393 (G3	0,000	0,018	0,000	0,000	0,071									
Solyc09g091000	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR000916 (PF	0,100	1,518	1,153	1,244	3,207									
Solyc09g091010	Transmembrane protein, putative (AHRD V3.3 *** G7I6P2_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	23,385	23,411	8,393	8,087	13,103			0,636	0,032				up	
Solyc09g091020	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7KYK1_MEDTR)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	61,342	60,845	94,834	110,969	103,332									
Solyc09g091030	Beta-amylase 1		P:GO:0000272; F:G(	P:polysaccharide ca	EC:3.2.1.2	Beta-amylase	IPR001371 (PRINTS): IPR001554 (PF	195,243	316,507	435,880	496,422	466,986									
Solyc09g091040	Late embryogenesis abundant protein (AHRD V3.3 *** F2YQ25_9MAGN)						mobidb-lite (MOBIDB_LITE): IPR0396:	0,019	0,000	0,000	0,047	0,096									
Solyc09g091050	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *-* AT5G04220.1)		P:GO:0006629	P:lipid metabolic process			IPR035892 (G3DSA:2.60.40.GENE3D	82,231	68,661	271,775	247,888	257,572									
Solyc09g091060	UPF0329 protein ECU01_0100/ECU01_1510/ECU08_0030, putative isoform 2 (AHRD V3.3 *** A0A061ELC2_THECC)						PTHR37226 (PANTHER)	0,693	0,496	0,358	0,309	0,093									
Solyc09g091070	Malate dehydrogenase (AHRD V3.3 *** A0A061G4A3_THECC)		P:GO:0005975; P:G(	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR015955 (G3DSA:3.90.110.GENE3I	19,509	25,893	69,128	73,534	77,085									
Solyc09g091080	myosin XI A (AHRD V3.3 *** AT1G04600.1)		F:GO:0003774; F:G(	F:motor activity; F:a	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PFAM): G3DSA:1.20.58.5	0,097	0,080	0,000	0,000	0,024									
Solyc09g091090	flavin monooxygenase-like protein		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.:	Flavin-containing mo	PR00368 (PRINTS): PR00469 (PRINT	0,063	0,772	0,093	0,212	0,164									
Solyc09g091100	coenzyme F420 hydrogenase_dehydrogenase beta subunit-like		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR007516 (PFAM): IPR007525 (PFA	18,915	21,091	17,413	20,777	25,644			0,557	0,002				up	
Solyc09g091120	Heavy meromyosin-like protein, putative (AHRD V3.3 *** A0A072VST2_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	36,269	36,154	32,087	34,367	33,623									
Solyc09g091140	Glutathione s-transferase, putative (AHRD V3.3 *** B9RWR5_RICCO)	GSTU48	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): IPR00	0,000	0,021	0,022	0,050	0,023									
Solyc09g091150	F-box family protein (AHRD V3.3 *-* A0A061EM39_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	10,319	13,369	8,507	8,875	9,415									
Solyc09g091160	F-box domain containing protein (AHRD V3.3 *-* B6TYX2_MAIZE)		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE)	11,475	17,947	9,984	11,817	11,058									
Solyc09g091170	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 (AHRD V3.3 *** A0A151U305_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR009346 (PFAM): IPR009346 (PAN	68,504	68,265	113,121	98,300	104,419									
Solyc09g091180	Chaperonin CPN60, mitochondrial (AHRD V3.3 *** CH60A_ARATH)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR027409 (G3	98,968	124,305	170,187	150,172	155,794									
Solyc09g091190	PHD finger protein ING (AHRD V3.3 *** K4CWE5_SOLLC)		C:GO:0005634; P:G(	C:nucleus; P:chromatin organization; F:methylated histone bindi			IPR013083 (G3DSA:3.30.40.GENE3D	15,246	13,794	24,388	21,286	21,916									
Solyc09g091220	F-box associated interaction domain-containing protein (AHRD V3.3 *-* A0A103XHT5_CYNCS)		C:GO:0016021	C:integral component of membrane			PTHR44355 (PANTHER)	0,019	0,021	0,025	0,025	0,024									
Solyc09g091230	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein, putative (AHRD V3.3 *** A0A06		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): mobidb-lite (MOBI	5,464	5,251	3,983	3,516	4,051									
Solyc09g091240	GDT1-like protein (AHRD V3.3 *** A0A072VSW1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001727 (PFAM): mobidb-lite (MOBI	14,522	20,085	28,357	29,597	32,600									
Solyc09g091250	GATA transcription factor, putative (AHRD V3.3 *** B9RWP4_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transı			IPR013088 (G3DS GATA	24,064	26,871	19,839	17,554	19,614									
Solyc09g091260	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CWF2_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM): IPR032675 (G3D	3,463	3,737	2,536	3,089	2,570									
Solyc09g091270	cotton fiber protein (AHRD V3.3 *** AT5G13880.2)						IPR008480 (PFAM): PTHR33450 (PAI	1,825	1,088	0,570	0,875	0,613									

Solyc09g091280	Retinoblastoma-related protein 1 (AHRD V3.3 *** H9E8V1_SOLLC)		P:GO:0000082; C:G(	P:G1/S transition of mitotic cell cycle; C:nucleus; P:regulation o			IPR024599 (PFAM); IPR002720 (PFA	35,483	34,896	38,317	30,505	31,695									
Solyc09g091290	LOW QUALITY:Plant self-incompatibility S1 (AHRD V3.3 *** A0A118JZS1_CYNCS)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF5	0,021	0,000	0,000	0,000	0,000									
Solyc09g091300	LOW QUALITY:S-protein homologue (AHRD V3.3 *** Q9AVU9_SOLLC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF5	0,019	0,081	0,000	0,000	0,000									
Solyc09g091320	LOW QUALITY:Plant self-incompatibility S1 (AHRD V3.3 *** A0A118JZS1_CYNCS)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF1	0,103	0,253	0,000	0,000	0,000									
Solyc09g091340	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT3G17080.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF5	0,021	0,132	0,000	0,000	0,000									
Solyc09g091350	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT3G17080.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF5	0,038	0,174	0,000	0,000	0,000									
Solyc09g091370	holliday junction resolvase (AHRD V3.3 *** AT1G04650.1)						IPR027902 (PFAM); PTHR36702 (PAI	2,353	1,678	0,865	0,759	0,964									
Solyc09g091380	LOW QUALITY:WUSCHEL-related homeobox 3A (AHRD V3.3 --* WOX3A_MAIZE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	11,068	7,094	0,173	0,325	0,000									
Solyc09g091390	GATA transcription factor 18 (AHRD V3.3 --* GAT18_ORYSJ)						PTHR34463 (PANTHER); PTHR34463	0,150	0,307	0,000	0,000	0,000									
Solyc09g091400	Receptor protein kinase (AHRD V3.3 *** Q9FEU2_PINSY)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS); IPR032675 (G3D	0,399	0,519	0,000	0,025	0,023									
Solyc09g091410	LOW QUALITY:Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3		F:GO:0003989; F:G(	F:acetyl-CoA carbo	EC:6.4.1.2	Acetyl-CoA carboxyla	PTHR42995:SF3 (PANTHER); PTHR4:	0,019	0,081	0,075	0,201	0,188									
Solyc09g091420	Inosine triphosphate pyrophosphatase (AHRD V3.3 *** K4CWG8_SOLLC)		P:GO:0009143; F:G(	P:nucleoside tripho:	EC:3.6.1.19	Acting on acid anhyd	IPR002637 (PFAM); IPR029001 (G3D	2,791	4,997	0,945	1,333	1,010									
Solyc09g091430	Pectate lyase (AHRD V3.3 *** M1CWG5_SOLTU)		F:GO:0030570; P:G(	F:pectate lyase act	EC:4.2.2.2	Pectate lyase	IPR018082 (PRINTS); IPR012334 (G3	6,809	8,115	154,389	191,565	114,929									
Solyc09g091440	Histone deacetylase (AHRD V3.3 *** K4CWH0_SOLLC)		F:GO:0004407; P:G(	F:histone deacetyla	EC:3.5.1.98	Histone deacetylase	IPR003084 (PRINTS); IPR000286 (PF	81,341	83,715	141,162	144,218	135,956									
Solyc09g091450	DNA polymerase delta subunit 4 family (AHRD V3.3 *** D7KJU8_ARALL)		C:GO:0005634; P:G(	C:nucleus; P:DNA replication			IPR007218 (PFAM); mobidb-lite (MOB	24,434	23,070	35,123	31,926	30,475									
Solyc09g091460	Kinase family protein (AHRD V3.3 *-* D7KE69_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PRINTS); G3DSA:3.30.2(	2,179	6,357	1,033	0,533	0,919	1,571	0,001					up		
Solyc09g091470	3-ketoacyl-CoA thiolase (AHRD V3.3 *** P93112_9ROSI)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR016039 (G3DSA:3.40.47 GENE3D	248,842	258,420	2625,174	2597,546	2535,059									
Solyc09g091480	RING/U-box superfamily protein (AHRD V3.3 *** AT1G04790.1)		F:GO:0016874	F:ligase activity			IPR001841 (PFAM); IPR013083 (G3D	10,234	10,116	12,435	10,301	11,672									
Solyc09g091490	Transcription factor jumonji domain-containing protein (AHRD V3.3 *** D7M504_ARALL)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			IPR018866 (PFAM); mobidb-lite (MOB	0,119	0,208	0,025	0,025	0,000									
Solyc09g091500	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT5G48870.1)		F:GO:0003723; C:G(	F:RNA binding; C:spliceosomal complex; C:U6 snRNP; P:mRNA			IPR001163 (PFAM); G3DSA:2.30.30.1	11,296	11,476	21,078	20,752	19,779									
Solyc09g091510	chalcone synthase 1	CHS-1	P:GO:0009058; F:G(	P:biosynthetic process; F:transferase activity, transferring acyl			IPR001099 (PFAM); IPR011141 (PIRS	17,610	17,212	994,897	1097,736	1005,568									
Solyc09g091520	60S acidic ribosomal protein P0 (AHRD V3.3 *** K4CWH8_SOLLC)		C:GO:0005622; P:G(	C:intracellular; P:ribosome biogenesis			G3DSA:3.90.105.20 (GENE3D); IPR0(	0,000	0,021	0,170	0,984	0,070									
Solyc09g091530	Salicylic acid/benzoic acid carboxyl methyltransferase (AHRD V3.3 *** A4URY9_9SOLA)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM); G3DSA:3.40.50.1	0,040	0,039	0,047	0,000	0,000									
Solyc09g091550	S-adenosyl-L-methionine: salicylic acid carboxyl methyltransferase (AHRD V3.3 *** D2Y3T9_SOLLC)		F:GO:0008168	F:methyltransferase activity			IPR005299 (PFAM); G3DSA:3.40.50.1	0,140	0,340	0,000	0,000	0,000									
Solyc09g091560	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A118JU06_CYNCS)		F:GO:0005515	F:protein binding			IPR021832 (PFAM); IPR036770 (G3D	20,015	29,566	15,790	15,694	16,780									
Solyc09g091580	ABC1 protein kinase 6 (AHRD V3.3 *** Q9LRN0_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR004147 (PFAM); mobidb-lite (MOB	17,776	17,628	53,653	48,136	54,546									
Solyc09g091590	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT3G07030.5)		F:GO:0003676	F:nucleic acid binding			IPR036882 (G3DSA:3.30.110.GENE3	21,850	20,941	22,061	19,346	19,788									
Solyc09g091600	Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *** A0A061EKH3_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,078	4,869	19,238	27,379	19,051									
Solyc09g091610	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9RWK6_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			IPR001388 (PRINTS); IPR001388 (PF	0,000	0,000	0,000	0,000	0,024									
Solyc09g091620	Protein disulfide-isomerase (AHRD V3.3 --* PDI_MAIZE)							0,000	0,112	0,047	0,000	0,000									
Solyc09g091635	LOW QUALITY:F-box family protein (AHRD V3.3 *** A0A061EN61_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR015915 (G3D	0,718	0,383	0,025	0,025	0,000									
Solyc09g091650	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G04730.1)		F:GO:0005524	F:ATP binding			IPR003959 (PFAM); G3DSA:1.10.8.6(	6,056	5,689	5,504	3,740	4,645									
Solyc09g091660	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG46	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR029481 (PFAM); IPR013581 (PFA	45,021	209,290	12,930	16,714	26,581	2,234	0,007	1,036	0,001			up	up	
Solyc09g091670	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG47	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR013581 (PFA	1,181	0,750	3,248	3,869	6,129									
Solyc09g091690	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYN(		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR017451 (TIGF	24,120	19,694	18,886	13,043	18,128									
Solyc09g091700	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** I3SE71_MEDTR)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.40.50.720 (GENE3D); G3DS	0,075	1,122	0,293	0,432	0,329									
Solyc09g091710	F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYNCS)						IPR017451 (TIGRFAM); PTHR44355 (	14,181	14,569	19,220	17,215	14,833									
Solyc09g091730	Pectinesterase (AHRD V3.3 *** K4CWJ9_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3	1,386	1,188	5,524	2,444	2,048									
Solyc09g091740	60S ribosomal protein L13a-like protein (AHRD V3.3 *** Q3HRW1_SOLTU)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR005822 (PIRSF); IPR036899 (G3D	126,826	134,302	91,935	80,800	81,834									
Solyc09g091750	26S proteasome non-ATPase regulatory subunit 1 (AHRD V3.3 *** A0A0B2Q963_GLYSO)		C:GO:0000502; F:G(	C:proteasome complex; F:enzyme regulator activity; P:regulatio			IPR011989 (G3DSA:1.25.10.GENE3D	120,894	117,829	202,344	202,050	183,373									
Solyc09g091770	LOW QUALITY:Protein NRT1/ PTR FAMILY 1.2 (AHRD V3.3 --* PTR6_ARATH)							0,019	0,018	0,072	0,145	0,167									
Solyc09g091780	LES441249 p27KIP1-related-protein 1	krp1	F:GO:0004861; C:G(	F:cyclin-dependent protein serine/threonine kinase inhibitor acti			IPR003175 (PFAM); G3DSA:4.10.365	10,984	10,764	12,304	9,507	9,681									
Solyc09g091790	E3 ubiquitin-protein ligase PRT1-like protein (AHRD V3.3 *** A0A0B0PZL6_GOSAR)		F:GO:0008270	F:zinc ion binding			G3DSA:3.30.60.90 (GENE3D); PF139	47,243	36,152	84,312	70,744	70,489									
Solyc09g091800	LOW QUALITY:Fatty acid hydroxylase superfamily protein (AHRD V3.3 --* AT3G02590.2)							32,853	24,205	0,000	0,022	0,000									
Solyc09g091810	LOW QUALITY:CLAVATA3/ESR-related protein (AHRD V3.3 --* A0A0A0LNB8_CUCSA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,274	0,752	0,025	0,072	0,000									
Solyc09g091820	Type 1 membrane protein, putative isoform 1 (AHRD V3.3 *** A0A061EKE4_THECC)		C:GO:0016021	C:integral component of membrane			PTHR37735 (PANTHER)	167,502	151,592	215,847	210,371	192,983									
Solyc09g091830	plastid transcriptionally active 5 (AHRD V3.3 *** AT4G13670.1)		C:GO:0000427; F:G(	C:plastid-encoded r	EC:5.3.4.1	Protein disulfide-ison	IPR002477 (PFAM); IPR036366 (G3D	5,696	8,299	24,729	21,449	20,798									
Solyc09g091840	Glutathione Reductase (AHRD V3.3 *** A0A089ZXK5_GENTR)	GR	F:GO:0004362; P:G(	F:glutathione-disulfi	EC:1.8.1.7	Glutathione-disulfide	PR00411 (PRINTS); PR00368 (PRINT	100,063	100,020	117,469	109,698	116,353									
Solyc09g091850	Non-lysosomal glucosylceramidase (AHRD V3.3 *** K4CWL1_SOLLC)		F:GO:0004553	F:hydrolase activity, hydrolyzing O-glycosyl compounds			IPR024462 (PFAM); IPR012341 (G3D	26,108	19,192	26,038	28,223	27,413									
Solyc09g091855	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 --* AT2G35710.1)							3,848	2,869	3,500	4,230	3,816									
Solyc09g091860	Poly(A) RNA polymerase GLD2-A (AHRD V3.3 *** M7ZLW5_TRIUA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	11,030	8,501	7,168	5,692	8,269									
Solyc09g091870	Flavin-containing monooxygenase (AHRD V3.3 *** M1DF47_SOLTU)		F:GO:0004499; F:G(	F:N,N-dimethylanilir	EC:1.14.13.8; EC:1.	Flavin-containing mo	PR00368 (PRINTS); PR00469 (PRINT	0,291	0,566	0,099	0,126	0,000									
Solyc09g091880	Myb family transcription factor APL (AHRD V3.3 *** A0A0B0NIP7_GOSAR)		F:GO:0003677; F:G(	F:DNA binding; F:protein binding			IPR022617 (PFAM G2-like	1,936	0,839	0,000	0,025	0,048									
Solyc09g091890	Small ubiquitin-related modifier (AHRD V3.3 *** A0A0V0GJJ5_SOLCH)		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D); IPR02:	0,646	0,380	0,172	0,189	0,118									
Solyc09g091900	ER lumen protein-retaining receptor (AHRD V3.3 *** K4CWL6_SOLLC)		P:GO:0006621; C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS); IPR000133 (PF	24,317	26,467	35,793	46,000	33,962					0,364	0,036			up
Solyc09g091910	Purple acid phosphatase (AHRD V3.3 *** K4CWL7_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR008963 (G3DSA:2.60.40.GENE3D	0,412	0,800	0,150	0,163	0,071									
Solyc09g091920	Glucan endo-1,3-beta-glucosidase 1 (AHRD V3.3 *** A0A151QZ89_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR012946 (PFAM); mobidb-lite (MOB	0,021	0,000	0,000	0,000	0,000									
Solyc09g091930	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** G7JA39_MEDTR)		F:GO:0008270; P:G(	F:zinc ion binding; F	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001607 (PFAM); G3DSA:3.90.70.1	26,007	22,346	26,992	26,479	25,818									
Solyc09g091940	LOW QUALITY:Protein DETOXIFICATION (AHRD V3.3 --* M0X270_HORVD)							0,301	0,344	0,169	0,188	0,377									
Solyc09g091945	4F5 family protein (AHRD V3.3 *-* G7LFV3_MEDTR)						IPR007513 (PFAM); mobidb-lite (MOB	0,019	0,160	0,051	0,047	0,071									
Solyc09g091950	Ethylene-responsive transcription factor ERF062 (AHRD V3.3 *** ERF62_ARATH)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,021	0,022	0,000	0,024									
Solyc09g091960	High mobility group B-like protein (AHRD V3.3 *** G7KWP7_MEDTR)		F:GO:0003677	F:DNA binding			IPR036431 (G3DSA:1.10.150 GENE3	7,189	8,050	0,312	0,632	0,703									
Solyc09g091970	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G21280.2)		F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D); IPR0(	2,495	5,277	2,983	4,305	9,471	1,107	0,009	1,665	0,000			up	up	
Solyc09g091980	N-acetyltransferase mak3, putative (AHRD V3.3 *** B9RGX2_RICCO)		F:GO:0004596; P:G(	F:peptide alpha-N-a	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR000182 (PFAM); G3DSA:3.40.630	83,596	71,770	58,788	48,974	54,122									
Solyc09g091990	Kinase family protein (AHRD V3.3 *-* B9IJH3_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); G3DS	23,249	36,170	19,135	14,447	18,997									
Solyc09g092010	Kinase family protein (AHRD V3.3 *-* B9IJH3_POPTR)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	PTHR27007 (PANTHER); PTHR27007	9,177	16,533	8,389	5,886	7,778	0,873	0,019					up		
Solyc09g092020	Calcium-binding EF-hand family protein isoform 3 (AHRD V3.3 *** A0A061EJV0_THECC)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM); IPR002048 (PFA	0,097	0,335	0,000	0,051	0,048									
Solyc09g092025	Small ubiquitin-related modifier (AHRD V3.3 *** M1D3F5_SOLTU)		C:GO:0005634; P:G(	C:nucleus; P:protein sumoylation; F:protein tag; F:ubiquitin-like			G3DSA:3.10.20.90 (GENE3D); IPR02:	0,000	0,019	0,000	0,000	0,000									
Solyc09g092030	UV radiation resistance-associated protein (AHRD V3.3 *** AT2G32760.1)		F:GO:0000149; C:G(	F:SNARE binding; C:endosome; C:cytosol; P:protein targeting t(			PTHR15157 (PANTHER); PTHR15157	11,920	11,002	14,484	18,589	13,630									
Solyc09g092040	Ubiquitin-associated domain-containing family protein (AHRD V3.3 *-* A9P9K4_POPTR)		F:GO:0003676	F:nucleic acid binding			G3DSA:1.20.58.2190 (GENE3D); IPR(	74,771	80,775	98,903	91,180	104,365									
Solyc09g092050	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GFV9_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,372	3,177	2,344	2,693	2,514									
Solyc09g092060	LOW QUALITY:F-box protein (AHRD V3.3 *-* A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); IPR(	0,021	0,000	0,000	0,076	0,000									
Solyc09g092070	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G13730.1)						IPR000195 (PFAM); G3DSA:1.10.472	39,912	38,843	59,165	56,993	54,457									
Solyc09g092075	LOW QUALITY:Isoflavone reductase (AHRD V3.3 --* IFR_PEA)		C:GO:0005737; F:G(	C:cytoplasm; F:oxidoreductase activity, acting on the CH-CH gr			IPR005720 (PFAM)	0,162	0,039	0,126	0,123	0,047									
Solyc09g092080	Ribosomal protein l7ae (AHRD V3.3 *** A0A0A0LF58_CUCSA)		F:GO:0003723; C:G(	F:RNA binding; C:nucleolus			IPR018492 (PRINTS); IPR002415 (PF	15,120	16,203	7,279	5,499	5,860									
Solyc09g092090	50S ribosomal protein L13, putative (AHRD V3.3 *** B9RBL9_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005823 (TIGRFAM); IPR036899 ((	26,357	27,064	22,391	19,812	19,795									
Solyc09g092100	Histidine kinase-, DNA gyrase B (AHRD V3.3 *** G7LHV1_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:embryo development ending in seed dormancy; P:I			IPR036890 (G3DSA:3.30.565.GENE3	17,221	14,713	16,299	20,596	18,627									
Solyc09g092110	Light-regulated (AHRD V3.3 *** A0A0B0P5I2_GOSAR)		C:GO:0009507	C:chloroplast			IPR009856 (PFAM); IPR009856 (PAN	2,064	5,014	0,283	2,749	3,984			3,740	0,000	3,201	0,000		up	up
Solyc09g092120	Alkaline ceramidase 3 (AHRD V3.3 *** A0A0B0NPT2_GOSAR)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra			IPR008901 (PFAM); PTHR12956:SF5	21,525	21,225	25,788	24,892	21,227									
Solyc09g092130	Sucrose-phosphate synthase (AHRD V3.3 *** A0A0U1ZVB4_LYCBA)		P:GO:0005985; F:G(	P:sucrose metaboli	EC:2.4.1.14; EC:2.4.	Sucrose-phosphate s	IPR006380 (PFAM); G3DSA:3.40.50.2	12,085	11,815	6,492	5,690	5,324									
Solyc09g092140	Methyltransferase-like protein 13 (AHRD V3.3 *** W9QL05_9ROSA)		F:GO:0008168	F:methyltransferase activity			PF01564 (PFAM); IPR013216 (PFAM)	50,660	43,019	63,996	60,048	58,138									
Solyc09g092150	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YJT4_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,576	0,808	0,780	0,863	0,753									
Solyc09g092170	Beta-galactosidase (AHRD V3.3 *** A0A0V0IVF7_SOLCH)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS); IPR031330 (PF	20,331	16,559	35,715	36,574	36,702									
Solyc09g092180	RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 *** AT3G24255.2)						PTHR36037 (PANTHER)	6,198	5,286	5,305	6,658	5,665									
Solyc09g092210	Nuclear migration protein nudC (AHRD V3.3 *-* B6T728_MAIZE)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding; P:developmental process; F:unf(			IPR008978 (G3DSA:2.60.40.GENE3D	0,042	0,000	0,000	0,000	0,000									
Solyc09g092220	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM); PTHR12570:SF2	0,875	0,881	0,780	0,720	0,567									
Solyc09g092230	LOW QUALITY:Chlorophyll a-b binding protein of LHCII type I, chloroplastic (AHRD V3.3 --* CB2_DUNSA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				1,322	1,144	0,458	0,481	0,379									
Solyc09g092240	Small subunit processome component 20 like (AHRD V3.3 *** A0A0B2RDD2_GLYSO)		C:GO:0005730; C:G(	C:nucleolus; C:90S preribosome; C:small-subunit processome			IPR011430 (PFAM); PTHR17695 (PAI	62,201	48,404	45,993	48,498	44,192									
Solyc09g092250	Zinc finger transcription factor 55	C3H55	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (PFAM); IPR012677 (G3D	96,498	74,254	92,459	92,912	91,247									
Solyc09g092260	chaperone protein dnaJ 20		C:GO:0009507; P:G(	C:chloroplast; P:chaperone-mediated protein folding			IPR001623 (PRINTS); IPR036869 (G:	17,073	19,230	3,983	5,382	7,449			0,905	0,019				up	
Solyc09g092270	Transferase family protein (AHRD V3.3 *** B9GFT7_POPTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM); IPR023213 (G3D	0,398	0,813	5,854	5,884	4,262									
Solyc09g092280	Ph-3 resistance protein (AHRD V3.3 *** A0A060D304_SOLPI)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR002182 (PFA	0,247	1,160	0,047	0,145	0,094									
Solyc09g092290	Ph-3 resistance protein (AHRD V3.3 *** A0A060D304_SOLPI)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); G3DSA:1.10.8.4:	0,307	1,025	0,025	0,025	0,069									
Solyc09g092310	Ph-3 resistance protein (AHRD V3.3 *** A0A060D304_SOLPI)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR032675 (G3D	1,271	3,342	0,165	0,143	0,140	1,413	0,036					up		
Solyc09g092320	RNA binding protein (AHRD V3.3 *** O23793_NICSY)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM); IPR012677 (G3D	18,797	17,534	7,179	3,835	5,300					-0,901	0,042			down
Solyc09g092330	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE6	F:GO:0003824; C:G(	F:catalytic activity; C:integral component of membrane; F:coenz			PR01713 (PRINTS); IPR016040 (PFA	146,225	125,362	29,399	19,108	24,413					-0,620	0,011			down
Solyc09g092340	Werner Syndrome-like exonuclease (AHRD V3.3 *** A0A0B2QQZ2_GLYSO)		F:GO:0003676; P:G(	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR036397 (G3DSA:3.30.420.GENE3	7,946	6,816	0,877	0,796	1,455									
Solyc09g092360	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103XFT4_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	11,206	12,487	23,469	24,759	20,166									
Solyc09g092370	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT5G12060.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM); PTHR31232:SF5	0,987	0,378	0,025	0,050	0,024									
Solyc09g092380	S-adenosyl-l-homocysteine hydrolase	sahh	F:GO:0004013; P:G(	F:adenosylhomocys	EC:3.3.1.1	Adenosylhomocystei	IPR000043 (PFAM); IPR000043 (TIGF	2095,441	1942,557	19415,500	18304,655	15796,485									
Solyc09g092390	Adenosylhomocysteinase (AHRD V3.3 *** SAHH_NICSY)		F:GO:0004013; P:G(	F:adenosylhomocys	EC:3.3.1.1	Adenosylhomocystei	IPR015878 (PFAM); G3DSA:3.40.50.1	446,290	531,685	140,528	103,615	103,307									
Solyc09g092400	Apyrase (AHRD V3.3 *** APY_SOLTU)		F:GO:0016787	F:hydrolase activity			IPR000407 (PFAM); G3DSA:3.30.420	0,000	0,000	0,000	0,025	0,000									
Solyc09g092410	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.2)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS); IPR035897 (G3D	0,038	0,000	0,000	0,000	0,023									
Solyc09g092420	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1740.10 (GENE3D); IPR(	0,261	0,267	0,162	0,219	0,234									
Solyc09g092430	Selenium binding family protein (AHRD V3.3 *** B9GFI5_POPTR)		F:GO:0008430	F:selenium binding			IPR008826 (PFAM); PTHR23300:SF0	71,052	74,697	11,801	9,263	14,729									
Solyc09g092450	Long-chain acyl-CoA synthetase (AHRD V3.3 *** A0A061R0V4_9CHLO)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D); IPI	39,466	37,841	20,748	16,279	19,438									
Solyc09g092460	Receptor protein kinase, putative (AHRD V3.3 *** B9T5F6_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0	19,440	13,593	51,854	52,988	52,857									
Solyc09g092480	Glycosyltransferase (AHRD V3.3 *** K4CWS4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM); G3DSA:3.40.50.2	7,877	6,606	12,181	19,365	19,669			0,689	0,003	0,672	0,022		up	up
Solyc09g092490	Glycosyltransferase (AHRD V3.3 *-* B6EWX4_LYCBA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); G3D	3,133	4,304	30,736	31,946	34,172									
Solyc09g092500	Glycosyltransferase (AHRD V3.3 *** K4CWS6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR(	90,791	60,544	572,144	589,860	590,704									
Solyc09g092510	Pyrroline-5-carboxylate reductase (AHRD V3.3 *-* A0A1D1ZGA1_9ARAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,960	4,269	0,665	0,237	0,586									
Solyc09g092520	xyloglucan endotransglycosylase	br1	F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucc	G3DSA:2.60.120.200 (GENE3D); IPR(	45,079	21,659	4,300	11,285	6,698	-1,025	0,025			1,391	0,000	down		up
Solyc09g092530	Protein TIC 22-like, chloroplastic (AHRD V3.3 *** A0A0B0MXE6_GOSAR)		P:GO:0015031	P:protein transport			IPR007378 (PFAM); G3DSA:3.40.135(	33,740	46,558	34,917	27,397	31,730									
Solyc09g092540	LOW QUALITY:F-box family protein (AHRD V3.3 *** AT1G19160.1)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM); IPR013187 (F	0,099	0,059	0,047	0,025	0,047									
Solyc09g092550	30S ribosomal S5 (AHRD V3.3 *-* A0A0B0MR18_GOSAR)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	55,688	50,386	33,420	31,627	34,823									
Solyc09g092580	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,040	0,037	0,075	0,022	0,192									
Solyc09g092600	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc09g092605	Cytochrome P450, putative (AHRD V3.3 *-* A0A061FE03_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR036396 (G3	0,021	0,076	0,000	0,000	0,000									
Solyc09g092620	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,037	0,039	0,025	0,025	0,094									
Solyc09g092640	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,057	0,208	0,022	0,000	0,213									
Solyc09g092670	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,057	0,039	0,025	0,047	0,000									
Solyc09g092680	Protein transport protein sec23, putative (AHRD V3.3 *** B9RRN0_RICCO)		P:GO:0006886; F:G(	P:intracellular protein transport; F:zinc ion binding; C:COPII vesi			G3DSA:1.20.120.730 (GENE3D); IPR(	21,235	21,461	23,330	23,470	21,043									
Solyc09g092690	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NXQ5_ZOSMR)		F:GO:0005515	F:protein binding			G3DSA:3.30.1670.20 (GENE3D); IPR(	3,959	1,443	4,945	4,172	8,748									
Solyc09g092710	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)						IPR010800 (PFAM); PTHR37389:SF3	2,299	2,740	0,420	0,523	0,373									
Solyc09g092720	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)						IPR010800 (PFAM); PTHR37389:SF3	0,021	0,018	0,000	0,000	0,000									
Solyc09g092740	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT3G13300.3)						mobidb-lite (MOBIDB_LITE)	0,021	0,021	0,000	0,000	0,024									
Solyc09g092760	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT2G41060.3)							0,021	0,021	0,000	0,000	0,000									
Solyc09g097760	Glycine rich protein (AHRD V3.3 *-* Q94CG1_TOBAC)		F:GO:0003899; P:G(	F:DNA-directed 5'-3' RNA polymerase activity; P:RNA biosynthe			IPR010800 (PFAM); mobidb-lite (MOB	17,911	13,493	4,225	8,969	17,912			2,074	0,011				up	
Solyc09g097770	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)						IPR010800 (PFAM)	0,640	1,308	4,044	9,575	23,398			2,525	0,009				up	
Solyc09g097780	Glycine-rich protein (AHRD V3.3 *-* GRP1_TOBAC)						PR01228 (PRINTS); IPR010800 (PFA	9,017	15,378	1,237	1,229	0,841									
Solyc09g097820	RNA helicase family protein		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR007502 (PFAM); IPR001650 (PFA	21,010	17,577	32,820	35,013	30,370									
Solyc09g097825	Zn-dependent exopeptidases superfamily protein (AHRD V3.3 --* AT5G20660.3)		P:GO:0006493; F:G(	P:protein O-linked glycosylation; F:transferase activity, transfer			mobidb-lite (MOBIDB_LITE); mobidb-lit	4,398	3,094	4,655	4,826	4,144									
Solyc09g097830	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT3G04240.1)		F:GO:0005515	F:protein binding			IPR019734 (PFAM); IPR011990 (G3D	99,210	80,641	115,762	112,355	114,268									
Solyc09g097840	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XYK9_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	12,632	12,578	5,611	5,958	6,780									
Solyc09g097850	Cysteine proteinase inhibitor (AHRD V3.3 *** K4CWV7_SOLLC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			G3DSA:3.10.450.10 (GENE3D); IPR0(	41,229	37,887	45,641	51,408	41,513									
Solyc09g097860	Kinesin-like protein (AHRD V3.3 *** F4J464_ARATH)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (PF	0,195	0,411	0,047	0,000	0,023									
Solyc09g097865	Kinesin-like protein (AHRD V3.3 *** A0A0D2U096_GOSRA)		F:GO:0003777; P:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE); mobidb-lit	1,330	1,380	0,214	0,166	0,304									
Solyc09g097870	bHLH transcription factor 062		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR036638 (G3DS bHLH	35,946	16,320	15,288	17,083	18,348	-1,109	0,000					down		
Solyc09g097880	DNA topoisomerase (AHRD V3.3 *** K4CWW0_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:5.99.1.2	DNA topoisomerase	IPR013497 (PRINTS); IPR013826 (G3	30,327	24,691	34,229	29,734	34,762									
Solyc09g097900	Ras family (AHRD V3.3 *** A0A191UMR0_SOLDE)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); G3DSA:3.40.50.3	8,812	9,195	5,782	5,974	6,568									
Solyc09g097910	30S ribosomal protein S1 (AHRD V3.3 *** W9RML0_9ROSA)		F:GO:0003676	F:nucleic acid binding			G3DSA:2.40.50.140 (GENE3D); IPR0(	20,847	25,337	32,433	38,514	48,252			0,571	0,001				up	

Solyc09g097915	dCTP pyrophosphatase 1 (AHRD V3.3 --* A0A0B2PTE7_GLYSO)							1,845	1,815	2,166	1,846	2,164									
Solyc09g097920	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT1G74120.1)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR038538 (G3DSA:1.25.70.GENE3D	7,476	6,695	10,532	9,238	10,059									
Solyc09g097930	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A0B0PZH5_GOSAR)		P:GO:0009143; F:G(	P:nucleoside tripho:	EC:3.6.1.19	Acting on acid anhyd	G3DSA:1.10.287.1080 (GENE3D): IPI	0,558	0,513	0,150	0,198	0,094									
Solyc09g097950	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *-* G7KTT7_MEDTR)						IPR023210 (PFAM): IPR036812 (G3D	0,000	0,021	0,000	0,022	0,023									
Solyc09g097960	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60710.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR023210 (PFAM): IPR036812 (G3D	0,499	4,427	3,909	8,070	16,335	3,143	0,004	2,053	0,000	1,043	0,040	up	up	up
Solyc09g097970	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60710.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR036812 (G3DSA:3.20.20.GENE3D	4,254	5,824	2,259	1,974	3,658									
Solyc09g097980	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60710.1)						IPR036812 (G3DSA:3.20.20.GENE3D	1,306	2,256	1,006	1,190	1,013									
Solyc09g098000	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60690.1)						IPR036812 (G3DSA:3.20.20.GENE3D	0,019	0,000	0,022	0,000	0,000									
Solyc09g098030	Cytochrome P450 (AHRD V3.3 *** A0A103Y530_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS): IPR002401 (PF	0,279	0,213	0,412	0,148	0,163									
Solyc09g098040	Phosphoglucan, water dikinase (AHRD V3.3 *** A0A072UBU6_MEDTR)		F:GO:0005524; F:G(	F:ATP binding; F:kinase activity; P:phosphorylation; F:starch bir			IPR013815 (G3DSA:3.30.1490.GENE	214,433	215,082	257,541	235,960	269,946									
Solyc09g098050	Ankyrin repeat-containing protein (AHRD V3.3 *** A0A0B2SGR8_GLYSO)		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	1,247	0,844	6,708	8,770	5,514									
Solyc09g098060	Ankyrin repeat family protein (AHRD V3.3 *** B9ICR0_POPTR)		F:GO:0005515	F:protein binding			IPR026961 (PFAM): IPR036770 (G3D	0,244	0,158	0,000	0,045	0,047									
Solyc09g098070	MACPF domain protein (AHRD V3.3 *** G7LHB4_MEDTR)		C:GO:0005886; P:G(	C:plasma membrane; P:plant-type hypersensitive response			IPR020864 (PFAM): PTHR33199:SF2	69,296	70,168	128,313	129,945	118,000									
Solyc09g098080	Glycosyltransferase (AHRD V3.3 *** K4CWX9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,429	0,493	10,514	17,073	18,103			0,784	0,001	0,706	0,017		up	up
Solyc09g098090	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *-* AT1G60690.1)						IPR023210 (PFAM): IPR036812 (G3D	1,749	1,517	1,368	1,051	1,254									
Solyc09g098095	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60690.1)						IPR036812 (G3DSA:3.20.20.GENE3D	25,682	21,321	19,908	18,194	18,017									
Solyc09g098100	CC-NBS-LRR_Solyc09g098100		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	28,610	19,379	17,151	17,899	16,568									
Solyc09g098110	bHLH transcription factor 092	bHLH092	F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM bHLH	5,667	4,604	4,242	3,428	3,279									
Solyc09g098115	Voltage-gated hydrogen channel 1 (AHRD V3.3 *** A0A151T9W1_CAJCA)		C:GO:0005887; F:G(	C:integral component of plasma membrane; F:voltage-gated pro			IPR027359 (G3DSA:1.20.120.GENE3	0,114	0,080	0,000	0,000	0,000									
Solyc09g098120	Oil body-associated protein 1A (AHRD V3.3 *** OBP1A_ARATH)						IPR010686 (PFAM): mobidb-lite (MOB	23,872	33,156	7,352	17,436	1,137									
Solyc09g098130	CC-NBS-LRR gene	sw5	F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	10,244	9,583	7,286	9,275	9,444									
Solyc09g098140	centrosomal protein (AHRD V3.3 *** AT1G79390.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR363	22,709	20,812	43,323	33,494	35,661					-0,368	0,016			down
Solyc09g098150	Metacaspase (AHRD V3.3 *** K4CWY6_SOLLC),Pfam:PF00656	mca1					PF00656 (PFAM): G3DSA:3.40.50.14	91,335	90,568	152,190	135,552	121,399									
Solyc09g098160	pirin	pirin	C:GO:0005634	C:nucleus			IPR012093 (PIRSF): IPR008778 (PFA	1,366	2,735	1,871	2,115	1,418									
Solyc09g098170	Ras family (AHRD V3.3 *** A0A191UMR0_SOLDE)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	25,477	24,155	18,976	17,572	16,889									
Solyc09g098180	Pirin (AHRD V3.3 *** A0A191UMQ8_SOLDE)						IPR012093 (PIRSF): IPR008778 (PFA	0,774	1,045	0,190	0,125	0,142									
Solyc09g098190	Signal peptide peptidase-like protein (AHRD V3.3 *-* A0A072TX77_MEDTR)		F:GO:0004190; C:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	G3DSA:3.50.30.30 (GENE3D): IPR00	1,819	1,398	0,524	0,383	0,588									
Solyc09g098210	LOW QUALITY:NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9Q9_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	0,021	0,019	0,000	0,000	0,000									
Solyc09g098220	Mitotic spindle assembly checkpoint protein MAD2B (AHRD V3.3 *** A0A151S2V7_CAJCA)		P:GO:0006974; P:G(	P:cellular response to DNA damage stimulus; P:response to UV-			IPR003511 (PFAM): IPR036570 (G3D	1,505	1,307	2,972	3,287	2,585									
Solyc09g098225	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT1G79120.2)						IPR021099 (PFAM): PTHR31476:SF1	3,935	4,484	15,216	16,954	13,385									
Solyc09g098230	ATP-dependent DNA helicase 2 subunit Ku70-like protein (AHRD V3.3 *** AT1G16970.1)		P:GO:0000723; F:G(	P:telomere mainten	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036465 (G3DSA:3.40.50.GENE3D	25,284	23,311	33,284	35,400	29,632									
Solyc09g098240	Importin-like protein (AHRD V3.3 *** G7KT01_MEDTR)		P:GO:0006886; F:G(	P:intracellular protein transport; F:Ran GTPase binding			IPR013713 (PFAM): IPR001494 (PFA	211,254	217,558	163,522	145,757	152,148									
Solyc09g098260	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9NPN7_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C:nucleus			G3DSA:2.30.30.140 (GENE3D): G3DS	34,554	27,928	38,734	38,443	38,259									
Solyc09g098265	Phosphatidylinositol 3-kinase, nodule isoform (AHRD V3.3 --* PI3K2_SOYBN)							0,184	0,230	0,359	0,292	0,238									
Solyc09g098270	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G23460.1)	PG12-1	F:GO:0004650; P:G(	F:polygalacturonas(	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	0,553	0,561	0,241	0,192	0,236									
Solyc09g098280	Eukaryotic translation initiation factor 3 subunit H (AHRD V3.3 *** K4CWZ8_SOLLC)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; C:eukary			G3DSA:3.40.140.10 (GENE3D): IPR0	35,590	36,509	53,244	59,438	51,779									
Solyc09g098290	Receptor protein kinase, putative (AHRD V3.3 *** B9RWV4_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): G3DSA:3.30.200	38,731	35,029	3,875	3,412	5,578									
Solyc09g098300	proline-rich family protein (AHRD V3.3 *-* AT2G41420.1)		C:GO:0005886; P:G(	C:plasma membrane; P:megasporogenesis; C:integral compone			PR00239 (PRINTS): IPR028144 (PFA	79,610	95,484	59,822	63,425	60,320									
Solyc09g098310	Adhesive/proline-rich protein homolog (AHRD V3.3 *** Q8L8M2_ARATH)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	104,585	199,521	105,518	108,986	104,376	0,956	0,023					up		
Solyc09g098320	LOW QUALITY:12-oxophytodienoate reductase-like protein (AHRD V3.3 *-* OPRL_SOLLC)		F:GO:0010181; F:G(	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc09g098330	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G56190.3)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	37,429	30,202	31,687	32,224	30,461									
Solyc09g098340	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G05840.1)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	13,010	12,334	13,124	14,147	13,808									
Solyc09g098360	RNA polymerase II transcription mediator (AHRD V3.3 --* AT1G55325.4)							22,465	24,112	16,371	14,757	14,565									
Solyc09g098370	Zinc ion binding,nucleic acid binding,hydrolases, putative isoform 1 (AHRD V3.3 *** A0A061EJ21_THECC)		F:GO:0003676; F:G(	F:nucleic acid binding; F:nuclease activity; F:protein binding; F:			IPR014883 (PFAM): IPR001810 (PFA	13,573	14,112	16,689	19,096	16,144									
Solyc09g098380	Transmembrane amino acid transporter family protein (AHRD V3.3 *-* G7JBE3_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM): PTHR22950:SF2	0,000	0,000	0,000	0,069	0,118									
Solyc09g098390	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G43370.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	12,871	11,698	11,728	11,375	11,591									
Solyc09g098400	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT1G51890.4)						mobidb-lite (MOBIDB_LITE): PTHR373	0,000	0,021	0,000	0,100	0,000									
Solyc09g098420	Leucine-rich repeat receptor protein kinase EXS (AHRD V3.3 *** A0A1D1XPP4_9ARAE)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	6,785	3,985	0,505	0,443	0,708									
Solyc09g098440	ROP-interactive CRIB motif protein (AHRD V3.3 *** G7KTT6_MEDTR)						IPR036936 (G3DSA:3.90.810.GENE3	0,135	0,559	1,440	1,123	1,363									
Solyc09g098445	ATPase, V0 complex, subunit E (AHRD V3.3 *** A0A0K9Q325_ZOSMR)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR008389 (PFAM): IPR008389 (PAN	8,937	8,449	14,631	12,968	13,084									
Solyc09g098450	Sn1-specific diacylglycerol lipase (AHRD V3.3 *-* A0A0K9NK42_ZOSMR)		P:GO:0006629	P:lipid metabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	37,696	32,126	26,336	25,434	25,062									
Solyc09g098460	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ERH8_THECC)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM): G3DSA:3.40.50.1	0,019	0,039	0,000	0,025	0,000									
Solyc09g098490	Clathrin interactor EPSIN 3 (AHRD V3.3 *** EPN3_ARATH)		F:GO:0005515	F:protein binding			IPR013809 (PFAM): IPR008942 (G3D	3,026	3,244	0,778	0,660	0,401									
Solyc09g098500	Got1/Sft2-like vescicle transport protein family (AHRD V3.3 *** AT1G05785.7)		P:GO:0016192	P:vesicle-mediated transport			IPR007305 (PFAM): PTHR21493:SF9	2,409	2,665	3,466	3,638	3,705									
Solyc09g098510	Extensin (Class I) (AHRD V3.3 *-* Q01945_SOLLC)		F:GO:0005199; P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			PR01217 (PRINTS): IPR006706 (PFA	45,796	68,344	38,266	24,173	30,100									
Solyc09g098520	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT2G43240.1)		C:GO:0000139; F:G(	C:Golgi membrane; F:pyrimidine nucleotide-sugar transmembrar			IPR007271 (PFAM): IPR007271 (PIRS	32,312	32,176	19,841	22,789	20,842									
Solyc09g098530	phosphoribosylformylglycinamidine synthase (AHRD V3.3 *** AT2G43235.1)		C:GO:0016021	C:integral component of membrane			PTHR35830 (PANTHER)	11,174	12,580	27,362	27,542	28,273									
Solyc09g098540	Chitinase family protein (AHRD V3.3 *** AT1G05850.2)		F:GO:0004568; P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	G3DSA:3.30.20.10 (GENE3D): G3DS	1349,029	853,008	117,437	78,074	92,285			-0,351	0,038	-0,586	0,000		down	down
Solyc09g098550	Ubx domain-containing, putative (AHRD V3.3 *** B9SX29_RICCO)		F:GO:0005515	F:protein binding			G3DSA:3.10.20.90 (GENE3D): IPR00	114,016	92,916	87,624	81,609	82,055									
Solyc09g098580	Rela-spot homolog family protein (AHRD V3.3 *** B9I9P5_POPTR)		P:GO:0015969	P:guanosine tetraphosphate metabolic process			IPR004095 (PFAM): G3DSA:3.30.460	2,848	3,543	2,963	3,336	3,818									
Solyc09g098590	sucrose synthase	SUS4	P:GO:0005985; P:G(	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	G3DSA:3.40.50.2000 (GENE3D): G3D	70,328	62,605	60,034	54,396	64,409									
Solyc09g098610	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS): IPR001128 (PF	0,038	0,266	0,025	0,076	0,072									
Solyc10g005000	SUN-like protein 27	SUN27	F:GO:0005515	F:protein binding			IPR000048 (PFAM): IPR025064 (PFA	4,114	3,637	0,645	0,627	0,845									
Solyc10g005010	NAC domain-containing protein, putative (AHRD V3.3 *** B9SVG2_RICCO)	NAC083	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	4,052	4,199	0,218	0,165	0,403									
Solyc10g005020	DUF4228 domain protein (AHRD V3.3 *** G7LHF9_MEDTR)						IPR025322 (PFAM): PTHR33148:SF9	0,593	1,485	0,250	0,142	0,165	1,340	0,042					up		
Solyc10g005030	Pseudo-response regulator 9 (AHRD V3.3 *** D0PPG9_CASSA)		P:GO:0000160; F:G(	P:phosphorelay signal transduction system; F:protein binding			G3DSA:3.40.50.2300 (GENE3D): IPR(	35,539	20,753	24,106	26,551	25,927	-0,748	0,025					down		
Solyc10g005040	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT4G01410.1)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM): mobidb-lite (MOB	2,363	3,508	8,568	16,155	7,895					0,915	0,001			up
Solyc10g005050	Thylakoid membrane phosphoprotein, chloroplastic (AHRD V3.3 *** A0A1D1Z1Z5_9ARAE)		C:GO:0009579	C:thylakoid			IPR025564 (PFAM): IPR033344 (PAN	61,655	118,953	32,228	34,597	66,487	0,975	0,003	1,041	0,000			up	up	
Solyc10g005060	Caffeic acid O-methyltransferase (AHRD V3.3 *** A0A072TEU0_MEDTR)		F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity			IPR016461 (PIRSF): IPR036388 (G3D	3,008	3,252	6,691	7,545	5,598									
Solyc10g005080	Late elongated hypocotyl (AHRD V3.3 *** J9PV71_NICAT)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI MYB_related	34,838	34,174	28,251	34,466	30,999									
Solyc10g005090	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7M1C9_ARALL)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	3,740	3,276	2,673	2,848	2,610									
Solyc10g005100	plasma-membrane associated cation-binding protein 1 (AHRD V3.3 *** AT4G20260.6)		C:GO:0046658	C:anchored component of plasma membrane			IPR008469 (PFAM): mobidb-lite (MOB	316,679	219,203	393,833	389,919	376,166									
Solyc10g005110	Coproporphyrinogen III oxidase (AHRD V3.3 *** AT1G03475.1)	HEMF/CPOX	F:GO:0004109; P:G(	F:coproporphyrinog	EC:1.3.3.3	Coproporphyrinogen	IPR001260 (PRINTS): IPR001260 (PF	30,227	61,576	78,279	74,263	95,177	1,054	0,000					up		
Solyc10g005120	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G16330.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,056	0,124	0,025	0,000	0,000									
Solyc10g005130	Dicer-like 1	DCL1	F:GO:0003677; F:G(	F:DNA binding; F:rit	EC:3.1.3; EC:3.1.26;	Acting on ester bond:	G3DSA:3.30.160.20 (GENE3D): G3DS	53,225	74,869	36,560	36,275	42,175									
Solyc10g005140	Protein kinase superfamily protein (AHRD V3.3 *** AT2G46850.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:2.10.25.10 (GENE3D): G3DS/	0,000	0,021	0,025	0,025	0,000									
Solyc10g005150	Purine permease-related family protein (AHRD V3.3 *** B9GYR4_POPTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	0,082	0,155	0,000	0,000	0,000									
Solyc10g005170	Purine permease-related family protein (AHRD V3.3 *** B9GYR4_POPTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): IPR030182 (PANTH	0,866	1,246	0,022	0,047	0,118									
Solyc10g005180	Ycf3-interacting protein 1, chloroplastic (AHRD V3.3 *** Y3IP1_TOBAC)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:photosystem I assembly; F			mobidb-lite (MOBIDB_LITE): mobidb-lit	34,407	55,710	28,283	29,159	47,451	0,723	0,001	0,742	0,000			up	up	
Solyc10g005195	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,000	0,022	0,000									
Solyc10g005200	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT5G44670.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR008166 (PFAM): PTHR21461:SF1	44,641	49,452	7,697	5,539	7,670									
Solyc10g005210	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9SVU2_RICCO)		P:GO:0006284; F:G(	P:base-excision rep	EC:3.2.2.21; EC:3.2.	DNA-3-methyladenine	IPR005019 (PFAM): G3DSA:1.10.340	6,551	4,754	0,072	0,000	0,094									
Solyc10g005220	RING/U-box superfamily protein (AHRD V3.3 *-* A0A061DVK0_THECC)						IPR013083 (G3DSA:3.30.40.GENE3D	0,019	0,036	0,000	0,000	0,000									
Solyc10g005230	Excitatory amino acid transporter 1 (AHRD V3.3 *** A0A0B0PDB0_GOSAR)						PTHR36052 (PANTHER)	34,387	30,941	40,307	31,165	37,684									
Solyc10g005240	R2R3MYB transcription factor 67	R2R3MYB67	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 MYB	0,000	0,079	0,000	0,047	0,023									
Solyc10g005250	LOW QUALITY:AT hook, DNA-binding motif-containing protein (AHRD V3.3 *-* A0A103YJM2_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,023									
Solyc10g005260	RNA-binding family protein (AHRD V3.3 *** A0A061FD24_THECC)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	104,231	106,752	72,280	74,020	84,640									
Solyc10g005290	Cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 *** B9RXN8_RIC(		P:GO:0008654; C:G(	P:phospholipid biosynthetic process; C:membrane; F:phosphotr			G3DSA:1.20.120.1760 (GENE3D): IPI	13,182	13,476	15,211	15,415	15,209									
Solyc10g005300	Kinase family protein (AHRD V3.3 *** U5GUL9_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	2,628	3,252	7,881	7,871	9,468									
Solyc10g005310	Adenosine deaminase, putative (AHRD V3.3 *** B9RXP2_RICCO)		F:GO:0019239	F:deaminase activity			IPR001365 (PFAM): PTHR11409:SF4	22,063	23,006	13,090	12,218	14,583									
Solyc10g005320	Tryptophan synthase (AHRD V3.3 *** K4CX65_SOLLC)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.2.1.2	Tryptophan synthase	G3DSA:3.40.50.1100 (GENE3D): IPR(	1,055	8,442	0,413	0,098	0,166	3,015	0,000					up		
Solyc10g005330	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GU68_POPTR)		F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			G3DSA:1.10.10.60 HD-ZIP	18,026	19,367	3,941	6,527	5,446					0,724	0,018			up
Solyc10g005340	ROP-interactive CRIB motif protein (AHRD V3.3 *-* A0A072U2K9_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR036936 (G3DSA:3.90.810.GENE3	2,088	1,805	3,322	4,187	3,680									
Solyc10g005350	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CX68_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xylogluco:	IPR008264 (PRINTS): IPR016455 (PII	0,021	0,000	0,025	0,000	0,024									
Solyc10g005360	Gibberellin 2-beta-dioxygenase (AHRD V3.3 *** G7K109_MEDTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,181	0,524	2,583	6,617	2,800					1,353	0,000			up
Solyc10g005370	Pyruvate, phosphate dikinase regulatory protein, putative (AHRD V3.3 *** A0A072VR94_MEDTR)		F:GO:0005524; F:G(	F:ATP binding; F:transferase activity, transferring phosphorus-c			IPR005177 (PFAM): mobidb-lite (MOB	76,794	57,521	153,744	135,258	139,173									
Solyc10g005380	Transmembrane protein, putative (AHRD V3.3 *** G7K108_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR34064:SF4 (PANTHER): PTHR3	0,640	0,871	0,536	0,632	0,658									
Solyc10g005390	Linalool/nerolidol synthase (AHRD V3.3 *** G5CV39_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,018	0,000	0,000	0,000									
Solyc10g005410	Terpene synthase (AHRD V3.3 *** G5CV41_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion binding; F:terpene synthase activity			IPR036965 (G3DSA:1.50.10.GENE3D	0,000	0,000	0,025	0,025	0,000									
Solyc10g005430	Quinone reductase family protein (AHRD V3.3 *** AT4G27270.3)		F:GO:0003955; F:G(	F:NAD(P)H dehydro	EC:1.6.5.2	NAD(P)H dehydroger	IPR005025 (PFAM): IPR010089 (TIGF	0,733	1,594	0,000	0,000	0,000									
Solyc10g005440	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IWF8_SOLCH)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (PFAM): IPR003609 (PFA	0,000	0,041	0,000	0,000	0,000									
Solyc10g005450	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H200_POPTR)		F:GO:0005337; C:G(	F:nucleoside transmembrane transporter activity; C:integral con			IPR002259 (PIRSF): IPR002259 (PFA	0,524	0,281	0,025	0,022	0,000									
Solyc10g005460	MYB transcription factor (AHRD V3.3 *** A0A0U3IU11_MESCR)	R2R3MYB74	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 MYB	0,042	0,039	0,050	0,025	0,000									
Solyc10g005470	receptor-interacting protein (AHRD V3.3 *** AT4G21445.1)						PTHR36382 (PANTHER)	0,432	1,618	0,115	0,451	0,656	1,900	0,001					up		
Solyc10g005480	F-box family protein (AHRD V3.3 *** B9H220_POPTR)						PTHR34049:SF1 (PANTHER): PTHR3	20,387	17,903	2,241	1,947	2,673									
Solyc10g005490	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *** A0A072TQ60_MEDTR)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR039187 (PFAM): IPR019787 (PFA	80,764	72,105	78,004	75,780	78,222									
Solyc10g005500	Cation efflux family protein (AHRD V3.3 *** AT1G16310.1)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;			IPR027470 (PFAM): IPR027469 (G3D	0,317	0,344	0,269	0,361	0,356									
Solyc10g005510	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4CX83_SOLLC)		P:GO:0006006; F:G(	P:glucose metabolic process; F:oxidoreductase activity, acting			IPR020831 (PRINTS): IPR006424 (TI(	66,777	87,780	79,686	70,702	71,621									
Solyc10g005520	RNA helicase DEAD30	DEAD30	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	16,926	16,996	21,581	22,821	20,071									
Solyc10g005530	ABH1 (AHRD V3.3 *** A0A097PNP2_SOLLC)		F:GO:0000339; F:G(	F:RNA cap binding; F:protein binding; C:nuclear cap binding con			IPR016021 (G3DSA:1.25.40.GENE3D	88,242	79,033	77,003	70,614	74,424									
Solyc10g005540	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9RHZ5_RICCO)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			IPR010719 (PFAM): G3DSA:3.40.50.1	0,675	0,667	0,094	0,116	0,211									
Solyc10g005550	R2R3MYB transcription factor 63	R2R3MYB10	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 MYB	0,000	0,000	0,025	0,000	0,000									
Solyc10g005560	Ubiquitin, putative (AHRD V3.3 *** B9RI09_RICCO)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): IPR000626 (PF	111,329	109,621	127,536	114,160	111,891									
Solyc10g005580	Interactor of constitutive active ROPs 2 (AHRD V3.3 *** A0A061FHC7_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	19,537	16,106	14,616	14,117	14,322									
Solyc10g005590	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT1G73530.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D	76,608	81,449	93,743	78,659	79,202									
Solyc10g005600	BTB/POZ domain-containing protein 1 (AHRD V3.3 *** S5ZYZ0_SOLTU)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0(	16,543	18,645	10,790	12,064	13,587									
Solyc10g005610	serine/arginine repetitive matrix-like protein (AHRD V3.3 *** AT1G56020.1)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,360	1,674	0,769	0,783	1,174									
Solyc10g005620	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT1G56000.1)						PR00419 (PRINTS): G3DSA:3.90.660	4,933	7,116	3,135	2,597	4,496									
Solyc10g005630	Kinase family protein (AHRD V3.3 *** B9NAB5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PIRS	1,370	1,117	0,522	0,877	0,777									
Solyc10g005640	Kinase family protein (AHRD V3.3 *-* B9NAB5_POPTR)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11; EC:3.1.3.	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): IPR0	7,433	5,895	4,056	3,981	4,094									
Solyc10g005650	Peroxisomal targeting signal 1 receptor (AHRD V3.3 *** Q9ZTK6_TOBAC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	117,779	99,553	186,237	183,213	174,651									
Solyc10g005660	Eukaryotic translation initiation factor 3 subunit F (AHRD V3.3 *** A0A0D6R1D0_ARACU)		P:GO:0000338; F:G(	P:protein deneddylation; F:protein binding; C:COP9 signalosom			IPR024969 (PFAM): IPR000555 (PFA	16,935	18,904	27,750	29,413	25,721									
Solyc10g005670	4-hydroxy-4-methyl-2-oxoglutarate aldolase (AHRD V3.3 *** M1ASF0_SOLTU)		F:GO:0008428; P:G(	F:ribonuclease inhibitor activity; P:regulation of RNA metabolic ı			IPR005493 (PFAM): IPR010203 (TIGF	58,957	57,963	85,132	83,825	84,493									
Solyc10g005690	Chloride channel protein (AHRD V3.3 *** K4CXA1_SOLLC)		F:GO:0005247; P:G(	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR001807 (PRINTS): IPR014743 (G3	31,593	23,880	2,096	1,730	2,365									
Solyc10g005700	BnaA03g48040D protein (AHRD V3.3 *** A0A078HW77_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	60,750	61,905	39,118	35,385	39,726									
Solyc10g005710	LOW QUALITY:SIN3-like 3 (AHRD V3.3 --* AT1G24190.3)							0,122	0,140	0,072	0,000	0,073									
Solyc10g005720	ATP-dependent DNA helicase Q-like 1 (AHRD V3.3 --* RQL1_ARATH)							18,135	14,701	13,729	13,007	11,822									
Solyc10g005730	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G13340.3)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	111,803	104,797	161,465	169,627	154,118									
Solyc10g005740	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G55690.5)						IPR001251 (PFAM): IPR036865 (G3D	0,864	0,496	0,124	0,000	0,024									
Solyc10g005750	Calcium-dependent protein kinase (AHRD V3.3 *** A0A0K9PJH9_ZOSMR)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	3,251	2,785	2,112	2,780	1,793									
Solyc10g005770	Protein kinase (AHRD V3.3 *** Q02494_MAIZE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR005366 (PFAM): IPR000719 (PFA	80,019	49,585	83,450	87,823	81,054	-0,662	0,022					down		
Solyc10g005780	ER membrane protein complex subunit-like protein (AHRD V3.3 *** G7KEJ5_MEDTR)		C:GO:0072546	C:ER membrane protein complex			IPR005366 (PFAM): G3DSA:3.40.140	1,741	1,163	1,457	1,378	1,650									
Solyc10g005790	transmembrane protein C9orf5 protein (AHRD V3.3 *** AT5G55960.1)		C:GO:0016021	C:integral component of membrane			IPR002549 (PFAM): PTHR21716:SF4	9,025	5,429	3,828	3,290	3,992									
Solyc10g005800	Protein CWC15 like (AHRD V3.3 *** A0A0B2SG97_GLYSO)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:spliceosomal complex			IPR006973 (PFAM): mobidb-lite (MOB	148,286	140,468	162,269	165,179	150,008									
Solyc10g005820	Farnesyl diphosphate synthase (AHRD V3.3 *** A0A0H5AZB7_NICBE)		F:GO:0004161; F:G(	F:dimethylallyltranst	EC:2.5.1.1; EC:2.5.1	(2E,6E)-farnesyl diph	IPR000092 (PFAM): IPR008949 (G3D	7,813	6,358	9,443	9,494	7,467									
Solyc10g005830	ureidoglycolate hydrolase (AHRD V3.3 *** AT2G35820.2)		F:GO:0004848	F:ureidoglycolate hy	EC:3.5.3.19	Acting on carbon-nitr	IPR024060 (G3DSA:2.60.120.GENE3	20,272	18,334	19,087	22,154	21,375									
Solyc10g005840	Farnesyl diphosphate synthase (AHRD V3.3 *** Q5S267_9APIA)		F:GO:0004161; F:G(	F:dimethylallyltranst	EC:2.5.1.1; EC:2.5.1	(2E,6E)-farnesyl diph	IPR008949 (G3DSA:1.10.600.GENE3	17,610	15,558	16,068	16,491	20,705									
Solyc10g005850	WW domain-containing protein (AHRD V3.3 *** AT3G13225.2)		F:GO:0005515	F:protein binding			IPR001202 (PFAM): G3DSA:2.20.70.1	28,443	32,674	26,807	25,935	24,562									
Solyc10g005860	WW domain-containing protein, putative isoform 4 (AHRD V3.3 *-* A0A061FBS1_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,320	2,178	1,602	1,724	1,955									
Solyc10g005870	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 *** A0A061F3L0_THECC)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	G3DSA:3.10.50.40 (GENE3D): PTHR4	5,499	7,801	2,737	3,132	5,731			1,064	0,006				up	
Solyc10g005880	Uridine kinase (AHRD V3.3 *** A0A022QIW2_ERYGU)		F:GO:0005524; P:G(	F:ATP binding; P:nucleoside metabolic process; F:kinase activit			PR00988 (PRINTS): G3DSA:3.40.50.2	27,934	35,448	15,748	13,334	17,248									

Solyc10g005890	DNA damage-inducible protein 1 (AHRD V3.3 *** A0A0B2RHB2_GLYSO)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	57,466	60,650	117,142	117,432	103,713									
Solyc10g005900	BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins) (AHRD '		C:GO:0000439; P:G(	C:transcription factor TFIIH core complex; P:nucleotide-excisior			IPR005607 (PFAM): IPR027079 (PAN	41,757	41,113	49,634	49,941	48,727									
Solyc10g005910	LOW QUALITY:GTPase Der (AHRD V3.3 *** A0A022QX40_ERYGU)		F:GO:0005525	F:GTP binding			IPR016484 (TIGRFAM): IPR032859 (F	6,664	5,009	5,041	5,896	5,844									
Solyc10g005920	Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *-* A0A0B2S7S2_GLYSO)		F:GO:0005515	F:protein binding			IPR032401 (PFAM): IPR001680 (PFA	36,213	27,003	22,601	20,571	25,434									
Solyc10g005925	Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *-* W9QQU0_9ROSA)		C:GO:0000932; P:G(	C:P-body; P:deadenylation-independent decapping of nuclear-tr			G3DSA:1.10.220.100 (GENE3D): PTH	34,904	28,851	22,687	20,051	23,984									
Solyc10g005930	histidine biosynthesis bifunctional protein (HISIE) (AHRD V3.3 *** AT1G31860.1)		P:GO:0000105; F:G(	P:histidine biosynth	EC:3.6.1.31; EC:3.5.	Phosphoribosyl-ATP	IPR038019 (G3DSA:3.10.20.GENE3D	15,695	16,953	37,558	34,819	35,602									
Solyc10g005950	Nudix hydrolase (AHRD V3.3 *** A0A061F5Q1_THECC)		F:GO:0016787	F:hydrolase activity			IPR003293 (PRINTS): IPR020476 (PF	6,224	10,216	9,350	9,276	9,312									
Solyc10g005955	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 --* AT1G79120.2)							0,000	0,021	0,044	0,025	0,000									
Solyc10g005960	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** A0A072UY96_MEDTR)		C:GO:0016021; C:G(	C:integral component of membrane; C:anchored component of r			IPR000782 (PFAM): IPR036378 (G3D	80,393	81,203	2,006	1,393	2,338									
Solyc10g005970	phospholipase-like protein (PEARLI 4) family protein (AHRD V3.3 --* AT2G20960.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,061	0,094	0,025	0,022	0,000									
Solyc10g005980	LOW QUALITY:RNA-binding protein, putative (AHRD V3.3 *** B9S9T2_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D	0,140	0,039	0,025	0,022	0,023									
Solyc10g005990	Tuftelin-interacting protein 11 (AHRD V3.3 *** A0A0B2RLS8_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR024933 (PIRSF): IPR022159 (PFA	32,955	33,726	40,272	33,742	37,270									
Solyc10g006000	Protein DEK (AHRD V3.3 *** A0A0B2PUB3_GLYSO)		C:GO:0005634; F:G(	C:nucleus; F:histone binding; P:regulation of double-strand brea			IPR014876 (PFAM): G3DSA:1.10.10.6	2,931	3,245	0,115	0,165	0,214									
Solyc10g006010	Outward rectifying potassium channel protein (AHRD V3.3 *** AT5G55630.2)		F:GO:0005267; C:G(	F:potassium channel activity; C:membrane; P:potassium ion tra			IPR003280 (PRINTS): G3DSA:1.10.28	15,832	20,453	17,758	18,861	14,669									
Solyc10g006020	Mitochondrial import inner membrane translocase subunit TIM50 (AHRD V3.3 *** A0A1D1YE49_9ARAE)		C:GO:0005744; P:G(	C:TIM23 mitochondrial import inner membrane translocase com			IPR004274 (PFAM): IPR023214 (G3D	18,408	22,860	30,759	32,349	29,115									
Solyc10g006030	Ribosomal protein S10 (AHRD V3.3 *** A0A103Y4F5_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001848 (PRINTS): IPR027486 (PF	14,249	25,595	13,445	15,678	23,764	0,873	0,001	0,817	0,000			up	up	
Solyc10g006040	Serine acetyltransferase (AHRD V3.3 *** Q6STL5_NICPL)		C:GO:0005737; P:G(	C:cytoplasm; P:cys	EC:2.3.1.3	Serine O-acetyltrans	IPR010493 (PFAM): G3DSA:1.10.313	2,836	3,698	2,249	1,922	2,328									
Solyc10g006050	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	78,739	66,114	62,650	59,369	57,350									
Solyc10g006070	40S ribosomal protein S8 (AHRD V3.3 *** K4CXD9_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001047 (TIGRFAM): G3DSA:2.40.	230,633	218,437	195,069	167,320	174,185									
Solyc10g006080	Sodium/hydrogen exchanger (AHRD V3.3 *** A0A067F4C6_CITSI)		C:GO:0005774; P:G(	C:vacuolar membrane; P:sodium ion transport; P:regulation of p			IPR004709 (PRINTS): IPR006153 (PF	3,369	2,943	0,826	1,213	0,778									
Solyc10g006090	ENHANCED DOWNY MILDEW 2 (AHRD V3.3 *** AT5G55390.3)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:signal t			IPR013083 (G3DSA:3.30.40.GENE3D	54,056	43,249	68,009	70,108	64,594									
Solyc10g006100	Transcription initiation factor TFIID subunit-like protein (AHRD V3.3 *** G7KXV7_MEDTR)		C:GO:0000124; C:G(	C:SAGA complex; C:transcription factor TFIID complex; P:regula			IPR009072 (G3DSA:1.10.20.GENE3D	20,805	19,712	26,083	23,237	22,997									
Solyc10g006110	EH domain-containing protein 1 (AHRD V3.3 *** EHD1_ARATH)		F:GO:0005509; F:G(	F:calcium ion binding; F:protein binding; F:GTP binding			G3DSA:1.10.268.20 (GENE3D): IPR0	0,000	0,060	0,000	0,000	0,000									
Solyc10g006120	extracellular ligand-gated ion channel protein (DUF3537) (AHRD V3.3 *** AT3G20300.1)		C:GO:0016021	C:integral component of membrane			IPR021924 (PFAM): PTHR31963:SF4	1,452	0,912	0,846	0,610	0,896									
Solyc10g006130	EAR motif SlERF36	ERF.F1	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN' ERF	252,857	93,873	66,821	181,309	80,003	-1,405	0,000			1,443	0,000	down		up
Solyc10g006140	Acid phosphatase/vanadium-dependent haloperoxidase-related protein (AHRD V3.3 *** AT3G21610.1)		F:GO:0004601; C:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR003832 (PFAM): PTHR31446:SF7	59,480	47,048	40,245	32,157	35,260									
Solyc10g006150	DUF4408 domain protein (AHRD V3.3 *** G7K8L0_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR008480 (PFAM): PTHR36887 (PAN	1,043	0,649	0,644	0,701	0,375									
Solyc10g006153	Rcd1-like cell differentiation family protein (AHRD V3.3 *-* B9GJH1_POPTR)		C:GO:0000932; P:G(	C:P-body; P:negative regulation of translation; C:CCR4-NOT co			PF04078 (PFAM): IPR011989 (G3DS	2,588	2,045	3,177	3,229	3,349									
Solyc10g006155	GATA transcription factor 26 (AHRD V3.3 --* AT4G17570.3)						mobidb-lite (MOBIDB_LITE)	6,394	4,835	6,378	8,616	7,204									
Solyc10g006157	Rcd1-like cell differentiation family protein (AHRD V3.3 *-* B9GJH1_POPTR)		C:GO:0000932; P:G(	C:P-body; P:negative regulation of translation; C:CCR4-NOT co			G3DSA:3.30.160.20 (GENE3D): PF14	0,118	0,135	0,174	0,192	0,095									
Solyc10g006170	Rcd1-like cell differentiation family protein (AHRD V3.3 *-* B9GJH1_POPTR)		C:GO:0000932; P:G(	C:P-body; P:negative regulation of translation; C:CCR4-NOT co			IPR011989 (G3DSA:1.25.10.GENE3D	0,084	0,061	0,025	0,000	0,072									
Solyc10g006180	DNA repair protein recA-1-like protein (AHRD V3.3 --* W9QMN4_9ROSA)							0,019	0,000	0,000	0,000	0,000									
Solyc10g006190	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)		C:GO:0000932; P:G(	C:P-body; P:negative regulation of translation; C:CCR4-NOT co			IPR011989 (G3DSA:1.25.10.GENE3D	4,018	3,705	2,699	3,601	2,686									
Solyc10g006200	Ribonuclease 3-like protein 2 (AHRD V3.3 *** A0A061F5X1_THECC)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	PF14709 (PFAM): IPR036389 (G3DS	1,100	0,732	0,634	0,809	0,692									
Solyc10g006215	Cell differentiation protein RCD1 like (AHRD V3.3 *-* A0A0B2PXT8_GLYSO),Pfam:PF04078						IPR011989 (G3DSA:1.25.10.GENE3D	0,000	0,039	0,000	0,000	0,000									
Solyc10g006220	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)						PF04078 (PFAM): IPR011989 (G3DS	4,017	3,464	2,481	3,003	2,893									
Solyc10g006230	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** A0A0V0HM25_SOLCH)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	449,017	856,154	257,679	361,360	650,851	0,959	0,023	1,333	0,000			up	up	
Solyc10g006240	Proline synthase co-transcribed bacterial (AHRD V3.3 *** A0A1D1ZCG0_9ARAE)		F:GO:0030170	F:pyridoxal phosphate binding			IPR001608 (PFAM): IPR011078 (TIGF	34,421	35,592	39,433	38,081	40,961									
Solyc10g006250	Protein suppressor of white apricot (AHRD V3.3 *-* A0A151U2B3_CAJCA)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing			IPR019147 (PFAM): mobidb-lite (MOB	13,192	11,719	11,639	10,799	11,386									
Solyc10g006260	SWAP (Suppressor-of-white-APricot)/surp domain protein, putative (AHRD V3.3 *** A0A072UG97_MEDTR)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing			IPR035967 (G3DSA:1.10.10.GENE3D	93,322	94,419	90,513	80,020	83,948									
Solyc10g006270	Autophagy-related protein (AHRD V3.3 *** K4CXF8_SOLLC)		C:GO:0005737; P:G(	C:cytoplasm; P:autophagy; P:cellular response to nitrogen starv			IPR004241 (PFAM): G3DSA:3.10.20.9	43,811	34,256	53,304	48,657	46,777									
Solyc10g006275	Senescence regulator (AHRD V3.3 *** G7IY27_MEDTR)		C:GO:0009506	C:plasmodesma			IPR007608 (PFAM): PTHR33083 (PAN	0,021	0,000	0,000	0,000	0,000									
Solyc10g006290	constitutive plastid-lipid associated protein	chrdc	C:GO:0005829; F:G(	C:cytosol; F:deaminase activity; P:organonitrogen compound ca			IPR006175 (PFAM): IPR035959 (G3D	45,654	50,868	137,087	122,768	126,954									
Solyc10g006295	Purple acid phosphatase (AHRD V3.3 *-* K4CXG1_SOLLC)		F:GO:0003993; P:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase		0,243	0,059	0,068	0,099	0,234									
Solyc10g006300	Purple acid phosphatase (AHRD V3.3 *** K4CXG1_SOLLC)		F:GO:0003993; F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR025733 (PFAM): IPR029052 (G3D	2,510	1,971	2,485	3,323	2,349									
Solyc10g006310	Transmembrane proteins 14C (AHRD V3.3 *** A0A061F6B6_THECC)		C:GO:0016020	C:membrane			G3DSA:1.20.58.1140 (GENE3D): IPR(	3,973	5,145	3,127	3,467	4,039									
Solyc10g006320	Vacuolar protein sorting-associated protein (AHRD V3.3 *** K4CXG3_SOLLC)		C:GO:0000814; P:G(	C:ESCRT II complex; P:multivesicular body sorting pathway			IPR036388 (G3DSA:1.10.10.GENE3D	21,082	22,889	32,679	29,702	29,665									
Solyc10g006330	Plastid movement impaired protein (AHRD V3.3 *** G7LD87_MEDTR)		P:GO:0009902	P:chloroplast relocation			IPR019448 (PFAM): mobidb-lite (MOB	43,938	38,634	21,621	23,404	43,743			1,012	0,000				up	
Solyc10g006340	Kinase family protein (AHRD V3.3 *** U5GUL9_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): PIRSF000654 (P	0,019	0,000	0,000	0,000	0,000									
Solyc10g006350	CONSTANS interacting protein 7	CIP7	C:GO:0005874; F:G(	C:microtubule; F:microtubule binding			IPR011989 (G3DSA:1.25.10.GENE3D	26,968	24,452	30,326	26,866	25,355									
Solyc10g006360	Hexon (AHRD V3.3 *** A0A0B0PIL4_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,290	2,258	6,503	7,955	5,116									
Solyc10g006370	Lhcp translocation defect-like protein (AHRD V3.3 *** A0A0B0PFC4_GOSAR)		C:GO:0009570; P:G(	C:chloroplast stroma; P:granum assembly			IPR036770 (G3DSA:1.25.40.GENE3D	10,733	14,896	16,740	16,485	21,144									
Solyc10g006380	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G54840.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0(	0,155	0,194	0,000	0,025	0,000									
Solyc10g006390	FHA domain-containing protein		F:GO:0005515	F:protein binding			G3DSA:2.60.200.20 (GENE3D): IPR0(	55,176	47,683	40,272	37,947	42,188									
Solyc10g006400	Tryptophan synthase (AHRD V3.3 *** K4CXH1_SOLLC)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.2.1.2	Tryptophan synthase	IPR001926 (PFAM): G3DSA:3.40.50.1	38,448	43,566	73,924	63,679	74,464									
Solyc10g006410	AP-5 complex subunit zeta-1 (AHRD V3.3 *** AT3G15160.1)		C:GO:0044599	C:AP-5 adaptor complex			IPR028222 (PFAM): PTHR12181:SF2	22,644	18,362	26,287	28,872	25,987									
Solyc10g006430	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G61660.7)		P:GO:0010089	P:xylem development			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,060	0,018	0,000	0,000	0,000									
Solyc10g006440	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G27100.2)		F:GO:0005096; C:G(	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (PFAM): G3DSA:1.10.8.27	1,599	0,720	0,436	0,369	0,444									
Solyc10g006450	COBRA-like protein (AHRD V3.3 *** L0AUC5_POPTO)		P:GO:0010215; P:G(	P:cellulose microfibril organization; P:cell growth; C:anchored co			IPR006918 (PFAM): PTHR31052 (PAN	0,471	0,710	0,196	0,212	0,166									
Solyc10g006460	DDRGK domain-containing protein 1 (AHRD V3.3 *** A0A1D1YPH7_9ARAE)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane			IPR019153 (PFAM): IPR036388 (G3D	34,635	32,454	46,910	45,341	44,165									
Solyc10g006470	Protein translation factor SUI1 homolog (AHRD V3.3 *** SUI1_ORYSJ)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			IPR001950 (PFAM): G3DSA:3.30.780	87,548	102,973	164,746	183,241	158,238									
Solyc10g006480	Polyubiquitin (AHRD V3.3 *** UBI1P_NICSY)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): G3DSA:3.10.20	639,817	651,792	559,457	581,832	518,372									
Solyc10g006490	Trafficking protein particle complex subunit 3 (AHRD V3.3 *** A0A1D1YVK5_9ARAE)		C:GO:0030008; P:G(	C:TRAPP complex; P:Golgi vesicle transport			IPR016721 (PIRSF): G3DSA:3.30.138	61,677	55,644	62,377	51,229	58,244									
Solyc10g006500	Hexosyltransferase (AHRD V3.3 *** K4CXI1_SOLLC)	GAUT12-1	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR029044 (G3DSA:3.90.550.GENE3	1,061	0,955	0,123	0,047	0,118									
Solyc10g006510	bHLH transcription factor152		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM bHLH	7,614	8,682	12,456	12,959	11,687									
Solyc10g006520	Thioredoxin-related family protein (AHRD V3.3 *** B9MVK1_POPTR)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	3,989	3,665	4,281	4,224	3,844									
Solyc10g006525	Protein DETOXIFICATION (AHRD V3.3 --* K7M2A8_SOYBN)							0,768	0,633	0,661	0,579	0,686									
Solyc10g006530	Photosynthetic NDH subcomplex L 3 (AHRD V3.3 *** A0A0F7CYJ0_9ROSI)		F:GO:0005509; C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR008797 (PFAM): G3DSA:1.20.120	0,323	0,933	0,068	0,119	0,354									
Solyc10g006540	Formin-like protein (AHRD V3.3 *** K4CXI5_SOLLC)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.58.2220 (GENE3D): G3D	70,840	104,794	57,215	62,948	69,592									
Solyc10g006550	Protein DETOXIFICATION (AHRD V3.3 --* A0A0D3HQG4_9ORYZ)							1,859	1,481	0,821	0,848	0,633									
Solyc10g006560	Histone H2A (AHRD V3.3 *** A0A0V0H7M3_SOLCH)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimer			IPR002119 (PRINTS): IPR032454 (PF	38,670	43,792	66,684	56,269	52,285									
Solyc10g006570	LOW QUALITY:Protein JTB (AHRD V3.3 -** A0A0B0PSQ1_GOSAR)						PTHR35318:SF2 (PANTHER): PTHR3	2,153	2,033	2,000	1,529	1,436									
Solyc10g006580	ribosomal protein L2	rpl2	F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022666 (PFAM): IPR022669 (PFA	207,953	223,816	147,278	127,420	130,735									
Solyc10g006590	transmembrane protein, putative (Protein of unknown function, DUF538) (AHRD V3.3 *** AT3G07470.3)		C:GO:0016021	C:integral component of membrane			IPR007493 (PFAM): IPR036758 (G3D	0,021	0,021	0,025	0,000	0,000									
Solyc10g006600	Gluconokinase (AHRD V3.3 *** M1CC61_SOLTU)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:kinase activity			G3DSA:3.40.50.300 (GENE3D): IPR0(	2,766	1,948	2,509	2,823	3,059									
Solyc10g006610	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT5G54510.1)						IPR004993 (PFAM): IPR004993 (PAN	0,061	0,043	0,050	0,124	0,071									
Solyc10g006640	bHLH transcription factor153		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	0,493	0,716	0,349	0,346	0,493									
Solyc10g006650	Quinone reductase family protein (AHRD V3.3 *** AT4G27270.1)		F:GO:0003955; F:G(	F:NAD(P)H dehydro	EC:1.6.5.2	NAD(P)H dehydroger	IPR005025 (PFAM): IPR029039 (G3D	53,045	47,361	126,582	115,422	108,794									
Solyc10g006660	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	213,809	64,484	53,305	215,527	83,846	-1,705	0,000			2,018	0,000	down		up
Solyc10g006670	Serine/threonine-protein kinase (AHRD V3.3 *-* V4TXK0_9ROSI)		F:GO:0005488; P:G(	F:binding; P:cellular process; F:kinase activity			G3DSA:1.10.510.10 (GENE3D): G3DS	0,021	0,000	0,000	0,000	0,023									
Solyc10g006680	lectin protein kinase family protein (AHRD V3.3 *-* AT3G16030.8)		F:GO:0004672; P:G(	F:protein kinase activity; P:protein phosphorylation			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,019	0,021	0,000	0,047	0,070									
Solyc10g006690	Serine/threonine-protein kinase (AHRD V3.3 *** M5WN54_PRUPE)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:1.10.510.10 (GENE3D): IPR0(	1,512	1,885	0,967	1,648	0,958									
Solyc10g006700	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	208,969	71,912	51,350	191,497	70,183	-1,515	0,000			1,901	0,000	down		up
Solyc10g006710	Serine/threonine-protein kinase (AHRD V3.3 *** U5GTQ6_POPTR)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR001480 (PFAM): IPR024171 (PIRS	42,920	68,515	105,467	125,674	113,459									
Solyc10g006720	Serine/threonine-protein kinase (AHRD V3.3 *** M1CC72_SOLTU)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000858 (PFAM): IPR001245 (PFA	0,081	0,754	2,099	2,348	2,515									
Solyc10g006730	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GVT5_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	13,304	10,273	11,979	12,186	12,038									
Solyc10g006740	Calcium-binding family protein (AHRD V3.3 *** B9I910_POPTR)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	0,717	0,915	1,336	2,329	2,234									
Solyc10g006750	ABC-2 and Plant PDR ABC-type transporter family protein (AHRD V3.3 --* AT4G152	BBX26						0,563	0,762	1,830	2,293	1,865									
Solyc10g006755	LOW QUALITY:Zinc finger, B-box (AHRD V3.3 *-* A0A103Y479_CYNCS)		F:GO:0008270	F:zinc ion binding			IPR000315 (PFAM): mobidb-lite (MOB	0,021	0,000	0,025	0,045	0,000									
Solyc10g006760	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)						IPR006015 (PRINTS): IPR014729 (G3	30,708	35,379	40,169	34,683	33,724									
Solyc10g006770	FACT complex subunit SPT16 (AHRD V3.3 *** W9RSN6_9ROSA)		C:GO:0035101	C:FACT complex			IPR013719 (PFAM): IPR011993 (G3D	62,656	44,716	93,774	90,840	83,876									
Solyc10g006780	Telomere length regulation protein TEL2 like (AHRD V3.3 *** A0A0B2RBY7_GLYSO)						IPR038528 (G3DSA:1.25.40.GENE3D	33,309	26,398	42,218	49,206	44,209									
Solyc10g006790	mitogen-activated protein kinase 16 (AHRD V3.3 --* AT5G19010.1)							22,484	24,391	33,787	31,820	30,263									
Solyc10g006800	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9SIE1_RICCO)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR014710 (G3DSA:2.60.120.GENE3	0,422	1,455	0,363	1,139	1,381									
Solyc10g006820	Myosin VIII-2 (AHRD V3.3 *** B0CN63_NICBE)		F:GO:0003774; F:G(	F:motor activity; F:(	EC:3.6.1.15	Nucleoside-triphosph	IPR001609 (PRINTS): G3DSA:1.20.58	35,146	34,752	26,261	26,114	32,232									
Solyc10g006830	B3 domain-containing protein family (AHRD V3.3 *-* A0A151T7I8_CAJCA)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM): IPR015300 (G3D	12,490	11,381	15,420	15,734	14,917									
Solyc10g006840	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT1G72660.3)							0,945	1,266	1,699	1,828	1,318									
Solyc10g006850	Arf GTPase activating protein (AHRD V3.3 *** A0A103YJY6_CYNCS)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (PF	11,530	12,122	11,523	9,659	10,653									
Solyc10g006860	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G17845.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	26,652	28,793	73,163	66,383	103,535									
Solyc10g006880	NAC domain protein (AHRD V3.3 *** Q56UP7_SOLLC)	NOR	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	3,523	7,030	282,630	375,242	246,812					0,412	0,031			up
Solyc10g006890	WD-repeat protein, putative (AHRD V3.3 *** B9T7M5_RICCO)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	47,760	40,041	58,523	75,273	57,508									
Solyc10g006900	light dependent NADH:protochlorophyllide oxidoreductase 3 s2	POR3	F:GO:0016630; P:G(	F:protochlorophyllid	EC:1.3.1.33	Protochlorophyllide re	IPR002347 (PRINTS): IPR005979 (TI	16,918	76,349	3,987	4,736	10,529	2,201	0,000	1,395	0,000			up	up	
Solyc10g006910	50S ribosomal protein L16, chloroplastic (AHRD V3.3 *** RK16_SOLBU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR016180 (PFAM): IPR036920 (G3D	0,218	0,682	0,558	0,794	0,606									
Solyc10g006920	CBS domain-containing protein (AHRD V3.3 *** A0A061GEK1_THECC)						IPR000644 (PFAM): mobidb-lite (MOB	2,382	1,511	0,124	0,126	0,048									
Solyc10g006930	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT3G15410.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	65,730	54,053	91,990	90,207	89,632									
Solyc10g006940	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G62760.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,023									
Solyc10g006950	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT2G22040.1)							1,447	1,634	3,022	3,082	3,701									
Solyc10g006960	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G58030.4)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	2,049	1,605	4,622	3,891	4,590									
Solyc10g006970	Thioredoxin (AHRD V3.3 *** A0A118K131_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS): IPR013766 (PFA	7,395	12,840	31,791	28,608	37,853	0,823	0,008					up		
Solyc10g006980	3-deoxy-manno-octulosonate cytidylyltransferase (AHRD V3.3 *** A0A072VK14_MEDTR)		F:GO:0008690	F:3-deoxy-manno-o	EC:2.7.7.38	3-deoxy-manno-octul	IPR029044 (G3DSA:3.90.550.GENE3	47,153	41,257	43,529	40,609	37,560									
Solyc10g006990	nucleotidyltransferase family protein		F:GO:0016779	F:nucleotidyltransferase activity			G3DSA:3.30.460.10 (GENE3D): G3DS	29,710	31,055	48,234	45,707	44,165									
Solyc10g007000	Ubiquitin conjugating enzyme, putative (AHRD V3.3 *** B9T0E4_RICCO)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin conjugating enzyme activity			IPR016135 (G3DSA:3.10.110.GENE3	6,305	7,776	18,182	19,414	16,071									
Solyc10g007010	Cytochrome c oxidase copper chaperone, putative (AHRD V3.3 *** B9T0E6_RICCO)		C:GO:0005758; P:G(	C:mitochondrial intermembrane space; P:copper ion transport; F			IPR007745 (PFAM): G3DSA:1.10.287	2,920	3,037	4,713	4,240	4,689									
Solyc10g007020	Protein kinase superfamily protein (AHRD V3.3 --* AT2G25220.5)						mobidb-lite (MOBIDB_LITE)	1,175	1,801	1,951	2,599	2,140									
Solyc10g007030	Transmembrane protein, putative (AHRD V3.3 *** G7IPT2_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR34274 (PANTHER): PTHR34274	21,558	23,315	11,059	8,585	9,357									
Solyc10g007040	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** F4JIW2_ARATH		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): mobidb-lite (MOB	1,835	1,244	22,016	24,493	14,683			-0,587	0,047				down	
Solyc10g007050	Methylthioribulose 1-phosphate dehydratase / enolase-phosphatase E1 (AHRD V3.3 *-* A0A061R779_9CHL		F:GO:0000287; P:G(	F:magnesium ion bi	EC:3.1.3.77	Acireductone synthas	IPR023214 (G3DSA:3.40.50.GENE3D	2,563	5,605	1,508	1,538	2,068	1,156	0,022					up		
Solyc10g007060	Phenylalanyl-tRNA synthetase alpha chain, putative (AHRD V3.3 *-* G7JG63_MEDTR)		F:GO:0000049; F:G(	F:tRNA binding; F:p	EC:6.1.1.2	Phenylalanine--tRNA	G3DSA:1.10.10.2330 (GENE3D): G3D	7,932	9,089	4,540	4,689	5,247									
Solyc10g007065	Phenylalanyl-tRNA synthetase alpha chain, putative (AHRD V3.3 *-* G7JG63_MEDTR)		F:GO:0000049; F:G(	F:tRNA binding; F:p	EC:6.1.1.2	Phenylalanine--tRNA	G3DSA:3.30.930.10 (GENE3D): IPR0(	14,885	16,287	10,415	8,759	9,254									
Solyc10g007070	Early nodulin-like protein (AHRD V3.3 *** A0A072VAV5_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	7,698	5,675	5,316	4,890	4,893									
Solyc10g007080	Protein DETOXIFICATION (AHRD V3.3 *-* K4CXP0_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): PTHR11206 (PAN	8,609	4,345	1,314	0,728	0,915									
Solyc10g007090	Protein DETOXIFICATION (AHRD V3.3 *-* K4CXP0_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): PTHR11206 (PAN	1,509	0,739	0,121	0,167	0,094									
Solyc10g007100	Protein DETOXIFICATION (AHRD V3.3 *** K4CXP0_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	8,747	4,639	12,570	14,158	14,107	-0,882	0,046					down		
Solyc10g007103	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)		F:GO:0003677	F:DNA binding			IPR000047 (PRINTS): IPR001356 (PF	0,019	0,000	0,025	0,000	0,047									
Solyc10g007107	Nucleic acid-binding, OB-fold (AHRD V3.3 *-* A0A103XEX3_CYNCS)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D): PTHR	0,118	0,211	0,068	0,095	0,142									
Solyc10g007110	Tyrosine aminotransferase (AHRD V3.3 *** E2JFA7_PERFR)	TAT1	P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR015422 (G3DSA:3.90.1150.GENE	13,640	23,159	426,027	619,802	565,073					0,545	0,005			up
Solyc10g007120	transmembrane protein (AHRD V3.3 *** AT3G15110.1)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of mem			IPR021434 (PFAM): mobidb-lite (MOB	7,853	11,848	8,514	7,315	11,735									
Solyc10g007125	Zinc finger MYM-type protein 5 (AHRD V3.3 --* A0A151T4M1_CAJCA)							2,271	4,084	2,546	2,496	3,844									
Solyc10g007130	Sequence-specific DNA-binding transcription factor (AHRD V3.3 *** G7LDQ2_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:chromatin binding			IPR032001 (PFAM HB-other	29,780	26,040	29,709	29,888	31,632									
Solyc10g007140	RING/U-box superfamily protein (AHRD V3.3 *** AT1G53190.2)		C:GO:0005634; P:G(	C:nucleus; P:protein ubiquitination; F:ligase activity; F:ubiquitin			IPR013083 (G3DSA:3.30.40.GENE3D	20,830	16,844	35,104	34,488	33,659									
Solyc10g007150	Apoptosis inhibitory 5 (AHRD V3.3 *** A0A103XEZ4_CYNCS)		F:GO:0003729; C:G(	F:mRNA binding; C:nucleus; P:regulation of programmed cell dea			IPR008383 (PFAM): mobidb-lite (MOB	38,728	33,561	50,556	50,967	47,847									
Solyc10g007156	Actin cytoskeleton-regulatory complex protein pan1, putative isoform 1 (AHRD V3.3 *** A0A061F777_THECC		F:GO:0003700	F:DNA-binding transcription factor activity			PTHR33388:SF1 (PANTHER): PTHR3	0,019	0,000	0,000	0,000	0,023									
Solyc10g007158	Transcription factor GTE4 (AHRD V3.3 --* A0A0B2PJL2_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,018	0,000	0,000	0,000									
Solyc10g007160	Transcription factor GTE4 (AHRD V3.3 --* A0A0B2PJL2_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,285	0,144	0,000	0,000	0,000									
Solyc10g007170	Transcription factor GTE4-like protein (AHRD V3.3 *-* A0A0B0NA54_GOSAR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,468	0,322	0,000	0,000	0,000									
Solyc10g007180	DAG protein (AHRD V3.3 *** A0A0K9PW98_ZOSMR)		P:GO:0016554	P:cytidine to uridine editing			mobidb-lite (MOBIDB_LITE): mobidb-lit	102,063	100,158	163,229	133,993	143,821									
Solyc10g007190	Zinc finger BED domain-containing protein RICESLEEPER 2 (AHRD V3.3 *-* A0A199W0P7_ANACO)		F:GO:0003677	F:DNA binding			IPR003656 (PFAM): PTHR34396:SF1	9,992	12,530	16,049	14,324	14,207									
Solyc10g007200	Hexosyltransferase (AHRD V3.3 *** K4CXQ0_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			IPR002659 (PFAM): PTHR11214:SF1	17,383	17,545	30,696	27,377	26,393									
Solyc10g007220	tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *-* AT5G65160.1)		F:GO:0005515	F:protein binding			IPR013105 (PFAM): IPR011990 (G3D	0,019	0,037	0,000	0,000	0,000									
Solyc10g007225	TPR repeat thioredoxin TTL1-like protein (AHRD V3.3 *-* A0A072V9X4_MEDTR)		F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): IPR01	0,019	0,076	0,000	0,000	0,000									
Solyc10g007230	TPR repeat thioredoxin TTL1-like protein (AHRD V3.3 *** A0A072V9X4_MEDTR)		F:GO:0005515; P:G(	F:protein binding; P:cell redox homeostasis			PF13432 (PFAM): IPR011990 (G3DS	0,253	0,458	0,000	0,000	0,000									

Solyc10g007255	RELA/SPOT homolog 1 (AHRD V3.3 --* AT4G02260.4)							0,000	0,041	0,025	0,000	0,000									
Solyc10g007260	Ubiquitin-conjugating enzyme (AHRD V3.3 *** H6VUT0_9FABA)		F:GO:0005524: C:G(	F:ATP binding; C:nucleus; C:cytosol; C:plasma membrane; P:po			IPR016135 (G3DSA:3.10.110.GENE3	27,128	30,592	48,173	51,896	47,635									
Solyc10g007280	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding			IPR025753 (PFAM); G3DSA:3.40.50.3	9,235	54,182	2,991	2,863	4,759	2,570	0,001					up		
Solyc10g007290	Phosphoenolpyruvate carboxylase (AHRD V3.3 *** CAPP_TOBAC)		P:GO:0006099; F:G(	P:tricarboxylic acid	EC:4.1.1.31; EC:4.1.	Phosphoenolpyruvate	IPR021135 (PRINTS); G3DSA:1.20.14	57,913	58,546	14,470	5,598	8,541			-0,764	0,048	-1,369	0,000		down	down
Solyc10g007300	succinate dehydrogenase 2-1 (AHRD V3.3 --* AT3G27380.2)							1,705	1,066	1,064	1,515	1,198									
Solyc10g007310	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM); mobidb-lite (MOB	136,581	118,609	327,588	347,634	273,295									
Solyc10g007320	Uroporphyrinogen decarboxylase (AHRD V3.3 *** K4CXR1_SOLLC)	HEME/UROD	F:GO:0004853; P:G(	F:uroporphyrinogen	EC:4.1.1.37	Uroporphyrinogen de	IPR000257 (PFAM); IPR038071 (G3D	28,308	45,788	66,097	60,501	69,408	0,721	0,006					up		
Solyc10g007330	peptide:N-glycanase	PNGase	F:GO:0000224; C:G(	F:peptide-N4-(N-ac	EC:3.5.1.52	Peptide-N(4)-(N-acet	IPR021102 (PFAM); IPR021102 (PAN	13,441	9,006	11,983	9,224	9,711									
Solyc10g007340	Methylthioribose-1-phosphate isomerase (AHRD V3.3 *-* A0A0B0PHV1_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	21,526	21,259	22,487	21,280	22,325									
Solyc10g007345	LOW QUALITY:Ribonuclease H (AHRD V3.3 *** Q2HU20_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM); IPR036397 (G3D	0,102	0,132	0,000	0,092	0,024									
Solyc10g007350	Multiprotein bridging factor 1a (AHRD V3.3 *** Q152U9_SOLLC)		F:GO:0043565	F:sequence-specific DNA binding			IPR001387 (PFAM); IPR013729 (PFA	55,838	60,403	81,390	81,230	80,093									
Solyc10g007360	Protein DETOXIFICATION (AHRD V3.3 *** A5B677_VITVI)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM); IPR002528 (F	7,172	7,275	16,967	15,840	16,416									
Solyc10g007390	Protein transport protein Sec61 subunit alpha (AHRD V3.3 *** A0A151RBI9_CAJCA)		P:GO:0015031; C:G(	P:protein transport; C:membrane			IPR002208 (PIRSF); IPR023201 (G3D	127,956	126,640	137,368	135,825	124,857									
Solyc10g007400	DNA polymerase delta subunit 3 (AHRD V3.3 *** A0A0B0NMF9_GOSAR)		C:GO:0005634; P:G(	C:nucleus; P:DNA replication			G3DSA:1.10.10.1300 (GENE3D); IPR(	5,675	5,825	7,737	5,938	6,726									
Solyc10g007410	gamma-glutamylhydrolase 2		F:GO:0008242	F:omega peptidase	EC:3.4.19	Acting on peptide bor	IPR011697 (PFAM); IPR029062 (G3D	16,965	15,878	19,517	19,555	20,552									
Solyc10g007420	gamma-glutamylhydrolase		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,068	3,469	2,286	2,764	2,349									
Solyc10g007430	LOW QUALITY:TPR repeat thioredoxin TTL1-like protein (AHRD V3.3 *-* A0A072V9X4_MEDTR)		F:GO:0005515	F:protein binding			PF14559 (PFAM); IPR011990 (G3DS/	0,040	0,037	0,000	0,000	0,024									
Solyc10g007440	Zinc finger family protein, putative (AHRD V3.3 *-* A0A061F333_THECC)						PTHR23111:SF24 (PANTHER); PTHR:	8,114	8,000	11,328	12,389	11,798									
Solyc10g007450	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM); IPR026057 (PFA	0,019	0,077	0,000	0,000	0,000									
Solyc10g007460	Zinc finger protein (AHRD V3.3 *-* W9RJ16_9ROSA)						PTHR23111:SF24 (PANTHER); PTHR:	4,815	4,424	5,109	5,136	4,914									
Solyc10g007470	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR003656 (PFAM); IPR008906 (PFA	20,796	17,697	27,663	28,422	29,058									
Solyc10g007480	NAD-dependent epimerase/dehydratase family protein (AHRD V3.3 *** AT1G53500.1)		F:GO:0008460; P:G(	F:dTDP-glucose 4,6	EC:4.2.1.46	dTDP-glucose 4,6-de	IPR029903 (PFAM); IPR016040 (PFA	410,619	378,733	285,274	304,518	280,385									
Solyc10g007500	mitogen-activated protein kinase 10	mapk10	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	63,425	64,933	51,357	55,676	53,412									
Solyc10g007505	Mitogen-activated protein kinase (AHRD V3.3 *** M1BWT4_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	17,805	15,297	13,387	15,301	13,851									
Solyc10g007510	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0NBZ5_GOSAR)		F:GO:0016787	F:hydrolase activity			G3DSA:1.20.58.1040 (GENE3D); IPR(	0,019	0,120	0,000	0,000	0,000									
Solyc10g007520	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K158_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,542	5,854	4,061	4,030	3,113									
Solyc10g007550	RNA helicase DEAD31	DEAD31	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			IPR001650 (PFAM); G3DSA:3.40.50.3	29,939	32,926	25,866	23,498	23,195									
Solyc10g007570	Gibberellin 2-oxidase 2 (AHRD V3.3 *** I0B5A7_PETHY)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	4,333	4,590	1,864	1,126	1,276									
Solyc10g007580	VQ motif-containing protein (AHRD V3.3 *-* AT1G78410.2)						IPR008889 (PFAM); IPR039608 (PAN	0,021	0,021	0,000	0,000	0,000									
Solyc10g007590	CTC-interacting domain protein (AHRD V3.3 *** A0A072V9E0_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR009818 (PFAM); PTHR44161:SF3	39,114	39,362	84,397	78,535	72,563									
Solyc10g007600	glycolate oxidase	glo2.1	F:GO:0010181; F:G(	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	355,248	496,856	1384,826	1392,226	2034,011			0,551	0,011				up	
Solyc10g007610	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT3G14410.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM); IPR040189 (PAN	20,175	29,978	15,655	17,658	17,662									
Solyc10g007650	DNA-directed RNA polymerases I, II, and III subunit RPABC4 (AHRD V3.3 *** A0A0B2QXH3_GLYSO)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR006591 (PFAM); G3DSA:2.20.28.3	24,303	25,148	29,248	22,649	23,687					-0,367	0,041			down
Solyc10g007660	CASP-like protein (AHRD V3.3 *** K4CXU5_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006459 (TIGRFAM); IPR006702 (F	1,185	1,399	1,519	1,033	0,756									
Solyc10g007670	NifU-like protein 3, chloroplastic (AHRD V3.3 *** A0A1D1XGL9_9ARAE)		F:GO:0005506; P:G(	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl			IPR034904 (G3DSA:3.30.300.GENE3	0,237	0,408	0,125	0,069	0,330									
Solyc10g007680	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** AT5G48330.2)						IPR000408 (PRINTS); PF13540 (PFAI	9,451	7,813	14,538	13,914	14,803									
Solyc10g007690	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4CXU8_SOLLC)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE:	293,002	489,650	83,489	105,794	199,490			1,253	0,000				up	
Solyc10g007700	Ras-related protein (AHRD V3.3 *** W9R1W6_9ROSA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); G3DSA:3.40.50.3	42,969	30,085	57,509	52,867	48,378									
Solyc10g007710	Protein glycosylationmyb-like TTH transcriptional regulator (AHRD V3.3 *** A0A077SLG9_9MAGN)		P:GO:0006629; F:G(	P:lipid metabolic process; F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,021	0,041	0,000	0,000	0,000									
Solyc10g007720	Conserved oligomeric Golgi complex subunit 5 (AHRD V3.3 *** A0A118JSM3_CYNCS)		P:GO:0006891; C:G(	P:intra-Golgi vesicle-mediated transport; C:Golgi transport comp			IPR019465 (PFAM); IPR019465 (PAN	27,114	30,528	19,155	18,181	19,165									
Solyc10g007730	Type II inositol 3,4-bisphosphate 4-phosphatase (AHRD V3.3 *** A0A1D1XN75_9ARAE)		C:GO:0009507	C:chloroplast			PTHR37174 (PANTHER)	3,118	4,119	7,954	8,119	7,443									
Solyc10g007740	Magnesium transporter CorA family protein (AHRD V3.3 *** A0A061DJX1_THECC)		C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane			IPR002523 (PFAM); mobidb-lite (MOB	25,591	22,611	28,674	27,698	27,767									
Solyc10g007760	Ribose-phosphate pyrophosphokinase, putative (AHRD V3.3 *** B9T1G2_RICCO)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	G3DSA:3.40.50.2020 (GENE3D); IPR(	80,992	71,512	106,894	105,547	104,097									
Solyc10g007770	RNA-binding protein, putative (AHRD V3.3 *** B9T754_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	67,988	41,542	125,392	137,526	125,980	-0,684	0,004					down		
Solyc10g007780	Cortactin-binding 2 (AHRD V3.3 *** A0A0B0PEQ3_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	8,777	8,110	9,821	7,501	8,146									
Solyc10g007790	RING/U-box superfamily protein (AHRD V3.3 --* AT2G31760.1)							0,037	0,118	0,025	0,000	0,000									
Solyc10g007800	protodermal factor 1 (AHRD V3.3 *-* AT2G42840.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	6,600	6,034	0,516	1,435	0,209									
Solyc10g007810	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM); IPR025525 (PFA	9,310	9,098	12,633	12,711	11,134									
Solyc10g007820	HVA22-like protein (AHRD V3.3 *** K4CXW1_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004345 (PFAM); IPR004345 (PAN	0,000	0,198	0,000	0,048	0,023									
Solyc10g007830	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT3G24240.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR032675 (G3D	0,613	1,031	0,022	0,000	0,023									
Solyc10g007840	Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial (AHRD V3.3 *** K4CXW3_SOLL		F:GO:0004040; P:G(	F:amidase activity;	EC:3.5.1.4; EC:6.3.5	Amidase; Glutaminyl-	IPR023631 (PFAM); IPR036928 (G3D	11,916	12,642	17,727	18,921	18,731									
Solyc10g007850	Peptidase C13 family (AHRD V3.3 *** AT1G08750.3)		F:GO:0003923; P:G(	F:GPI-anchor transamidase activity; P:proteolysis; F:peptidase			IPR001096 (PRINTS); G3DSA:3.40.50	32,177	29,764	44,840	47,669	44,132									
Solyc10g007880	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	2,906	3,862	4,011	4,396	3,431									
Solyc10g007890	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,019	0,019	0,000	0,025	0,093									
Solyc10g007900	Cytochrome P450 (AHRD V3.3 *-* A0A124SAX2_CYNCS)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR002402 (PRINTS); IPR001128 (PF	0,078	0,461	0,025	0,224	0,915									
Solyc10g007930	Cytochrome P450 (AHRD V3.3 *-* A0A103XS13_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR036396 (G3	0,713	1,655	1,140	2,109	3,550			1,605	0,003				up	
Solyc10g007940	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U7E1K1_POPTR)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR002885 (PFAM); IPR011990 (G3D	0,639	0,767	0,530	0,466	0,471									
Solyc10g007950	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S8D6_RICCO)		F:GO:0003824; P:G(	F:catalytic activity; P:trehalose biosynthetic process			IPR003337 (TIGRFAM); G3DSA:3.40.5	21,104	15,018	26,370	27,020	24,823									
Solyc10g007960	Allene oxide synthase (AHRD V3.3 *** Q5NDE2_SOLTU)	CYP74C3	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3	0,171	0,059	0,025	0,025	0,000									
Solyc10g007970	WRKY transcription factor 77	WRKY77	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM WRKY	0,095	0,126	0,022	0,142	0,118									
Solyc10g007980	Ribosomal L5P family protein (AHRD V3.3 *** AT5G45775.2)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR031309 (PFAM); IPR031310 (PFA	116,163	134,019	111,244	106,737	103,166									
Solyc10g007990	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B2RH57_GLYSO)		F:GO:0016702; P:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR012864 (PFAM); PTHR22966 (PAN	44,447	37,445	83,051	86,226	74,226									
Solyc10g008000	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM); mobidb-lite (MOB	0,079	0,151	0,954	0,991	0,658									
Solyc10g008010	Proteasome subunit alpha type (AHRD V3.3 *** K4CXX8_SOLLC)		F:GO:0004298; P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	60,125	64,898	102,379	100,188	94,483									
Solyc10g008020	CMV 1a interacting protein 1 (AHRD V3.3 *** Q5DT22_TOBAC)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0	1,927	4,078	1,414	1,547	2,491	1,108	0,019					up		
Solyc10g008030	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM); IPR026057 (PFA	0,037	0,057	0,000	0,000	0,000									
Solyc10g008040	Late embryogenesis abundant protein-like (AHRD V3.3 *-* Q9LF88_ARATH)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,622	0,546	0,532	0,420	0,617									
Solyc10g008050	Transmembrane protein, putative (AHRD V3.3 *** G7JV20_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33834:SF2 (PANTHER); PTHR3:	0,319	0,446	0,365	0,270	0,283									
Solyc10g008060	diiron containing four-helix bundle family ferritin protein, putative (Protein of unknown function DUF455) (AHRD V3.3 *** AT1G06240.1)						IPR007402 (PFAM); mobidb-lite (MOB	5,652	5,161	5,852	5,749	6,041									
Solyc10g008065	inter alpha-trypsin inhibitor, heavy chain-like protein (AHRD V3.3 --* AT1G72500.3)							1,741	1,518	1,824	1,950	1,578									
Solyc10g008070	Transcription factor GTE4 (AHRD V3.3 *** A0A0B2R809_GLYSO)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS); IPR036427 (G3	39,820	34,083	36,123	37,862	38,175									
Solyc10g008080	RING/U-box superfamily protein (AHRD V3.3 *** AT2G42350.1)		C:GO:0016020	C:membrane			IPR001841 (PFAM); IPR013083 (G3D	0,037	0,098	0,025	0,092	0,071									
Solyc10g008090	Oligosaccharyltransferase complex/magnesium transporter family protein (AHRD V3.3 *** AT1G61790.2)		F:GO:0004579; C:G(	F:dolichyl-diphosph	EC:2.4.1.119	Glycosyltransferases	G3DSA:3.40.30.10 (GENE3D); IPR02	0,059	0,200	0,150	0,098	0,095									
Solyc10g008100	Glucosidase 2 subunit beta (AHRD V3.3 *** A0A0B0MJA2_GOSAR)		P:GO:0006491	P:N-glycan processing			IPR028146 (PFAM); IPR039794 (PAN	4,716	4,697	3,083	2,317	2,893									
Solyc10g008110	Acyl-coenzyme A oxidase (AHRD V3.3 *** M1APJ6_SOLTU)		F:GO:0003997; C:G(	F:acyl-CoA oxidase	EC:1.3.3.6	Acyl-CoA oxidase	G3DSA:1.20.140.10 (GENE3D); IPR0(	89,521	91,717	66,065	66,469	81,551									
Solyc10g008120	O-methyltransferase (AHRD V3.3 *** A0A1B4Z3W3_9ROSA)	ASMT10	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity			IPR016461 (PIRSF); IPR012967 (PFA	0,671	3,977	0,000	0,025	0,023	2,563	0,002					up		
Solyc10g008130	Pre-rRNA-processing protein esf2 (AHRD V3.3 *** A0A0B2SES6_GLYSO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	50,117	36,776	52,185	55,429	45,309									
Solyc10g008140	Prohibitin, putative (AHRD V3.3 *** B9RVS2_RICCO)		C:GO:0016020	C:membrane			IPR000163 (PRINTS); IPR001107 (PF	85,041	95,928	103,472	93,732	92,338									
Solyc10g008150	Glutaredoxin (AHRD V3.3 *** U3RBI7_CUCSA)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR002109 (PFAM); IPR011905 (TIGF	0,100	0,692	0,047	0,098	0,118									
Solyc10g008160	Two-component response regulator-like APRR2 (AHRD V3.3 *** A0A151SET7_CAJ	GLK2	F:GO:0003677; C:G(	F:DNA binding; C:nucleus			G3DSA:1.10.10.6(G2-like	23,943	27,303	15,938	9,328	19,290					-0,772	0,008			down
Solyc10g008170	26S proteasome regulatory subunit (AHRD V3.3 *-* I0YWJ7_COCSC)		C:GO:0008540; F:G(	C:proteasome regulatory particle, base subcomplex; F:enzyme r			IPR040892 (PFAM); mobidb-lite (MOB	0,138	0,062	0,025	0,025	0,000									
Solyc10g008180	26S proteasome regulatory subunit (AHRD V3.3 *** I0YWJ7_COCSC)		C:GO:0008540; F:G(	C:proteasome regulatory particle, base subcomplex; F:enzyme r			IPR011989 (G3DSA:1.25.10.GENE3D	0,276	0,097	0,022	0,070	0,000									
Solyc10g008200	Tyrosine aminotransferase, putative (AHRD V3.3 *** B9RVV0_RICCO)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3	0,942	2,859	0,355	0,147	0,351	1,616	0,017					up		
Solyc10g008205	Non-specific lipid-transfer protein (AHRD V3.3 *** B9RVV8_RICCO)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding; C:membrane; C:integral compor			G3DSA:1.10.110.10 (GENE3D); PTHF	1,467	0,372	0,000	0,000	0,000									
Solyc10g008210	Targeting protein for Xklp2 (AHRD V3.3 *** A0A0B2QW97_GLYSO)		C:GO:0005819; C:G(	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027330 (PFAM); IPR027329 (PFA	0,413	0,371	0,025	0,022	0,000									
Solyc10g008220	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); G3DSA:1.10.8.43	10,893	22,330	16,228	17,844	16,428	1,061	0,000					up		
Solyc10g008230	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); G3DSA:3.40.50.3	6,911	5,716	4,335	4,970	4,501									
Solyc10g008240	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); G3DSA:3.40.50.3	11,563	10,318	10,851	12,871	10,542									
Solyc10g008245	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT4G20970.1)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase			IPR036638 (G3DSA:4.10.280.GENE3	0,000	0,000	0,025	0,000	0,000									
Solyc10g008250	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0H3YBT5_SALMI)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase			IPR036638 (G3DS bHLH	0,101	1,458	0,173	0,098	0,141									
Solyc10g008280	Protein kinase superfamily protein (AHRD V3.3 *** AT1G53050.2)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); G3DS	85,841	134,795	87,112	76,883	85,126									
Solyc10g008300	Mannan endo-1,4-beta-mannosidase 1 (AHRD V3.3 *** MAN1_ORYSJ)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001547 (PFAM); G3DSA:3.20.20.8	53,387	46,272	25,839	30,964	27,874									
Solyc10g008310	LOW QUALITY:pyrroline-5-carboxylate reductase (AHRD V3.3 *** AT4G03600.1)		C:GO:0016021	C:integral component of membrane			PTHR34656 (PANTHER); PTHR34656	5,339	3,896	4,904	4,518	4,004									
Solyc10g008320	LOW QUALITY:phosphatidic acid phosphatase 1 (AHRD V3.3 --* AT2G01180.6)						mobidb-lite (MOBIDB_LITE); mobidb-lit	7,473	9,451	2,794	1,975	2,335									
Solyc10g008330	MLP protein (AHRD V3.3 *** A0A0B0N0M0_GOSAR)		P:GO:0006952	P:defense response			IPR000916 (PFAM); IPR023393 (G3D	0,021	0,037	0,000	0,000	0,071									
Solyc10g008340	Structural constituent of cell wall, putative (AHRD V3.3 *** B9RVZ9_RICCO)						IPR010820 (PFAM); mobidb-lite (MOB	29,436	44,051	34,724	31,321	31,770	0,608	0,029					up		
Solyc10g008350	50S ribosomal protein L20, chloroplastic (AHRD V3.3 --* RK20_PHAAO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,494	4,744	1,185	1,960	1,850									
Solyc10g008360	GPI-anchored protein LORELEI (AHRD V3.3 *** A0A0B2RL44_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR039307 (PANTHER); PTHR31533:	0,040	0,021	0,025	0,000	0,024									
Solyc10g008390	Thioredoxin (AHRD V3.3 *** A7LNX7_9CARY)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidoredu			PR00421 (PRINTS); IPR013766 (PFA	4,466	6,227	3,930	5,891	5,214									
Solyc10g008400	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G74990.1)		F:GO:0046872	F:metal ion binding			IPR018957 (PFAM); IPR013083 (G3D	106,073	56,009	33,095	105,718	48,784	-0,894	0,019			1,678	0,000	down		up
Solyc10g008410	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G19310.1)		F:GO:0046872	F:metal ion binding			IPR018957 (PFAM); IPR013083 (G3D	0,254	0,823	0,051	0,100	0,469									
Solyc10g008420	acyl-UDP-N-acetylglucosamine O-acyltransferase (AHRD V3.3 *** AT4G28260.2)		F:GO:0003676	F:nucleic acid binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	26,663	20,287	33,132	30,903	28,094									
Solyc10g008450	F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYNCS)						IPR017451 (TIGRFAM); IPR006527 (F	2,235	1,688	0,551	0,526	0,515									
Solyc10g008460	LanC-like protein 2 (AHRD V3.3 *** A0A0B2RC28_GLYSO)		F:GO:0003824	F:catalytic activity			IPR020464 (PRINTS); IPR007822 (PF	9,086	12,101	4,922	3,828	6,006									
Solyc10g008470	ELMO/CED-12 family protein (AHRD V3.3 *** AT1G03620.9)						IPR006816 (PFAM); PTHR12771:SF4:	2,533	1,949	43,901	46,239	37,092									
Solyc10g008480	Plant/F9H3-4 protein (AHRD V3.3 *** A0A072VLR0_MEDTR)						IPR008507 (PFAM); PTHR31343:SF3	4,355	4,889	8,947	10,990	8,735									
Solyc10g008490	Phosphatase 2C family protein (AHRD V3.3 *** U5FGH9_POPTR)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR036457 (G3DSA:3.60.40.GENE3D	0,040	0,041	0,000	0,095	0,000									
Solyc10g008500	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT4G03410.2)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM); IPR007248 (PAN	13,812	13,508	38,515	41,671	34,734									
Solyc10g008510	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 *** AT1G03560.1)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	4,790	2,969	1,861	1,890	1,950									
Solyc10g008515	respiratory burst oxidase-like protein (AHRD V3.3 --* AT1G09090.2)							1,357	0,711	0,528	0,313	0,234									
Solyc10g008520	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT4G03400.2)						IPR004993 (PFAM); PTHR31901:SF1	14,169	11,438	0,340	0,296	0,520									
Solyc10g008540	Multidrug resistance 3 (AHRD V3.3 *** A0A0B0MAA3_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,115	1,804	1,489	1,196	1,342									
Solyc10g008550	Secretory carrier-associated membrane protein (AHRD V3.3 *** A0A072VLP1_MEDTR)		P:GO:0015031; C:G(	P:protein transport; C:integral component of membrane			IPR007273 (PFAM); mobidb-lite (MOB	0,021	0,000	0,050	0,000	0,000									
Solyc10g008560	UPF0420 C16orf58-like protein (AHRD V3.3 *** A0A072UUJ6_MEDTR)						IPR006968 (PFAM); IPR006968 (PAN	46,063	43,467	48,750	57,526	52,625									
Solyc10g008570	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SD53_CYNCS)		F:GO:0005515; C:G(	F:protein binding; C:membrane; P:vesicle-mediated transport			IPR002885 (TIGRFAM); IPR006011 (F	3,572	5,528	4,123	3,697	3,268									
Solyc10g008580	F-box family protein (AHRD V3.3 *** S1SIA6_THECC)		F:GO:0005515	F:protein binding			IPR006527 (PFAM); G3DSA:1.20.128	4,958	3,991	2,717	2,756	2,688									
Solyc10g008590	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RB17_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	0,804	1,202	1,261	1,078	1,272									
Solyc10g008600	embryo defective 1923 (AHRD V3.3 *** AT4G28210.1)		P:GO:0009409; C:G(	P:response to cold; C:integral component of membrane				6,370	7,219	15,685	15,534	14,707									
Solyc10g008610	LOW QUALITY:Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHRD V3.3 --* AT5G19420.2)							0,369	0,351	0,270	0,333	0,236									
Solyc10g008620	LOW QUALITY:Unknown protein (AHRD V3.3)							0,469	0,561	0,713	0,464	0,587									
Solyc10g008630	External alternative NAD(P)H-ubiquinone oxidoreductase B1, mitochondrial (AHRD V3.3 *** ENDB1_SOLTU		F:GO:0005509; F:G(	F:calcium ion binding; F:oxidoreductase activity; P:oxidation-rec			PR00368 (PRINTS); G3DSA:3.50.50.1	47,288	52,036	138,637	141,953	135,673									
Solyc10g008640	Diacylglycerol kinase (AHRD V3.3 *** K4CY41_SOLLC)		F:GO:0003951; F:G(	F:NAD+ kinase acti	EC:2.7.1.23; EC:2.7.	NAD(+) kinase; Diacy	IPR000756 (PFAM); IPR017438 (G3D	37,887	35,126	48,512	51,050	46,825									
Solyc10g008650	LOW QUALITY:Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* A0A0B2REP2_GLYSO)		F:GO:0047165	F:flavonol-3-O-beta	EC:2.3.1.116	Flavonol-3-O-beta-gl	IPR023213 (G3DSA:3.30.559.GENE3	0,615	0,631	1,583	1,120	1,391									
Solyc10g008655	Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* A0A0B2SWD3_GLYSO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM); IPR023213 (G3D	8,265	6,123	14,993	13,340	12,666									
Solyc10g008660	Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* A0A0B2REP2_GLYSO)		F:GO:0047165	F:flavonol-3-O-beta	EC:2.3.1.116	Flavonol-3-O-beta-gl	IPR023213 (G3DSA:3.30.559.GENE3	0,000	0,000	0,022	0,000	0,023									
Solyc10g008670	Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* ANTA_GENTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM); IPR023213 (G3D	0,000	0,037	0,000	0,000	0,000									
Solyc10g008680	Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *** ANTA_GENTR)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	2,784	3,631	0,467	0,554	1,028									
Solyc10g008720	GDSL esterase/lipase (AHRD V3.3 *** A0A199VJD6_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	0,019	0,060	0,000	0,000	0,000									
Solyc10g008730	Transmembrane protein, putative (AHRD V3.3 *** G7IKA1_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33834:SF2 (PANTHER); PTHR3:	3,450	3,063	0,924	1,968	1,103					1,069	0,046			up
Solyc10g008740	Mg-protoporphyrin IX chelatase (AHRD V3.3 *** K4CY51_SOLLC)	CHLH/I/D	F:GO:0005524; P:G(	F:ATP binding; P:ch	EC:6.6.1.1	Magnesium chelatas	G3DSA:1.10.8.80 (GENE3D); IPR011	49,359	109,046	78,427	88,838	164,971	1,172	0,000	1,069	0,000			up	up	
Solyc10g008750	Nudix hydrolase-like protein (AHRD V3.3 *** G7IK84_MEDTR)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D); IPR00	2,755	2,866	3,536	3,440	2,851									
Solyc10g008760	Nudix hydrolase (AHRD V3.3 *** A0A061GLW3_THECC)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D); IPR00	16,426	12,806	11,554	12,619	9,870									
Solyc10g008770	nudix hydrolase homolog 15 (AHRD V3.3 *** AT1G28960.5)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D); IPR00	18,551	16,960	17,484	15,082	16,364									
Solyc10g008780	LOW QUALITY:TCP transcription factor 30	TCP30					IPR017887 (PFAM TCP	0,000	0,000	0,022	0,000	0,000									
Solyc10g008790	SUN-like protein 28	SUN28	F:GO:0005515	F:protein binding			IPR000048 (PFAM); mobidb-lite (MOB	26,405	17,517	18,310	15,023	20,320	-0,566	0,031					down		
Solyc10g008800	Apoptosis inhibitory 5 (AHRD V3.3 *** A0A103XEZ4_CYNCS)		F:GO:0003729; C:G(	F:mRNA binding; C:nucleus; P:regulation of programmed cell dea			IPR008383 (PFAM); mobidb-lite (MOB	33,695	32,242	41,734	40,499	40,067									
Solyc10g008810	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SKJ1_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	0,000	0,019	0,065	0,050	0,093									
Solyc10g008840	Rab family GTPase (AHRD V3.3 *** D8RE14_SELML)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); IPR005225 (TIGF	0,104	0,099	0,075	0,123	0,116									
Solyc10g008850	transmembrane protein (AHRD V3.3 *** AT1G28540.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	8,787	8,065	9,051	8,731	8,119									
Solyc10g008860	Glycosyltransferase (AHRD V3.3 *** K4CY62_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); G3D	0,386	0,305	0,000	0,025	0,000									
Solyc10g008870	Transcription elongation factor 1 homolog (AHRD V3.3 *** ELOF1_ORYSJ)		F:GO:0000993; F:G(	F:RNA polymerase II complex binding; F:translation elongation f			IPR007808 (PFAM); IPR038567 (G3D	141,071	140,006	163,959	155,139	157,547									

Solyc10g008880	Zinc finger transcription factor 56	C3H56	P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:positive regulati	IPR039277 (PANT VOZ	102,544	110,418	42,866	49,837	57,400									
Solyc10g008890	Optic atrophy 3 protein (OPA3) (AHRD V3.3 *** AT1G28510.1)		C:GO:0005739; P:G(	C:mitochondrion; P:regulation of lipid metabolic process	IPR010754 (PFAM): IPR010754 (PAN	3,742	3,556	5,738	6,338	5,441									
Solyc10g008910	Histone H3 (AHRD V3.3 *** A0A068VC55_COFCA)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS): IPR007125 (PF	27,753	30,581	5,752	1,989	4,520					-1,526	0,012			down
Solyc10g008920	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *-* W9SHV7_9ROSA)		F:GO:0003676	F:nucleic acid binding	IPR036397 (G3DSA:3.30.420.GENE3I	0,040	0,062	0,025	0,025	0,000									
Solyc10g008930	Glutaredoxin-like family protein (AHRD V3.3 *** B9H2P7_POPTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR011905 (TIGRFAM): G3DSA:3.40.:	0,038	0,000	0,000	0,000	0,000									
Solyc10g008950	Guanylate-binding family protein (AHRD V3.3 *** B9H2Q0_POPTR)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	G3DSA:1.20.1000.10 (GENE3D): IPR(	47,372	40,545	40,668	39,379	40,298									
Solyc10g008960	Kinase family protein (AHRD V3.3 *** U5FVU7_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): G3DS	0,061	0,021	0,000	0,000	0,094									
Solyc10g008980	triose phosphate translocator		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR004853 (PFAM): IPR004696 (TIGF	226,955	320,728	95,116	119,413	183,471			0,945	0,000				up	
Solyc10g008990	UPF0533 protein C5orf44 like (AHRD V3.3 *-* A0A0B2PQR4_GLYSO)				IPR010378 (PFAM): IPR010378 (PAN	38,859	37,658	43,086	42,035	40,647									
Solyc10g009000	snRNA-activating protein complex subunit (AHRD V3.3 *** X5BXX0_NICBE)				IPR022042 (PFAM): IPR022042 (PAN	8,591	8,810	7,700	7,415	7,977									
Solyc10g009010	CBS domain-containing protein (AHRD V3.3 *** A0A061GEK1_THECC)				IPR000644 (PFAM): PTHR13780:SF5	0,137	0,236	0,000	0,000	0,046									
Solyc10g009020	RING finger protein (AHRD V3.3 *** A0A0B0PIZ1_GOSAR)		F:GO:0016874	F:ligase activity	IPR013083 (G3DSA:3.30.40.GENE3D	5,722	5,308	6,410	5,835	5,910									
Solyc10g009030	sphingolipid delta 4 desaturase	des1	C:GO:0016021; P:G(	C:integral component of membrane; P:sphingolipid biosynthetic	IPR013866 (PFAM): IPR011388 (PIRS	16,026	14,605	5,750	5,328	6,736									
Solyc10g009040	defensin-like protein (AHRD V3.3 --* AT4G21720.3)				mobidb-lite (MOBIDB_LITE): PTHR360	4,689	4,792	4,047	4,465	3,980									
Solyc10g009045	subtilase 4.12 (AHRD V3.3 --* AT5G59090.3)					2,950	2,747	2,134	3,231	2,740									
Solyc10g009050	DUF616 family protein (AHRD V3.3 *** A0A072UMP6_MEDTR)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membra	IPR006852 (PFAM): mobidb-lite (MOB	8,177	7,473	12,091	15,233	10,924									
Solyc10g009055	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR025525 (PFAM): IPR008906 (PFA	0,019	0,000	0,000	0,000	0,000									
Solyc10g009060	MAP kinase kinase kinase 72	MAPKKK72	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): IPR0(	19,820	14,855	10,143	14,943	10,353					0,559	0,008			up
Solyc10g009070	RNA helicase DEAD32	DEAD32	F:GO:0003723; F:G(	F:RNA binding; F:A EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	47,391	42,084	29,997	28,892	30,670									
Solyc10g009080	Squamosa promoter binding protein 3		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; C:nu	IPR036893 (G3DS SBP	8,564	11,428	4,284	3,966	6,270									
Solyc10g009090	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT2G33820.1)		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	2,157	2,941	0,404	0,144	0,492									
Solyc10g009100	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G45210.4)					0,480	0,539	0,122	0,118	0,189									
Solyc10g009110	ethylene response factor F.5	ERF.F5	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	216,526	172,375	67,026	109,666	94,036					0,712	0,010			up
Solyc10g009120	LOW QUALITY:DNA repair (Rad51) family protein (AHRD V3.3 --* AT2G28560.6)					16,844	14,244	5,515	8,097	7,687									
Solyc10g009130	nuclear fusion defective 6 (AHRD V3.3 *-* AT2G20585.5)		P:GO:0000741	P:karyogamy	IPR033251 (PTHR33156:PANTHER):	3,976	4,320	2,089	1,878	1,929									
Solyc10g009140	Hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *-* AT1G61080.6)		C:GO:0016020	C:membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,039	0,000	0,025	0,023									
Solyc10g009150	Organ-specific protein S2 (AHRD V3.3 *** F2VPS2_SOLNI)				IPR024489 (PFAM): mobidb-lite (MOB	0,334	0,329	0,000	0,193	0,000									
Solyc10g009160	Bromodomain 4, putative (AHRD V3.3 *** A0A061GG17_THECC)		F:GO:0005515	F:protein binding	IPR036427 (G3DSA:1.20.920.GENE3I	12,135	11,697	11,633	11,337	10,222									
Solyc10g009170	lysine ketoglutarate reductase trans-splicing-like protein (DUF707) (AHRD V3.3 *** AT1G11170.7)		C:GO:0016021	C:integral component of membrane	IPR007877 (PFAM): PTHR31210:SF1	0,291	1,142	0,269	0,657	0,095									
Solyc10g009180	Secretory carrier membrane protein (AHRD V3.3 *** B3TLU6_ELAGV)		P:GO:0015031; C:G(	P:protein transport; C:integral component of membrane	IPR007273 (PFAM): mobidb-lite (MOB	50,011	54,169	45,504	49,107	46,510									
Solyc10g009190	LOW QUALITY:glycine-rich protein (AHRD V3.3 *-* AT4G21620.2)		C:GO:0016021	C:integral component of membrane	PTHR34789 (PANTHER): PTHR34789	6,662	7,417	0,699	0,437	0,609									
Solyc10g009200	Nucleolar protein 12 (AHRD V3.3 *** A0A103XU68_CYNCS)		F:GO:0003697; F:G(	F:single-stranded DNA binding; F:protein binding; C:nucleolus; P	IPR019186 (PFAM): mobidb-lite (MOB	1,424	1,550	2,381	2,051	1,511									
Solyc10g009210	Calmodulin-binding protein (AHRD V3.3 *** A0A072V4D6_MEDTR)		F:GO:0005516	F:calmodulin binding	IPR012416 (PFAM): IPR019186 (PFA	98,184	174,844	46,526	51,115	64,841			0,475	0,023				up	
Solyc10g009220	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT4G00830.6)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	62,180	64,167	71,606	67,607	68,233									
Solyc10g009240	3-ketoacyl-CoA synthase (AHRD V3.3 *** B9GRP8_POPTR)		P:GO:0006633; C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a	IPR012392 (PIRSF): IPR016039 (G3D	0,154	0,404	0,236	0,299	0,164									
Solyc10g009260	LOW QUALITY:Cytochrome b5 isoform 1 (AHRD V3.3 -** M8A0M0_TRIUA)		C:GO:0016020	C:membrane	IPR032238 (PFAM): PTHR35165 (PAN	0,042	0,021	0,097	0,025	0,048									
Solyc10g009270	bHLH transcription factor154		F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DS bHLH	0,000	0,000	0,022	0,000	0,000									
Solyc10g009280	GRF1-interacting factor-like protein (AHRD V3.3 *** A0A072TYG4_MEDTR)		F:GO:0003713	F:transcription coactivator activity	IPR007726 (PFAM): mobidb-lite (MOB	15,548	14,489	15,956	15,790	15,505									
Solyc10g009290	bHLH transcription factor155		F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DS bHLH	1,493	3,041	0,075	0,164	0,070									
Solyc10g009310	Cytochrome P450 (AHRD V3.3 *** F4YF83_9APIA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,000	0,018	0,025	0,025	0,000									
Solyc10g009320	NAD-dependent protein deacetylase HST1-like protein (AHRD V3.3 *** AT2G46640.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,043	0,000	0,000	0,000									
Solyc10g009330	Arginine/serine-rich splicing factor, putative (AHRD V3.3 *** B9SBD0_RICCO)		P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spli	IPR012677 (G3DSA:3.30.70.GENE3D	48,923	47,270	62,617	53,332	53,985									
Solyc10g009350	MAP kinase kinase kinase 73	MAPKKK73	F:GO:0004674; F:G(	F:protein serine/thre EC:2.7.11 Transferring phospho	G3DSA:1.10.510.10 (GENE3D): IPR0(	1,354	1,445	0,563	1,091	1,012									
Solyc10g009360	Dof zinc finger protein (AHRD V3.3 *** W9RTF5_9ROSA)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003851 (PFAM Dof	0,276	0,478	0,025	0,101	0,118									
Solyc10g009380	arginine N-methyltransferase, putative (DUF688) (AHRD V3.3 --* AT2G30990.5)				PTHR34371 (PANTHER): PTHR34371	14,591	14,210	2,090	1,457	1,601									
Solyc10g009390	Cytochrome P450 (AHRD V3.3 *** Q9MBF5_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	0,000	0,000	0,000	0,000	0,023									
Solyc10g009400	S-adenosyl-L-methionine-dependent methyltransferase (AHRD V3.3 *-* A0A0R4XC65_9MYRT)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	IPR019410 (PFAM): PTHR14614:SF9	5,896	4,798	2,626	3,300	3,224									
Solyc10g009410	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G01300.1)		F:GO:0004190; P:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR001461 (PRINTS): IPR021109 (G3	74,650	101,209	18,004	27,171	19,467					0,596	0,028			up
Solyc10g009420	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4CYB8_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal	IPR018121 (PFAM): IPR013083 (G3D	4,996	4,263	6,803	7,064	8,451									
Solyc10g009430	O-acyltransferase WSD1 (AHRD V3.3 *** W9R027_9ROSA)		F:GO:0004144; P:G(	F:diacylglycerol O-a EC:2.3.1.2 Diacylglycerol O-acy	IPR004255 (PFAM): IPR009721 (PFA	0,601	1,124	6,379	13,420	8,457					1,074	0,000			up
Solyc10g009440	Transcription factor (AHRD V3.3 *-* A0A0H5LIB4_COFCA)		F:GO:0046982	F:protein heterodimerization activity	PR00615 (PRINTS NF-YB	3,062	2,016	0,000	0,000	0,000									
Solyc10g009450	F-box protein (AHRD V3.3 *** A0A0P0CKG2_CITMA)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): IPR006527 (PFA	0,021	0,000	0,000	0,000	0,000									
Solyc10g009460	F-box protein (AHRD V3.3 *** W9QUQ9_9ROSA)		F:GO:0005515	F:protein binding	IPR017451 (TIGRFAM): IPR006527 (F	0,037	0,000	0,000	0,000	0,000									
Solyc10g009480	Cytochrome b561/ferric reductase transmembrane with DOMON related domain-containing protein (AHRD V:		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce	IPR005018 (PFAM): IPR006593 (PFA	0,258	0,078	0,000	0,000	0,000									
Solyc10g009487	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G46494.1)		C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc10g009490	Poly(A) RNA polymerase cid14 (AHRD V3.3 *** W9RAG3_9ROSA)		F:GO:0016779	F:nucleotidyltransferase activity	G3DSA:1.10.1410.10 (GENE3D): IPR(	55,975	46,485	63,002	65,388	64,786									
Solyc10g009550	LOW QUALITY:WRKY transcription factor 42	WRKY42	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR036576 (G3DS WRKY	68,345	29,764	2,713	5,553	5,893	-1,175	0,002	1,108	0,014			down	up	
Solyc10g009560	LOW QUALITY:DNA-binding storekeeper protein-related transcriptional regulator (AHRD V3.3 --* A0A0K9Q2		C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding		0,316	0,200	0,072	0,273	0,237									
Solyc10g009570	thylakoid rhodanese-like protein (AHRD V3.3 *** AT4G01050.1)		F:GO:0008410	F:CoA-transferase activity	IPR036873 (G3DSA:3.40.250.GENE3I	44,820	81,839	28,449	36,587	64,788	0,897	0,012	1,184	0,000			up	up	
Solyc10g009580	Glycosyltransferase (AHRD V3.3 *** K4CYD4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	8,377	7,232	1,242	1,536	2,483									
Solyc10g009590	Trichome birefringence-like protein (AHRD V3.3 *-* A0A072TUJ8_MEDTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding	IPR026057 (PFAM): IPR025724 (PFA	0,000	0,019	0,000	0,000	0,000									
Solyc10g009610	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR004993 (PAN	0,206	0,319	0,072	0,075	0,048									
Solyc10g009620	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR004993 (PAN	1,436	1,572	0,000	0,000	0,000									
Solyc10g009640	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR004993 (PAN	0,080	0,153	0,000	0,000	0,000									
Solyc10g010650	Auxin-responsive GH3 family protein (AHRD V3.3 *-* AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR004993 (PAN	0,037	0,018	0,000	0,000	0,000									
Solyc10g011650	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR004993 (PAN	0,019	0,076	0,000	0,000	0,000									
Solyc10g011660	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT2G46370.4)		P:GO:0009611; P:G(	P:response to wounding; P:jasmonic acid metabolic process; P:	IPR004993 (PFAM): IPR031110 (PTH	8,485	8,382	4,327	3,669	6,232									
Solyc10g011670	Mitochondrial substrate carrier family protein (AHRD V3.3 *** B9I8V0_POPTR)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS): IPR018108 (PF	63,677	52,312	88,420	74,512	80,178									
Solyc10g011680	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_LEMMI)				mobidb-lite (MOBIDB_LITE)	0,617	0,655	0,046	0,022	0,046									
Solyc10g011690	Ubiquitin ligase protein cop1, putative (AHRD V3.3 *** B9T343_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR020472 (PRINTS): IPR015943 (G3	16,809	13,027	13,970	17,320	15,866									
Solyc10g011700	RNA-binding KH domain-containing protein (AHRD V3.3 --* AT1G14170.3)					4,549	4,400	4,217	4,925	4,321									
Solyc10g011710	LOW QUALITY:Subtilisin-like protease (AHRD V3.3 *-* W9RY09_9ROSA)		F:GO:0004252; P:G(	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR036852 (G3DSA:3.40.50.GENE3D	0,019	0,000	0,094	0,000	0,000									
Solyc10g011730	Arabinogalactan peptide 20 (AHRD V3.3 *** AGP20_ARATH)		C:GO:0016021	C:integral component of membrane	IPR009424 (PFAM): PTHR33374:SF9	2,313	2,158	0,168	0,073	0,189									
Solyc10g011740	Ubiquitin-conjugating enzyme E2, putative (AHRD V3.3 *** B9T334_RICCO)		F:GO:0005524; P:G(	F:ATP binding; P:protein ubiquitination; F:ligase activity; F:ubiqu	IPR000608 (PFAM): IPR016135 (G3D	110,817	158,129	44,522	66,871	66,736									
Solyc10g011750	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR312	5,995	4,321	1,681	1,173	2,010									
Solyc10g011760	Aldose 1-epimerase, putative (AHRD V3.3 *** B9RE17_RICCO)		P:GO:0005975; F:G(	P:carbohydrate metabolic process; F:isomerase activity; F:carb	IPR008183 (PFAM): IPR014718 (G3D	3,247	4,620	1,873	1,967	1,643									
Solyc10g011770	Protein CURVATURE THYLAKOID 1A, chloroplastic (AHRD V3.3 *** CUT1A_ARATH	CURT1	C:GO:0009579	C:thylakoid	IPR025564 (PFAM): PTHR33222:SF4	20,292	37,584	18,993	25,453	37,063	0,916	0,000	0,961	0,000	0,426	0,026	up	up	up
Solyc10g011790	BTB/POZ domain-containing family protein (AHRD V3.3 *** B9I8T4_POPTR)		F:GO:0005515	F:protein binding	G3DSA:1.25.40.420 (GENE3D): G3DS	32,608	42,172	47,287	32,068	44,787					-0,558	0,000			down
Solyc10g011810	Fatty acid/sphingolipid desaturase (AHRD V3.3 *-* AT2G46210.1)		P:GO:0006629	P:lipid metabolic process	IPR005804 (PFAM): PTHR19353:SF2	0,951	4,248	0,416	0,549	1,037	2,183	0,000					up		
Solyc10g011815	Desaturase/cytochrome b5 protein (AHRD V3.3 *-* Q9ZTY9_RICCO)		P:GO:0006629; C:G(	P:lipid metabolic process; C:integral component of membrane; F	IPR001199 (PFAM): IPR036400 (G3D	0,139	0,969	0,000	0,097	0,165									
Solyc10g011820	Fatty acid/sphingolipid desaturase (AHRD V3.3 *** AT2G46210.1)		P:GO:0006629; C:G(	P:lipid metabolic process; C:integral component of membrane; F	IPR001199 (PFAM): IPR005804 (PFA	5,344	6,126	1,114	1,854	2,802			1,307	0,005				up	
Solyc10g011840	phosphopantothenate-cysteine ligase-like protein (AHRD V3.3 *** AT5G02080.7)		F:GO:0016874	F:ligase activity	IPR035929 (G3DSA:3.40.50.GENE3D	0,114	0,064	0,025	0,025	0,047									
Solyc10g011870	Reticulon-like protein (AHRD V3.3 *** K4CYG5_SOLLC)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me	IPR003388 (PFAM): mobidb-lite (MOB	63,320	64,315	86,136	82,635	77,362									
Solyc10g011880	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61550.1)		C:GO:0016021	C:integral component of membrane	IPR001841 (PFAM): IPR013083 (G3D	1,987	2,643	0,587	0,717	0,797									
Solyc10g011910	WRKY transcription factor 25	WRKY25	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR036576 (G3DS WRKY	3,053	2,996	1,368	4,041	2,793					1,561	0,001			up
Solyc10g011920	Phenylalanine ammonia-lyase (AHRD V3.3 *** A0A124SBF6_CYNCS)	PAL	C:GO:0005737; P:G(	C:cytoplasm; P:L-phenylalanine catabolic process; F:ammonia-l	IPR024083 (G3DSA:1.10.275.GENE3I	1,226	1,093	2,608	3,721	2,770									
Solyc10g011940	chromatin remodeling factor (AHRD V3.3 *-* AT4G31900.3)		F:GO:0003677; F:G(	F:DNA binding; F:he EC:3.6.1.15 Nucleoside-triphosph	IPR038718 (G3DSA:3.40.50.GENE3D	12,686	8,341	0,122	0,170	0,211									
Solyc10g011943	S-locus-specific glycoprotein S14 (AHRD V3.3 --* SLSG4_BRAOL)					0,059	0,000	0,000	0,000	0,000									
Solyc10g011950	phosphatidylinositol 4-kinase gamma-like protein (AHRD V3.3 --* AT5G24240.2)		F:GO:0003677; F:G(	F:DNA binding; F:he EC:3.6.1.15 Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	1,562	1,049	0,046	0,000	0,023									
Solyc10g011960	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT1G01490.2)		F:GO:0016787; P:G(	F:hydrolase activity; P:metal ion transport; F:metal ion binding	G3DSA:3.30.70.100 (GENE3D): mobic	9,080	7,014	0,924	1,154	0,707									
Solyc10g011980	Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** AT1G01500.1)		F:GO:0004617; P:G(	F:phosphoglycerate EC:1.1.1.95 Phosphoglycerate de	PTHR42938 (PANTHER): PTHR42938	23,591	38,885	17,132	16,986	18,102	0,746	0,012					up		
Solyc10g011985	Zinc finger, RING/FYVE/PHD-type (AHRD V3.3 --* A0A103XI32_CYNCS)				PTHR34451 (PANTHER): PTHR34451	0,173	0,036	0,025	0,000	0,000									
Solyc10g012000	LOW QUALITY:DUF4283 domain protein (AHRD V3.3 --* G7I744_MEDTR)				IPR025558 (PFAM): PTHR34427 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc10g012005	LOW QUALITY:HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2R149_ORYSJ)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR025525 (PFAM): IPR008906 (PFA	0,021	0,000	0,022	0,000	0,000									
Solyc10g012030	Chorismate synthase (AHRD V3.3 *** A0A0B0NMD4_GOSAR)		F:GO:0003729; C:G(	F:mRNA binding; C:mRNA cap binding complex	mobidb-lite (MOBIDB_LITE): mobidb-lit	59,386	53,299	67,200	66,348	65,255									
Solyc10g012050	Mechanosensitive ion channel protein (AHRD V3.3 *** AT4G00290.1)		C:GO:0016020; P:G(	C:membrane; P:transmembrane transport	IPR006685 (PFAM): IPR023408 (G3D	0,440	0,643	0,387	0,395	0,284									
Solyc10g012060	Mechanosensitive ion channel protein (AHRD V3.3 *** AT4G00290.1)		C:GO:0016020; P:G(	C:membrane; P:transmembrane transport	IPR006685 (PFAM): IPR023408 (G3D	9,985	9,973	11,334	12,149	10,973									
Solyc10g012080	PLAC8 family protein (AHRD V3.3 *** AT4G23470.3)		F:GO:0016874	F:ligase activity	PTHR31152:SF6 (PANTHER): PTHR3	21,851	41,046	18,678	25,959	26,874									
Solyc10g012090	LOW QUALITY:Ferredoxin-thioredoxin reductase catalytic chain, chloroplastic (AHRD V3.3 --* FTRC_MAIZE		C:GO:0043231; F:G(	C:intracellular membrane-bounded organelle; F:2 iron, 2 sulfur cluster binding		0,000	0,043	0,075	0,070	0,070									
Solyc10g012100	LOW QUALITY:CoA ligase (AHRD V3.3 *-* A0A0K9PM15_ZOSMR)		F:GO:0003824	F:catalytic activity	IPR025110 (PFAM): IPR000873 (PFA	0,252	0,309	0,112	0,172	0,211									
Solyc10g012110	Non-specific lipid-transfer protein (AHRD V3.3 *** K4AY52_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding	G3DSA:1.10.110.10 (GENE3D): IPR0	3,636	4,635	0,000	0,096	0,000									
Solyc10g012120	Non-specific lipid-transfer protein (AHRD V3.3 *** NLTP_PINTA)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding	IPR016140 (PFAM): G3DSA:1.10.110.	1,274	2,361	0,000	0,025	0,000									
Solyc10g012130	LOW QUALITY:Non-specific lipid-transfer protein (AHRD V3.3 *** A0A151RUH1_CAJCA)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding	IPR016140 (PFAM): G3DSA:1.10.110.	2,491	4,276	0,000	0,000	0,000									
Solyc10g012137	LOW QUALITY:HAT family dimerisation domain containing protein (AHRD V3.3 *** Q7XET1_ORYSJ)		F:GO:0046983	F:protein dimerization activity	IPR008906 (PFAM): mobidb-lite (MOB	0,038	0,057	0,000	0,151	0,142									
Solyc10g012160	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G22800.1)		F:GO:0008168	F:methyltransferase activity	IPR013216 (PFAM): G3DSA:3.40.50.1	9,180	8,759	15,347	15,283	14,856									
Solyc10g012170	Kinase family protein (AHRD V3.3 *** U5G9B2_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	13,786	23,183	35,413	41,419	34,423	0,775	0,034					up		
Solyc10g012180	LOW QUALITY:Transcription factor, MADS-box (AHRD V3.3 *-* A0A118JYH5_CYNCS)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR002100 (PFAM M-type_MADS	0,021	0,000	0,000	0,000	0,000									
Solyc10g012190	ABC transporter family protein (AHRD V3.3 *** A0A097P9R9_HEVBR)	ABCF5	F:GO:0005524; F:G(	F:ATP binding; F:AT EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003439 (PFAM): IPR003439 (PFA	0,040	0,041	0,050	0,025	0,000									
Solyc10g012200	LOW QUALITY:Transcription factor, MADS-box (AHRD V3.3 *-* A0A118JYH5_CYNCS)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR002100 (PFAM M-type_MADS	0,021	0,019	0,000	0,000	0,000									
Solyc10g012210	AT-rich interactive domain protein (AHRD V3.3 *** Q2HUC6_MEDTR)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus	mobidb-lite (MOBIDB_LITE): PTHR229	0,902	1,200	3,321	2,476	2,854									
Solyc10g012230	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR008543 (PFAM): IPR008543 (PAN	0,000	0,021	0,025	0,050	0,024									
Solyc10g012240	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A1D1ZAB9_9ARAE)		F:GO:0005524; P:G(	F:ATP binding; P:ubiquitin-dependent protein catabolic process;	IPR000608 (PFAM): IPR016135 (G3D	65,657	45,681	207,256	191,436	189,314									
Solyc10g012253	Rhomboid-like protein (AHRD V3.3 *** K4CM51_SOLLC)		F:GO:0004252; C:G(	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR035952 (G3DSA:1.20.1540.GENE	0,000	0,000	0,050	0,000	0,023									
Solyc10g012270	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A072TZ92_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:integral component of membrane; F:transferas	IPR000608 (PFAM): IPR016135 (G3D	0,216	0,094	0,118	0,119	0,141									
Solyc10g012280	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT1G69550.1)		F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,057	0,123	0,000	0,094									
Solyc10g012290	Disease resistance protein (AHRD V3.3 *-* A0A068EX82_SOLHA)		F:GO:0043531	F:ADP binding	G3DSA:3.40.50.300 (GENE3D): PTHF	0,061	0,158	0,000	0,270	0,258									
Solyc10g012300	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G38350.1)		F:GO:0043531	F:ADP binding	G3DSA:3.40.50.300 (GENE3D): PTHF	0,000	0,064	0,025	0,022	0,023									
Solyc10g012310	Rhomboid-like protein (AHRD V3.3 *-* K4CM51_SOLLC)		F:GO:0004252; C:G(	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR022764 (PFAM): IPR035952 (G3D	0,078	0,154	0,121	0,151	0,095									
Solyc10g012320	Ubiquitin-conjugating enzyme (AHRD V3.3 *** A0A072TZ92_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:integral component of membrane; F:transferas	IPR000608 (PFAM): IPR016135 (G3D	0,000	0,019	0,025	0,000	0,000									
Solyc10g012330	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G69550.1)		F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,025	0,025	0,023									
Solyc10g012340	Disease resistance protein (AHRD V3.3 *-* A0A068EX82_SOLHA)		F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,022	0,024									
Solyc10g012350	NBS resistance protein RGA22 (AHRD V3.3 *** A0A0E3T826_TOBAC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:ADP bindin	PTHR23155:SF877 (PANTHER): PTHI	0,176	0,359	0,231	0,292	0,374									
Solyc10g012360	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1		F:GO:0016740	F:transferase activity	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,050	0,000									
Solyc10g012370	Cysteine synthase (AHRD V3.3 *** K4CYL4_SOLLC)		F:GO:0004124; C:G(	F:cysteine synthase EC:4.4.1.9; EC:2.5.1 L-3-cyanoalanine syi	IPR005856 (TIGRFAM): G3DSA:3.40.!	42,249	37,359	252,928	257,608	215,283									
Solyc10g012380	LOW QUALITY:Transcription factor, MADS-box (AHRD V3.3 *-* A0A118JYH5_CYNCS)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR036879 (G3DS M-type_MADS	0,019	0,039	0,000	0,000	0,000									
Solyc10g012400	LDLR chaperone MESD (AHRD V3.3 *** A0A1D1YKF8_9ARAE)		P:GO:0006457	P:protein folding	IPR019330 (PFAM): G3DSA:3.30.70.2	1,419	0,770	1,701	0,823	1,157									
Solyc10g012410	ribosomal RNA small subunit methyltransferase G (AHRD V3.3 *** AT2G45990.2)		F:GO:0000149; P:G(	F:SNARE binding; P:SNARE complex assembly	PTHR15157:SF15 (PANTHER): PTHR	4,874	6,627	3,086	3,801	4,877									
Solyc10g012420	Mesoderm induction early response protein 1, putative isoform 1 (AHRD V3.3 *** A0A061DT69_THECC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	26,453	20,939	42,421	40,276	34,509									
Solyc10g012430	Signal peptide peptidase-like protein (AHRD V3.3 *** G7LBR2_MEDTR)		F:GO:0004190; C:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR007369 (PFAM): IPR003137 (PFA	6,101	13,303	5,323	3,971	5,697	1,148	0,045					up		
Solyc10g017490	MAP kinase kinase kinase 74	MAPKKK74	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR020683 (PFAM): IPR000719 (PFA	0,317	0,317	0,124	0,025	0,048									
Solyc10g017495	Dual specificity protein kinase splA (AHRD V3.3 *-* W9RSM8_9ROSA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	0,077	0,080	0,000	0,025	0,000									
Solyc10g017500	LOW QUALITY:Gamma-aminobutyrate transaminase 1, mitochondrial (AHRD V3.3 --* GATP1_ORYSI)					0,000	0,000	0,050	0,000	0,000									
Solyc10g017510	Cytochrome P450, putative (AHRD V3.3 *** B9S9Q2_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR002401 (PRINTS): IPR001128 (PF	1,218	1,472	0,194	0,070	0,117									
Solyc10g017520	Pollen-specific SF3 (AHRD V3.3 *** A0A0B0PMH4_GOSAR)		F:GO:0046872	F:metal ion binding	IPR001781 (PFAM): G3DSA:2.10.110.	0,040	0,037	0,000	0,022	0,000									
Solyc10g017530	RNA helicase DEAD33	DEAD33	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR001650 (PFAM): G3DSA:3.40.50.3	91,912	87,501	92,823	90,765	91,853									
Solyc10g017540	Remorin, putative (AHRD V3.3 *** B9RDP4_RICCO)				IPR005516 (PFAM): mobidb-lite (MOB	0,134	0,149	0,125	0,628	0,093									
Solyc10g017570	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)		P:GO:0055114	P:oxidation-reduction process	IPR002347 (PRINTS): IPR002347 (PF	0,000	0,021	0,025	0,000	0,000									
Solyc10g017580	Digalactosyldiacylglycerol synthase (AHRD V3.3 *** A2Q3N6_MEDTR)		F:GO:0008194; C:G(	F:UDP-glycosyltransferase activity; C:chloroplast outer membra	G3DSA:3.40.50.2000 (GENE3D): PF1	24,298	24,534	17,915	16,258	15,639									
Solyc10g017590	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G61050.2		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:lipid binding	IPR000008 (PRINTS): IPR000008 (PF	0,040	0,019	0,000	0,000	0,000									
Solyc10g017600	Hexosyltransferase (AHRD V3.3 *** M1AND6_SOLTU)	GAUT2	F:GO:0047262	F:polygalacturonate EC:2.4.1.43 Polygalacturonate 4-	IPR029044 (G3DSA:3.90.550.GENE3I	20,393	20,364	22,757	26,096	22,155									
Solyc10g017610	LOW QUALITY:Mechanosensitive ion channel protein 9 (AHRD V3.3 --* MSL9_ARATH)					0,097	0,055	0,000	0,072	0,024									

Solyc10g017630	MADS-box transcription factor (AHRD V3.3 *** Q1EMR8_PLAMJ)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM); PTHR11945 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc10g017655	Phospholipase D (AHRD V3.3 *-* Q9AWB6_SOLLC)		F:GO:0003824	F:catalytic activity			G3DSA:3.30.870.10 (GENE3D); IPR0;	0,021	0,000	0,000	0,000	0,000									
Solyc10g017750	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G61660.3)						PTHR33499:SF7 (PANTHER); PTHR3:	0,019	0,021	0,075	0,000	0,047									
Solyc10g017810	ATPase ASNA1 homolog (AHRD V3.3 *** K4CYQ6_SOLLC)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR025723 (PFAM); IPR016300 (TIGF	13,935	11,949	17,089	17,829	15,934									
Solyc10g017830	LOW QUALITY:Kinase family protein (AHRD V3.3 *** D7MH12_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,159	0,039	0,000	0,000	0,024									
Solyc10g017850	Peroxisomal membrane protein 11-1 (AHRD V3.3 *** PX111_ORYSJ)		C:GO:0005779; P:G(	C:integral component of peroxisomal membrane; P:peroxisome			IPR008733 (PFAM); PTHR12652:SF1(	35,775	49,875	43,153	55,825	55,251					0,375	0,026			up
Solyc10g017880	F-box protein (AHRD V3.3 *** A0A0B2RBZ5_GLYSO)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); PTH	41,756	38,167	51,571	50,172	46,128									
Solyc10g017890	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_POPAL)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,077	0,288	0,223	0,661	0,401									
Solyc10g017900	Photosystem I P700 chlorophyll a apoprotein A1 family (AHRD V3.3 *-* A0A151R2J4_CAJCA)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PRINTS); IPR001280 (PF	0,061	0,334	0,101	0,437	0,235									
Solyc10g017910	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_DAUCA)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,083	0,025	0,348	0,095									
Solyc10g017920	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR037034 (G3DSA:3.90.1110.GENE	0,019	0,064	0,072	0,122	0,093									
Solyc10g017930	Cytochrome b6/f complex subunit VIII (AHRD V3.3 *** A0A172W6Y6_9SOLA)		C:GO:0009507	C:chloroplast				0,000	0,101	0,000	0,075	0,141									
Solyc10g017940	Photosystem II CP43 reaction center protein (AHRD V3.3 *** PSBC_CICAR)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM); G3DSA:1.10.10.6	0,078	0,367	0,099	0,174	0,095									
Solyc10g017950	Photosystem II reaction center protein Z (AHRD V3.3 *** K4CYR9_SOLLC)		C:GO:0009539; P:G(	C:photosystem II reaction center; P:photosystem II stabilization			IPR002644 (TIGRFAM); IPR036512 ((	0,000	0,120	0,025	0,075	0,116									
Solyc10g017960	F-box protein PP2-A13 (AHRD V3.3 *** P2A13_ARATH)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); IPR(	0,377	1,105	2,357	7,058	3,857					1,579	0,000			up
Solyc10g017970	Chitinase (AHRD V3.3 *-* Q9SQL3_POAPR)		F:GO:0008061	F:chitin binding			IPR001002 (PRINTS); IPR036861 (G3	157,328	572,290	3652,840	5029,880	5753,888	1,890	0,049					up		
Solyc10g017980	Chitinase (AHRD V3.3 *-* B8QVJ5_ZEAMP)		F:GO:0008061	F:chitin binding			IPR001002 (PRINTS); IPR001002 (PF	21,520	104,349	706,803	808,920	1057,613	2,306	0,017					up		
Solyc10g017990	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ9_SOLLC)		P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	IPR006094 (PFAM); IPR016170 (G3D	0,000	0,018	0,022	0,000	0,093									
Solyc10g018010	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 --* AT2G21230.4)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,628	1,127	0,849	1,286	1,157									
Solyc10g018100	RNA-binding domain CCCH-type zinc finger protein (AHRD V3.3 *-* G7JUR4_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	0,061	0,021	0,025	0,098	0,000									
Solyc10g018120	neuronal PAS domain protein (AHRD V3.3 *** AT2G40390.1)		C:GO:0016021	C:integral component of membrane			PTHR31439 (PANTHER); PTHR31439	1,113	0,964	5,130	9,962	7,521					0,961	0,000			up
Solyc10g018130	LOW QUALITY:Cystathionine beta-synthase (CBS) protein (AHRD V3.3 --* AT1G69800.2)							0,000	0,000	0,097	0,094	0,071									
Solyc10g018140	Dihydroflavonol-4-reductase-like (AHRD V3.3 *** A0A0N6XTN7_LYCRU)	DFR	F:GO:0003854; P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D); IPR0(	2,212	3,813	22,397	28,834	22,023									
Solyc10g018150	SlCytochromeP450		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,000	0,000	0,025	0,000	0,000									
Solyc10g018160	S-acyltransferase (AHRD V3.3 *** K4CYU0_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM); mobidb-lite (MOB	12,829	13,870	20,989	22,733	20,620									
Solyc10g018190	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G24530.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,000	0,021	0,000	0,000	0,000									
Solyc10g018196	ALBINO OR PALE-GREEN 13 (AHRD V3.3 --* AT1G63680.3)							0,037	0,000	0,000	0,000	0,000									
Solyc10g018250	40S ribosomal protein S13 (AHRD V3.3 *** RS13_SOYBN)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.287.10 (GENE3D); IPR0(	63,228	64,221	74,635	65,663	67,512									
Solyc10g018260	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE3-like2	F:GO:0003824; F:G(	F:catalytic activity; F:coenzyme binding			PR01713 (PRINTS); IPR001509 (PFA	1,717	1,078	0,383	0,489	0,496									
Solyc10g018290	LOW QUALITY:NHL repeat-containing family protein (AHRD V3.3 *-* B9HJT0_POPTR)		C:GO:0016021	C:integral component of membrane			PTHR13833:SF42 (PANTHER); PTHR	0,876	0,784	0,000	0,097	0,000									
Solyc10g018300	Transketolase (AHRD V3.3 *** AT3G60750.1)	TKT	F:GO:0004802	F:transketolase act	EC:2.2.1.1	Transketolase	IPR005478 (TIGRFAM); G3DSA:3.40.!	102,992	214,397	77,503	98,311	228,939	1,085	0,004	1,559	0,000			up	up	
Solyc10g018310	LOW QUALITY:regulatory components of ABA receptor 3 (AHRD V3.3 --* AT5G53160.2)							0,510	0,572	0,172	0,189	0,189									
Solyc10g018340	Small auxin up-regulated RNA71	SAUR71	P:GO:0009733	P:response to auxin			IPR003676 (PFAM); PTHR31374:SF5(	0,000	0,150	0,047	0,216	0,140									
Solyc10g018350	Vesicle-associated 1-1-like protein (AHRD V3.3 *** A0A0B0MV36_GOSAR)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR000535 (PFAM); IPR016763 (PIRS	14,328	15,802	13,054	13,177	14,732									
Solyc10g018390	Tryptophan synthase (AHRD V3.3 *** K4CYW3_SOLLC)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.2.1.2	Tryptophan synthase	IPR001926 (PFAM); G3DSA:3.40.50.1	0,000	0,018	0,000	0,000	0,000									
Solyc10g018393	Polyprotein (AHRD V3.3 *-* A0A151RXE0_CAJCA)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding; F:rRNA (guanine) metl			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,082	0,039	0,090	0,000	0,023									
Solyc10g018397	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SA73_CAJCA)						IPR019557 (PFAM); PTHR44194 (PAN	0,000	0,037	0,000	0,000	0,000									
Solyc10g018420	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SA73_CAJCA)						IPR019557 (PFAM); PTHR44194 (PAN	0,056	0,115	0,000	0,000	0,000									
Solyc10g018510	bHLH transcription factor 063		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (PFAM bHLH	0,094	0,057	0,022	0,095	0,047									
Solyc10g018520	3'-5' exonuclease domain-containing family protein (AHRD V3.3 *** B9I623_POPTR)		F:GO:0000166; C:G(	F:nucleotide binding; C:nuclear exosome (RNase complex); F:nu			G3DSA:1.10.150.80 (GENE3D); IPR0(	94,819	74,827	95,210	82,684	92,148									
Solyc10g018530	DNA mismatch repair protein MutS (AHRD V3.3 *** G7K3K2_MEDTR)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			G3DSA:3.40.50.300 (GENE3D); IPR0(	5,893	5,060	3,509	3,859	3,323									
Solyc10g018540	DNA mismatch repair protein MutS (AHRD V3.3 *-* G7K3K2_MEDTR)		F:GO:0005524; P:G(	F:ATP binding; P:mismatch repair; F:mismatched DNA binding			IPR007696 (PFAM); G3DSA:1.10.142(	2,982	2,115	1,608	1,968	2,097									
Solyc10g018590	Plastid lipid-associated protein (AHRD V3.3 *** A0A072TY66_MEDTR)						IPR006843 (PFAM); IPR039633 (PAN	6,941	6,862	11,162	11,764	10,759									
Solyc10g018600	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RD13_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1740.10 (GENE3D); IPR(	37,194	34,585	46,723	45,127	50,198									
Solyc10g018610	50S ribosomal protein L2, chloroplastic (AHRD V3.3 *-* RK2_TOBAC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022669 (PFAM); IPR014726 (G3D	0,253	0,379	0,075	0,118	0,141									
Solyc10g018640	Zinc finger protein (AHRD V3.3 *** A0A0B0MVF4_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,245	0,204	0,000	0,025	0,000									
Solyc10g018670	LOW QUALITY:DNA glycosylase (AHRD V3.3 *-* A0A103XC49_CYNCS)		P:GO:0006284; F:G(	P:base-excision rep	EC:3.2.2.21; EC:3.2.	DNA-3-methyladenine	IPR005019 (PFAM); G3DSA:1.10.340	0,019	0,000	0,000	0,000	0,000									
Solyc10g018710	LOW QUALITY:TCP transcription factor 1 (AHRD V3.3 *** G3BGU2_SOLLC)						IPR017887 (PFAM TCP	0,038	0,019	0,000	0,000	0,000									
Solyc10g018750	Metalloendoproteinase 1, putative (AHRD V3.3 *-* B9RD50_RICCO)		F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR021190 (PRINTS); IPR001818 (PF	0,040	0,018	0,197	0,269	0,047									
Solyc10g018760	Metalloendoproteinase 1, putative (AHRD V3.3 *** B9RD50_RICCO)		F:GO:0008237	F:metallopeptidase activity			IPR002477 (PFAM); IPR024079 (G3D	0,042	0,085	0,100	0,172	0,188									
Solyc10g018770	LOW QUALITY:dentin sialophosphoprotein-like protein (AHRD V3.3 --* AT5G07940.3)							0,019	0,000	0,022	0,050	0,000									
Solyc10g018780	Squamosa promoter binding protein 8a		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			IPR004333 (PFAM SBP	31,293	28,822	0,356	0,556	0,678									
Solyc10g018790	LOW QUALITY:embryo defective 1303 (AHRD V3.3 --* AT1G56200.2)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,041	0,000	0,000	0,000									
Solyc10g018810	60S ribosomal protein L7A-like protein (AHRD V3.3 *-* Q2XPW4_SOLTU)		P:GO:0000470; F:G(	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large ribo			IPR001921 (PRINTS); IPR038524 (G3	0,832	1,492	0,869	0,771	0,704									
Solyc10g018820	LOW QUALITY:histone acetyltransferase of the CBP family 5 (AHRD V3.3 --* AT3G12980.2)							0,969	0,873	0,836	0,907	0,727									
Solyc10g018840	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_LACSA)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM); IPR000932 (PAN	0,076	0,043	0,125	0,222	0,119									
Solyc10g018850	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9SFP3_RICCO)		F:GO:0016787	F:hydrolase activity			IPR002925 (PFAM); IPR029058 (G3D	8,938	5,249	17,836	18,737	14,112	-0,741	0,047					down		
Solyc10g018870	Melanoma-associated antigen G1, putative (AHRD V3.3 *** B9RJL0_RICCO)						G3DSA:1.10.10.1210 (GENE3D); IPR(	7,213	4,966	7,218	8,249	7,052									
Solyc10g018880	LOW QUALITY:kinase with adenine nucleotide alpha hydrolases-like domain-containing protein (AHRD V3.3 --* AT1G78940.3)							0,115	0,119	0,150	0,346	0,167									
Solyc10g018885	Melanoma-associated antigen G1 (AHRD V3.3 *-* A0A151RLN9_CAJCA)						IPR002190 (PFAM); G3DSA:1.10.10.1	4,935	3,931	5,623	5,486	5,023									
Solyc10g018900	Histone-lysine N-methyltransferase ATX5 (AHRD V3.3 --* A0A151TS84_CAJCA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	4,368	3,289	4,856	5,101	4,943									
Solyc10g018903	SPT4 homolog 2 (AHRD V3.3 --* AT5G63670.1)							0,252	1,398	0,046	0,727	0,428	2,424	0,001					up		
Solyc10g018907	LOW QUALITY:Chaperonin 60 subunit beta 1, chloroplastic (AHRD V3.3 --* CPNB1_ARATH)		F:GO:0005488	F:binding			IPR025558 (PFAM); mobidb-lite (MOB	1,916	1,359	1,341	1,672	1,718									
Solyc10g018930	LOW QUALITY:Beige/BEACH and WD40 domain-containing protein (AHRD V3.3 --* AT4G02660.3)							0,120	0,080	0,423	0,022	0,188									
Solyc10g018945	Ribosomal protein S13 (AHRD V3.3 *** A0A142I0Y0_NICSY)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR001892 (PFAM); IPR027437 (G3D	0,000	0,000	0,022	0,000	0,000									
Solyc10g018980	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM); IPR008543 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc10g018990	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM); IPR008543 (PAN	0,000	0,000	0,000	0,124	0,000									
Solyc10g019000	Protein Ycf2 (AHRD V3.3 *-* YCF2_SPIOL)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PANTHER); IPR027417 (!	0,019	0,039	0,000	0,245	0,070									
Solyc10g019020	LOW QUALITY:Anthranilate O-methyltransferase 1 (AHRD V3.3 --* AAMT1_MAIZE)							0,021	0,000	0,000	0,000	0,000									
Solyc10g019030	Interactor of constitutive active ROPs 3-like protein (AHRD V3.3 *-* A0A0B0N2C1_GOSAR)		F:GO:0051219	F:phosphoprotein binding			IPR029688 (PANTHER); IPR029688 (I	0,000	0,021	0,000	0,000	0,023									
Solyc10g019037	Cycloartenol synthase (AHRD V3.3 --* CAS1_LUFAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,000	0,025	0,047									
Solyc10g019040	Kinetochore protein nuf2, putative (AHRD V3.3 *** B9STF6_RICCO)		C:GO:0031262	C:Ndc80 complex			IPR005549 (PFAM); IPR038275 (G3D	56,550	50,353	60,572	65,698	56,848									
Solyc10g019050	LOW QUALITY:Farnesyl pyrophosphate synthase 1 (AHRD V3.3 --* FPPS1_LUPAL)							0,433	0,400	0,416	0,336	0,495									
Solyc10g019130	exocyst complex component sec10 (AHRD V3.3 *-* AT5G12370.3)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis; P:vesicle docking			IPR009976 (PFAM); IPR009976 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc10g019140	exocyst complex component sec10 (AHRD V3.3 *** AT5G12370.3)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis; P:vesicle docking			IPR009976 (PFAM); IPR033960 (PTH	0,019	0,000	0,000	0,000	0,000									
Solyc10g019170	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT4G16820.1)							1,644	2,662	2,083	3,050	2,137									
Solyc10g019177	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4DEU6_SOLLC)		F:GO:0005524	F:ATP binding			IPR041569 (PFAM); G3DSA:3.40.50.3	0,000	0,018	0,000	0,000	0,023									
Solyc10g019190	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4DEU6_SOLLC)		F:GO:0005524	F:ATP binding			IPR003959 (PFAM); IPR041569 (PFA	0,199	0,158	0,364	0,270	0,421									
Solyc10g019210	Sulfotransferase (AHRD V3.3 *** K4CZ39_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,473	0,269	0,000	0,000	0,000									
Solyc10g019220	Sulfotransferase (AHRD V3.3 *** K4CZ40_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM); G3DSA:3.40.50.3	0,475	0,343	0,000	0,000	0,000									
Solyc10g019270	Multidrug resistance protein ABC transporter family (AHRD V3.3 *** A0A061FKD3_1	ABCC10	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR011527 (PFA	0,021	0,018	0,184	0,242	0,070									
Solyc10g024320	Lon protease homolog, mitochondrial (AHRD V3.3 *** A0A0V0IX74_SOLCH)		F:GO:0004176; F:G(	F:ATP-dependent pe	EC:3.4.21; EC:3.6.1.	Acting on peptide bor	PR00830 (PRINTS); G3DSA:1.20.58.1	31,867	34,077	33,658	33,233	32,400									
Solyc10g024330	Ankyrin repeat domain containing protein 2 (AHRD V3.3 *** A0A0A7EAV4_NICBE)		F:GO:0030941; C:G(	F:chloroplast targeting sequence binding; C:integral component			IPR041243 (PFAM); IPR036770 (G3D	0,063	0,107	0,025	0,022	0,093									
Solyc10g024360	Potassium channel (AHRD V3.3 *** Q9SSV3_NICPA)		F:GO:0005249; F:G(	F:voltage-gated potassium channel activity; F:protein binding; P			IPR003938 (PRINTS); IPR002110 (PF	1,466	1,555	1,306	2,173	1,885									
Solyc10g024370	Phospholipase D (AHRD V3.3 *** K4CZ56_SOLLC)		F:GO:0004630; F:G(	F:phospholipase D ;	EC:3.1.4.4	Phospholipase D	IPR025202 (PFAM); IPR000008 (PFA	0,561	0,371	0,336	0,701	0,398									
Solyc10g024410	Ribose-phosphate pyrophosphokinase family protein (AHRD V3.3 *** B9IB48_POPTR)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.6.1	Ribose-phosphate di	G3DSA:3.40.50.2020 (GENE3D); IPR(	112,987	130,933	73,193	58,838	71,001									
Solyc10g024415	RNA 2'-phosphotransferase, Tpt1 / KptA family (AHRD V3.3 --* AT2G45330.2)							0,343	0,079	0,072	0,097	0,094									
Solyc10g024420	ABC transporter family protein (AHRD V3.3 *** B9IB53_POPTR)	ABCC11	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0(	28,548	22,066	667,132	1023,934	658,538					0,621	0,000			up
Solyc10g024430	TUDOR-SN protein 1 (AHRD V3.3 --* AT5G07350.2)							0,000	0,000	0,268	0,349	0,282									
Solyc10g024470	Chromo domain protein LHP1 (AHRD V3.3 *-* LHP1_SOLLC)		C:GO:0005634	C:nucleus			IPR023780 (PFAM); G3DSA:2.40.50.4	29,294	26,543	52,226	51,464	48,113									
Solyc10g024490	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM); IPR000109 (PAN	1,012	0,780	3,474	7,097	5,756			0,724	0,035	1,031	0,002		up	up
Solyc10g026527	Cytochrome P450, putative (AHRD V3.3 *-* B9S4U7_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR036396 (G3DSA:1.10.630.GENE3I	0,158	0,158	0,022	0,025	0,023									
Solyc10g031550	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR038120 (G3DSA:1.10.132.GENE3	0,000	0,058	0,025	0,175	0,023									
Solyc10g031560	LOW QUALITY:DNA-directed RNA polymerase subunit (AHRD V3.3 *-* M1CW95_SOLTU)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR007066 (PFAM); G3DSA:1.10.274.	0,000	0,128	0,074	0,145	0,070									
Solyc10g033560	LOW QUALITY:Signal recognition particle subunit SRP72 (AHRD V3.3 *-* K4D938_SOLLC)		P:GO:0006614; F:G(	P:SRP-dependent cotranslational protein targeting to membrane			IPR013699 (PFAM); mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc10g037890	ELMO domain-containing protein A (AHRD V3.3 *-* M7YWT9_TRIUA)						mobidb-lite (MOBIDB_LITE); PTHR360	37,171	42,169	37,855	41,716	48,132									
Solyc10g037897	L-aspartate oxidase (AHRD V3.3 *-* AT5G14760.1)		F:GO:0008734; P:G(	F:L-aspartate oxida	EC:1.4.3.16; EC:1.4.	L-aspartate oxidase;	IPR036188 (G3DSA:3.50.50.GENE3D	0,042	0,021	0,000	0,025	0,000									
Solyc10g037910	Kinase family protein (AHRD V3.3 *-* D7M6L5_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,335	0,199	0,025	0,166	0,164									
Solyc10g037930	coiled-coil protein (AHRD V3.3 *-* AT3G48860.1)		P:GO:0000911	P:cytokinesis by cell plate formation			IPR040321 (PANTHER)	0,084	0,041	0,090	0,000	0,024									
Solyc10g037940	fas-binding factor-like protein (AHRD V3.3 *-* AT4G08630.2)		P:GO:0000911	P:cytokinesis by cell plate formation			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,140	0,145	0,215	0,000	0,094									
Solyc10g037950	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G48020.1)		F:GO:0051213; P:G(	F:dioxygenase activity; P:oxidation-reduction process			IPR026992 (PFAM); IPR027443 (G3D	22,678	21,344	34,394	29,225	30,397									
Solyc10g037960	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT5G48020.1)						IPR027443 (G3DSA:2.60.120.GENE3I	15,608	15,710	25,901	24,335	24,938									
Solyc10g037980	Thioredoxin-like family protein (AHRD V3.3 *** V5IV10_HEVBR)		C:GO:0005829; F:G(	C:cytosol; F:protein	EC:1.8.1.8	Protein-disulfide redu	IPR010357 (PFAM); G3DSA:3.40.30.1	23,424	22,500	50,734	46,891	50,444									
Solyc10g037990	LOW QUALITY:Maturase K (AHRD V3.3 --* C0KEH0_9MAGN)							0,000	0,000	0,000	0,025	0,000									
Solyc10g038000	Zinc finger transcription factor 57	C3H57	F:GO:0046872	F:metal ion binding			IPR001841 (PFAM C3H	21,191	16,717	22,664	20,872	21,287									
Solyc10g038005	E3 ubiquitin-protein ligase makorin (AHRD V3.3 --* C3H41_ORYSJ)		F:GO:0016874; F:G(	F:ligase activity; F:metal ion binding				4,113	3,399	4,536	3,297	3,328									
Solyc10g038020	Cellulose synthase family protein (AHRD V3.3 *-* AT5G17420.1)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR005150 (PFAM); PTHR13301 (PAN	0,057	0,043	0,051	0,502	0,046									
Solyc10g038030	Zinc finger family protein (AHRD V3.3 *-* B9MXH1_POPTR)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:response to abscisic acid; F:metal			PTHR23111 (PANTHER); PTHR23111	0,040	0,000	0,000	0,000	0,071									
Solyc10g038060	Ribosomal protein L28 (AHRD V3.3 *** A0A103XZR0_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR026569 (PFAM); IPR037147 (G3D	2,652	2,937	2,843	1,849	2,324									
Solyc10g038080	Shikimate dehydrogenase, 3-dehydroquinate dehydratase (AHRD V3.3 *** A0A0K9PLS3_ZOSMR)		F:GO:0003855; F:G(	F:3-dehydroquinate	EC:1.1.1.25; EC:4.2.	Shikimate dehydroge	G3DSA:3.40.50.10860 (GENE3D); IPF	2,875	3,707	71,578	96,357	72,483					0,433	0,044			up
Solyc10g038120	Coatomer subunit delta (AHRD V3.3 *** W9SBM6_9ROSA)		P:GO:0006890; C:G(	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			G3DSA:3.30.450.60 (GENE3D); G3DS	73,939	74,353	154,078	142,312	141,112									
Solyc10g038130	Pectinacetylesterase family protein (AHRD V3.3 *** AT2G46930.1)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM); PTHR21562:SF5	42,365	40,424	24,775	21,972	25,954									
Solyc10g038150	Zinc finger family protein (AHRD V3.3 --* B9MXH1_POPTR)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:response to abscisic acid; F:metal			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,022	0,000	0,000									
Solyc10g038190	Kinase family protein (AHRD V3.3 *** B9GP63_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); PTHR24351 (PAN	13,041	14,861	21,336	25,882	22,422									
Solyc10g039190	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** AT3G21540.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR015943 (G3	48,682	50,249	42,402	34,383	38,961									
Solyc10g039195	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 --* A0A0K1ZDF5_VERTH)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR33144 (PANTHER); PTHR33144	0,019	0,000	0,000	0,000	0,000									
Solyc10g039217	Nucleic acid-binding, OB-fold (AHRD V3.3 *-* A0A103XN23_CYNCS)						G3DSA:2.40.50.140 (GENE3D)	0,000	0,021	0,000	0,045	0,000									
Solyc10g039230	S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61490.7)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,237	0,227	0,193	0,124	0,096									
Solyc10g039270	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9PKM9_ZOSMR)		P:GO:0000413; F:G(	P:protein peptidyl-pr	EC:5.2.1.8	Peptidylprolyl isomer	IPR001179 (PFAM); G3DSA:3.10.50.4	8,087	10,144	6,987	6,890	9,465									
Solyc10g039280	Protein-tyrosine phosphatase mitochondrial 1 (AHRD V3.3 *** A0A0B0MXE1_GOSAR)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR029021 (G3DSA:3.90.190.GENE3I	4,540	4,901	2,540	2,473	2,750									
Solyc10g039290	Nitrate transporter protein 1.2-like protein (AHRD V3.3 *** A0A0H3WEV3_CAMSI)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM); G3DSA:1.20.125(	3,808	3,428	1,053	0,885	1,010									
Solyc10g039295	Basic helix-loop-helix DNA-binding superfamily protein (AHRD V3.3 --* A0A061EC23_THECC)						mobidb-lite (MOBIDB_LITE)	0,136	0,082	0,025	0,050	0,046									
Solyc10g039360	DUF1639 family protein (AHRD V3.3 *-* G7JHQ0_MEDTR)						IPR012438 (PFAM); mobidb-lite (MOB	31,088	34,281	29,567	30,744	30,649									
Solyc10g039367	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* AT2G18600.2)		F:GO:0005524; F:G(	F:ATP binding; F:NEDD8 transferase activity; P:protein neddyla			IPR000608 (PFAM); IPR016135 (G3D	0,019	0,019	0,025	0,000	0,070									
Solyc10g039380	TSA: Wollemia nobilis Ref_Wollemi_Transcript_16394_661 transcribed RNA sequence (AHRD V3.3 *** A0A0C9RRW7_9SPER)						IPR039491 (PFAM); IPR039491 (PAN	15,817	16,418	20,738	16,707	19,001									
Solyc10g039390	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT1G29000.2)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); IPR0(	0,000	0,019	0,000	0,022	0,046									
Solyc10g039393	Cytochrome C oxidase subunit II-like, transmembrane domain-containing protein (AHRD V3.3 --* ATMG0128		C:GO:0005886	C:plasma membrane			PTHR31149:SF4 (PANTHER); PTHR3:	2,322	2,818	3,836	3,233	3,141									
Solyc10g039430	Tripartite motif-containing 29 (AHRD V3.3 *** A0A0B0P7U5_GOSAR)		C:GO:0005886	C:plasma membrane			G3DSA:2.60.40.2700 (GENE3D); mob	31,338	26,832	29,332	31,364	31,124									
Solyc10g044450	Regulator of nonsense transcripts 3A (AHRD V3.3 *** A0A151T884_CAJCA)		P:GO:0000184; F:G(	P:nuclear-transcribed mRNA catabolic process, nonsense-medi			IPR005120 (PFAM); IPR012677 (G3D	22,236	24,164	36,810	38,796	37,867									
Solyc10g044470	Chloride channel protein (AHRD V3.3 *** M1AL73_SOLTU)		F:GO:0005247; P:G(	F:voltage-gated chloride channel activity; P:chloride transport; (			IPR001807 (PRINTS); IPR002251 (PF	228,228	179,525	133,626	235,287	214,646			0,681	0,004	0,818	0,000		up	up
Solyc10g044480	Transmembrane 9 superfamily member (AHRD V3.3 *** K4CZH3_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM); PTHR10766:SF8	64,879	61,923	67,725	70,521	68,141									
Solyc10g044495	LOB domain-containing protein 35 (AHRD V3.3 --* AT5G35900.1)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity				0,038	0,000	0,000	0,000	0,000									
Solyc10g044510	MLO-like protein (AHRD V3.3 *** K4CZH6_SOLLC)		P:GO:0006952; C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM); PTHR31942 (PAN	10,231	6,695	6,061	7,439	7,181									
Solyc10g044517	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic (AHRD V3.3 --* ACCD_LEPVR)							0,060	0,000	0,025	0,047	0,000									
Solyc10g044520	Ferredoxin (AHRD V3.3 *** A0A0K0PWX6_SOLLC)		F:GO:0009055; P:G(	F:electron transfer activity; P:electron transport chain; F:2 iron,			IPR010241 (TIGRFAM); IPR012675 ((	0,019	0,021	0,000	0,000	0,000									
Solyc10g044530	Auxin transporter-like protein 5 (AHRD V3.3 --* LAX5_MEDTR)							0,042	0,039	0,025	0,025	0,046									
Solyc10g044540	ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_PANGI)		F:GO:0005524; C:G(	F:ATP binding; C:ch	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.12240 (GENE3D); PT	0,119	0,260	0,025	0,100	0,070									
Solyc10g044543	ATP synthase subunit b, chloroplastic (AHRD V3.3 *** ATPF_SOLBU)		C:GO:0016020; C:G(	C:membrane; C:intracellular part			PTHR34264 (PANTHER); PTHR34264	0,391	1,575	0,200	0,617	0,444	1,994	0,002					up		
Solyc10g044547	Formin-like protein (AHRD V3.3 *-* K4CXI5_SOLLC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc10g044640	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM); mobidb-lite (MOB	15,933	15,992	20,125	19,565	18,464									
Solyc10g044670	phytochrome A	PHYA	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR001294 (PRINTS); IPR003594 (PF	76,054	70,112	151,748	165,739	173,567									

Solyc10g044680	R2R3MYB transcription factor 55	R2R3MYB55	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	4,075	1,533	0,025	0,166	0,167									
Solyc10g044690	Annexin (AHRD V3.3 *** K4CZJ0_SOLLC)		F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS); IPR037104 (G3	0,195	0,075	0,115	0,000	0,000									
Solyc10g044700	LOW QUALITY:Calcium-binding EF-hand (AHRD V3.3 *** A0A103XMB3_CYNCS)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D); IPR0(	0,000	0,019	0,025	0,000	0,000									
Solyc10g044710	TPR repeat protein (AHRD V3.3 *** G7I8S7_MEDTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	6,327	7,227	6,453	7,831	9,122									
Solyc10g044720	inositol requiring 1-1 (AHRD V3.3 --* AT5G24360.3)							4,646	4,581	6,055	7,899	6,072									
Solyc10g044730	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G02780.3)							0,000	0,000	0,025	0,000	0,000									
Solyc10g044740	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** G7JCS6_MEDTR)		F:GO:0004190; P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS); IPR032799 (PF	33,142	30,283	38,725	34,953	33,805									
Solyc10g044745	ENTH/VHS/GAT family protein (AHRD V3.3 *-* A0A061GKP2_THECC)		C:GO:0005623; P:G(	C:cell; P:intracellular protein transport			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,063	0,060	0,025	0,047	0,023									
Solyc10g044780	cell cycle checkpoint control protein family (AHRD V3.3 *** AT3G05480.1)		P:GO:0000077; P:G(	P:DNA damage checkpoint; P:DNA repair; C:checkpoint clamp c			G3DSA:3.70.10.10 (GENE3D); IPR02(	18,845	17,829	18,322	15,111	19,514									
Solyc10g044783	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 --* A0A0L9TDG0_PHAAN)							0,019	0,000	0,000	0,000	0,000									
Solyc10g044840	yacP-like NYN domain protein (AHRD V3.3 *** AT2G02410.1)						IPR010298 (PFAM); IPR010298 (PAN	7,061	10,561	2,999	2,193	4,607									
Solyc10g044880	LOW QUALITY:oxidoreductase/transition metal ion-binding protein (AHRD V3.3 *** AT2G31940.1)		C:GO:0016021	C:integral component of membrane			PTHR33306 (PANTHER); PTHR33306	0,082	0,140	0,050	0,269	0,143									
Solyc10g044900	Ion channel DMI1 (AHRD V3.3 *** DMI1_MEDTR)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.720 (GENE3D); IPR0'	43,910	38,056	21,099	20,454	26,532									
Solyc10g044910	etoposide-induced protein (AHRD V3.3 *** AT4G06676.1),Pfam:PF07264		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:integral component of membrane; P			PF07264 (PFAM); IPR009890 (PANTH	12,589	11,306	19,974	22,311	20,036									
Solyc10g044915	LOW QUALITY:Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 --* AT4G35770.(		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR002156 (PFAM); IPR036397 (G3D	1,408	1,473	1,758	2,733	1,863									
Solyc10g044920	Stromal processing peptidase, chloroplastic (AHRD V3.3 --* SPP_ARATH)							0,000	0,060	1,905	2,731	2,843									
Solyc10g044960	Emsy N terminus domain-containing family protein (AHRD V3.3 *** B9HPS6_POPTR)		P:GO:0050832	P:defense response to fungus			IPR005491 (PFAM); G3DSA:1.10.124(	32,295	32,065	50,318	47,444	42,739									
Solyc10g044990	26S proteasome non-ATPase regulatory subunit 3 (AHRD V3.3 *-* G7J5U6_MEDTR)		C:GO:0000502; P:G(	C:proteasome complex; P:ubiquitin-dependent protein catabolic			PTHR10758 (PANTHER); PTHR10758	0,019	0,000	0,000	0,000	0,000									
Solyc10g045040	Protein DETOXIFICATION (AHRD V3.3 --* A0A0E0B5H8_9ORYZ)							0,061	0,000	0,000	0,000	0,047									
Solyc10g045050	LOW QUALITY:Enolase (AHRD V3.3 *-* A0A103XBT6_CYNCS)		C:GO:0000015; F:G(	C:phosphopyruvate	EC:4.2.1.11	Phosphopyruvate hy(	IPR000941 (PRINTS); IPR029017 (G3	0,019	0,124	0,050	0,120	0,023									
Solyc10g045100	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT3G05170.1)		F:GO:0003824	F:catalytic activity			PIRSF000709 (PIRSF); IPR013078 (F	0,000	0,019	0,000	0,000	0,000									
Solyc10g045105	Kinesin-like protein (AHRD V3.3 *-* M1AK12_SOLTU)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,237	0,181	0,144	0,216	0,238									
Solyc10g045107	importin alpha isoform 2 (AHRD V3.3 --* AT4G16143.2)						PTHR33499:SF1 (PANTHER); PTHR3:	0,037	0,059	0,068	0,025	0,000									
Solyc10g045150	LOW QUALITY:oxidoreductase, zinc-binding dehydrogenase family protein (AHRD V3.3 --* AT4G21580.2)							1,441	1,426	0,277	0,169	0,352									
Solyc10g045153	ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 --* A0A0B0NED8_GOSAR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,864	5,295	0,516	0,652	0,962									
Solyc10g045170	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT3G45440.4)							0,450	0,388	0,801	0,452	0,822									
Solyc10g045175	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G60080.1)		F:GO:0003824	F:catalytic activity			IPR013083 (G3DSA:3.30.40.GENE3D	7,025	7,794	8,218	7,647	7,726									
Solyc10g045180	E3 ubiquitin-protein ligase (AHRD V3.3 --* A0A0F7G5V7_9ROSI)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga:			mobidb-lite (MOBIDB_LITE)	0,164	0,119	0,046	0,072	0,047									
Solyc10g045190	RNA-DIRECTED DNA METHYLATION 1 (AHRD V3.3 *** AT3G22680.1)		C:GO:0005634; P:G(	C:nucleus; P:regulation of DNA methylation			IPR036319 (G3DSA:1.20.120.GENE3I	60,900	62,643	35,069	39,654	36,383									
Solyc10g045240	Beta-glucosidase (AHRD V3.3 *** L0ASF2_POPTO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001360 (PRINTS); G3DSA:3.20.2(	0,236	0,096	0,000	0,047	0,047									
Solyc10g045250	LOW QUALITY:RNA-binding KH domain-containing protein (AHRD V3.3 *-* AT3G13230.2)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA binding; C:nucleolus			PTHR12826 (PANTHER)	0,000	0,424	0,000	0,000	0,116									
Solyc10g045270	Protein kinase family protein (AHRD V3.3 *** X5I191_IPONI)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF); G3DSA:1.10.5	3,210	3,071	0,851	0,699	1,125									
Solyc10g045290	Kinase interacting (KIP1-like) family protein, putative (AHRD V3.3 *** A0A061DQM7_THECC)		F:GO:0003779	F:actin binding			IPR011684 (PFAM); PTHR32258:SF6	1,629	2,228	0,382	0,491	0,754									
Solyc10g045310	Oxidoreductase/ transition metal ion binding protein (AHRD V3.3 *** D7MCM0_ARALL)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA po	IPR021920 (PFAM); mobidb-lite (MOB	16,236	20,894	17,873	13,784	18,593									
Solyc10g045320	ATP binding cassette subfamily B4 (AHRD V3.3 --* AT2G47000.7)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,968	3,330	2,298	1,745	2,256									
Solyc10g045350	ecotropic viral integration site protein (AHRD V3.3 *** AT2G44360.1)		P:GO:0008150	P:biological_process			mobidb-lite (MOBIDB_LITE); mobidb-lit	6,926	6,642	5,286	4,187	4,831									
Solyc10g045380	Vacuolar protein sorting-associated protein 62 (AHRD V3.3 *** A0A103Y146_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR009291 (PFAM); PTHR42656:SF5	8,063	9,325	1,366	0,797	1,016									
Solyc10g045390	Histone acetyltransferase gcn5, putative (AHRD V3.3 *** B9S4R6_RICCO)		F:GO:0004402; F:G(	F:histone acetyltrar	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	IPR001487 (PRINTS); IPR036427 (G3	33,628	31,271	33,123	32,587	36,284									
Solyc10g045420	O-fucosyltransferase family protein (AHRD V3.3 *** AT2G44500.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:chloroplast; C:integral componer			IPR024709 (PIRSF); IPR019378 (PFA	44,902	60,980	13,558	17,077	22,804			0,746	0,009				up	
Solyc10g045430	Phosphoglycerate mutase family protein (AHRD V3.3 *** AT3G05170.1)		F:GO:0003824	F:catalytic activity			IPR013078 (PFAM); IPR029033 (G3D	6,242	7,353	10,180	10,573	9,757									
Solyc10g045433	DEAD-box ATP-dependent RNA helicase 32 (AHRD V3.3 --* RH32_ORYSJ)						mobidb-lite (MOBIDB_LITE)	3,133	2,681	1,113	2,597	2,423			1,095	0,010	1,200	0,003		up	up
Solyc10g045457	Ubiquitin, putative (AHRD V3.3 *-* B9SWD7_RICCO)		C:GO:0005634; C:G(	C:nucleus; C:ribosome; P:cellular protein metabolic process; C:i			G3DSA:3.10.20.90 (GENE3D)	6,044	6,171	1,332	1,507	1,599									
Solyc10g045480	LOW QUALITY:calmodulin-binding protein (DUF1645) (AHRD V3.3 *** AT2G15760.1)		C:GO:0005886	C:plasma membrane			IPR012442 (PFAM); mobidb-lite (MOB	0,223	0,282	2,368	2,841	1,775									
Solyc10g045500	Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 *-* AT1G08860.1)		F:GO:0005544; P:G(	F:calcium-dependent phospholipid binding; P:negative regulatior			IPR010734 (PFAM); IPR031116 (PTH	0,000	0,000	1,342	2,988	1,644					1,158	0,044			up
Solyc10g045540	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G56440.1)		F:GO:0005515	F:protein binding			IPR019734 (PFAM); IPR025986 (PFA	34,543	36,333	57,191	56,122	55,940									
Solyc10g045550	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); IPR001806 (PFA	17,407	17,859	16,819	16,880	14,264									
Solyc10g045555	Glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial (AHRD V3.3 --* GATB_OSTTA)							0,059	0,041	0,000	0,000	0,000									
Solyc10g045560	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,116	0,057	0,000	0,000	0,000									
Solyc10g045580	Cytochrome c oxidase subunit 5C (AHRD V3.3 *** Q9ZTN1_PETHY)		C:GO:0005746	C:mitochondrial respirasome			PTHR34372:SF2 (PANTHER); IPR008	0,119	0,218	0,000	0,000	0,000									
Solyc10g045600	Transmembrane receptor, eukaryota (AHRD V3.3 *** A0A118JVM3_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR009637 (PFAM); mobidb-lite (MOB	74,339	72,988	60,479	69,156	64,881									
Solyc10g045610	Protein kinase-like protein (AHRD V3.3 *** Q8W248_CAPAN)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,144	0,250	0,093	0,025	0,024									
Solyc10g045620	plant/protein%2C putative (DUF3411) (AHRD V3.3 *** AT5G24690.1)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast inner membrane; C:integral com			IPR021825 (PFAM); mobidb-lite (MOB	32,394	36,212	55,183	52,825	54,271									
Solyc10g045623	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *** A0A061FD65_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM); IPR025525 (PFA	0,000	0,019	0,000	0,000	0,000									
Solyc10g045630	plant/protein%2C putative (DUF3411) (AHRD V3.3 *** AT5G24690.1)		C:GO:0005739; C:G(	C:mitochondrion; C:chloroplast inner membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	25,830	26,221	42,636	41,559	43,217									
Solyc10g045640	Transmembrane emp24 domain-containing 10 (AHRD V3.3 *** A0A0B0Q0Q7_GOSAR)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of me			IPR009038 (PFAM); IPR015720 (PAN	32,198	27,509	55,883	44,236	46,034									
Solyc10g045650	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A1D1YY40_9ARAE)		C:GO:0000943	C:retrotransposon nucleocapsid			IPR039537 (PANTHER); PTHR11439:	0,019	0,021	0,000	0,025	0,000									
Solyc10g045720	Syntaxin-like protein (AHRD V3.3 --* D5K191_BAUPU)		F:GO:0000149; F:G(	F:SNARE binding; F:SNAP receptor activity; P:intracellular protein transport; P:vesicle fusion; C:endom				0,019	0,000	0,000	0,000	0,000									
Solyc10g045725	NADH-ubiquinone oxidoreductase chain 5 (AHRD V3.3 *-* NU5M_ARATH)		C:GO:0005743; F:G(	C:mitochondrial inne	EC:1.6.99.5; EC:1.6.	Acting on NADH or NADPH; NADH dehydrogenase; NADH:ub		0,000	0,000	0,000	0,025	0,000									
Solyc10g045775	HSP20-like chaperones superfamily protein (AHRD V3.3 --* AT4G02450.2)							0,080	0,019	0,000	0,000	0,000									
Solyc10g046770	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *-* B9S8D6_RICCO)		F:GO:0003824; P:G(	F:catalytic activity; P:trehalose biosynthetic process			IPR003337 (PFAM); PTHR10788 (PAN	2,567	2,888	1,716	2,127	1,904									
Solyc10g046860	RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 --* AT3G24255.1)							0,000	0,000	0,050	0,000	0,047									
Solyc10g046880	LOW QUALITY:WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)							0,271	0,424	0,047	0,050	0,071									
Solyc10g046930	FtsJ-like methyltransferase family protein (AHRD V3.3 *** AT4G25730.1)		P:GO:0001510; C:G(	P:RNA methylation; C:nucleus; P:rRNA processing; F:methyltrar			IPR024576 (PFAM); IPR012920 (PFA	148,159	133,428	105,805	96,236	101,124									
Solyc10g046970	Tubby-like F-box protein (AHRD V3.3 *** K4CZW2_SOLLC)		F:GO:0005515	F:protein binding			IPR000007 (PRINTS); IPR000007 (PF	34,101	45,211	38,907	42,522	41,691									
Solyc10g047000	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G80670.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR001680 (PF	48,652	47,758	66,143	63,499	61,819									
Solyc10g047030	LEXYL1 protein	xyl1	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS); IPR036881 (G3	1,755	1,734	16,967	25,796	9,614			-0,823	0,008				down	
Solyc10g047040	zinc finger protein	C3H58	F:GO:0046872	F:metal ion binding			G3DSA:4.10.1000_C3H	9,011	7,792	8,214	9,335	6,920									
Solyc10g047050	Dynamin family protein, putative, expressed (AHRD V3.3 *** Q2QWX6_ORYSJ)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS); G3DSA:3.40.5(	34,003	34,071	20,731	20,720	27,141									
Solyc10g047090	LOW QUALITY:50S ribosomal protein L2, chloroplastic (AHRD V3.3 *-* RK2_SOLBU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.50.140 (GENE3D); IPR0:	0,419	0,916	0,346	0,367	0,446									
Solyc10g047110	Peroxidase (AHRD V3.3 *** K4CZX5_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS); IPR000823 (PF	0,019	0,000	0,025	0,000	0,000									
Solyc10g047120	tRNA (Guanine(10)-N2)-methyltransferase (AHRD V3.3 *** A0A0B0N5L8_GOSAR)		F:GO:0008168	F:methyltransferase activity			IPR000241 (PFAM); G3DSA:3.40.50.1	17,367	18,099	26,383	27,208	25,748									
Solyc10g047130	Glycine-rich RNA-binding protein (AHRD V3.3 *** A0A0B0NTU5_GOSAR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			G3DSA:4.10.60.10 (GENE3D); IPR01:	95,078	94,909	75,061	59,606	66,076									
Solyc10g047140	Receptor-like kinase (AHRD V3.3 *** A0A0K9PIY0_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:signaling receptor binding; F:ATP bir			IPR032675 (G3DSA:3.80.10.GENE3D	27,988	38,428	30,431	27,166	30,484									
Solyc10g047150	LOW QUALITY:50S ribosomal L4 (AHRD V3.3 *-* A0A0B0Q1P8_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR023574 (G3DSA:3.40.1370.GENE:	0,220	0,057	0,194	0,410	0,328									
Solyc10g047200	LOW QUALITY:Lycopene beta/epsilon cyclase protein (AHRD V3.3 --* AT5G57030.1)							9,755	10,154	8,947	10,442	9,836									
Solyc10g047210	LOW QUALITY:hyccin (AHRD V3.3 *-* AT5G64090.1)		C:GO:0005886	C:plasma membrane			IPR018619 (PFAM); IPR018619 (PAN	14,665	17,521	15,667	16,233	15,099									
Solyc10g047220	Plant/MHJ24-14 protein (AHRD V3.3 *** I3SQK3_MEDTR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	35,550	34,174	53,212	49,823	47,040									
Solyc10g047240	annexin 9	AnnSl9	F:GO:0005509; F:G(	F:calcium ion binding; F:calcium-dependent phospholipid binding			IPR001464 (PRINTS); IPR009118 (PF	27,293	18,261	2,662	2,093	3,019									
Solyc10g047260	LOW QUALITY:magnesium transporter 7 (AHRD V3.3 --* AT5G09690.4)							3,038	2,635	1,292	1,715	1,827									
Solyc10g047270	Potassium transporter (AHRD V3.3 *** M1AY13_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM); IPR003855 (TIGF	28,918	26,148	36,043	39,440	35,685									
Solyc10g047290	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G34750.3)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM); IPR036457 (G3D	27,453	34,086	39,905	42,726	41,139									
Solyc10g047300	Translocon at the outer membrane of chloroplasts 64-V isoform 1 (AHRD V3.3 *** A0A061E2D6_THECC)		F:GO:0004040; F:G(	F:amidase activity;	EC:3.5.1.4	Amidase	IPR023631 (PFAM); IPR036928 (G3D	18,675	31,549	26,397	25,170	23,681	0,783	0,005					up		
Solyc10g047320	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072TW48_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR041118 (PFA	32,837	50,872	11,300	17,281	16,117	0,658	0,030	0,507	0,043	0,612	0,016	up	up	up
Solyc10g047330	LOW QUALITY:DNA topoisomerase, type IA, core (AHRD V3.3 --* AT4G31210.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	5,595	5,174	5,379	4,410	4,712									
Solyc10g047340	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G09430.1)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS); IPR000073 (PF	9,096	8,914	15,315	13,528	13,581									
Solyc10g047360	Polyadenylate-binding protein 2 (AHRD V3.3 *** W9QVE2_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM); IPR012677 (G3D	29,079	28,887	12,601	10,254	14,173									
Solyc10g047370	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y3G7_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	27,952	25,618	20,971	19,622	21,253									
Solyc10g047400	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001135 (PFAM); IPR038290 (G3D	0,059	0,083	0,025	0,174	0,189									
Solyc10g047410	Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_SOLLC)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR001135 (PFAM); IPR038290 (G3D	0,098	0,561	0,326	0,584	0,354									
Solyc10g047420	LOW QUALITY:NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 *-* NU4C_SOLTU)		F:GO:0008137; P:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR022997 (PTHR43507:PANTHER);	0,000	0,080	0,000	0,051	0,000									
Solyc10g047430	LOW QUALITY:Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* Q6SSH3_9SPER)		F:GO:0000287	F:magnesium ion binding			IPR036376 (G3DSA:3.20.20.GENE3D	0,061	0,000	0,000	0,075	0,071									
Solyc10g047470	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit H, chloroplastic (AHRD V3.3 *-* NDHH_TOBAC)		F:GO:0016651; F:G(	F:oxidoreductase activity, acting on NAD(P)H; F:quinone bindin			IPR001135 (PFAM); IPR038290 (G3D	0,000	0,000	0,050	0,000	0,069									
Solyc10g047500	transmembrane protein (AHRD V3.3 *** AT4G33600.1)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM); IPR007657 (PAN	0,536	0,191	0,000	0,000	0,000									
Solyc10g047530	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G64330.1)		F:GO:0005515; P:G(	F:protein binding; P:protein ubiquitination			IPR027356 (PFAM); G3DSA:3.30.710	0,000	0,019	0,000	0,000	0,000									
Solyc10g047540	Basic helix loop helix protein, putative (AHRD V3.3 *-* A0A072TTF3_MEDTR)						mobidb-lite (MOBIDB_LITE); IPR0402(	0,600	0,629	0,139	0,122	0,116									
Solyc10g047570	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G17150.1)	PG36	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM); IPR012334 (G3D	0,076	0,386	0,000	0,000	0,000									
Solyc10g047610	Arginine/serine-rich splicing factor, putative (AHRD V3.3 --* B9SGV2_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR035979 (SUPERFAMILY)	0,138	0,137	0,075	0,097	0,047									
Solyc10g047630	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (AHRD V3.3 *** AT5G12040		P:GO:0006807	P:nitrogen compound metabolic process			IPR003010 (PFAM); IPR036526 (G3D	52,535	48,494	71,995	69,948	68,324									
Solyc10g047640	GATA transcription factor, putative (AHRD V3.3 *** B9S9L8_RICCO)		F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; F:protein binding; P:i			IPR000679 (PFAM GATA	17,202	15,928	19,391	18,037	18,221									
Solyc10g047643	CHCH-like protein (AHRD V3.3 *** A0A103XM78_CYNCS)		C:GO:0005634; C:G(	C:nucleus; C:mitochondrion; P:mitochondrion organization			IPR010625 (PFAM); PTHR13523:SF9	0,116	0,402	0,190	0,486	0,213									
Solyc10g047670	HVA22-like protein (AHRD V3.3 *-* M0ZZ84_SOLTU)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding; C:integral component			PF12874 (PFAM); G3DSA:3.30.160.6(	29,362	28,726	23,039	24,758	24,217									
Solyc10g047680	Clade XVII lectin receptor kinase (AHRD V3.3 *** K4D030_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); G3DS	0,000	0,019	0,000	0,000	0,024									
Solyc10g047720	B3 domain protein (AHRD V3.3 -** AT5G26805.1)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus			PTHR36264 (PANTHER)	0,000	0,039	0,000	0,000	0,000									
Solyc10g047730	LOW QUALITY:receptor-like protein kinase 2 (AHRD V3.3 --* AT3G02130.2)						mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,046	0,000	0,023									
Solyc10g047778	LOW QUALITY:HAT family dimerisation domain containing protein, expressed (AHRD V3.3 *-* Q8S6T7_ORY		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); mobidb-lite (MOB	0,000	0,018	0,000	0,025	0,000									
Solyc10g047823	Ulp1 protease family protein (DUF1985) (AHRD V3.3 --* AT3G31910.1)						IPR015410 (PFAM); mobidb-lite (MOB	0,019	0,039	0,000	0,000	0,000									
Solyc10g047827	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G02340.2)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,023									
Solyc10g047890	LOW QUALITY:Ribonuclease H-like superfamily protein (AHRD V3.3 *** AT2G02650.1)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3I	0,038	0,062	0,000	0,000	0,000									
Solyc10g047900	S-acyltransferase (AHRD V3.3 --* W9SEE1_9ROSA)							2,359	2,259	1,171	0,785	1,129									
Solyc10g047930	Methionine sulfoxide reductase, putative (AHRD V3.3 *** B9RX37_RICCO)		P:GO:0006979; P:G(	P:response to oxida	EC:1.8.4.12	Peptide-methionine (.	G3DSA:2.170.150.20 (GENE3D); IPR(	31,167	47,182	40,328	41,498	54,038	0,625	0,010	0,420	0,012			up	up	
Solyc10g047950	Inorganic pyrophosphatase (AHRD V3.3 *** A0A124SF20_CYNCS)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.1	Inorganic diphosphat	IPR036649 (G3DSA:3.90.80.GENE3D	35,710	35,140	22,778	21,178	24,069									
Solyc10g047960	transmembrane protein (AHRD V3.3 *** AT5G65810.1)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.50.150 (GENE3D); PTHF	33,120	33,332	18,437	18,551	17,769									
Solyc10g048010	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2SPP5_GLYSO)		C:GO:0016021	C:integral component of membrane			G3DSA:3.10.580.10 (GENE3D); IPR0(	0,019	0,000	0,000	0,000	0,000									
Solyc10g048030	Major latex-like protein (AHRD V3.3 *** B5THI3_PANGI)		P:GO:0006952	P:defense response			IPR000916 (PFAM); IPR023393 (G3D	0,181	0,000	0,268	0,049	0,000									
Solyc10g048050	LOW QUALITY:Developmentally-regulated GTP-binding protein (AHRD V3.3 *-* A0A059Q004_9POAL)		P:GO:0002181; F:G(	P:cytoplasmic translation; F:GTP binding; C:cytoplasm			IPR012675 (G3DSA:3.10.20.GENE3D	0,075	0,079	0,072	0,072	0,094									
Solyc10g048055	Major latex-like protein (AHRD V3.3 *** B5THI3_PANGI)		P:GO:0006952	P:defense response			IPR000916 (PFAM); IPR023393 (G3D	0,040	0,019	0,000	0,025	0,000									
Solyc10g048060	myosin XI D (AHRD V3.3 --* AT2G33240.5)		C:GO:0005739	C:mitochondrion			PTHR37773 (PANTHER)	5,357	3,872	6,255	13,269	10,006					1,090	0,017			up
Solyc10g048065	Transport membrane protein (AHRD V3.3 *** A0A0C5ARU2_HYONI)		C:GO:0016021	C:integral component of membrane			IPR002033 (PFAM); IPR003319 (PFA	0,117	0,120	0,152	0,296	0,071									
Solyc10g048070	DUF1005 family protein (AHRD V3.3 *** G7J413_MEDTR)						IPR010410 (PFAM); IPR010410 (PAN	0,019	0,019	0,000	0,025	0,000									
Solyc10g048120	DUF1005 family protein (DUF1005) (AHRD V3.3 *** AT4G29310.1)						IPR010410 (PFAM); PTHR31317:SF3	0,571	0,493	0,022	0,022	0,047									
Solyc10g048140	Zinc finger protein 385D (AHRD V3.3 *** A0A0B2SEZ1_GLYSO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			PF12874 (PFAM); G3DSA:3.30.160.6(	0,000	0,019	0,000	0,000	0,000									
Solyc10g048150	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G30250.2)							0,038	0,059	0,000	0,000	0,000									
Solyc10g048155	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A151RL39_CAJCA)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D); IPR0'	0,000	0,000	0,000	0,025	0,000									
Solyc10g048190	Thymocyte nuclear protein 1 (AHRD V3.3 *** A0A0B2RF18_GLYSO)		C:GO:0005634	C:nucleus			G3DSA:3.10.590.10 (GENE3D); IPR0(	0,756	0,652	0,119	0,022	0,000									
Solyc10g049200	D-3-phosphoglycerate dehydrogenase 3, chloroplastic (AHRD V3.3 --* SERA3_ARATH)							0,021	0,000	0,000	0,000	0,000									
Solyc10g049210	Serine carboxypeptidase, putative (AHRD V3.3 *** B9S819_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); G3DSA:3.40.5(	34,059	29,833	23,540	18,721	28,148									
Solyc10g049215	Pyruvate, phosphate dikinase 1, chloroplastic (AHRD V3.3 --* PPDK1_MAIZE)						mobidb-lite (MOBIDB_LITE)	0,278	0,376	2,028	2,570	2,081									
Solyc10g049230	LOW QUALITY:Nbs-lrr resistance protein, putative (AHRD V3.3 --* A0A061FM42_THECC)		F:GO:0043531	F:ADP binding			IPR027417 (SUPERFAMILY)	0,000	0,079	1,394	1,823	1,532									
Solyc10g049260	ADP-ribosylation factor (AHRD V3.3 *-* ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PFAM); G3DSA:3.40.50.3	0,101	0,325	0,047	0,000	0,116									
Solyc10g049270	Serine carboxypeptidase, putative (AHRD V3.3 *** B9S819_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	0,784	0,414	0,147	0,488	0,310									
Solyc10g049280	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM); IPR029949 (PTH	0,000	0,043	0,000	0,000	0,000									
Solyc10g049300	Glycine-rich protein A3 (AHRD V3.3 --* GRP3_DAUCA)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,057	0,022	0,000	0,000									
Solyc10g049330	isopentenyltransferase 5 (AHRD V3.3 --* AT5G19040.3)		C:GO:0016021	C:integral component of membrane			PTHR33499 (PANTHER); PTHR33499	0,000	0,019	0,000	0,000	0,000									
Solyc10g049360	cyclin A3_6	CycA3_6	C:GO:0005634	C:nucleus			G3DSA:1.10.472.10 (GENE3D); IPR0(	21,778	19,738	19,667	24,094	22,004									
Solyc10g049370	Pectinesterase (AHRD V3.3 *** K4D094_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	1,151	1,558	0,000	0,000	0,000									
Solyc10g049420	TRAF-like superfamily protein (AHRD V3.3 --* AT5G52330.4)							0,497	0,347	0,368	0,507	0,496									
Solyc10g049430	Pectinesterase (AHRD V3.3 *** K4D0A0_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	0,513	0,519	0,087	0,022	0,000									
Solyc10g049440	Pectinesterase (AHRD V3.3 *** K4D0A1_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	0,103	0,037	0,000	0,000	0,000									
Solyc10g049450	Pectinesterase (AHRD V3.3 *** K4D0A2_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	0,613	0,452	0,071	0,215	0,023									
Solyc10g049470	Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM); PTHR33163:SF1:	0,341	0,198	0,172	0,170	0,071									
Solyc10g049477	LOW QUALITY:F-box domain-containing protein (AHRD V3.3 *-* A4UV34_SOLTU)						IPR006527 (PFAM); PTHR44355 (PAN	0,000	0,021	0,000	0,000	0,023									

Solyc10g049480	Abc transporter family protein (AHRD V3.3 *-* D7LIF8_ARALL)		F:GO:0003677	F:DNA binding		G3DSA:2.40.50.140 (GENE3D): IPR0	0,000	0,019	0,000	0,048	0,000									
Solyc10g049530	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** AT5G05800.5)					IPR024752 (PFAM): mobidb-lite (MOB	0,296	0,350	0,122	0,216	0,023									
Solyc10g049533	ATP-dependent helicase/deoxyribonuclease subunit B (AHRD V3.3 --* A0A0B0NKU1_GOSAR)						0,550	0,691	0,574	0,173	0,492									
Solyc10g049560	ARM repeat superfamily protein (AHRD V3.3 --* AT1G60190.1)						2,202	2,311	2,160	1,233	1,530									
Solyc10g049565	fanconi anemia group F protein (FANCF) (AHRD V3.3 --* AT5G44010.3)						0,000	0,000	0,000	0,025	0,000									
Solyc10g049570	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RFN9_RICCO)		F:GO:0005515	F:protein binding		IPR002885 (TIGRFAM): IPR011990 ((	10,435	10,469	9,523	9,284	9,551									
Solyc10g049580	Arabinogalactan protein (AHRD V3.3 --* Q9FUL8_NICAL)		F:GO:0005199	F:structural constituent of cell wall		mobidb-lite (MOBIDB_LITE): mobidb-lit	1,775	1,921	0,239	0,221	0,282									
Solyc10g049590	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_NYMAL)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP synthesis c		IPR038662 (G3DSA:1.20.20.GENE3D	0,119	0,261	0,437	0,299	0,141									
Solyc10g049600	Progesterone 5-beta-reductase (AHRD V3.3 *** D6NIX2_ATRBE)		F:GO:0003854: F:G(	F:3-beta-hydroxy-de EC:1.1.1.145; EC:1.:	3-beta-hydroxy-Delta	G3DSA:3.40.50.720 (GENE3D): PTHF	2,809	3,938	0,150	0,240	0,351									
Solyc10g049610	F-box/RNI-like superfamily protein (AHRD V3.3 --* AT4G22280.1)						0,000	0,019	0,000	0,000	0,023									
Solyc10g049620	Progesterone 5-beta-reductase (AHRD V3.3 *** D6NIX2_ATRBE)		F:GO:0003824: F:G(	F:catalytic activity; F:coenzyme binding		IPR001509 (PFAM): G3DSA:3.40.50.7	93,754	87,695	110,787	106,321	108,386									
Solyc10g049630	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G33920.1)		F:GO:0004722: P:G(	F:protein serine/thre EC:3.1.3.16	Protein-serine/threon	IPR001932 (PFAM): IPR036457 (G3D	117,919	94,022	68,953	144,074	118,008			0,772	0,004	1,064	0,000		up	up
Solyc10g049640	Amino acid permease family protein (AHRD V3.3 *** AT3G19553.1)		C:GO:0016020: F:G(	C:membrane; F:transmembrane transporter activity; P:transmem		G3DSA:1.20.1740.10 (GENE3D): IPR(	1,677	1,427	0,736	0,712	1,219									
Solyc10g049650	Histone deacetylase 6 (AHRD V3.3 *** W9SEY2_9ROSA)		F:GO:0008270	F:zinc ion binding		IPR013083 (G3DSA:3.30.40.GENE3D	3,866	4,500	4,822	5,808	4,862									
Solyc10g049660	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** B9HMY5_POPTR)		F:GO:0005515: P:G(	F:protein binding; P:positive gravitropism		IPR027356 (PFAM): IPR000210 (PFA	0,042	0,096	0,000	0,000	0,000									
Solyc10g049710	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4D0C8_SOLLC)		F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): G3DSA:3.90.22	106,897	162,331	358,278	360,118	408,219	0,629	0,017					up		
Solyc10g049750	Helicase protein with RING/U-box domain-containing protein (AHRD V3.3 *** AT1G05120.1)		F:GO:0005524	F:ATP binding		IPR013083 (G3DSA:3.30.40.GENE3D	1,441	1,055	0,165	0,098	0,163									
Solyc10g049760	Signal anchor, putative (AHRD V3.3 *-* A0A072UJ16_MEDTR)		C:GO:0009507	C:chloroplast			0,099	0,147	0,025	0,047	0,185									
Solyc10g049770	LOW QUALITY:Basic helix-loop-helix transcription factor (AHRD V3.3 *-* A0A0H3YC47_SALMI)		F:GO:0001228: C:G(	F:DNA-binding transcription activator activity, RNA polymerase		mobidb-lite (MOBIDB_LITE): PTHR162	0,021	0,039	0,000	0,000	0,000									
Solyc10g049790	DUF936 family protein (AHRD V3.3 *-* A0A072VCI3_MEDTR)					IPR010341 (PFAM): IPR010341 (PAN	4,925	4,112	4,183	4,299	3,912									
Solyc10g049800	DUF936 family protein (AHRD V3.3 *-* A0A072VCI3_MEDTR)					IPR010341 (PFAM): mobidb-lite (MOB	5,396	3,527	3,948	3,938	3,939									
Solyc10g049820	B3 domain-containing protein family (AHRD V3.3 --* A0A151QXP1_CAJCA)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,278	0,280	0,169	0,117	0,165									
Solyc10g049840	LOW QUALITY:DnaJ-like protein (AHRD V3.3 *-* A0A0B2QWH0_GLYSO)					IPR024593 (PFAM): PTHR44137:SF5	0,019	0,060	0,000	0,000	0,166									
Solyc10g049850	TIP41-like family protein (AHRD V3.3 *** AT4G34270.1)	TIP4.1				IPR007303 (PFAM): PTHR21021 (PAN	34,469	35,121	47,803	41,163	44,604									
Solyc10g049860	LOW QUALITY:HVA22 homologue B (AHRD V3.3 --* AT5G62490.1)						0,000	0,018	0,025	0,050	0,023									
Solyc10g049870	Zinc finger protein, putative (AHRD V3.3 *** B9SNA3_RICCO)		F:GO:0003676	F:nucleic acid binding		G3DSA:3.30.160.6 C2H2	2,257	1,437	0,411	0,505	0,467									
Solyc10g049890	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** K4D0E5_SOLLC)		F:GO:0004617: P:G(	F:phosphoglycerate EC:1.1.1.95	Phosphoglycerate de	G3DSA:3.30.70.260 (GENE3D): G3DS	35,515	27,870	16,154	11,071	10,278			-0,656	0,004	-0,542	0,034		down	down
Solyc10g049900	LOW QUALITY:diiron containing four-helix bundle family ferritin protein, putative (Protein of unknown function DUF455) (AHRD V3.3 *-* AT1G06240.1)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc10g049910	Kynurenine formamidase (AHRD V3.3 *-* A0A0B0MST0_GOSAR)		F:GO:0004061: P:G(	F:arylformamidase : EC:3.5.1.9	Arylformamidase	IPR037175 (G3DSA:3.50.30.GENE3D	0,019	0,000	0,025	0,000	0,000									
Solyc10g049920	Aldose 1-epimerase (AHRD V3.3 --* K4BBT5_SOLLC)						8,758	7,287	9,471	9,314	8,388									
Solyc10g049940	LOW QUALITY:Myb/SANT-like DNA-binding domain protein (AHRD V3.3 --* AT5G05800.5)					IPR035513 (G3DSA:1.20.140.GENE3	0,883	0,961	0,000	0,000	0,000									
Solyc10g049970	Kynurenine formamidase (AHRD V3.3 *** A0A151RRB2_CAJCA)		F:GO:0004061: P:G(	F:arylformamidase : EC:3.5.1.9	Arylformamidase	IPR037175 (G3DSA:3.50.30.GENE3D	28,202	37,300	32,382	31,960	38,631									
Solyc10g049980	LOW QUALITY:serine carboxypeptidase-like 16 (AHRD V3.3 --* AT3G12220.3)						0,275	0,291	0,247	0,314	0,235									
Solyc10g049996	60S ribosomal protein L3 (AHRD V3.3 --* W9S5Y9_9ROSA)		F:GO:0003690: P:G(	F:double-stranded DNA binding; P:regulation of transcription, DNA-templated			0,099	0,000	0,759	0,337	0,071									
Solyc10g050050	LOW QUALITY:Nucleotide binding site-leucine rich repeat protein (AHRD V3.3 *-* A0A0H5AGV4_SOLPI)		F:GO:0043531	F:ADP binding		IPR002182 (PFAM): PTHR44061:SF1	0,000	0,019	0,000	0,050	0,000									
Solyc10g050060	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT4G34150.1)					IPR000008 (PFAM): IPR035892 (G3D	88,027	102,690	53,407	84,746	67,628					0,668	0,000			up
Solyc10g050063	Transcription complex (AHRD V3.3 --* A0A059Q1V3_9POAL)						0,000	0,238	0,000	0,051	0,000									
Solyc10g050087	cytochrome P450, family 705, subfamily A, polypeptide 30 (AHRD V3.3 --* AT3G20940.1)						1,082	0,563	0,072	0,000	0,024									
Solyc10g050095	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G36290.2)		F:GO:0000166: F:G(	F:nucleotide binding; F:ATP binding; C:membrane; C:integral component of membrane; F:ATPase activit			0,000	0,021	0,000	0,000	0,000									
Solyc10g050110	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PL83_ZOSMR)					IPR032675 (G3DSA:3.80.10.GENE3D	44,345	21,075	1,723	0,973	1,133									
Solyc10g050160	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_ZINVI)		F:GO:0008171	F:O-methyltransferase activity		G3DSA:3.40.50.150 (GENE3D): IPR0	7,612	10,344	3,403	3,007	3,375									
Solyc10g050170	RING/U-box superfamily protein (AHRD V3.3 *** AT2G15530.7)		F:GO:0016874	F:ligase activity		IPR001841 (PFAM): IPR013083 (G3D	74,386	62,128	107,222	108,569	98,732									
Solyc10g050180	LOW QUALITY:L-galactono-1,4-lactone dehydrogenase 1, mitochondrial (AHRD V3.3 --* GLDH1_ORYSJ)					mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,000	0,023									
Solyc10g050200	LOW QUALITY:transmembrane protein, putative (DUF679 domain membrane protein 2) (AHRD V3.3 *** AT3		P:GO:0010256: C:G(	P:endomembrane system organization; C:integral component of		IPR007770 (PFAM): IPR007770 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc10g050210	Abscisic acid responsive element-binding factor 1 family protein (AHRD V3.3 *** U5GLH1_POPTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans		G3DSA:1.20.5.17(bZIP	0,000	0,021	0,000	0,025	0,000									
Solyc10g050220	cold regulated protein 27 (AHRD V3.3 *** AT5G42900.2)					PTHR33676 (PANTHER): PTHR33676	0,670	0,737	0,810	0,556	0,680									
Solyc10g050230	Alpha 1,3 fucosyltransferase (AHRD V3.3 *** Q5DTC9_MEDSA)		P:GO:0006486: F:G(	P:protein glycosylation; F:fucosyltransferase activity; C:membra		IPR001503 (PFAM): IPR038577 (G3D	15,339	17,139	25,354	24,611	24,298									
Solyc10g050290	LOW QUALITY:PIF1-like helicase (AHRD V3.3 *** A0A072V1R7_MEDTR)		P:GO:0000723: F:G(	P:telomere mainten EC:3.6.1.15	Nucleoside-triphosph	PTHR45355 (PANTHER): IPR027417 (	0,078	0,000	0,025	0,000	0,023									
Solyc10g050307	Triose phosphate/phosphate translocator, chloroplastic (AHRD V3.3 --* TPT_SPIOL)						0,593	0,374	0,147	0,434	0,279									
Solyc10g050310	LOW QUALITY:SPX domain-containing family protein (AHRD V3.3 *-* B9GW54_POPTR)		C:GO:0016020	C:membrane		PTHR23510:SF21 (PANTHER): PTHR:	0,332	0,173	0,072	0,283	0,071									
Solyc10g050320	LOW QUALITY:SPX domain-containing protein (AHRD V3.3 *-* D7MDY2_ARALL)		C:GO:0016020	C:membrane		PTHR23510:SF21 (PANTHER): PTHR:	0,195	0,117	0,047	0,196	0,024									
Solyc10g050325	Kinesin-like calmodulin-binding protein like (AHRD V3.3 *-* A0A0B2PXL0_GLYSO)					IPR004252 (PFAM): PTHR33499:SF1	6,374	7,052	4,358	7,720	5,146									
Solyc10g050370	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A118JUD2_CYNCS)					G3DSA:2.40.50.140 (GENE3D): G3D(	0,000	0,000	0,000	0,025	0,000									
Solyc10g050420	two-component response regulator (AHRD V3.3 *-* AT3G62670.1)		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.6(ARR-B	0,000	0,019	0,000	0,000	0,000									
Solyc10g050440	transmembrane protein (Protein of unknown function DUF2359, transmembrane) (AHRD V3.3 --* AT1G23170.1)					mobidb-lite (MOBIDB_LITE): mobidb-lit	43,791	67,896	11,665	14,554	26,245	0,660	0,024	1,164	0,000			up	up	
Solyc10g050450	CSL zinc finger protein, putative (AHRD V3.3 *** G7JEX8_MEDTR)		P:GO:0002098: C:G(	P:tRNA wobble uridine modification; C:nucleus; C:cytosol; C:int(		PTHR21454 (PANTHER): PTHR21454	3,562	4,060	4,030	4,385	3,944									
Solyc10g050465	zinc ion binding/nucleic acid binding/hydrolase (AHRD V3.3 --* AT1G48360.4)						0,000	0,000	0,000	0,050	0,000									
Solyc10g050510	LOW QUALITY:transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)					mobidb-lite (MOBIDB_LITE): mobidb-lit	0,038	0,036	0,000	0,025	0,023									
Solyc10g050540	Cleavage stimulation factor subunit 3 (AHRD V3.3 *** W9R731_9ROSA)		F:GO:0005515: C:G(	F:protein binding; C:nucleus; P:mRNA processing		PF13428 (PFAM): IPR008847 (PFAM)	35,110	34,329	41,095	40,319	39,027									
Solyc10g050550	La-related protein 7 (AHRD V3.3 *** W9S6D8_9ROSA)		F:GO:0003723: C:G(	F:RNA binding; C:nucleus; P:RNA processing; C:integral compo		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,056	0,018	0,000	0,000	0,000									
Solyc10g050560	MADS-box transcription factor family protein (AHRD V3.3 --* AT1G65330.1)						0,000	0,000	0,000	0,000	0,023									
Solyc10g050570	LOW QUALITY:hydrolases, acting on ester bond (AHRD V3.3 --* AT3G27325.3)						0,082	0,080	0,000	0,022	0,024									
Solyc10g050670	LOW QUALITY:LOB domain-containing protein 7 (AHRD V3.3 --* AT1G72980.1)						5,643	6,317	1,054	0,900	1,296									
Solyc10g050690	Plastocyanin-like domain protein (AHRD V3.3 *** G7JMH1_MEDTR)		F:GO:0009055	F:electron transfer activity		IPR008972 (G3DSA:2.60.40.GENE3D	0,019	0,000	0,000	0,000	0,000									
Solyc10g050735	Sodium channel modifier 1 (AHRD V3.3 *** A0A0B0PQ63_GOSAR)		P:GO:0008380	P:RNA splicing		IPR031622 (PFAM): IPR031625 (PFA	6,529	5,561	4,681	5,421	4,943									
Solyc10g050750	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT5G17680.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:ADP bindin		IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,019	0,000	0,000	0,000									
Solyc10g050753	LRR and NB-ARC domains-containing disease resistance protein, putative (AHRD V3.3 *-* A0A061EIS9_TH		C:GO:0016020: F:G(	C:membrane; F:ADP binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,018	0,000	0,000	0,000									
Solyc10g050757	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)		F:GO:0016787	F:hydrolase activity		IPR004963 (PFAM): IPR004963 (PAN	0,019	0,000	0,022	0,000	0,023									
Solyc10g050760	LOW QUALITY:Non-specific lipid-transfer protein (AHRD V3.3 --* A0A0N9E6M0_PLAAC)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,000	0,025	0,000									
Solyc10g050770	LOW QUALITY:Mitogen activated protein kinase kinase kinase-like protein (AHRD V3.3 --* AT3G58640.2)						0,063	0,062	0,172	0,070	0,095									
Solyc10g050840	Dipeptidyl peptidase family member 6 (AHRD V3.3 *** A0A151SBS0_CAJCA)		P:GO:0006508: F:G(	P:proteolysis; F:serine-type peptidase activity		IPR029058 (G3DSA:3.40.50.GENE3D	87,429	81,734	138,522	129,107	132,915									
Solyc10g050850	Galactose-1-phosphate uridylyltransferase (AHRD V3.3 *** A0A061F9R4_THECC)		F:GO:0008108: F:G(	F:UDP-glucose:hex EC:2.7.7.12	UDP-glucose--hexos	IPR005849 (PFAM): IPR036265 (G3D	12,887	10,050	4,473	2,847	4,940									
Solyc10g050860	DNA-binding protein AY506544		F:GO:0003676	F:nucleic acid binding		IPR000504 (PFAM): IPR012677 (G3D	232,867	193,812	130,166	114,234	127,416									
Solyc10g050870	Sulfotransferase (AHRD V3.3 *** M1CFY4_SOLTU)		F:GO:0008146: C:G(	F:sulfotransferase activity; C:integral component of membrane		G3DSA:3.40.50.300 (GENE3D): PTHF	7,876	6,954	10,683	12,405	10,722									
Solyc10g050880	Alpha/beta-Hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061E1M8_THECC)		F:GO:0016787	F:hydrolase activity		IPR013094 (PFAM): IPR029058 (G3D	0,019	0,125	0,320	0,464	1,105									
Solyc10g050890	nitrite reductase 2	nii2	F:GO:0016491: F:G(	F:oxidoreductase activity; F:heme binding; F:iron-sulfur cluster l		IPR006066 (PRINTS): IPR006067 (PF	64,166	45,593	68,627	77,025	55,288									
Solyc10g050905	Long chain acyl-CoA synthetase 4 (AHRD V3.3 --* LACS4_ARATH)					mobidb-lite (MOBIDB_LITE): mobidb-lit	1,626	1,303	1,561	1,706	1,436									
Solyc10g050910	LOW QUALITY:(Z)-3-hexen-1-ol acetyltransferase (AHRD V3.3 --* CHAT_ARATH)						0,701	0,455	0,550	0,688	0,493									
Solyc10g050920	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT3G22150.2)					mobidb-lite (MOBIDB_LITE)	3,417	4,255	1,024	1,414	1,877									
Solyc10g050960	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9R7J5_9ROSA)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of trans		IPR017392 (PIRSF): IPR036955 (G3D	0,215	0,100	0,169	0,337	0,210									
Solyc10g050970	Ethylene Response Factor D.4	ERF_D_4	F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec		IPR001471 (PRIN ERF	6,457	4,249	2,976	6,851	3,542					1,199	0,005			up
Solyc10g050980	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 (AHRD V3.3 -** A0A1D1XPR6_9ARAE)					PTHR38222 (PANTHER)	0,358	0,241	0,671	0,738	0,854									
Solyc10g050990	Pyruvate kinase (AHRD V3.3 --* A9TZX1_PHYPA)					PTHR38222 (PANTHER)	3,639	3,067	4,952	6,937	7,603									
Solyc10g050997	Mitochondrial import receptor subunit TOM6-like protein (AHRD V3.3 *-* A0A0B0NUA5_GOSAR)		C:GO:0005742	C:mitochondrial outer membrane translocase complex		IPR034554 (PANTHER)	0,779	0,715	0,000	0,000	0,000									
Solyc10g051010	Cytochrome P450 (AHRD V3.3 *-* A9ZT56_COPJA)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR002401 (PRINTS): IPR001128 (PF	1,453	1,488	0,891	1,146	0,916									
Solyc10g051020	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)		F:GO:0005506: F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do		IPR002401 (PRINTS): IPR001128 (PF	1,121	4,082	3,421	5,860	4,605	1,878	0,047			0,778	0,027	up		up
Solyc10g051030	electron transporter%2C putative (Protein of unknown function%2C DUF547) (AHRD V3.3 *** AT5G66600.9)					IPR006869 (PFAM): IPR025757 (PFA	1,636	1,670	0,999	0,830	0,948									
Solyc10g051050	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding		PR00364 (PRINTS): G3DSA:3.40.50.3	1,794	2,341	0,449	0,814	0,585									
Solyc10g051070	LOW QUALITY:NAC domain-containing protein (AHRD V3.3 --* A0A060A1G1_BOENI)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter		mobidb-lite (MOBIDB_LITE)	0,607	2,253	0,318	0,318	0,280	1,910	0,002					up		
Solyc10g051080	Low temperature and salt responsive protein family (AHRD V3.3 -** AT1G57550.1)						0,784	1,191	0,287	0,740	0,470									
Solyc10g051090	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151R878_CAJCA)					IPR019557 (PFAM): PTHR44194 (PAN	0,019	0,000	0,000	0,000	0,000									
Solyc10g051095	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G18890.1)		C:GO:0009941: C:G(	C:chloroplast envelope; C:chloroplast thylakoid membrane prote		G3DSA:3.40.50.720 (GENE3D): IPR0	36,933	64,357	17,903	22,808	38,849	0,829	0,003	1,115	0,000			up	up	
Solyc10g051120	Mitochondrial pyruvate carrier (AHRD V3.3 *-* M1AEY6_SOLTU)		C:GO:0005743: P:G(	C:mitochondrial inner membrane; P:mitochondrial pyruvate trans		IPR005336 (PFAM): PTHR14154:SF1	2,948	2,353	31,710	34,672	26,429									
Solyc10g051130	Protein DETOXIFICATION (AHRD V3.3 *** K4D0R6_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpo		IPR002528 (PFAM): IPR002528 (TIGF	0,082	0,120	0,579	0,736	0,494									
Solyc10g051135	Protein DETOXIFICATION (AHRD V3.3 *-* K4D0R6_SOLLC)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpo		PTHR11206:SF181 (PANTHER): PTHI	0,000	0,000	0,022	0,097	0,048									
Solyc10g051140	Enhanced downy mildew 2, putative isoform 1 (AHRD V3.3 *** A0A061DLT4_THECC)		C:GO:0016021	C:integral component of membrane		mobidb-lite (MOBIDB_LITE): mobidb-lit	1,231	1,488	0,255	0,485	0,663									
Solyc10g051150	DNA (Cytosine-5)-methyltransferase 1, replication foci domain-containing protein (AHRD V3.3 *-* A0A124SE69_CYNCS)					IPR022702 (PFAM): PTHR22884:SF4	0,497	0,371	0,025	0,199	0,094									
Solyc10g051200	cytochrome c biogenesis protein family (AHRD V3.3 *** AT1G49380.1)		C:GO:0016021	C:integral component of membrane		IPR007816 (PFAM): mobidb-lite (MOB	26,836	28,667	58,302	56,030	65,808									
Solyc10g051220	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		C:GO:0016021: P:G(	C:integral component of membrane; P:oxidation-reduction proce		IPR032675 (G3DSA:3.80.10.GENE3D	0,758	0,537	0,690	0,586	0,992									
Solyc10g051225	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 --* AT4G20270.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane		IPR032675 (G3DSA:3.80.10.GENE3D	0,140	0,890	0,065	0,022	0,024									
Solyc10g051230	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT4G26540.1)		C:GO:0016020	C:membrane			0,042	0,164	0,000	0,022	0,000									
Solyc10g051240	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 --* AT4G08850.2)		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	0,143	0,389	0,000	0,075	0,024									
Solyc10g051250	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		C:GO:0016021: F:G(	C:integral component of membrane; F:kinase activity; P:phosph		IPR032675 (G3DSA:3.80.10.GENE3D	0,063	0,064	0,000	0,000	0,000									
Solyc10g051253	Cf-2.1 (AHRD V3.3 *-* Q41397_SOLPI)		C:GO:0016021: F:G(	C:integral component of membrane; F:kinase activity; P:phosphorylation			0,182	0,244	0,000	0,000	0,000									
Solyc10g051270	RING/U-box superfamily protein (AHRD V3.3 *** AT2G23780.3)		P:GO:0006511: C:G(	P:ubiquitin-dependent protein catabolic process; C:integral com		IPR013083 (G3DSA:3.30.40.GENE3D	16,865	18,513	13,419	11,012	11,467									
Solyc10g051300	HVA22-like protein (AHRD V3.3 *** K4D0T2_SOLLC)		C:GO:0016020	C:membrane		IPR004345 (PFAM): IPR004345 (PAN	11,536	10,722	16,805	16,922	15,784									
Solyc10g051310	clp-like energy-dependent protease	TOMCLPP	F:GO:0004252: P:G(	F:serine-type endo(EC:3.4.21	Acting on peptide bor	IPR001907 (PRINTS): IPR023562 (PF	40,277	50,681	93,055	89,051	98,071									
Solyc10g051340	Adenylyl cyclase-associated protein (AHRD V3.3 *** K4D0T6_SOLLC)		P:GO:0000902: F:G(	P:cell morphogenesis; F:actin binding; P:cytoskeleton organizati		IPR016098 (G3DSA:2.160.20.GENE3	126,926	140,569	135,607	129,569	128,271									
Solyc10g051350	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 *** NDHI_AETGR)		C:GO:0016020: F:G(	C:membrane; F:oxidoreductase activity, acting on NAD(P)H; F:		IPR017896 (PFAM): IPR010226 (TIGF	44,796	47,883	37,740	27,094	34,240					-0,475	0,010			down
Solyc10g051380	Glycine-rich RNA-binding protein (AHRD V3.3 *** GRP1_DAUCA)		F:GO:0003676	F:nucleic acid binding		IPR012677 (G3DSA:3.30.70.GENE3D	27,520	26,261	15,923	18,924	22,518			0,498	0,015				up	
Solyc10g051390	RNA-binding glycine-rich protein (AHRD V3.3 *** D6PZY6_TOBAC)		F:GO:0003676	F:nucleic acid binding		IPR000504 (PFAM): IPR012677 (G3D	181,912	281,615	260,542	214,691	220,653	0,658	0,030					up		
Solyc10g052470	Myb family transcription factor family protein (AHRD V3.3 *** B9H0R6_POPTR)		F:GO:0003677	F:DNA binding		G3DSA:1.10.10.6(MYB_related	0,000	0,000	0,025	0,000	0,000									
Solyc10g052480	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G02340.2)		F:GO:0008270: F:G(	F:zinc ion binding; F:ligase activity; F:metal ion binding		IPR001841 (PFAM): IPR013083 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc10g052490	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU)		C:GO:0005737: F:G(	C:cytoplasm; F:oxidoreductase activity; P:oxidation-reduction p		G3DSA:3.40.50.720 (GENE3D): IPR(	7,647	5,893	50,982	74,779	48,746					0,554	0,008			up
Solyc10g052500	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU)		C:GO:0005737: F:G(	C:cytoplasm; F:oxidoreductase activity; P:oxidation-reduction p		G3DSA:3.40.50.720 (GENE3D): IPR(	0,155	0,080	0,075	0,222	0,046									
Solyc10g052510	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU)		C:GO:0005737: F:G(	C:cytoplasm; F:oxidoreductase activity; P:oxidation-reduction p		IPR008030 (PFAM): G3DSA:3.90.25.1	5,623	4,247	10,192	11,006	11,182									
Solyc10g052520	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G61050.2		P:GO:0006355	P:regulation of transcription, DNA-templated		IPR035892 (G3DSA:2.60.40.GENE3D	0,632	0,313	0,525	0,384	0,472									
Solyc10g052540	Small auxin up-regulated RNA73	SAUR73	P:GO:0009733	P:response to auxin		IPR003676 (PFAM): PTHR31929:SF1	0,000	0,019	0,000	0,000	0,000									
Solyc10g052545	Auxin-responsive family protein (AHRD V3.3 *-* B9HRD2_POPTR)		P:GO:0009733	P:response to auxin		PTHR31929:SF14 (PANTHER): PTHR:	0,000	0,000	0,000	0,025	0,000									
Solyc10g052550	Small auxin up-regulated RNA74	SAUR74	P:GO:0009733	P:response to auxin		IPR003676 (PFAM): PTHR31175 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc10g052560	Small auxin up-regulated RNA75	SAUR75	P:GO:0009733	P:response to auxin		IPR003676 (PFAM): PTHR31175 (PAN	0,038	0,000	0,025	0,779	0,141									
Solyc10g052580	Small auxin up-regulated RNA76	SAUR76	P:GO:0009733	P:response to auxin		IPR003676 (PFAM): PTHR31929:SF1	0,038	0,094	0,000	0,000	0,000									
Solyc10g052600	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity		G3DSA:3.40.50.150 (GENE3D): IPR0	0,118	0,352	0,025	0,000	0,117									
Solyc10g052605	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2QRD1_ORYSJ)		F:GO:0046983	F:protein dimerization activity		IPR008906 (PFAM): PTHR23272:SF5	0,000	0,043	0,000	0,000	0,024									
Solyc10g052643	ABC-2 and Plant PDR ABC-type transporter family protein (AHRD V3.3 --* AT4G15236.1)						0,000	0,019	0,000	0,094	0,000									
Solyc10g052650	F-box protein (AHRD V3.3 *-* A0A0B2RZB4_GLYSO)		P:GO:0010099	P:regulation of photomorphogenesis		PTHR36062:SF1 (PANTHER): IPR037	3,956	9,975	0,650	1,188	2,348	1,358	0,000	1,833	0,001			up	up	
Solyc10g052660	ribosomal protein S25		C:GO:0005840	C:ribosome		G3DSA:1.10.10.2780 (GENE3D): IPR(	112,383	126,532	125,961	114,029	113,526									
Solyc10g052710	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9HMA7_POPTR)		F:GO:0005515	F:protein binding		G3DSA:1.20.1280.50 (GENE3D): IPR(	0,077	0,041	0,000	0,000	0,000									
Solyc10g052740	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_POPAL)		C:GO:0009522: P:G(	C:photosystem I; P:photosynthesis; C:integral component of me		IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,126	0,175	0,470	0,262									
Solyc10g052745	Sesquiterpene synthase (AHRD V3.3 *-* G8H5N0_SOLHA)		F:GO:0000287: F:G(	F:magnesium ion binding; F:terpene synthase activity		IPR005630 (PFAM): IPR008949 (G3D	2,862	2,369	3,105	2,479	2,537									
Solyc10g052790	LOW QUALITY:ATP synthase subunit a, chloroplastic (AHRD V3.3 *-* ATPI_PANGI)		C:GO:0005886: C:G(	C:plasma membran EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:1.10.510.10 (GENE3D): PTHF	0,076	0,085	0,149	0,072	0,187									
Solyc10g052795	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 *-* AT4G00960.1)		F:GO:0000166: F:G(	F:nucleotide binding; F:protein kinase activity; C:membrane; P:(		G3DSA:3.30.200.20 (GENE3D): PTHF	0,000	0,000	0,000	0,022	0,000									
Solyc10g052810	LOW QUALITY:NAC domain protein 13 (AHRD V3.3 --* AT1G32870.2)					PTHR33499 (PANTHER): PTHR33499	0,000	0,062	0,000	0,050	0,024									
Solyc10g052815	Seven transmembrane MLO family protein (AHRD V3.3 --* AT1G61560.3)						0,000	0,019	0,000	0,000	0,023									
Solyc10g052840	LOW QUALITY:Transposon protein, putative, CACTA, En/Spm sub-class (AHRD V3.3 *-* Q7G3C6_ORYSJ)					PTHR33499:SF7 (PANTHER): PTHR3:	0,000	0,018	0,000	0,000	0,000									
Solyc10g052869	Alpha N-terminal protein methyltransferase 1 (AHRD V3.3 --* NTM1_ORYSI)		F:GO:0005524	F:ATP binding			0,021	0,248	0,076	0,196	0,234									
Solyc10g052870	LOW QUALITY:Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 --* AT1G58400.3)					PTHR33499 (PANTHER): PTHR33499	0,037	0,000	0,000	0,000	0,000									
Solyc10g052880	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** A0A061DFG6		F:GO:0005515	F:protein binding		IPR032675 (G3DSA:3.80.10.GENE3D	14,967	30,964	8,215	11,235	17,535	1,075	0,005	1,090	0,002			up	up	
Solyc10g053880	disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G46260.1)						0,329	0,218	0,244	0,297	0,257									
Solyc10g053910	B-cell receptor-associated 31-like protein (AHRD V3.3 *** AT5G42570.1)		C:GO:0005783: P:G(	C:endoplasmic reticulum; P:intracellular protein transport; C:inte		mobidb-lite (MOBIDB_LITE): mobidb-lit	0,227	0,154	0,047	0,000	0,023									
Solyc10g053970	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT2G21520.1)		C:GO:0016021	C:integral component of membrane		PR00180 (PRINTS): IPR011074 (PFA	62,651	74,648	51,982	48,936	52,332									

Solyc10g053980	DHHC-type zinc finger family protein (AHRD V3.3 --* AT5G41060.4)							0,038	0,021	0,101	0,070	0,047									
Solyc10g054000	LOW QUALITY:ATP synthase subunit a (AHRD V3.3 *-* ATP6_TOBAC)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP synthesis c			IPR000568 (PFAM): PTHR11410 (PAI	0,019	0,000	0,000	0,000	0,000									
Solyc10g054010	LOW QUALITY:BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (PFAM): bZIP	8,615	9,644	2,578	2,318	2,407									
Solyc10g054030	RING/U-box superfamily protein (AHRD V3.3 *** AT4G39140.5)						IPR013083 (G3DSA:3.30.40.GENE3D	9,631	14,431	21,523	23,505	22,788									
Solyc10g054040	26S protease regulatory subunit (AHRD V3.3 *** A0A0K9PSD5_ZOSMR)		F:GO:0005524: C:G(	F:ATP binding; C:cytoplasm; F:hydrolase activity; P:protein cata			IPR003959 (PFAM): G3DSA:3.40.50.3	0,238	0,217	0,218	0,947	0,426									
Solyc10g054060	Ribosomal protein S21 family protein (AHRD V3.3 *** AT3G26360.2)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001911 (PFAM): PTHR37228 (PAI	12,669	13,401	23,625	22,768	21,476									
Solyc10g054070	Lateral root primordium protein-related (AHRD V3.3 *** A0A061E6J8_THECC),Pfam:PF05142		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; P:positive regulation of transcription,			IPR006511 (TIGR SRS	0,000	0,018	0,000	0,000	0,023									
Solyc10g054080	Kinesin-related protein (AHRD V3.3 *** D3YBF5_TRIRP)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	49,395	41,884	2,432	1,198	2,276									
Solyc10g054100	Protein DETOXIFICATION (AHRD V3.3 *** M0ZV31_SOLTU)		P:GO:0006855: F:G(	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	1,721	1,904	2,048	1,908	2,319									
Solyc10g054130	Squalene synthase (AHRD V3.3 *** FDFT_NICBE)		F:GO:0004310: P:G(	F:farnesyl-diphosph	EC:2.5.1.29; EC:2.5.	Geranylgeranyl diphc	IPR008949 (G3DSA:1.10.600.GENE3I	0,000	0,041	0,000	0,000	0,000									
Solyc10g054170	Nucleic acid-binding, OB-fold (AHRD V3.3 *-* A0A103XIY6_CYNCS)						G3DSA:2.40.50.140 (GENE3D): mobic	0,019	0,000	0,000	0,000	0,000									
Solyc10g054200	LOW QUALITY:Bifunctional levopimaradiene synthase, chloroplastic (AHRD V3.3 --* TPSD1_PICAB)						mobidb-lite (MOBIDB_LITE)	0,375	0,548	0,223	0,000	0,139									
Solyc10g054270	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103XN23_CYNCS)						IPR013955 (PFAM): G3DSA:2.40.50.1	0,076	0,134	0,000	0,466	0,140									
Solyc10g054272	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JVF5_MEDTR),Pfam:PF00702		F:GO:0016787	F:hydrolase activity			IPR023214 (G3DSA:3.40.50.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc10g054274	LOW QUALITY:Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *-* AT2G24960.2)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR024752 (PFAM): mobidb-lite (MOB	0,000	0,018	0,022	0,000	0,000									
Solyc10g054280	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JVF5_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR023214 (G3DSA:3.40.50.GENE3D	0,555	0,595	0,234	0,309	0,211									
Solyc10g054300	LOW QUALITY:Protein kinase-like (AHRD V3.3 *-* Q5QMM2_ORYSJ)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510.	0,000	0,021	0,000	0,000	0,000									
Solyc10g054320	Coiled-coil domain-containing 90B, mitochondrial (AHRD V3.3 *** A0A0B0NYS6_GOSAR)		C:GO:0005739: C:G(	C:mitochondrion; C:integral component of membrane			IPR024461 (PFAM): PTHR14360:SF1	5,254	9,515	4,746	8,215	5,836					0,794	0,001			up
Solyc10g054330	Zinc knuckle family protein (AHRD V3.3 *** B9H4I7_POPTR)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			PF13917 (PFAM): G3DSA:4.10.60.10	48,142	57,706	44,262	44,008	43,093									
Solyc10g054340	Fructose-bisphosphate aldolase (AHRD V3.3 *-* A0A0K9QFF9_SPIOL)		F:GO:0004332: P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc10g054350	Disease resistance protein (AHRD V3.3 *-* A0A124SFK9_CYNCS)		C:GO:0016021: F:G(	C:integral component of membrane; F:ADP binding			IPR041118 (PFAM): PTHR23155:SF8	0,000	0,019	0,000	0,000	0,000									
Solyc10g054380	Fructose-bisphosphate aldolase (AHRD V3.3 *-* B0FPD8_SOLTU)		F:GO:0004332: P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	0,511	0,712	0,368	0,390	0,637									
Solyc10g054383	LOW QUALITY:HAT dimerization domain-containing family protein (AHRD V3.3 --* B9I2P4_POPTR)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): IPR012337 (SUP	0,042	0,000	0,050	0,022	0,047									
Solyc10g054390	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4D137_SOLLC)		F:GO:0004332: P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR000741 (PFAM): IPR013785 (G3D	0,000	0,000	0,000	0,000	0,024									
Solyc10g054395	FRIGIDA interacting protein 1 (AHRD V3.3 --* AT2G06005.6)							0,000	0,000	0,050	0,022	0,095									
Solyc10g054400	Transcription initiation factor IIF subunit beta, putative (AHRD V3.3 *** B9T7T1_RICCO)		C:GO:0005674: P:G(	C:transcription factor TFIIF complex; P:transcription initiation fr(			IPR040450 (PFAM): IPR036388 (G3D	1,805	2,381	1,883	2,083	1,881									
Solyc10g054410	LOW QUALITY:NAC (No Apical Meristem) domain transcriptional regulator superfamily protein (AHRD V3.3 -		F:GO:0008270	F:zinc ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,106	0,025	0,000	0,000									
Solyc10g054420	PsbP-like protein 2 (AHRD V3.3 *** A0A061FNQ0_THECC)		F:GO:0005509: C:G(	F:calcium ion binding; C:photosystem II oxygen evolving comple			IPR016123 (G3DSA:3.40.1000.GENE	10,204	16,265	1,436	1,563	5,092			1,811	0,000				up	
Solyc10g054440	arginine decarboxylase 1	adc1	P:GO:0006527: P:G(	P:arginine catabolic	EC:4.1.1.19	Arginine decarboxyla	IPR002985 (PRINTS): IPR000183 (PF	363,135	708,687	119,602	141,399	216,491			0,853	0,022				up	
Solyc10g054450	LOW QUALITY:Protein kinase superfamily protein (AHRD V3.3 --* AT2G28940.1)		F:GO:0003723	F:RNA binding			mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,025	0,025	0,000									
Solyc10g054460	FAD-binding Berberine family protein, putative (AHRD V3.3 *-* A0A061G791_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			G3DSA:3.30.465.50 (GENE3D): IPR0(	0,060	0,021	0,075	0,072	0,093									
Solyc10g054470	FAD-binding Berberine family protein (AHRD V3.3 *-* A0A061E9C4_THECC)		F:GO:0016491: F:G(	F:oxidoreductase activity; F:flavin adenine dinucleotide binding;			IPR012951 (PFAM): G3DSA:3.30.465	0,101	0,237	0,099	0,198	0,094									
Solyc10g054480	FAD-binding Berberine family protein, putative (AHRD V3.3 *** A0A061G791_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR016167 (G3DSA:3.30.43.GENE3D	4,572	3,887	3,357	3,371	3,578									
Solyc10g054530	FAD-binding Berberine family protein, putative (AHRD V3.3 *-* A0A061G791_THECC)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			G3DSA:3.30.465.50 (GENE3D): G3DS	0,019	0,075	0,000	0,000	0,000									
Solyc10g054560	V-type proton ATPase proteolipid subunit (AHRD V3.3 *** Q3HVP1_SOLTU)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR000245 (PRINTS): G3DSA:1.20.12	86,505	91,543	87,926	88,168	84,096									
Solyc10g054570	V-type proton ATPase proteolipid subunit (AHRD V3.3 *** Q3HVP1_SOLTU)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR000245 (PRINTS): G3DSA:1.20.12	46,854	47,963	45,710	48,736	43,281									
Solyc10g054590	V-type proton ATPase proteolipid subunit (AHRD V3.3 *** Q3HVP1_SOLTU)		F:GO:0015078: P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR000245 (PRINTS): G3DSA:1.20.12	47,893	45,111	46,293	46,275	40,945									
Solyc10g054660	Carbohydrate-binding-like fold (AHRD V3.3 --* AT3G62360.2)							0,640	0,707	1,281	0,595	1,058									
Solyc10g054663	Unknown protein (AHRD V3.3)							0,377	0,370	1,218	1,176	1,133									
Solyc10g054665	Beta-1,3-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A072VIG3_MEDTR)		P:GO:0001709	P:cell fate determination			IPR040361 (PANTHER): PTHR33184::	0,096	0,249	0,000	0,000	0,000									
Solyc10g054667	Beta-1,3-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A072VIG3_MEDTR)		P:GO:0001709: F:G(	P:cell fate determination; F:transferase activity; F:transferase a			IPR040361 (PANTHER): PTHR33184::	0,141	0,440	0,000	0,000	0,000									
Solyc10g054725	TRAF-type zinc finger-like protein (AHRD V3.3 --* AT1G09920.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,769	0,627	0,514	0,560	0,446									
Solyc10g054730	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A061DZK4_THECC)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	0,716	0,709	0,722	0,700	0,615									
Solyc10g054780	Gibberellin receptor GID1A (AHRD V3.3 *** GID1A_ARATH)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	34,223	35,825	20,347	19,234	23,089									
Solyc10g054790	X-intrinsic protein 1.5	XIP1.5	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	0,942	1,202	0,121	0,845	0,117									
Solyc10g054800	X-intrinsic protein 1.4	XIP1.4	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,019	0,043	0,000	0,000	0,000									
Solyc10g054820	X-intrinsic protein 1.2	XIP1.2	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	2,020	2,838	0,000	0,000	0,000									
Solyc10g054840	X-intrinsic protein 1.1	XIP1.1	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	23,866	26,082	0,025	0,075	0,047									
Solyc10g054850	ER lumen protein retaining receptor family protein (AHRD V3.3 *** AT4G38790.1)		P:GO:0006621: C:G(	P:protein retention in ER lumen; C:integral component of membr			IPR000133 (PRINTS): IPR000133 (PF	10,548	8,616	5,275	4,555	4,214									
Solyc10g054860	Urb2/Npa2, putative isoform 2 (AHRD V3.3 *** A0A061E0C3_THECC)		C:GO:0005730: P:G(	C:nucleolus; P:ribosome biogenesis			IPR018849 (PFAM): mobidb-lite (MOB	30,052	27,958	26,708	26,772	23,472									
Solyc10g054870	triosephosphate isomerase (AHRD V3.3 *** AT2G21170.3)		F:GO:0004807: P:G(	F:triose-phosphate	EC:5.3.1.1	Triose-phosphate isc	IPR000652 (PFAM): IPR000652 (TIGF	2,048	9,867	0,000	0,222	0,164	2,290	0,000					up		
Solyc10g054880	Translocon-associated protein, alpha subunit, putative (AHRD V3.3 *-* B9STC6_RICCO)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR005595 (PFAM): PTHR12924 (PAI	33,473	38,466	32,143	29,300	29,138									
Solyc10g054900	Proline-rich protein (AHRD V3.3 *** Q9M6T7_NICGL)						PF01190 (PFAM): PTHR23201:SF16 (	298,710	262,624	2,575	4,706	0,280									
Solyc10g054910	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4D184_SOLLC)		P:GO:0000413: F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PFAM): IPR002130 (PF	12,029	12,134	13,470	12,316	10,184									
Solyc10g054915	Ethylene-responsive transcription factor (AHRD V3.3 *** F1DGA5_COFAR)		F:GO:0003677: F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINTS): IPR036955 (G3	0,000	0,000	0,000	0,000	0,023									
Solyc10g054930	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095: P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM): PTHR12570:SF1	13,765	16,252	20,398	21,855	21,340									
Solyc10g055110	LOW QUALITY:Disease resistance protein (AHRD V3.3 --* W9QH35_9ROSA)		F:GO:0043531	F:ADP binding			PTHR44061 (PANTHER): PTHR44061	0,042	0,057	0,050	0,022	0,024									
Solyc10g055120	Nucleotide binding site-leucine rich repeat protein (AHRD V3.3 *** A0A0H5AGV4_SOLPI)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,209	0,273	0,051	0,047	0,096									
Solyc10g055200	Dirigent protein (AHRD V3.3 *** K4D1B3_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAI	0,425	4,469	0,338	0,273	0,616	3,398	0,000					up		
Solyc10g055210	Dirigent protein (AHRD V3.3 *** K4D1B4_SOLLC)		C:GO:0005576	C:extracellular region			IPR004265 (PFAM): PTHR21495 (PAI	0,000	0,041	0,025	0,000	0,000									
Solyc10g055230	Dirigent protein (AHRD V3.3 *** K4D1B5_SOLLC)		C:GO:0048046	C:apoplast			IPR004265 (PFAM): PTHR21495 (PAI	0,000	0,039	0,000	0,000	0,000									
Solyc10g055240	1-phosphatidylinositol phosphodiesterase-related family protein (AHRD V3.3 *** B9H168_POPTR)		P:GO:0006629: F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR000909 (PFAM): IPR017946 (G3D	0,884	1,775	0,266	0,120	0,070									
Solyc10g055250	LOW QUALITY:cold shock domain protein 1 (AHRD V3.3 *** AT4G36020.2)		F:GO:0003676: F:G(	F:nucleic acid binding; F:zinc ion binding			IPR002059 (PRINTS): IPR002059 (PF	0,857	1,096	0,075	0,000	0,024									
Solyc10g055260	SILAX5		P:GO:0003333: F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): PTHR22950:SF3	0,123	0,019	0,000	0,000	0,000									
Solyc10g055270	LOW QUALITY:F-box protein interaction domain containing protein (AHRD V3.3 *-* Q60D10_SOLDE)		F:GO:0016740	F:transferase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,259	0,341	0,049	0,000	0,141									
Solyc10g055320	LOW QUALITY:F-box protein interaction domain containing protein (AHRD V3.3 *-* Q60D10_SOLDE)		F:GO:0016301	F:kinase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,181	0,060	0,025	0,000	0,023									
Solyc10g055330	Concanavalin A-like lectin protein kinase family protein (AHRD V3.3 --* AT5G59270.3)							0,021	0,037	0,000	0,000	0,024									
Solyc10g055370	Endo-1,4-beta-xylanase A (AHRD V3.3 *** A0A0B0MVH7_GOSAR)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb(			IPR001000 (PRINTS): G3DSA:3.20.2(	0,000	0,021	0,000	0,000	0,000									
Solyc10g055390	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9P7P6_ZOSMR)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM): G3DSA:1.20.125(	13,956	9,928	40,413	40,207	35,547									
Solyc10g055400	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_PINPU)						mobidb-lite (MOBIDB_LITE)	1,068	0,821	0,833	0,516	0,824									
Solyc10g055410	R2R3MYB transcription factor 32	R2R3MYB32/THM27	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	13,932	10,871	2,869	2,759	2,798									
Solyc10g055420	Malate dehydrogenase, cytoplasmic (AHRD V3.3 --* MDHC_MESCR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,432	2,345	0,146	0,195	0,497									
Solyc10g055450	E3 ubiquitin-protein ligase (AHRD V3.3 *** G7JNF2_MEDTR)		F:GO:0004842	F:ubiquitin-protein transferase activity			G3DSA:3.30.2160.10 (GENE3D): G3D	162,017	136,918	224,493	228,949	226,501									
Solyc10g055460	Peptidase M50 family protein (AHRD V3.3 --* AT4G20310.1)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus				0,466	0,508	0,345	0,265	0,377									
Solyc10g055470	Beta-galactosidase (AHRD V3.3 *** M1A6P4_SOLTU)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb(			IPR001944 (PRINTS): IPR041392 (PF	0,059	0,080	0,000	0,000	0,000									
Solyc10g055540	HAT transposon superfamily (AHRD V3.3 *-* A0A061G5I4_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): PTHR32166:SF5	2,628	1,815	1,252	0,775	0,749									
Solyc10g055545	Rac-like GTP binding protein (AHRD V3.3 *-* O65062_PICMA)		F:GO:0000166	F:nucleotide binding			G3DSA:3.40.50.300 (GENE3D): PTHF	0,224	0,081	0,022	0,050	0,071									
Solyc10g055550	BZIP transcription factor (AHRD V3.3 *** B7FIL7_MEDTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (PFAM bZIP	0,546	0,536	0,093	0,217	0,116									
Solyc10g055560	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT4G35070.1)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;			IPR017066 (PIRSF): IPR013083 (G3D	0,180	0,396	0,050	0,075	0,047									
Solyc10g055570	SKP1-like protein (AHRD V3.3 *** O82463_NICCL)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR016072 (PFAM): G3DSA:3.30.710	0,150	0,075	0,000	0,000	0,000									
Solyc10g055580	SKP1-like protein (AHRD V3.3 *** A0A0K0PTC5_NICBE)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR016897 (PIRSF): G3DSA:3.30.710	0,000	0,021	0,000	0,000	0,000									
Solyc10g055590	Skp1 (AHRD V3.3 *** Q49HP3_CAPAN)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR016073 (PFAM): G3DSA:3.30.710	0,038	0,018	0,000	0,000	0,000									
Solyc10g055610	SKP1-like protein (AHRD V3.3 *** O82463_NICCL)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process			IPR016897 (PIRSF): G3DSA:3.30.710	5,471	6,211	3,787	3,262	3,739									
Solyc10g055613	Glycine cleavage T-protein family (AHRD V3.3 --* AT1G60990.3)							0,078	0,043	0,000	0,000	0,000									
Solyc10g055617	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *-* A0A0B2QJR5_GLYSO)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane; F:transferase			PTHR31061:SF10 (PANTHER): PTHR:	0,179	0,059	0,025	0,025	0,024									
Solyc10g055620	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *** A0A0B2QJR5_GLYSO)		C:GO:0016021: F:G(	C:integral component of membrane; F:transferase activity			PTHR31061 (PANTHER): PTHR31061	7,322	6,093	4,208	5,478	6,074									
Solyc10g055630	plasma membrane intrinsic protein 2.9	PIP2.9	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (TI(	3,086	3,502	1,774	1,280	1,889									
Solyc10g055640	Pre-mRNA-splicing factor syf2, putative (AHRD V3.3 *** B9S5M2_RICCO)		C:GO:0000974: C:G(	C:Prp19 complex; C:catalytic step 2 spliceosome; C:post-mRN/			IPR013260 (PFAM): mobidb-lite (MOB	36,067	38,096	43,566	41,662	41,618									
Solyc10g055650	Protein phosphatase 2c, putative (AHRD V3.3 *** B9S5K3_RICCO)		F:GO:0004722: P:G(	F:protein serine/thr(	EC:3.1.3.16	Protein-serine/threor	IPR036457 (G3DSA:3.60.40.GENE3D	36,588	33,648	32,487	37,485	35,021									
Solyc10g055670	V-type proton ATPase subunit B2		F:GO:0005524: P:G(	F:ATP binding; P:ATP hydrolysis coupled proton transport; C:prc			IPR000194 (PFAM): G3DSA:3.40.50.1	90,850	84,018	64,330	52,164	63,309									
Solyc10g055680	Methyltransferase (AHRD V3.3 *** K4D1F8_SOLLC)		P:GO:0006694: F:G(	P:steroid biosynthetic process; F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): IPR0'	9,346	12,316	2,961	4,083	4,257									
Solyc10g055700	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XTC4_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	1,141	0,961	1,094	0,797	0,945									
Solyc10g055710	Mechanosensitive ion channel family protein (AHRD V3.3 *** AT2G17010.1)		C:GO:0016020: P:G(	C:membrane; P:transmembrane transport			IPR023408 (G3DSA:2.30.30.GENE3D	0,584	0,660	0,998	0,901	0,920									
Solyc10g055720	MAP kinase kinase kinase 75	MAPKKK75	F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): G3DSA:3.30.7(	38,850	27,508	63,221	74,625	58,166									
Solyc10g055740	Amino acid transporter, putative (AHRD V3.3 *** B9R8J4_RICCO)		P:GO:0003333: C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): PTHR22950 (PAI	1,063	2,395	1,326	2,444	1,703									
Solyc10g055750	Lysine/histidine transporter (AHRD V3.3 *** J9PGS6_PHYAN)		P:GO:0003333: C:G(	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM): mobidb-lite (MOB	0,000	0,000	0,025	0,000	0,000									
Solyc10g055760	NAC domain protein NAC6	NAC086	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	56,134	175,796	32,466	42,164	58,098	1,669	0,001	0,836	0,013			up	up	
Solyc10g055770	Hippocampus abundant transcript 1 (AHRD V3.3 *** A0A0B0P0P1_GOSAR)		F:GO:0005215: C:G(	F:transporter activity; C:integral component of membrane; P:tra			IPR001958 (PRINTS): IPR011701 (PF	27,972	32,763	1,937	0,664	1,713					-1,544	0,001			down
Solyc10g055780	Endochitinase (Chitinase) (AHRD V3.3 *** Q43184_SOLTU)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	G3DSA:1.10.530.10 (GENE3D): G3DS	0,061	0,188	0,097	0,000	0,000									
Solyc10g055790	Chitinase (AHRD V3.3 *-* B9VRK7_CAPAN)		F:GO:0008061	F:chitin binding			IPR001002 (PRINTS): IPR001002 (PF	0,000	0,021	0,050	0,025	0,000									
Solyc10g055800	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR001002 (PRINTS): IPR000726 (PF	9,890	16,511	130,079	85,042	93,564									
Solyc10g055810	chitinase Z15140		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR001002 (PRINTS): IPR016283 (PII	8,019	12,274	268,920	79,715	149,032					-1,753	0,000			down
Solyc10g055820	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR016283 (PIRSF): IPR000726 (PFA	0,500	1,019	30,534	11,334	11,198					-1,429	0,022			down
Solyc10g061830	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_SOLBU)		C:GO:0009521: P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM): G3DSA:1.10.10.6	0,059	0,081	0,025	0,221	0,119									
Solyc10g061860	Protein kinase superfamily protein (AHRD V3.3 *-* AT3G56760.1)		F:GO:0004672: F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	0,021	0,000	0,000	0,000	0,000									
Solyc10g061880	LOW QUALITY:Dihydrodipicolinate reductase, bacterial/plant (AHRD V3.3 --* AT3G59890.1)							0,060	0,064	0,047	0,025	0,070									
Solyc10g061940	Casein kinase II subunit beta (AHRD V3.3 *** A0A0V0HY87_SOLCH)		C:GO:0005956: F:G(	C:protein kinase CK2 complex; F:protein kinase regulator activi			IPR000704 (PRINTS): IPR016149 (G3	17,995	16,340	15,219	15,528	16,069									
Solyc10g061950	Light-independent protochlorophyllide reductase subunit B (AHRD V3.3 --* A0A097K POR-B							6,518	6,555	7,730	9,673	8,701									
Solyc10g061960	Phosphatidylinositol-4-phosphate 5-kinase 5-like protein (AHRD V3.3 *** A0A0B0PLQ6_GOSAR)		C:GO:0016021: F:G(	C:integral component of membrane; F:kinase activity; P:phosph			G3DSA:2.20.110.10 (GENE3D): IPR0(	19,200	15,558	19,644	20,902	19,491									
Solyc10g061970	60S ribosomal protein L37a (AHRD V3.3 *** RL37A_GOSHI)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR011331 (G3DSA:2.20.25.GENE3D	2,084	2,242	0,534	0,342	0,474									
Solyc10g061990	NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 *-* A0A142I0Y7_NICSY)		P:GO:0006120: F:G(	P:mitochondrial ele(	EC:1.6.99.5; EC:1.6.	Acting on NADH or N.	IPR000260 (PFAM): PTHR43507:SF6	0,040	0,000	0,025	0,025	0,000									
Solyc10g061995	NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 *-* A0A191TDL0_HORVD)		F:GO:0008137: P:G(	F:NADH dehydroge(	EC:1.6.99.5; EC:1.6.	Acting on NADH or N.	IPR001750 (PFAM): PTHR43507:SF6	0,042	0,021	0,000	0,000	0,000									
Solyc10g062130	LOW QUALITY:Auxin responsive SAUR protein (AHRD V3.3 --* A0A118JXA7_CYNCS)							0,081	0,081	0,000	0,072	0,071									
Solyc10g062160	Dynamin, putative (AHRD V3.3 *** B9SKH8_RICCO)		F:GO:0003924: F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR022812 (PRINTS): IPR003130 (PF	3,514	6,355	3,277	3,385	3,775									
Solyc10g062180	RNA binding protein, putative (AHRD V3.3 *** B9SKE9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	67,642	74,856	49,577	42,919	50,999									
Solyc10g062200	ELMO domain-containing protein, putative (AHRD V3.3 *-* B9SKK4_RICCO)						IPR006816 (PFAM): PTHR12771 (PAI	2,035	2,714	1,916	2,532	2,282									
Solyc10g062210	LOW QUALITY:importin alpha isoform 6 (AHRD V3.3 --* AT1G02690.2)							0,000	0,000	0,000	0,000	0,046									
Solyc10g062220	ELMO/CED-12 domain-containing protein (AHRD V3.3 *** Q8VZ78_ARATH)						IPR006816 (PFAM): PTHR12771 (PAI	4,523	6,438	5,069	5,947	4,825									
Solyc10g062330	Ycf1 (AHRD V3.3 *-* A0A0N7CFU2_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM): mobidb-lite (MOB	0,000	0,064	0,025	0,151	0,024									
Solyc10g062340	RNA binding protein, putative (AHRD V3.3 *** B9SKE9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	72,445	67,892	75,972	70,413	67,487									
Solyc10g068340	LOW QUALITY:F-box associated interaction domain-containing protein (AHRD V3.3 *** A0A103XHT5_CYN(		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM): IPR001810 (F	0,000	0,039	0,000	0,000	0,000									
Solyc10g068350	Endochitinase (Chitinase) (AHRD V3.3 *-* Q43184_SOLTU)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	G3DSA:1.10.530.10 (GENE3D): IPR0(	0,000	0,000	0,000	0,022	0,000									
Solyc10g074400	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR001002 (PFAM): IPR000726 (PFA	0,000	0,000	0,000	0,025	0,000									
Solyc10g074440	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)		F:GO:0004568: P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	IPR000726 (PFAM): IPR016283 (PIRS	0,021	0,039	0,000	0,000	0,000									
Solyc10g074450	LOW QUALITY:hydrolases, acting on ester bond (AHRD V3.3 --* AT3G27325.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,079	0,062	0,000	0,000	0,000									
Solyc10g074470	bZIP transcription factor (DUF630 and DUF632) (AHRD V3.3 *** AT2G27090.2)		P:GO:0071249	P:cellular response to nitrate			IPR006868 (PFAM): IPR006867 (PFA	22,490	18,191	5,510	4,327	5,361									
Solyc10g074490	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G20550.1)		P:GO:0006004: C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	0,502	0,579	0,000	0,000	0,000									
Solyc10g074500	mitochondrial NAD-dependent isocitrate dehydrogenase		F:GO:0004449: P:G(	F:isocitrate dehydrc	EC:1.1.1.41	Isocitrate dehydroge(	IPR004434 (TIGRFAM): IPR024084 (F	87,592	129,183	130,513	137,301	137,106									
Solyc10g074510	SEC1-family transport family protein (AHRD V3.3 *-* B9HPZ4_POPTR)		P:GO:0006904	P:vesicle docking involved in exocytosis			IPR027482 (G3DSA:3.40.50.GENE3D	1,279	1,862	1,473	1,238	1,313									
Solyc10g074520	SEC1 family transport protein (AHRD V3.3 *-* W9S8Q4_9ROSA)		P:GO:0006904	P:vesicle docking involved in exocytosis			G3DSA:3.90.830.10 (GENE3D): IPR0(	4,781	3,649	3,222	2,869	3,243									
Solyc10g074530	SEC1 family transport protein SLY1 (AHRD V3.3 --* A0A0B0NR49_GOSAR)		P:GO:0006904: P:G(	P:vesicle docking involved in exocytosis; P:vesicle-mediated transport				1,009	0,849	1,113	0,894	0,777									
Solyc10g074540	Phosphate-responsive 1 family protein (AHRD V3.3 *** D7L8T1_ARALL)						IPR006766 (PFAM): IPR006766 (PAN	139,041	37,334	9,039	9,273	15,393	-1,867	0,000					down		
Solyc10g074550	Unknown protein (AHRD V3.3)							3,966	2,840	0,930	0,605	0,800									
Solyc10g074560	Nucleolar complex 4 (AHRD V3.3 *** A0A0B0NPG2_GOSAR)		P:GO:0042254	P:ribosome biogenesis			IPR005612 (PFAM): mobidb-lite (MOB	15,709	13,644	10,809	10,210	9,457									
Solyc10g074570	Calcium-dependent protein kinase family protein (AHRD V3.3 *** AT2G17290.2)		F:GO:0004672: F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (PFAM): G3DSA:1.10.238	27,889	34,899	24,562	29,018	26,338									
Solyc10g074580	Glycerol kinase (AHRD V3.3 *** A0A0B0MP83_GOSAR)		C:GO:0009507	C:chloroplast			PTHR42936 (PANTHER)	25,477	27,012	61,941	59,373	60,681									
Solyc10g074590	pantothenate kinase (AHRD V3.3 *** AT4G35360.2)						IPR035073 (G3DSA:1.20.1700.GENE	50,570	49,056	104,009	99,940	99,956									
Solyc10g074600	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UEG7_ANACO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,963	1,792	2,738	2,819	3,277									
Solyc10g074610	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A0K9PTA0_ZOSMR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,213	4,447	5,301	4,731	6,111									
Solyc10g074620	Cellulose synthase, putative (AHRD V3.3 *** B9RKY2_RICCO)		C:GO:0016020: F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (l	PF14570 (PFAM): IPR005150 (PFAM)	0,021	0,000	0,000	0,049	0,024									
Solyc10g074630	ADP-ribosylation factor, putative (AHRD V3.3 *** B9R9D6_RICCO)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): G3DSA:3.40.5(	10,078	10,447	15,908	16,117	14,850									

Solyc10g074640	Disease resistance protein (AHRD V3.3 *-* W9R179_9ROSA)		F:GO:0043531	F:ADP binding			PTHR44061:SF1 (PANTHER): PTHR4	0,141	0,083	0,118	0,244	0,072								
Solyc10g074650	Hexosyltransferase (AHRD V3.3 *** K4D1Q7_SOLLC)	GAUT7	F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	34,627	27,639	32,454	33,965	34,414								
Solyc10g074680	Transcription factor GRAS (AHRD V3.3 *** A0A103Y639_CYNCS)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM) GRAS	0,315	0,082	0,000	0,000	0,000								
Solyc10g074690	retinal-binding protein (AHRD V3.3 *** AT5G01010.1)						G3DSA:2.60.120.680 (GENE3D): PTH	65,781	62,344	89,645	90,111	87,965								
Solyc10g074700	Ethanolamine-phosphate cytidylyltransferase (AHRD V3.3 *** PECT1_ARATH)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process			IPR014729 (G3DSA:3.40.50.GENE3D	26,355	29,546	52,055	51,583	46,962								
Solyc10g074710	Kinase family protein (AHRD V3.3 *** D7M6D0_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF): G3DSA:1.10.5	41,432	43,585	20,398	17,903	21,424								
Solyc10g074720	B1-type cyclin dependent kinase	cdkb1	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	3,197	3,253	0,508	0,564	0,703								
Solyc10g074730	cyclin dependent kinase		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): G3DSA:2.60.40.1	0,817	1,119	14,844	25,923	18,154					0,808	0,003			up
Solyc10g074740	Calcium-binding protein CAST (AHRD V3.3 *** CAST_SOLTU)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): G3DS	209,591	229,577	160,806	225,809	190,274					0,492	0,036			up
Solyc10g074745	Peroxidase (AHRD V3.3 --* K7VCN5_MAIZE)							7,776	8,860	8,186	9,343	7,511									
Solyc10g074790	Auxin efflux carrier family protein (AHRD V3.3 *** AT5G01990.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR004776 (PFAM): PTHR31419:SF1	776,438	400,117	461,176	382,715	394,955	-0,929	0,000					down		
Solyc10g074800	heat-inducible transcription repressor (AHRD V3.3 *-* AT5G01970.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,384	1,232	1,262	0,610	0,781									
Solyc10g074810	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01960.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity; F:metal io			IPR013083 (G3DSA:3.30.40.GENE3D	32,463	31,157	27,611	26,820	25,658									
Solyc10g074820	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT3G08600.1)		C:GO:0016021	C:integral component of membrane			IPR010605 (PFAM): mobidb-lite (MOB	6,840	5,851	1,830	1,649	1,857									
Solyc10g074830	LOW QUALITY:ER-based factor for assembly of V-ATPase (AHRD V3.3 *-* AT5G52980.1)		P:GO:0070072	P:vacuolar proton-transporting V-type ATPase complex assemb			IPR021013 (PANTHER)	0,019	0,021	0,047	0,000	0,000									
Solyc10g074850	Organic cation/carnitine transporter, putative (AHRD V3.3 *** G7LG12_MEDTR)		C:GO:0016020	C:membrane			G3DSA:1.20.1250.20 (GENE3D): PTH	0,000	0,000	0,000	0,025	0,000									
Solyc10g074860	Transmembrane protein 97, Putative (AHRD V3.3 --* AT1G05210.1)							69,942	71,585	96,734	87,216	88,707									
Solyc10g074870	KH domain-containing family protein (AHRD V3.3 *** B9MTT7_POPTR)		F:GO:0003723	F:RNA binding			IPR004088 (PFAM): IPR032377 (PFA	33,017	38,171	36,187	33,505	31,853									
Solyc10g074880	Protein RETICULATA-RELATED 3, chloroplastic (AHRD V3.3 *** RER3_ARATH)		C:GO:0016021	C:integral component of membrane			IPR021825 (PFAM): PTHR31620:SF5	9,564	8,623	20,604	28,894	19,550									
Solyc10g074890	Protein kinase-like protein (AHRD V3.3 *** A0A0K9Q444_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	10,432	12,659	18,702	21,110	17,778									
Solyc10g074900	Protein kinase-like protein (AHRD V3.3 *** A0A0K9Q444_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR032675 (G3DSA:3.80.10.GENE3D	7,580	5,923	4,515	4,446	5,193									
Solyc10g074910	N-acetyltransferase, putative (AHRD V3.3 *** B9T0N6_RICCO)		F:GO:0016740	F:transferase activity			IPR000182 (PFAM): G3DSA:3.40.630	8,342	10,930	11,987	12,454	14,557									
Solyc10g074920	Mannan endo-1,4-beta-mannosidase-like protein (AHRD V3.3 *** G7LAQ6_MEDTR)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	8,419	12,886	1,724	4,037	3,434					1,226	0,002			up
Solyc10g074930	serine/threonine protein kinase 2 (AHRD V3.3 *** AT3G08720.4)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (PFAM): G3DSA:1.10.510	49,131	64,631	26,730	30,348	34,589									
Solyc10g074935	myosin (AHRD V3.3 --* AT4G33200.4)							3,360	3,976	1,459	2,733	1,889									
Solyc10g074940	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A067JQP3_JATCU)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR006539 (TIGRFAM): PF00122 (PF	124,086	123,796	130,085	136,145	132,793									
Solyc10g074950	transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT5G43180.1)		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31881:SF5	2,729	2,163	1,633	2,152	1,636									
Solyc10g074960	ubiquitin-specific protease 15 (AHRD V3.3 --* AT1G17110.3)							81,593	48,876	96,438	86,448	83,027	-0,712	0,005					down		
Solyc10g074980	Vacuolar sorting receptor family protein (AHRD V3.3 *** B9HDJ2_POPTR)		F:GO:0005509; C:G(	F:calcium ion binding; C:endosome; C:trans-Golgi network; P:ub			G3DSA:2.10.25.10 (GENE3D): IPR00	261,601	287,605	268,534	254,878	257,721									
Solyc10g074990	Polynucleotidyl transferase isoform 1 (AHRD V3.3 *** A0A061G6C2_THECC)		P:GO:0006364	P:rRNA processing			IPR005227 (PFAM): IPR037027 (G3D	4,715	3,331	6,202	6,675	6,742									
Solyc10g075010	F-box family protein (AHRD V3.3 *** B9HMA7_POPTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR	0,495	0,500	0,116	0,097	0,000									
Solyc10g075020	Elongation factor P family protein (AHRD V3.3 *** A0A061EHF6_THECC)		F:GO:0003746; C:G(	F:translation elongation factor activity; C:cytoplasm; P:translatio			G3DSA:2.40.50.140 (GENE3D): IPR0(	8,654	14,650	6,421	6,328	11,170	0,787	0,007	0,790	0,010			up	up	
Solyc10g075030	B3 domain-containing protein (AHRD V3.3 *-* A0A0B2SFE8_GLYSO)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; F:zinc ion binding			mobidb-lite (MOBI[B3	14,357	12,398	11,819	14,833	15,650									
Solyc10g075035	B3 domain-containing protein (AHRD V3.3 *** A0A0B2SFE8_GLYSO)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR015300 (G3DSA:2.40.330.GENE3	11,883	10,998	8,679	10,966	13,052			0,583	0,013				up	
Solyc10g075040	Protein kinase atsik, putative (AHRD V3.3 *** B9SRS3_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	92,023	84,271	35,965	43,735	43,219									
Solyc10g075050	Non-specific lipid-transfer protein (AHRD V3.3 *** K4D1U7_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	2,125	2,520	0,075	0,554	0,023									
Solyc10g075067	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *-* AT2G18600.2)		F:GO:0005524; F:G(	F:ATP binding; F:ligase activity; F:NEDD8 transferase activity;			IPR016135 (G3DSA:3.10.110.GENE3	0,000	0,000	0,025	0,050	0,048									
Solyc10g075070	Non-specific lipid-transfer protein (AHRD V3.3 *** K4D1U9_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	786,623	541,060	52,165	44,416	35,228									
Solyc10g075080	LOW QUALITY:Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 --* A0A151SL68_CAJCA)		F:GO:0005488; C:G(	F:binding; C:membrane				0,038	0,019	0,000	0,025	0,000									
Solyc10g075090	Non-specific lipid-transfer protein (AHRD V3.3 *** Q4A1N0_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): G3DSA:1.10.11	232,784	251,952	140,115	108,251	133,320									
Solyc10g075100	Non-specific lipid-transfer protein (AHRD V3.3 *** Q4A1N1_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	413,962	298,671	182,898	165,146	164,412									
Solyc10g075110	Non-specific lipid-transfer protein (AHRD V3.3 *** M1AVB9_SOLTU)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	4,012	2,538	5,356	1,870	1,628			-1,718	0,000	-1,517	0,000		down	down
Solyc10g075130	Non-specific lipid-transfer protein (AHRD V3.3 *** K4D1W2_SOLLC)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): IPR016140 (PF	0,057	0,661	0,149	0,270	0,094									
Solyc10g075150	Non-specific lipid-transfer protein (AHRD V3.3 *** M1AVB3_SOLTU)		P:GO:0006869; F:G(	P:lipid transport; F:lipid binding			IPR000528 (PRINTS): G3DSA:1.10.11	12,824	55,155	142,576	309,943	411,927	2,127	0,000	1,526	0,000	1,126	0,000	up	up	up
Solyc10g075160	Ferredoxin (AHRD V3.3 *** A0A0K0PY61_NICBE)		F:GO:0009055; P:G(	F:electron transfer activity; P:electron transport chain; F:2 iron			IPR001041 (PFAM): IPR010241 (TIGF	17,759	44,512	4,477	6,155	13,602	1,353	0,004	1,602	0,000			up	up	
Solyc10g075170	Aspartate aminotransferase (AHRD V3.3 *-* A0A067JJ16_JATCU)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR015421 (G3DSA:3.40.640.GENE3	0,211	0,096	0,000	0,000	0,000									
Solyc10g075175	Aspartate aminotransferase (AHRD V3.3 *** B9HDA1_POPTR)		P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:transaminase activit			IPR000796 (PRINTS): IPR015421 (G3	0,213	0,099	0,000	0,000	0,024									
Solyc10g076180	ovate family protein 20	OFP20	F:GO:0003677; P:G(	F:DNA binding; P:negative regulation of transcription, DNA-temp			IPR006458 (TIGRFAM): IPR025830 (F	0,760	0,756	0,193	0,116	0,096									
Solyc10g076240	Peroxidase (AHRD V3.3 *** A0A0E0NC86_ORYRU)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	2,736	7,310	22,051	16,594	23,695									
Solyc10g076250	Alanine-glyoxylate aminotransferase, putative (AHRD V3.3 *** B9SZ94_RICCO)		F:GO:0008483; F:G(	F:transaminase activity; F:pyridoxal phosphate binding			IPR005814 (PIRSF): IPR005814 (PFA	13,429	16,889	5,780	6,471	8,961									
Solyc10g076260	Regulatory-associated protein of TOR protein (AHRD V3.3 *-* G7KW32_MEDTR)		P:GO:0031929; C:G(	P:TOR signaling; C:TORC1 complex			PR01547 (PRINTS): IPR029347 (PFA	16,686	10,266	9,024	14,413	12,367									
Solyc10g076270	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *-* I1HS93_BRADI)		F:GO:0005515; P:G(	F:protein binding; P:TOR signaling; C:TORC1 complex			IPR015943 (G3DSA:2.130.10.GENE3	30,535	26,515	23,052	26,116	25,714									
Solyc10g076280	Solute carrier family 40 member 1 (AHRD V3.3 *** A0A151RSH4_CAJCA)		F:GO:0005381; C:G(	F:iron ion transmembrane transporter activity; C:integral compo			IPR009716 (PFAM): PTHR11660:SF5	0,158	0,336	0,000	0,025	0,024									
Solyc10g076290	F-box/LRR protein (AHRD V3.3 *** A0A072UGE9_MEDTR)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	6,724	8,443	10,360	10,562	9,832									
Solyc10g076300	CASP-like protein (AHRD V3.3 *** K4D1X2_SOLLC)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006702 (PFAM): mobidb-lite (MOB	1,596	0,825	8,069	8,839	7,893									
Solyc10g076320	Protein phosphatase-2c, putative (AHRD V3.3 *** B9SL27_RICCO)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threon	IPR036457 (G3DSA:3.60.40.GENE3D	0,037	0,000	0,000	0,000	0,000									
Solyc10g076330	Kelch repeat-containing family protein (AHRD V3.3 *** B9IGK0_POPTR)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	0,000	0,000	0,000	0,022	0,000									
Solyc10g076350	Macrophage migration inhibitory factor (AHRD V3.3 *** A0A103YLB8_CYNCS)						IPR001398 (PFAM): IPR014347 (G3D	65,705	68,675	75,125	63,806	69,992									
Solyc10g076357	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 --* AT5G51930.2)							0,060	0,036	0,125	0,241	0,000									
Solyc10g076360	PRA1 family protein (AHRD V3.3 *** K4D1X8_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR19317:SF3	39,237	67,727	19,229	22,782	17,252	0,812	0,010					up		
Solyc10g076370	Dehydration-responsive element binding protein (AHRD V3.3 *-* G9JKP4_LEYCH)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PFAM) ERF	0,293	0,345	0,141	0,148	0,234									
Solyc10g076390	Beta-amylase (AHRD V3.3 *-* A0A0K9PI68_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:transcription, DNA			IPR008540 (PFAM) BES1	0,000	0,018	0,000	0,000	0,023									
Solyc10g076400	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFA	0,059	0,272	0,000	0,000	0,000									
Solyc10g076410	Abscisic acid receptor (AHRD V3.3 *** G7KT83_MEDTR)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm			IPR019587 (PFAM): IPR023393 (G3D	0,176	0,062	0,050	0,025	0,047									
Solyc10g076420	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT2G03350.1)		F:GO:0003674; C:G(	F:molecular_function; C:cellular_component; P:biological_proce			IPR007493 (PFAM): IPR036758 (G3D	28,167	24,273	31,099	32,755	30,719									
Solyc10g076450	Ethylene-overproduction protein 1 (AHRD V3.3 *** W9R4D2_9ROSA)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	4,504	3,128	3,071	2,641	2,781									
Solyc10g076460	MYB-like transcription factor family protein (AHRD V3.3 *** G7KSC8_MEDTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	0,040	0,232	0,000	0,022	0,141									
Solyc10g076480	Ammonium transporter (AHRD V3.3 *** K4D1Z0_SOLLC)		F:GO:0008519; C:G(	F:ammonium transmembrane transporter activity; C:membrane;			IPR002229 (PRINTS): IPR024041 (PF	5,679	20,986	1,880	1,659	2,510	1,907	0,005					up		
Solyc10g076485	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGQ2_ARATH)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,040	0,021	0,000	0,000	0,000									
Solyc10g076500	Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	0,082	2,075	0,025	0,022	0,046	4,563	0,000					up		
Solyc10g076510	Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion binding; F:carboxy-lyase activity; F:thiamine p			G3DSA:3.40.50.970 (GENE3D): G3DS	247,737	285,014	453,725	416,820	517,272									
Solyc10g076520	Ankyrin repeat family protein (AHRD V3.3 --* AT5G04700.1)							0,000	0,000	0,000	0,025	0,023									
Solyc10g076530	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:3.30.200.20 (GENE3D): G3DS	0,225	0,253	0,121	0,258	0,187									
Solyc10g076537	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT1G52470.3)							0,040	0,039	0,000	0,000	0,000									
Solyc10g076540	Kinase, putative (AHRD V3.3 --* B9RJQ3_RICCO)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	mobidb-lite (MOBIDB_LITE)	0,037	0,836	0,025	0,025	0,047									
Solyc10g076550	Protein kinase family protein (AHRD V3.3 *-* AT3G25490.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	0,178	3,814	0,025	0,314	0,447	4,366	0,000					up		
Solyc10g076555	UvrABC system C protein (AHRD V3.3 *** AT5G01350.1)						PTHR34966:SF3 (PANTHER): PTHR3	0,040	0,000	0,000	0,025	0,000									
Solyc10g076560	Kinase, putative (AHRD V3.3 *-* B9RJQ3_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,000	0,021	0,000	0,000	0,024									
Solyc10g076570	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT5G01360.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFA	0,078	0,080	0,025	0,049	0,047									
Solyc10g076590	Phosphoinositide phosphatase family protein (AHRD V3.3 *** B9IGB3_POPTR)		F:GO:0052866	F:phosphatidylinositol phosphate phosphatase activity			IPR002013 (PFAM): PTHR11200 (PAN	29,329	31,724	33,919	36,388	34,619									
Solyc10g076600	Acyl-coenzyme A oxidase 4 (AHRD V3.3 *** W9RND6_9ROSA)		F:GO:0016627; F:G(	F:oxidoreductase activity, acting on the CH-CH group of donors			G3DSA:2.40.110.10 (GENE3D): IPR0	52,882	45,440	278,553	284,778	295,823									
Solyc10g076610	lysyl-tRNA synthetase	lysrs	F:GO:0003676; F:G(	F:nucleic acid bindi	EC:6.1.1.6	Lysine--tRNA ligase	IPR018149 (PRINTS): IPR004364 (PF	0,000	0,135	1,834	2,466	1,065									
Solyc10g076635	AMP deaminase (AHRD V3.3 --* AMPD_ARATH)						mobidb-lite (MOBIDB_LITE)	0,098	0,018	0,142	0,047	0,023									
Solyc10g076640	F-box family protein (AHRD V3.3 *** AT3G06240.1)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR	0,000	0,000	0,000	0,000	0,023									
Solyc10g076650	dentin sialophosphoprotein (AHRD V3.3 *-* AT2G29620.6)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,807	0,827	0,639	0,613	0,959									
Solyc10g076660	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G05600.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR026992 (PFA	2,009	4,266	3,405	3,199	2,720									
Solyc10g076670	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G05600.1)		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR026992 (PFAM): IPR027443 (G3D	0,000	0,043	0,022	0,072	0,116									
Solyc10g076680	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT5G05600.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,000	0,018	0,022	0,022	0,023									
Solyc10g076690	PHD finger alfin-like protein (AHRD V3.3 *** A0A072UGM4_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR013083 (G3DSA:3.30.40.GENE3D	11,969	12,910	13,426	12,266	12,283									
Solyc10g076700	Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 *** A0A061EQB9_THECC)		P:GO:0009409; C:G(	P:response to cold; C:chloroplast thylakoid; C:chloroplast envel			IPR036873 (G3DSA:3.40.250.GENE3	0,858	1,580	0,336	0,543	1,056									
Solyc10g076710	Phosphoinositide phospholipase C (AHRD V3.3 *** A0A067L8K5_JATCU)		F:GO:0004435; P:G(	F:phosphatidylinosit	EC:3.1.4.11; EC:3.1.	Phosphoinositide ph(	IPR001192 (PRINTS): IPR000909 (PF	61,557	61,167	2,863	1,767	3,042									
Solyc10g076720	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --* AT3G21790.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,801	3,848	0,097	0,122	0,189	2,280	0,000					up		
Solyc10g076730	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061E		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (PFAM): IPR006501 (TIGF	0,273	0,332	0,000	0,022	0,024									
Solyc10g076740	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RQI9_CAJCA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	18,753	25,578	14,148	17,579	17,288									
Solyc10g076750	Protein yippee-like (AHRD V3.3 *** K4D217_SOLLC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	7,936	8,325	17,530	16,326	14,803									
Solyc10g076760	Kinase family protein (AHRD V3.3 *** B9IG83_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	11,057	9,644	10,117	9,508	10,146									
Solyc10g076780	LOW QUALITY:Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 *** A0A061EQG3_THECC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR007577 (PFAM): IPR007652 (PFA	0,226	0,283	0,072	0,025	0,024									
Solyc10g076790	SILAX4		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM): PTHR22950:SF3	1,097	1,648	0,221	0,173	0,256									
Solyc10g076800	Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase-like protein (AHRD V3.3 *** A0A0B0Q0L4_GOSAR		F:GO:0004377; C:G(	F:GDP-Man:Man3G	EC:2.4.1.131	GDP-Man:Man(3)Glc	G3DSA:3.40.50.2000 (GENE3D): IPR	10,182	12,257	14,131	13,383	13,149									
Solyc10g076810	LOW QUALITY:Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 -** AT2G36		F:GO:0003676	F:nucleic acid binding			IPR036397 (G3DSA:3.30.420.GENE3	3,630	3,864	3,213	2,537	2,713									
Solyc10g076820	Myb family transcription factor family protein (AHRD V3.3 *** B9HCK2_POPTR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI MYB	0,058	0,039	0,000	0,000	0,023									
Solyc10g076830	Laccase (AHRD V3.3 *** P93366_TOBAC)		F:GO:0005507; P:G(	F:copper ion bindin	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR011707 (PFAM): IPR008972 (G3D	0,061	0,290	0,000	0,000	0,024									
Solyc10g076840	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	6,957	8,147	4,401	4,884	5,125									
Solyc10g076845	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G20400.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	0,040	0,242	0,125	0,045	0,116									
Solyc10g076860	BTB/POZ domain-containing protein KCTD9, putative (AHRD V3.3 *** B9SI86_RICCO)		P:GO:0051260	P:protein homooligomerization			IPR001646 (PFAM): IPR003131 (PFA	19,384	19,710	23,864	21,821	23,534									
Solyc10g076870	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT2G44710.2)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	84,910	95,549	80,797	82,844	84,530									
Solyc10g076880	Heat shock family protein (AHRD V3.3 *-* U5GG61_POPTR)	Hsp15.5	C:GO:0016021	C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,040	0,000	0,000	0,000	0,000									
Solyc10g076890	RNA binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT5G32450.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	59,224	57,835	31,562	31,095	29,631									
Solyc10g076900	Calcium-dependent protein kinase (AHRD V3.3 *** H6UM43_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:1.10.510.10 (GENE3D): G3DS	0,777	1,574	0,165	0,022	0,071									
Solyc10g076910	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9SMB4_RICCO)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.6.1.15	Nucleoside-triphosph	IPR011709 (PFAM): IPR001650 (PFA	70,578	61,493	102,825	105,621	98,432									
Solyc10g076920	BZIP transcription factor (AHRD V3.3 *** A0A0K2JKR5_GOSHI)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			G3DSA:1.20.5.17(bZIP	11,290	12,446	10,809	9,858	11,252									
Solyc10g076930	RmlC-type cupin (AHRD V3.3 *** AT3G56820.1)		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network			IPR014710 (G3DSA:2.60.120.GENE3	0,019	0,000	0,025	0,000	0,000									
Solyc10g076990	Arf GTPase activating protein (AHRD V3.3 *-* A0A103YN54_CYNCS)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR015410 (PF	79,208	59,052	51,475	43,628	51,521									
Solyc10g077000	Transmembrane protein, putative (AHRD V3.3 *-* G7L2Q0_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	34,996	32,878	36,993	36,052	36,768									
Solyc10g077005	Calmodulin (AHRD V3.3 *** CALM_CAPAN)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	0,040	0,039	0,000	0,000	0,000									
Solyc10g077010	Calmodulin 3	CaM3	F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	125,185	141,452	156,760	139,169	146,958									
Solyc10g077020	Kinase family protein (AHRD V3.3 *** G7L2Q2_MEDTR)						G3DSA:1.10.510.10 (GENE3D): PTHF	0,981	0,558	0,850	0,444	0,656									
Solyc10g077030	Proteasome subunit alpha type (AHRD V3.3 *** A0A0V0HS34_SOLCH)		F:GO:0004298; P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000426 (PFAM): IPR001353 (PFA	40,552	42,852	68,886	65,065	59,659									
Solyc10g077040	putative magnesium-protoporphyrin monomethyl ester cyclase	CRD1	P:GO:0015979; P:G(	P:photosynthesis; F	EC:1.14.13.81; EC:1	Magnesium-protopor	IPR008434 (TIGRFAM): IPR003251 (F	125,998	244,651	92,119	93,377	165,056	0,985	0,029	0,837	0,003			up	up	
Solyc10g077050	S-acyltransferase (AHRD V3.3 *** K4D247_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	21,760	15,017	41,988	46,987	37,213									
Solyc10g077055	Casparian strip membrane protein 1 (AHRD V3.3 --* CASP1_HELAN)							6,014	6,688	8,806	8,188	7,257									
Solyc10g077060	S-acyltransferase (AHRD V3.3 *** K4D248_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): mobidb-lite (MOB	0,021	0,078	0,000	0,000	0,023									
Solyc10g077070	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1 (AHRD V3.3 *** SUVH1_TOBAC)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	G3DSA:2.170.270.10 (GENE3D): IPR(	113,252	108,320	132,053	134,825	137,277									
Solyc10g077080	Alpha-L-arabinofuranosidase (AHRD V3.3 *** Q76LU4_SOLLC)		P:GO:0046373; F:G(	P:L-arabinose meta	EC:3.2.1.55	Non-reducing end alp	IPR013780 (G3DSA:2.60.40.GENE3D	7,624	25,862	0,637	0,326	1,193									
Solyc10g077090	50S ribosomal protein 5, chloroplastic (AHRD V3.3 *** PSRP5_PEA)		C:GO:0005840; C:G(	C:ribosome; C:chloroplast thylakoid membrane; P:plastid transla			IPR040307 (PANTHER)	2,446	3,053	1,578	1,761	1,912									
Solyc10g077110	transcription factor IIIA	tf3a	F:GO:0003676	F:nucleic acid binding			IPR013087 (PFAM) C2H2	30,764	39,204	26,215	21,670	25,585									
Solyc10g077120	Photosystem II core complex proteins psbY (AHRD V3.3 *** A0A061EES6_THECC)		C:GO:0009523; P:G(	C:photosystem II; P:photosynthesis; C:integral component of m			IPR009388 (PFAM): IPR038760 (PAN	113,106	239,539	63,025	91,811	184,751	1,111	0,010	1,548	0,000	0,547	0,028	up	up	up
Solyc10g077130	LOW QUALITY:VQ motif-containing family protein (AHRD V3.3 *** B9IHK5_POPTR)		F:GO:0005516; P:G(	F:calmodulin binding; P:response to water deprivation; P:respor			IPR008889 (PFAM): mobidb-lite (MOB	30,792	24,345	6,764	11,296	9,748					0,738	0,021			up
Solyc10g078150	Nascent polypeptide-associated complex subunit alpha-like protein (AHRD V3.3 *** W9S3Y1_9ROSA)		C:GO:0005854	C:nascent polypeptide-associated complex			G3DSA:1.10.8.10 (GENE3D): IPR038	103,619	102,441	104,804	96,496	103,787									
Solyc10g078160	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT3G56590.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	29,920	18,891	3,325	2,252	1,855									
Solyc10g078170	Phosphatidylinositol 4-kinase (AHRD V3.3 *** J3R305_GOSBA)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			IPR000403 (PFAM): PTHR15245:SF2	0,615	0,682	1,123	0,542	0,711									
Solyc10g078173	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G40060.1)							0,063	0,141	0,149	0,098	0,048									
Solyc10g078177	Gamma-aminobutyrate transaminase 1, mitochondrial (AHRD V3.3 --* GATP1_ORYSI)							5,385	4,630	6,169	6,665	5,888									
Solyc10g078180	cyclinT1_1	CycT1_1	P:GO:0000079; P:G(	P:regulation of cyclin-dependent protein serine/threonine kinase			G3DSA:1.10.472.10 (GENE3D): IPR0(	106,640	104,527	121,893	120,267	112,129									
Solyc10g078190	cytosine-5 DNA methyltransferaseL1	DRM1L1	P:GO:0006306; F:G(	P:DNA methylation; F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	8,530	7,730	12,177	10,722	12,023									
Solyc10g078200	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHV7_9ROSA)		F:GO:0003676; P:G(	F:nucleic acid binding; P:nucleobase-containing compound meta			IPR036397 (G3DSA:3.30.420.GENE3	0,000	0,000	0,000	0,000	0,023									
Solyc10g078220	Cytochrome P450 (AHRD V3.3 *** A9ZT63_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,000	0,036	0,000	0,025	0,000									
Solyc10g078230	Cytochrome P450 (AHRD V3.3 *** A0A103VZI8_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,038	0,198	0,000	0,000	0,000									
Solyc10g078235	Cytochrome P450 (AHRD V3.3 *-* A9ZT63_COPJA)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PFAM): IPR036396 (G3D	0,042	0,000	0,000	0,000	0,000									
Solyc10g078240	Cytochrome P450 (AHRD V3.3 *** A0A103VZI8_CYNCS)	C3H	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	51,034	48,914	63,521	59,611	71,330									
Solyc10g078265	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9NXQ5_ZOSMR)		F:GO:0005515	F:protein binding			IPR001179 (PFAM): G3DSA:3.10.50.4	1,938	4,766	1,624	2,247	4,528	1,326	0,003	1,467	0,001			up	up	

Solyc10g078270	WAT1-related protein (AHRD V3.3 *** K4D269_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); PTHR31218:SF9	0,140	0,363	0,470	1,028	1,332									
Solyc10g078280	Cytochrome P450, putative (AHRD V3.3 *** A0A061FPW5_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(	IPR001128 (PRINTS); IPR002401 (PF	0,019	0,000	0,000	0,000	0,000									
Solyc10g078300	Single-stranded nucleic acid binding R3H (AHRD V3.3 *** A2Q6F7_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR001374 (PFAM); IPR024771 (PFAI	264,750	241,131	201,902	193,778	204,612									
Solyc10g078310	Two-component response regulator (AHRD V3.3 *** W9S6Z7_9ROSA)		F:GO:0003677	F:DNA binding	IPR001005 (PFAM G2-like	32,569	28,119	27,674	24,490	25,903									
Solyc10g078320	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524	F:ATP binding	G3DSA:1.10.8.60 (GENE3D); IPR041!	12,651	10,547	15,072	15,166	14,060									
Solyc10g078325	MSCS-like 2 (AHRD V3.3 --* AT5G10490.3)					0,077	0,000	0,193	0,069	0,070									
Solyc10g078330	B-type cyclin	cycb1d1	C:GO:0005634	C:nucleus	IPR039361 (PIRSF); G3DSA:1.10.472	0,292	0,382	0,000	0,025	0,047									
Solyc10g078340	Stomatal closure-related actin-binding protein 1 (AHRD V3.3 *** SCAB1_ARATH)		F:GO:0003779; P:G(	F:actin binding; P:actin filament organization; P:regulation of sto	IPR041144 (PFAM); PF16709 (PFAM)	5,437	6,914	14,264	15,767	14,103									
Solyc10g078350	Transcription elongation factor (TFIIS) family protein (AHRD V3.3 *** G7L5V3_MEDTR)		C:GO:0005634	C:nucleus	IPR035441 (G3DSA:1.20.930.GENE3I	0,196	0,254	0,025	0,047	0,095									
Solyc10g078370	Auxin Efflux Facilitator 9	PIN9	C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR004776 (PFAM); IPR014024 (TIGF	3,040	3,083	0,810	0,606	0,614									
Solyc10g078380	bHLH transcription factor 064		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR036638 (G3DS bHLH	0,178	0,297	0,098	0,170	0,024									
Solyc10g078390	Protein kinase superfamily protein (AHRD V3.3 *** AT3G56760.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.238.10 (GENE3D); G3DS	76,053	50,091	21,340	17,162	23,250									
Solyc10g078400	plant/protein (AHRD V3.3 *** AT2G41150.2)		C:GO:0005794; P:G(	C:Golgi apparatus; P:fucose metabolic process; C:integral comı	G3DSA:3.40.50.11350 (GENE3D); PT	8,012	7,059	12,516	12,131	10,845									
Solyc10g078410	F-box family protein (AHRD V3.3 *** AT2G32560.1)		F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D); IPR(	17,480	16,233	0,181	0,092	0,140									
Solyc10g078420	transmembrane protein (AHRD V3.3 *** AT5G09225.1)		C:GO:0016021	C:integral component of membrane	PTHR36392 (PANTHER)	9,399	8,972	16,229	16,436	15,205									
Solyc10g078430	Transcription factor DP (AHRD V3.3 *** AT5G03415.1)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:transcription facto	IPR003316 (PFAM E2F/DP	10,417	9,117	20,365	22,372	21,018									
Solyc10g078440	LOW QUALITY:VQ motif family protein (AHRD V3.3 *-* B6TQH0_MAIZE)		P:GO:0051091	P:positive regulation of DNA-binding transcription factor activity	IPR008889 (PFAM); mobidb-lite (MOB	7,477	4,824	3,537	7,183	5,079					1,019	0,000			up
Solyc10g078450	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT2G43810.3)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:small nucleolar ribonucleo	IPR001163 (PFAM); G3DSA:2.30.30.1	37,496	40,033	50,953	49,498	48,589									
Solyc10g078460	phosphatidylinositol- 4-phosphate 5-kinase 5 (AHRD V3.3 *** AT2G41210.1)		F:GO:0005524; F:G(	F:ATP binding; F:1-(EC:2.7.1.68 1-phosphatidylinosito	IPR027483 (G3DSA:3.30.810.GENE3I	0,038	0,057	0,000	0,000	0,000									
Solyc10g078470	Tryptophan/tyrosine permease (AHRD V3.3 *** AT2G33260.2)		P:GO:0003333; C:G(	P:amino acid transmembrane transport; C:integral component o(	IPR018227 (PFAM); IPR013059 (PAN	1,052	1,332	0,181	0,272	0,117									
Solyc10g078480	Chitobiosyldiphosphodolichol beta-mannosyltransferase (AHRD V3.3 *** A0A0B2R215_GLYSO)		F:GO:0000030	F:mannosyltransferase activity	PF13692 (PFAM); IPR028098 (PFAM)	25,009	26,349	33,134	32,263	31,533									
Solyc10g078490	ripening-related mRNA	SIP1.2	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS); IPR023271 (G3	10,136	14,745	12,991	11,029	11,885									
Solyc10g078495	Aquaporin SIP1-1 (AHRD V3.3 *-* W9R1G9_9ROSA)		F:GO:0015267; C:G(	F:channel activity; C:integral component of membrane; P:transn	IPR023271 (G3DSA:1.20.1080.GENE	0,734	1,013	0,265	0,070	0,095									
Solyc10g078510	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SHH6_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D); IPR01:	0,619	0,550	0,641	0,616	0,752									
Solyc10g078520	PHD finger protein ING (AHRD V3.3 *** K4D294_SOLLC)		C:GO:0005634; P:G(	C:nucleus; P:chromatin organization; F:methylated histone bindi	IPR013083 (G3DSA:3.30.40.GENE3D	8,143	6,742	9,390	9,225	8,861									
Solyc10g078530	Patatin (AHRD V3.3 *** M1C6Q0_SOLTU)		P:GO:0006629	P:lipid metabolic process	G3DSA:3.40.1090.10 (GENE3D); mob	35,833	48,168	3,646	7,888	5,270					1,115	0,000			up
Solyc10g078540	H/ACA ribonucleoprotein complex subunit 1-like protein 1, putative, expressed (AHRD V3.3 *-* Q2R242_ORY		P:GO:0001522; C:G(	P:pseudouridine synthesis; C:box H/ACA snoRNP complex; P:ri	IPR038664 (G3DSA:2.40.10.GENE3D	14,947	18,913	14,189	12,136	11,841									
Solyc10g078550	glutamate dehydrogenase	gdh1	P:GO:0006520; F:G(	P:cellular amino acid metabolic process; F:oxidoreductase activ	IPR006095 (PRINTS); IPR014362 (PII	0,019	0,019	0,000	0,047	0,023									
Solyc10g078560	Chaperone DnaJ-domain superfamily protein		C:GO:0005737; C:G(	C:cytoplasm; C:integral component of membrane; P:protein refo	IPR001623 (PRINTS); IPR001623 (PF	4,658	3,898	5,223	5,426	5,813									
Solyc10g078570	LOW QUALITY:Serine/Threonine kinase family protein (AHRD V3.3 --* G7K3Q2_MEDTR)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,257	0,277	0,094	0,237	0,259									
Solyc10g078580	Arabinogalactan peptide 14 (AHRD V3.3 *** AGP14_ARATH)		F:GO:0005515; C:G(	F:protein binding; C:integral component of membrane; C:anchor	PTHR34114:SF2 (PANTHER); IPR039	1,786	2,795	0,258	0,435	0,422									
Solyc10g078590	transmembrane protein (AHRD V3.3 *** AT5G18130.1)		C:GO:0016021	C:integral component of membrane	PTHR33646:SF2 (PANTHER); PTHR3:	60,846	50,450	54,247	55,363	50,596									
Solyc10g078600	Inorganic phosphate transporter 1-1 (AHRD V3.3 --* PHT11_ORYSJ)					22,065	26,409	20,514	28,114	22,941					0,460	0,033			up
Solyc10g078610	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RCL9_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg	IPR001471 (PRIN ERF	0,019	0,018	0,165	0,220	0,048									
Solyc10g078620	Ribosomal protein S5/S7 (AHRD V3.3 *** A0A103XH68_CYNCS)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos	IPR036823 (G3DSA:1.10.455.GENE3I	377,493	428,697	296,538	268,382	285,307									
Solyc10g078630	40S ribosomal protein S28 (AHRD V3.3 *-* W9SEX7_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR000289 (PFAM); G3DSA:2.40.50.1	262,467	294,602	213,539	196,553	199,385									
Solyc10g078660	60S ribosomal protein L24 (AHRD V3.3 *** B9MYJ4_POPTR)		P:GO:0000027; F:G(	P:ribosomal large subunit assembly; F:RNA binding; F:structural	IPR000988 (PFAM); IPR038630 (G3D	79,700	83,267	75,256	70,570	71,506									
Solyc10g078670	BZIP transcription factor family protein (AHRD V3.3 *** A0A061EYD6_THECC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	G3DSA:1.20.5.17(bZIP	1,515	2,955	1,341	4,269	1,487					1,671	0,000			up
Solyc10g078680	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072TGP1_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR035892 (G3DSA:2.60.40.GENE3D	4,221	4,323	0,025	0,145	0,071									
Solyc10g078690	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein (AHRD V3.3 ***		C:GO:0042721; P:G(	C:TIM22 mitochondrial import inner membrane insertion comple:	PF02466 (PFAM); PTHR14110:SF4 (F	109,423	111,066	177,120	149,544	163,144									
Solyc10g078700	Squamosa promoter binding protein 15		F:GO:0003677; C:G(	F:DNA binding; C:nucleus	IPR004333 (PFAM SBP	11,293	8,921	0,729	0,499	0,610									
Solyc10g078710	rho GTPase-activating gacO-like protein (AHRD V3.3 *** AT3G57930.2)		F:GO:0003677	F:DNA binding	IPR017956 (PRINTS); mobidb-lite (MO	35,625	33,773	24,421	22,263	25,713									
Solyc10g078720	Myb family transcription factor family protein (AHRD V3.3 *** B9HAD3_POPTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(G2-like	0,141	0,278	0,290	0,197	0,328									
Solyc10g078730	Non-structural maintenance of chromosome element 4 (AHRD V3.3 *** A0A103Y6P5_CYNCS)		C:GO:0005634; P:G(	C:nucleus; P:DNA repair; C:Smc5-Smc6 complex	IPR014854 (PFAM); mobidb-lite (MOB	6,231	6,818	5,596	5,272	5,798									
Solyc10g078740	Enoyl reductase (AHRD V3.3 *** P93062_BRANA)				IPR002347 (PRINTS); G3DSA:3.40.5(	48,452	48,189	43,503	47,447	53,027									
Solyc10g078750	Zinc finger transcription factor 59	C3H59	F:GO:0003723; F:G(	F:RNA binding; F:metal ion binding	IPR000571 (PFAM C3H	2,438	3,520	2,637	2,136	2,729									
Solyc10g078770	Seed maturation protein (AHRD V3.3 *** Q9LKC5_GLYTO)		P:GO:0009793	P:embryo development ending in seed dormancy	IPR005513 (PFAM); mobidb-lite (MOB	9,346	21,555	113,169	109,102	103,444									
Solyc10g078780	Seed maturation protein LEA 4 (AHRD V3.3 *** Q9FNX1_GLYCA)		P:GO:0009793	P:embryo development ending in seed dormancy	IPR005513 (PFAM); mobidb-lite (MOB	0,910	2,081	1,257	2,550	0,116									
Solyc10g078790	muniscin carboxy-terminal mu-like domain protein (AHRD V3.3 *** AT5G57460.1)		C:GO:0005886; C:G(	C:plasma membrane; C:chloroplast; P:pollen development; P:pr(	IPR018808 (PFAM); mobidb-lite (MOB	44,747	49,065	45,288	44,455	43,748									
Solyc10g078800	Protein phosphatase 2C family protein (AHRD V3.3 *-* AT5G06750.3)		F:GO:0004722; P:G(	F:protein serine/thr(EC:3.1.3.16 Protein-serine/threor	IPR001932 (PFAM); IPR036457 (G3D	0,000	0,019	0,025	0,000	0,000									
Solyc10g078820	Phosphatase 2C family protein (AHRD V3.3 *** A0A061F4N6_THECC)		F:GO:0004722; P:G(	F:protein serine/thr(EC:3.1.3.16 Protein-serine/threor	IPR001932 (PFAM); IPR036457 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc10g078830	Phosducin-like protein 3 (AHRD V3.3 *** A0A0K9PHG8_ZOSMR)				G3DSA:3.40.30.10 (GENE3D); IPR02(	39,990	43,923	53,772	47,679	45,657									
Solyc10g078840	Germin-like protein 1 (AHRD V3.3 *** B9N5Q7_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS); IPR014710 (G3	0,000	0,019	0,000	0,000	0,000									
Solyc10g078850	Germin-like protein 1 (AHRD V3.3 *** B9N5Q7_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS); IPR014710 (G3	0,021	0,000	0,000	0,000	0,000									
Solyc10g078860	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** K4D2C7_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA p(	IPR007641 (PFAM); G3DSA:3.90.107(	44,277	35,631	69,646	66,633	60,402									
Solyc10g078880	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** K4D2C9_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA p(	IPR007644 (PFAM); G3DSA:3.90.110(	0,920	1,093	1,709	0,980	1,443									
Solyc10g078890	Peroxidase (AHRD V3.3 *** K4D2D0_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS); IPR000823 (PF	0,678	3,573	0,000	0,000	0,000									
Solyc10g078900	Zinc finger family protein (AHRD V3.3 *** B9IIA0_POPTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity	mobidb-lite (MOBIDB_LITE); mobidb-lit	15,810	16,013	17,169	18,621	18,389									
Solyc10g078910	Protein trichome birefringence (AHRD V3.3 *** TBR_ARATH)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace	IPR025846 (PFAM); IPR026057 (PFA	113,848	91,885	26,481	31,432	33,660									
Solyc10g078920	Thioredoxin (AHRD V3.3 *** G7KVF9_MEDTR)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored(	G3DSA:3.40.30.10 (GENE3D); IPR01:	0,181	0,221	0,050	0,238	0,279									
Solyc10g078930	Activator of 90 kDa heat shock ATPase (AHRD V3.3 *** A0A0B0MWI3_GOSAR)		F:GO:0001671; F:G(	F:ATPase activator activity; F:chaperone binding; F:Hsp90 prot	IPR023393 (G3DSA:3.30.530.GENE3I	243,691	183,056	276,351	226,686	248,404									
Solyc10g078935	LOW QUALITY:low-molecular-weight cysteine-rich 37 (AHRD V3.3 -** AT4G13095.1)				IPR010851 (PFAM); IPR010851 (PAN	0,000	0,058	0,000	0,000	0,000									
Solyc10g078940	Kinase family protein (AHRD V3.3 *** B9HA11_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM); G3DSA:3.30.200	0,040	0,155	0,150	0,099	0,144									
Solyc10g078950	Carbon catabolite repressor 4-like protein (AHRD V3.3 *** A0A0B0P8G6_GOSAR)		F:GO:0004535; P:G(	F:poly(A)-specific ri EC:3.1.13; EC:3.1.1! Acting on ester bond:	IPR031615 (PFAM); IPR036691 (G3D	86,639	85,916	151,193	153,813	143,934									
Solyc10g078960	60S ribosomal protein L21-like protein (AHRD V3.3 *** Q3HVK5_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR036948 (G3DSA:2.30.30.GENE3D	453,301	487,899	356,052	328,564	342,478									
Solyc10g078980	Ankyrin repeat family protein (AHRD V3.3 --* AT3G18670.2)					0,097	0,079	0,093	0,047	0,000									
Solyc10g079000	LOW QUALITY:Transmembrane and coiled-coil domains protein (AHRD V3.3 *** K7W5R9_SOLTU)		F:GO:0005262; C:G(	F:calcium channel activity; C:integral component of endoplasmi(	IPR002809 (PFAM); IPR008559 (PIRS	16,479	18,243	24,243	25,034	23,968									
Solyc10g079010	Protein shisa-5 (AHRD V3.3 *** A0A0B0NQ09_GOSAR)		P:GO:0032259; F:G(	P:methylation; F:his EC:2.1.1.8 Histamine N-methyltr:	mobidb-lite (MOBIDB_LITE); mobidb-lit	70,928	72,886	67,432	67,916	70,294									
Solyc10g079050	BHLH transcription factor o95	bHLH095	F:GO:0046983	F:protein dimerization activity	IPR036638 (G3DS bHLH	1,356	0,876	15,418	14,383	12,353									
Solyc10g079070	bHLH transcription factor 065	bHLH065	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR036638 (G3DS bHLH	19,308	13,846	3,755	3,033	3,613									
Solyc10g079075	cellulose synthase like D4 (AHRD V3.3 --* AT4G38190.1)					0,594	0,194	0,047	0,025	0,000									
Solyc10g079080	stress-associated protein 5		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding	IPR000058 (PFAM); IPR035896 (G3D	66,574	63,660	85,266	85,689	74,357									
Solyc10g079090	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9SL79_RICCO)				IPR001623 (PRINTS); IPR001623 (PF	49,751	48,102	29,108	34,811	33,424									
Solyc10g079110	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** Q2Z1Y8_PRUMU)		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR002123 (PFAM); IPR032098 (PFA	10,840	11,145	4,307	3,249	5,023									
Solyc10g079120	Zinc finger transcription factor 60	C3H60	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding	IPR002110 (PRIN C3H	43,470	38,847	62,326	61,903	55,381									
Solyc10g079130	MAP kinase kinase kinase 76	MAPKKK76	F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR002048 (PFAM); G3DSA:1.10.238	155,083	203,503	40,869	58,624	67,460			0,720	0,005	0,521	0,014		up	up
Solyc10g079140	Guanylate kinase (AHRD V3.3 *** W9QSK2_9ROSA)		F:GO:0004385; F:G(	F:guanylate kinase EC:2.7.4.4; EC:2.7.4 Nucleoside-phosphat	IPR015915 (G3DSA:2.120.10.GENE3I	17,263	16,782	16,448	18,413	14,455									
Solyc10g079150	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR001289 (PRIN NF-YA	3,120	2,689	2,204	2,440	2,008									
Solyc10g079170	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072U3C5_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001611 (PFAM); IPR032675 (G3D	8,297	6,578	2,119	1,530	1,511									
Solyc10g079180	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G16580.1)		F:GO:0003824	F:catalytic activity	IPR001932 (PFAM); IPR036457 (G3D	0,057	0,085	0,025	0,050	0,000									
Solyc10g079190	Zinc finger transcription factor 61	C3H61	P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:nucleic acid binding; F:me	IPR012677 (G3DSA:3.30.70.GENE3D	55,058	40,504	36,610	33,734	34,965									
Solyc10g079200	Mitochondrial carrier protein (AHRD V3.3 *** B1N662_SOLLC)		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	11,232	16,122	4,248	4,583	5,205									
Solyc10g079210	glycosyltransferase-like protein		C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; C:plasma membrane; C:pl:	IPR008166 (PFAM); mobidb-lite (MOB	0,879	0,859	0,044	0,172	0,094									
Solyc10g079230	Unknown function		C:GO:0016021	C:integral component of membrane	IPR004158 (PFAM); PTHR31549:SF6	0,000	0,000	0,022	0,000	0,000									
Solyc10g079240	SUN-like protein 1	SUN1	F:GO:0005515	F:protein binding	IPR025064 (PFAM); IPR000048 (PFA	4,272	2,959	1,701	1,417	1,818									
Solyc10g079250	DNA repair protein recA (AHRD V3.3 *** A0A061GHC6_THECC)		F:GO:0003697; F:G(	F:single-stranded D EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR013765 (PRINTS); IPR013765 (TI(	6,933	5,572	8,971	11,146	9,732									
Solyc10g079260	uncharacterized protein		C:GO:0016020	C:membrane	IPR005349 (PFAM); G3DSA:1.20.58.1	22,400	24,048	32,831	33,510	30,645									
Solyc10g079280	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT5G04160.1)		C:GO:0005794; F:G(	C:Golgi apparatus; F:pyrimidine nucleotide-sugar transmembran	IPR004853 (PFAM); PTHR44010 (PAI	8,527	7,829	4,868	3,786	4,330									
Solyc10g079290	Outer envelope protein 80, chloroplastic (AHRD V3.3 *** OEP80_ARATH)		C:GO:0019867	C:outer membrane	G3DSA:2.40.160.50 (GENE3D); G3DS	6,519	6,218	6,997	5,756	6,847									
Solyc10g079300	Calcium-transporting ATPase (AHRD V3.3 *** M1AEH1_SOLTU)		F:GO:0005388; F:G(	F:calcium-transporti EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	IPR001757 (PRINTS); PR00119 (PRIN	0,371	0,527	0,000	0,170	0,070									
Solyc10g079310	tRNA-splicing endonuclease subunit Sen54 (AHRD V3.3 *** A0A0B0MEI8_GOSAR)		F:GO:0004519; P:G(	F:endonuclease activity; P:nucleic acid phosphodiester bond hy	IPR024336 (PFAM); mobidb-lite (MOB	5,196	5,636	5,487	6,542	5,603									
Solyc10g079320	Glycosyltransferase (AHRD V3.3 *** K4D2H3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); G3D	0,061	0,097	0,022	0,000	0,000									
Solyc10g079340	Glycosyltransferase (AHRD V3.3 *** K4D2H5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM); G3DSA:3.40.50.2	0,021	0,000	0,000	0,000	0,000									
Solyc10g079345	Glycosyltransferase (AHRD V3.3 *-* M1AEG6_SOLTU)		F:GO:0008194; F:G(	F:UDP-glycosyltransferase activity; F:transferase activity, trans	G3DSA:3.40.50.2000 (GENE3D); PTH	0,000	0,000	0,022	0,000	0,024									
Solyc10g079350	Glycosyltransferase (AHRD V3.3 *** K4D2H6_SOLLC)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:transferase acti	IPR000812 (PRINTS); G3DSA:1.10.47	1,819	1,757	1,252	0,995	1,035									
Solyc10g079360	Transcription initiation factor iib, putative (AHRD V3.3 *** B9T8A1_RICCO)		P:GO:0006355; P:G(	P:regulation of transcription, DNA-templated; P:transcription pre	IPR000812 (PRINTS); IPR013137 (PF	1,337	0,962	0,714	0,711	0,777									
Solyc10g079370	Transcription initiation factor IIB (AHRD V3.3 *** TF2B_SOYBN)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:TBP-class prote	IPR000812 (PRINTS); G3DSA:1.10.47	97,993	84,902	128,509	97,855	107,189					-0,391	0,026			down
Solyc10g079380	SolycHsfB3b	HSF-19	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR000232 (PRIN HSF	0,000	0,000	0,000	0,069	0,000									
Solyc10g079390	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT3G57400.1)		C:GO:0016021	C:integral component of membrane	PTHR34960 (PANTHER)	0,461	0,133	0,046	0,069	0,094									
Solyc10g079400	villin 2 (AHRD V3.3 *-* AT2G41740.2)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly	IPR007122 (PRINTS); IPR007123 (PF	0,019	0,000	0,000	0,000	0,000									
Solyc10g079405	villin 2 (AHRD V3.3 *** AT2G41740.2)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly	IPR007122 (PRINTS); IPR029006 (G3	0,058	0,062	0,000	0,000	0,000									
Solyc10g079410	Triacylglycerol lipase SDP1 (AHRD V3.3 *** W9RS42_9ROSA)		F:GO:0004806; P:G(	F:triglyceride lipase EC:3.1.1.1; EC:3.1.1 Carboxylesterase; Tr	IPR021771 (PFAM); IPR002641 (PFA	13,932	7,245	1,342	0,434	1,172	-0,912	0,009					down		
Solyc10g079420	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XQG1_CYNCS)		F:GO:0005509	F:calcium ion binding	IPR002048 (PFAM); G3DSA:1.10.238	275,742	116,981	43,638	97,620	70,119	-1,212	0,000	0,682	0,015	1,163	0,000	down	up	up
Solyc10g079430	U3 small nucleolar RNA-associated protein 11 (AHRD V3.3 *** A5B5S2_VITVI)		P:GO:0006364; C:G(	P:rRNA processing; C:small-subunit processome	IPR007144 (PFAM); IPR007144 (PIRS	10,668	13,580	9,163	8,311	8,669									
Solyc10g079440	FAD-dependent oxidoreductase family protein (AHRD V3.3 *** AT3G56840.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR006076 (PFAM); G3DSA:3.30.9.1(	5,189	4,863	4,081	3,993	4,536									
Solyc10g079450	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT3G10200.1)		F:GO:0008168	F:methyltransferase activity	IPR004159 (PFAM); G3DSA:3.40.50.1	28,480	26,075	30,734	33,575	28,670									
Solyc10g079460	BTB/POZ ankyrin repeat protein (AHRD V3.3 *** G8GTN4_MEDTR)		F:GO:0005515	F:protein binding	IPR036770 (G3DSA:1.25.40.GENE3D	0,042	0,037	0,000	0,000	0,000									
Solyc10g079470	gldhL-galactono-1,4-lactone dehydrogenase	GLDH	F:GO:0003885; C:G(	F:D-arabinono-1,4-l EC:1.1.3.37; EC:1.3. D-arabinono-1,4-lact(	IPR006094 (PFAM); IPR010031 (PIRS	35,844	35,962	18,108	15,738	18,811									
Solyc10g079480	Lycopene beta-cyclase (AHRD V3.3 *** A0A0U2DBC9_LYCCN)	B-LCY2	P:GO:0016117; F:G(	P:carotenoid biosynthetic process; F:oxidoreductase activity, a	IPR010108 (TIGRFAM); IPR036188 ((	1,146	1,169	0,097	0,169	0,282									
Solyc10g079490	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061E0L4_T		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM); PTHR19297:SF9:	11,308	10,938	6,582	7,358	8,632									
Solyc10g079500	Inosine-5'-monophosphate dehydrogenase (AHRD V3.3 *** K4D2J1_SOLLC)		F:GO:0003938; P:G(	F:IMP dehydrogena EC:1.1.1.25 IMP dehydrogenase	IPR005990 (PIRSF); IPR001093 (PFA	165,310	125,126	177,310	161,908	173,136									
Solyc10g079510	RAD3-like DNA-binding helicase protein (AHRD V3.3 *** AT1G20720.2)		F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR006555 (PFAM); mobidb-lite (MOB	2,131	1,746	0,426	0,234	0,141									
Solyc10g079515	RAD3-like DNA-binding helicase protein (AHRD V3.3 *-* AT1G20720.2)		F:GO:0005524	F:ATP binding	G3DSA:3.40.50.300 (GENE3D); mobic	0,313	0,152	0,025	0,025	0,070									
Solyc10g079520	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50170.1)		C:GO:0016021	C:integral component of membrane	IPR004158 (PFAM); PTHR31549:SF6	0,078	0,094	0,000	0,000	0,071									
Solyc10g079530	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50170.1)		C:GO:0016021	C:integral component of membrane	IPR004158 (PFAM); mobidb-lite (MOB	0,042	0,172	0,000	0,025	0,023									
Solyc10g079540	O-methyltransferase (AHRD V3.3 *** A0A1B4Z3W3_9ROSA)	ASMT11	F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity	IPR016461 (PIRSF); IPR012967 (PFA	0,021	0,021	0,025	0,000	0,000									
Solyc10g079550	Mitochondria fission 1 (AHRD V3.3 *** A0A0B0PYJ7_GOSAR)		P:GO:0000266; F:G(	P:mitochondrial fission; F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,641	1,975	0,611	0,578	0,589									
Solyc10g079560	Glutaredoxin family protein (AHRD V3.3 *** B9H950_POPTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	IPR002109 (PFAM); G3DSA:3.40.30.1	12,240	9,529	9,498	7,189	8,735									
Solyc10g079570	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR003480 (PFAM); IPR023213 (G3D	0,021	0,000	14,181	10,348	7,429			-0,934	0,013				down	
Solyc10g079580	RNA-binding region RNP-1 protein (AHRD V3.3 *** G7IZ45_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	26,623	25,412	54,069	52,230	51,349									
Solyc10g079590	LOW QUALITY:histidine-tRNA ligase (AHRD V3.3 *** AT3G10250.5)				IPR006476 (TIGRFAM); IPR006476 (F	0,909	0,745	0,173	0,151	0,024									
Solyc10g079600	Two-component response regulator (AHRD V3.3 *** W9RA85_9ROSA)	TRR 8A	P:GO:0000160	P:phosphorelay signal transduction system	G3DSA:3.40.50.2300 (GENE3D); IPR(	0,583	0,823	0,270	0,241	0,331									
Solyc10g079610	Strictosidine synthase, putative (AHRD V3.3 *** B9T2X5_RICCO)		P:GO:0009058; F:G(	P:biosynthetic proc EC:4.3.3.2 Strictosidine synthas	IPR018119 (PFAM); IPR011042 (G3D	30,086	24,922	47,925	46,572	42,954									
Solyc10g079620	haloacid dehalogenase		F:GO:0016787	F:hydrolase activity	IPR006439 (PRINTS); G3DSA:1.10.15	19,746	12,597	8,707	8,603	7,984									
Solyc10g079630	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G50940.1)		F:GO:0005524	F:ATP binding	IPR025753 (PFAM); G3DSA:3.40.50.3	0,098	0,228	0,000	0,000	0,000									
Solyc10g079640	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9RJ28_RICCO)		F:GO:0016787	F:hydrolase activity	G3DSA:3.40.630.10 (GENE3D); IPR0(	3,083	4,516	1,013	0,988	1,216									
Solyc10g079650	bHLH transcription factor 066	bHLH066	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase	IPR036638 (G3DS bHLH	0,000	0,021	0,000	0,000	0,000									
Solyc10g079660	bHLH transcription factor 067	bHLH067	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription by RNA polymerase	IPR036638 (G3DS bHLH	0,000	0,021	0,000	0,000	0,000									
Solyc10g079670	Zinc phosphodiesterase ELAC 2 (AHRD V3.3 *** A0A0B0NN53_GOSAR)		F:GO:0016891; P:G(	F:endoribonuclease EC:3.1.3; EC:3.1.26 Acting on ester bond:	IPR036866 (G3DSA:3.60.15.GENE3D	0,975	1,136	1,257	1,067	1,204									
Solyc10g079690	callose synthase 1 (AHRD V3.3 --* AT1G05570.4)				IPR037466 (PANTHER); PTHR38928:	0,588	0,985	17,535	25,380	12,340									
Solyc10g079700	Two-component response regulator (AHRD V3.3 *** A0A059T9P7_ROSCN)		P:GO:0000160	P:phosphorelay signal transduction system	G3DSA:3.40.50.2300 (GENE3D); IPR(	0,496	0,573	0,296	0,197	0,046									
Solyc10g079710	Two-component response regulator (AHRD V3.3 *-* W9RA85_9ROSA)		P:GO:0000160	P:phosphorelay signal transduction system	IPR006476 (TIGRFAM); IPR001789 (F	10,931	10,408	16,973	19,092	15,411									
Solyc10g079720	Cystathionine beta-lyase		F:GO:0004121; F:G(	F:cystathionine bet: EC:4.4.1.8 Cystathionine beta-ly	IPR015421 (G3DSA:3.40.640.GENE3I	25,732	28,026	56,334	54,672	52,115									
Solyc10g079730	Condensin complex subunit 1 (AHRD V3.3 *** K4D2L4_SOLLC)		C:GO:0005634; P:G(	C:nucleus; P:mitotic chromosome condensation	IPR024324 (PFAM); IPR007673 (PIRS	3,127	2,773	2,828	2,788	3,852									
Solyc10g079740	HAUS augmin-like complex subunit (AHRD V3.3 *** AT2G41350.1)		P:GO:0051225; C:G(	P:spindle assembly; C:HAUS complex	IPR026243 (PRINTS); IPR026243 (PA	23,486	22,385	26,098	26,419	24,147									
Solyc10g079750	BTB/POZ ankyrin repeat protein (AHRD V3.3 *** G8GTN4_MEDTR)		F:GO:0005515	F:protein binding	G3DSA:3.30.710.10 (GENE3D); IPR0:	0,754	0,667	0,022	0,122	0,117									
Solyc10g079755	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XQG1_CYNCS)		F:GO:0005509	F:calcium ion binding	G3DSA:1.10.238.10 (GENE3D); IPR0(	182,142	89,764	83,920	141,724	103,632	-0,993	0,000			0,759	0,000	down		up
Solyc10g079770	Triacylglycerol lipase SDP1 (AHRD V3.3 *** W9RS42_9ROSA)		F:GO:0004806; P:G(	F:triglyceride lipase EC:3.1.1.1; EC:3.1.1 Carboxylesterase; Tr	G3DSA:3.40.1090.10 (GENE3D); IPR(	28,395	29,426	35,102	35,849	34,776									
Solyc10g079780	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 (AHRD V3.3 -** DAD1_ORYSI)					0,341	0,332	0,356	0,612	0,329									
Solyc10g079790	Plant calmodulin-binding-like protein (AHRD V3.3 *-* G7KRQ7_MEDTR)		F:GO:0005516	F:calmodulin binding	IPR012417 (PFAM); mobidb-lite (MOB	6,466	5,168	0,966	0,657	0,844									
Solyc10g079810	LOW QUALITY:mediator of RNA polymerase II transcription subunit (AHRD V3.3 --* AT2G10440.2)				PTHR38223 (PANTHER)	0,084	0,369	0,428	1,006	0,423									

Solyc10g079820	Dehydration-induced protein ERD15 (AHRD V3.3 *** Q9LKW3_SOLLC)						IPR009818 (PFAM): mobidb-lite (MOB	232,691	248,555	199,242	207,620	200,358									
Solyc10g079830	7,8-dihydroneopterin aldolase (AHRD V3.3 *** A0A068UQN4_COFCA)		F:GO:0004150; P:G(	F:dihydroneopterin :	EC:4.1.2.25	Dihydroneopterin ald	G3DSA:3.30.1130.10 (GENE3D): IPR(	21,968	19,641	15,400	12,640	13,782									
Solyc10g079840	Peptide chain release factor 2 (AHRD V3.3 *** A0A0B0MIC9_GOSAR)		F:GO:0003747; P:G(	F:translation release factor activity; P:translational termination			IPR000352 (PFAM); G3DSA:3.30.70.1	3,915	6,376	1,866	2,094	3,221									
Solyc10g079850	AP-5 complex subunit beta-like protein (AHRD V3.3 *** AT3G19870.2)		P:GO:0016197	P:endosomal transport			mobidb-lite (MOBIDB_LITE): mobidb-lit	36,533	30,957	50,098	56,590	51,205									
Solyc10g079860	LEQB L.esculentum TomQ'b beta(1,3)glucanase	tomqb	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00(	0,648	3,504	22,867	43,531	63,546			1,469	0,005	0,932	0,017		up	up
Solyc10g079870	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUR0_SOLLC)		P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	IPR015345 (PFAM): IPR016169 (G3D	0,752	1,221	3,414	9,346	6,755			0,983	0,002	1,458	0,000		up	up
Solyc10g079880	Eukaryotic translation initiation factor 3 subunit E (AHRD V3.3 *** K4D2M9_SOLLC)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:eukaryotic translation in			G3DSA:1.25.40.570 (GENE3D): IPR0	122,342	137,719	121,944	119,058	116,101									
Solyc10g079890	Calcium-binding EF-hand family protein (AHRD V3.3 *** AT3G10300.3)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM); G3DSA:1.10.238	102,928	170,894	114,609	115,179	111,210									
Solyc10g079900	Rho termination factor (AHRD V3.3 --* AT4G18740.4)		P:GO:0006353	P:DNA-templated transcription, termination			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,219	0,158	0,022	0,022	0,000									
Solyc10g079910	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT5G04160.1)		C:GO:0005794; F:G(	C:Golgi apparatus; F:pyrimidine nucleotide-sugar transmembran			IPR004853 (PFAM); PTHR44010:SF2	0,337	0,280	0,097	0,025	0,144									
Solyc10g079920	Transmembrane protein, putative (AHRD V3.3 *** G7L3Y1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR029164 (PFAM); PTHR36485 (PAN	7,125	7,513	4,190	4,833	4,584									
Solyc10g079930	Glycosyltransferase (AHRD V3.3 *** K4D2N4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	21,183	45,310	9,547	11,038	18,268	1,119	0,020	0,931	0,000			up	up	
Solyc10g079940	LOW QUALITY:Glycosyltransferase (AHRD V3.3 *-* K4D2N4_SOLLC)		F:GO:0008194; F:G(	F:UDP-glycosyltransferase activity; F:transferase activity, trans			SSF53756 (SUPERFAMILY)	0,331	0,549	0,959	1,215	1,177									
Solyc10g079950	Glycosyltransferase (AHRD V3.3 *** K4D2N6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	24,855	25,951	68,429	80,681	72,981									
Solyc10g079960	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (AHRD V3.3 *-* A0A151RD44_C		F:GO:0000829; F:G(	F:inositol heptakisp	EC:2.7.4.24; EC:2.7.	Diphosphoinositol-pe	IPR040557 (PFAM); G3DSA:3.40.50.1	0,933	1,003	0,823	0,770	0,894									
Solyc10g079970	Transmembrane 19 (AHRD V3.3 *** A0A0B0P5R4_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR002794 (PFAM): IPR002794 (PAN	47,407	32,866	28,379	25,872	28,713									
Solyc10g079980	Glycosyltransferase (AHRD V3.3 *** K4D2N9_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	3,626	6,018	0,264	0,187	0,404									
Solyc10g079990	Transcription initiation factor IIB (AHRD V3.3 *** TF2B_SOYBN)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:TBP-class prote			IPR000812 (PRINTS); G3DSA:1.10.47	12,270	13,063	8,132	9,189	8,567									
Solyc10g080000	Folylpolyglutamate synthetase family protein (AHRD V3.3 --* AT5G41480.1)							0,000	0,000	0,025	0,022	0,000									
Solyc10g080010	Glycosyltransferase (AHRD V3.3 *** Q5QPZ6_MEDTR)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR007657 (PFAM); PTHR20961:SF3(	10,108	4,324	6,269	11,339	11,738	-1,199	0,048	0,896	0,040	0,851	0,031	down	up	up
Solyc10g080020	F-box/LRR protein (AHRD V3.3 *** AT5G63520.1)						IPR019494 (PFAM); PTHR14939:SF7	22,658	14,804	52,539	45,874	49,354	-0,585	0,033					down		
Solyc10g080030	MADS-box transcription factor (AHRD V3.3 *** A0A072VJL7_MEDTR)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINT MIKC_MADS	1,067	1,352	0,237	0,096	0,516									
Solyc10g080040	Ribonuclease III family protein (AHRD V3.3 *-* AT4G37510.1)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bond	IPR036389 (G3DSA:1.10.1520.GENE	4,014	5,354	8,858	7,858	8,127									
Solyc10g080045	Ribonuclease III family protein (AHRD V3.3 *-* AT4G37510.1)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bond	IPR036389 (G3DSA:1.10.1520.GENE	3,809	4,563	7,994	7,644	8,806									
Solyc10g080050	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT2G41660.1)						IPR006460 (PFAM); IPR006460 (TIGF	0,021	0,000	0,000	0,025	0,000									
Solyc10g080060	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *-* AT2G41660.1)						IPR006460 (TIGRFAM); IPR006460 (F	0,000	0,039	0,000	0,000	0,000									
Solyc10g080070	Mitochondrial GTPase 1 (AHRD V3.3 *** A0A0B0PKU7_GOSAR)		F:GO:0005525	F:GTP binding			IPR006073 (PFAM); IPR023179 (G3D	5,656	6,938	8,979	7,298	7,672									
Solyc10g080090	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061G8Z6_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR025525 (PFAM); IPR008906 (PFA	15,825	18,076	23,527	25,131	22,746									
Solyc10g080100	villin 2 (AHRD V3.3 *** AT2G41740.2)		F:GO:0051015; P:G(	F:actin filament binding; P:actin filament bundle assembly			IPR007122 (PRINTS); IPR003128 (PF	15,211	14,330	6,192	8,875	7,052									
Solyc10g080110	Cytoplasmic tRNA 2-thiolation protein 2 (AHRD V3.3 *-* K4D2Q2_SOLLC)		F:GO:0000049; P:G(	F:tRNA binding; P:tRNA wobble uridine modification; P:tRNA thic			IPR019407 (PFAM); IPR019407 (PAN	8,154	8,704	12,436	10,668	10,432									
Solyc10g080115	Cytoplasmic tRNA 2-thiolation protein 2 (AHRD V3.3 *** K4D2Q2_SOLLC)		F:GO:0000049; P:G(	F:tRNA binding; P:tRNA wobble uridine modification; P:tRNA thic			IPR014729 (G3DSA:3.40.50.GENE3D	8,041	7,458	12,121	11,776	11,121									
Solyc10g080120	LOW QUALITY:NADH-ubiquinone oxidoreductase chain 5 (AHRD V3.3 *-* NU5M_OENBE)		C:GO:0005743; F:G(	C:mitochondrial inne	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM); PTHR42829 (PAN	0,000	0,000	0,025	0,025	0,024									
Solyc10g080130	Exosome complex component RRP43 (AHRD V3.3 *** A0A0B2Q2J1_GLYSO)		C:GO:0005829	C:cytosol			IPR001247 (PFAM); IPR027408 (G3D	5,928	4,020	4,034	2,785	1,862			-1,120	0,008				down	
Solyc10g080140	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT4G13030.3)						PTHR34799 (PANTHER)	0,019	0,021	0,000	0,000	0,000									
Solyc10g080150	Methyltransferase (AHRD V3.3 *** K4D2Q6_SOLLC)		P:GO:0006694; F:G(	P:steroid biosynthetic process; F:methyltransferase activity			IPR013216 (PFAM); G3DSA:3.40.50.1	2,970	3,709	1,634	1,526	2,176									
Solyc10g080160	Ribosomal protein S9, putative (AHRD V3.3 *** B9RIU9_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000754 (PFAM); IPR014721 (G3D	38,434	41,766	51,123	46,764	46,040									
Solyc10g080180	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G14050.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM); IPR015943 (G3D	29,069	34,202	26,177	24,873	22,890									
Solyc10g080190	LOW QUALITY:Ozone-responsive stress related protein (AHRD V3.3 *** I0J1A1_ORYRU)		C:GO:0016021	C:integral component of membrane			IPR009515 (PFAM); IPR009515 (PAN	42,397	39,398	99,218	87,702	96,689									
Solyc10g080200	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 16 (AHRD V3.3 *** W9RRL3_9ROS		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			PF13894 (PFAM): C2H2	9,791	9,146	8,733	8,528	9,319									
Solyc10g080210	polygalacturonase	PG14 (pTOM6)	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3I	15,093	59,006	11740,023	14526,518	11421,865									
Solyc10g080220	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061EY03_THECC)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR032867 (PFAM); IPR002885 (PFA	2,054	2,248	1,848	2,508	2,471									
Solyc10g080230	Remorin family protein (AHRD V3.3 *** A0A061F452_THECC)						IPR005516 (PFAM); mobidb-lite (MOB	43,914	45,179	22,229	27,160	28,282									
Solyc10g080240	Remorin family protein (AHRD V3.3 *-* A0A061F452_THECC)						IPR005516 (PFAM); PTHR31471:SF7	13,959	15,969	8,194	9,345	10,025									
Solyc10g080250	cyclin-dependent kinase inhibitor (AHRD V3.3 --* AT5G02220.1)		P:GO:0032875	P:regulation of DNA endoreduplication			IPR040389 (PANTHER); PTHR33142:	0,000	0,021	0,196	0,289	0,071									
Solyc10g080260	Zinc finger transcription factor 62	C3H62	F:GO:0005515; F:G(	F:protein binding; F:metal ion binding			G3DSA:1.10.150.8 C3H	19,175	25,477	32,808	37,466	34,996									
Solyc10g080280	RING/FYVE/PHD zinc finger superfamily protein, putative (AHRD V3.3 *** A0A061GYX1_THECC)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 (GENE3D): IPR01:	43,659	48,602	33,599	30,138	34,455									
Solyc10g080310	Dehydration responsive element binding transcription factor (AHRD V3.3 *-* W6FTE8_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINT ERF	0,081	0,099	0,118	0,100	0,070									
Solyc10g080320	Adenylosuccinate synthetase, chloroplastic (AHRD V3.3 *** K4D2S2_SOLLC)		F:GO:0004019; F:G(	F:adenylosuccinate	EC:6.3.4.4	Adenylosuccinate sy	G3DSA:3.40.440.10 (GENE3D): IPR0(	78,579	77,290	88,815	82,006	81,019									
Solyc10g080330	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S1X9_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR011990 (G3D	0,670	0,448	0,860	0,656	0,992									
Solyc10g080340	Protein DETOXIFICATION (AHRD V3.3 *** K4D2S4_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM); IPR002528 (F	0,974	1,089	0,193	0,025	0,162									
Solyc10g080350	DNA-directed RNA polymerase subunit (AHRD V3.3 *** K4D2S5_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:3.30.1490.180 (GENE3D): G3	55,260	50,543	57,954	55,045	54,180									
Solyc10g080370	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 -** G7IZE0_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR33659 (PANTHER); PTHR33659	1,529	2,351	1,033	1,446	1,571									
Solyc10g080380	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 -** A0A072VTU6_MEDTR)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			PTHR33659:SF2 (PANTHER); PTHR3:	0,161	0,105	0,050	0,094	0,093									
Solyc10g080390	Kinase family protein (AHRD V3.3 *-* B9GW98_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	44,327	29,279	2,847	2,244	2,950									
Solyc10g080393	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 --* AT1G14130.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM); IPR027443 (G3D	0,196	0,205	0,000	0,000	0,000									
Solyc10g080397	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q2R149_ORYSJ)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); PTHR23272 (PAN	0,021	0,021	0,000	0,000	0,000									
Solyc10g080400	Uv-b-insensitive 4, putative (AHRD V3.3 *** A0A061EX89_THECC)		C:GO:0005634; P:G(	C:nucleus; P:regulation of nuclear division; P:negative regulatio			mobidb-lite (MOBIDB_LITE): mobidb-lit	3,172	4,531	0,975	0,223	0,212									
Solyc10g080410	BZIP family transcription factor (AHRD V3.3 *** G7KUH7_MEDTR)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM bZIP	2,390	1,926	0,287	0,271	0,141									
Solyc10g080420	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072TGP1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR035892 (G3DSA:2.60.40.GENE3D	111,744	95,533	85,036	80,168	79,149									
Solyc10g080430	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072TGP1_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR013583 (PFAM); IPR035892 (G3D	0,538	0,575	0,165	0,145	0,118									
Solyc10g080440	Tubulin binding cofactor C domain-containing protein (AHRD V3.3 *** AT3G57890.1)		P:GO:0000902	P:cell morphogenesis			IPR012945 (PFAM); IPR016098 (G3D	104,174	99,133	147,075	137,511	132,144									
Solyc10g080450	rho GTPase-activating gacO-like protein (AHRD V3.3 *** AT3G57930.2)		F:GO:0003677	F:DNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	13,828	13,039	9,933	8,012	7,586									
Solyc10g080460	Myb family transcription factor family protein (AHRD V3.3 *** B9HAD3_POPTR)		F:GO:0003677	F:DNA binding			IPR025756 (PFAM G2-like	0,000	0,083	0,025	0,025	0,023									
Solyc10g080480	Zinc finger transcription factor 63	C3H63	F:GO:0003723; F:G(	F:RNA binding; F:metal ion binding			G3DSA:4.10.1000 C3H	9,723	11,096	11,693	9,663	9,082									
Solyc10g080490	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT2G42130.4)						IPR006843 (PFAM); PTHR31906:SF1(	5,587	8,290	9,355	7,077	10,169									
Solyc10g080500	actin		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS); G3DSA:3.90.64	91,821	108,025	55,488	63,452	72,546			0,384	0,039				up	
Solyc10g080510	clade XII lectin receptor kinase		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:3.30.200	0,000	0,021	0,000	0,000	0,000									
Solyc10g080520	catalase chaperon NCA1-like		F:GO:0005515	F:protein binding			PF13920 (PFAM); IPR013083 (G3DS/	84,070	90,792	100,453	97,450	97,120									
Solyc10g080530	Growth-regulating factor (AHRD V3.3 --* A0A072U430_MEDTR)		C:GO:0005634; P:G(	C:nucleus; P:transcription, DNA-templated; P:developmental prc			IPR014977 (PFAM); mobidb-lite (MOB	2,408	2,690	0,551	0,537	0,823									
Solyc10g080540	homeobox leucine zipper protein (AHRD V3.3 *** AT5G06710.1)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003106 (PFAM HD-ZIP	1,120	0,619	0,069	0,050	0,095									
Solyc10g080550	Protein trichome birefringence (AHRD V3.3 *** TBR_ARATH)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM); IPR025846 (PFA	6,994	6,717	10,270	5,907	10,222					-0,794	0,001			down
Solyc10g080560	DNA-3-methyladenine glycosylase (AHRD V3.3 *** A0A0B2SK54_GLYSO)		F:GO:0003677; F:G(	F:DNA binding; F:all	EC:3.2.2.21	DNA-3-methyladenine	IPR003180 (TIGRFAM); IPR003180 (F	1,569	2,046	4,082	3,165	4,060									
Solyc10g080570	E3 ubiquitin-protein ligase (AHRD V3.3 *** K4D2U7_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal			IPR008974 (G3DSA:2.60.210.GENE3I	0,237	0,161	0,190	0,072	0,141									
Solyc10g080580	Kinase family protein (AHRD V3.3 *** B9HA11_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,000	0,021	0,000	0,025	0,000									
Solyc10g080590	60S ribosomal protein L21-like protein (AHRD V3.3 *** Q3HVK5_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001147 (PFAM); IPR036948 (G3D	87,796	87,800	66,330	57,358	59,832									
Solyc10g080600	Zinc finger family protein (AHRD V3.3 *** B9HA00_POPTR)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM); G3DSA:3.30.160.6(	0,078	0,222	0,000	0,000	0,000									
Solyc10g080610	F-box/kelch-repeat protein (AHRD V3.3 *** A0A172MAC1_VITPS)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	221,257	233,101	64,183	40,803	70,428					-0,651	0,006			down
Solyc10g080620	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2 A, chloroplastic (AHRD V3.3 --* NU2C1_HORVU)							0,373	0,405	0,000	0,000	0,000									
Solyc10g080630	ripening related X72734		F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; C:nucleus			IPR015943 (G3DSA:2.130.10.GENE3I	75,666	61,946	95,106	104,111	93,562									
Solyc10g080640	calmodulin-binding family protein (AHRD V3.3 *** AT3G13600.2)						mobidb-lite (MOBIDB_LITE): PTHR312	0,021	0,021	0,000	0,000	0,000									
Solyc10g080660	Eukaryotic translation initiation factor 4E (AHRD V3.3 *** G7KPL2_MEDTR)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:cytoplasm; P:translation			IPR001040 (PFAM); IPR023398 (G3D	110,058	107,185	122,006	126,459	128,096									
Solyc10g080670	Transmembrane protein, putative (AHRD V3.3 *** A2Q5V9_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR33646:SF2 (PANTHER); PTHR3:	17,615	23,550	58,203	81,641	59,739					0,491	0,028			up
Solyc10g080680	Adenylyl-sulfate kinase (AHRD V3.3 *** K4D2V8_SOLLC)		P:GO:0000103; F:G(	P:sulfate assimilatic	EC:2.7.1.25	Adenylyl-sulfate kinas	G3DSA:3.40.50.300 (GENE3D): PF01	11,874	13,762	15,630	15,119	14,713									
Solyc10g080690	Patatin (AHRD V3.3 *** K4D2V9_SOLLC)		P:GO:0006629	P:lipid metabolic process			IPR002641 (PFAM); G3DSA:3.40.109	7,085	33,902	0,910	0,786	1,056	2,287	0,000					up		
Solyc10g080700	Protein kinase family protein (AHRD V3.3 *** AT3G03940.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:1.10.510	147,639	137,755	127,295	107,367	121,456									
Solyc10g080710	asparaginyl-tRNA synthetase	ats1	F:GO:0003676; F:G(	F:nucleic acid bindi	EC:6.1.1.22	Asparagine--tRNA lig	IPR002312 (PRINTS); G3DSA:2.40.5(	170,082	139,115	172,998	155,921	154,371									
Solyc10g080715	Kinesin-like protein (AHRD V3.3 --* V4SQ41_9ROSI)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,740	1,898	0,850	0,659	1,035									
Solyc10g080720	Polypyrimidine tract-binding-like protein (AHRD V3.3 *** G7IBX9_MEDTR)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:mRNA processing			IPR000504 (PFAM); PF13893 (PFAM)	21,872	21,763	29,148	27,524	25,958									
Solyc10g080730	Thioredoxin, putative (AHRD V3.3 *** B9SHJ2_RICCO)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D): IPR01:	2,426	2,480	0,662	0,921	1,291									
Solyc10g080740	Telomerase activating protein Est1 (AHRD V3.3 *** A0A072UH06_MEDTR)		F:GO:0005515	F:protein binding			IPR019458 (PFAM); IPR011990 (G3D	124,237	119,018	132,874	140,415	141,010									
Solyc10g080750	phosphatidylinositol- 4-phosphate 5-kinase 5 (AHRD V3.3 *** AT2G41210.1)		F:GO:0005524; F:G(	F:ATP binding; F:1-(	EC:2.7.1.68	1-phosphatidylinosito	IPR027483 (G3DSA:3.30.810.GENE3I	0,000	0,043	0,000	0,000	0,000									
Solyc10g080760	Nudix hydrolase-like protein (AHRD V3.3 *** G7LGT1_MEDTR)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D): IPR00(	4,039	3,801	2,276	2,285	2,120									
Solyc10g080770	NPR1-interactor protein 1	npr1	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR004827 (PFAM bZIP	43,758	69,077	73,422	85,493	80,197									
Solyc10g080780	bZIP transcription factor family protein (AHRD V3.3 *** AT5G06950.5)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM); PTHR22952:SF2	17,808	16,967	20,452	18,916	19,215									
Solyc10g080810	Ubiquitin-associated domain-containing family protein (AHRD V3.3 *** B9H936_POPTR)		F:GO:0004252; F:G(	F:serine-type endo(	EC:3.4.21	Acting on peptide bor	IPR015940 (PFAM); IPR035952 (G3D	14,008	11,292	21,502	23,948	20,710									
Solyc10g080813	Cytochrome P450 (AHRD V3.3 *-* A2PZD4_IPONI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR036396 (G3DSA:1.10.630.GENE3I	0,115	0,092	0,022	0,069	0,164									
Solyc10g080815	Cytochrome P450 (AHRD V3.3 *-* A0A103Y9U2_CYNCS)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; C:integral compor			PTHR24296:SF1 (PANTHER); PTHR2	0,115	0,099	0,022	0,075	0,094									
Solyc10g080817	Cytochrome P450 (AHRD V3.3 *** A2PZD4_IPONI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,177	0,515	0,119	0,100	0,400									
Solyc10g080840	Cytochrome P450 (AHRD V3.3 *** A2PZD4_IPONI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS); IPR002401 (PF	37,411	15,761	716,535	1320,643	772,734	-1,219	0,002			0,887	0,000	down		up
Solyc10g080850	LOW QUALITY:plant U-box 17 (AHRD V3.3 --* AT1G29340.1)							0,000	0,000	0,046	0,271	0,000									
Solyc10g080855	Cytochrome P450 (AHRD V3.3 *-* A2PZD4_IPONI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR036396 (G3DSA:1.10.630.GENE3I	0,140	0,099	0,731	1,076	0,541									
Solyc10g080870	Cytochrome P450 (AHRD V3.3 *** A2PZD4_IPONI)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR002401 (PRINTS); IPR001128 (PF	0,084	0,043	4,472	4,627	2,227			-1,007	0,021				down	
Solyc10g080880	SIPIN7	PIN7	C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR014024 (TIGRFAM); IPR004776 (F	6,767	4,244	16,985	19,810	18,231									
Solyc10g080890	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G63380.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	8,097	6,341	19,179	23,032	16,949									
Solyc10g080900	ripening related X72730		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	4,508	9,030	974,877	1408,456	810,811					0,535	0,016			up
Solyc10g080910	LOW QUALITY:Serine/threonine-protein kinase WNK (With No Lysine)-like protein (AHRD V3.3 --* AT1G64625.1)							0,021	0,039	0,000	0,000	0,000									
Solyc10g080920	Myb family transcription factor family protein (AHRD V3.3 *** B9GRM8_POPTR)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB_related	0,279	0,213	0,346	0,690	0,189									
Solyc10g080930	Transcription elongation factor (TFIIS) family protein (AHRD V3.3 *** G7L5V2_MEDTR)		C:GO:0005634	C:nucleus			IPR017923 (PFAM); IPR035441 (G3D	21,530	24,179	43,196	47,209	41,821									
Solyc10g080940	Tubulin beta chain (AHRD V3.3 *** TBB_HORVU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002453 (PRINTS); IPR000217 (PF	699,431	531,916	208,027	126,017	192,586					-0,721	0,006			down
Solyc10g080950	cyclinB1_2	CycB1_2	C:GO:0005634	C:nucleus			IPR004367 (PFAM); IPR039361 (PIRS	0,354	0,433	0,000	0,025	0,000									
Solyc10g080960	Two-component response regulator (AHRD V3.3 *** W9S6Z7_9ROSA)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	2,700	2,428	0,883	1,901	1,359					1,114	0,048			up
Solyc10g080970	Methylenetetrahydrofolate dehydrogenase, putative (AHRD V3.3 *** B9T0V4_RICCO)		F:GO:0004488; P:G(	F:methylenetetrahy	EC:1.5.1.5	Methylenetetrahydrot	IPR000672 (PRINTS); IPR020630 (PF	31,135	38,905	35,858	28,785	33,421									
Solyc10g080980	WAT1-related protein (AHRD V3.3 *** K4D2Y5_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM); PTHR31218:SF9	0,647	0,833	0,316	0,487	0,354									
Solyc10g080990	WAT1-related protein (AHRD V3.3 *** K4D2Y6_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM); PTHR31218:SF9	0,475	0,134	0,072	0,047	0,073									
Solyc10g081000	LOW QUALITY:sequence-specific DNA binding transcription factor ATNDX (AHRD V3.3 --* AT4G03090.5)		F:GO:0004672; P:G(	F:protein kinase activity; P:protein phosphorylation; F:kinase ac			mobidb-lite (MOBIDB_LITE): mobidb-lit	47,558	38,975	40,222	38,620	36,663									
Solyc10g081010	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT3G56590.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	24,282	27,443	0,365	0,194	0,306									
Solyc10g081020	Transcription elongation factor SPT6 (AHRD V3.3 *** A0A151TAP5_CAJCA)		F:GO:0003676; P:G(	F:nucleic acid binding; P:positive regulation of transcription elor			IPR028231 (PFAM); IPR035420 (PFA	246,311	203,527	213,221	212,180	220,904									
Solyc10g081030	Nascent polypeptide-associated complex subunit alpha-like protein (AHRD V3.3 *** W9S3Y1_9ROSA)		C:GO:0005854	C:nascent polypeptide-associated complex			IPR016641 (PIRSF); IPR038187 (G3D	168,103	180,061	214,621	204,463	192,781									
Solyc10g081040	arginine/serine-rich 45 (AHRD V3.3 --* AT1G16610.7)							140,929	113,739	80,872	181,166	118,383					1,166	0,000			up
Solyc10g081050	LOW QUALITY:YqaJ-like viral recombinase domain-containing protein						IPR011604 (G3DSA:3.90.320.GENE3I	8,151	8,556	10,188	8,510	11,336									
Solyc10g081060	Syntaxin-51 (AHRD V3.3 *** A0A0B2QVT0_GLYSO)		F:GO:0005484; C:G(	F:SNAP receptor activity; C:cell; P:intracellular protein transport			G3DSA:1.20.5.110 (GENE3D): IPR00(	23,352	21,853	26,125	26,544	24,575									
Solyc10g081080	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G03140.9)							14,322	13,716	16,749	14,782	15,268									
Solyc10g081085	50S ribosomal protein L18, chloroplast, putative (AHRD V3.3 -** B9S9B8_RICCO)		C:GO:0005840; C:G(	C:ribosome; C:chloroplast thylakoid membrane; P:plastid transla			IPR040307 (PANTHER)	9,103	16,837	14,095	16,975	22,677	0,912	0,010	0,684	0,000			up	up	
Solyc10g081100	Splicing factor 3B subunit 1 (AHRD V3.3 *** A0A1D1YF64_9ARAE)		P:GO:0000245; F:G(	P:spliceosomal complex assembly; F:mRNA binding			IPR011989 (G3DSA:1.25.10.GENE3D	88,945	72,896	88,660	83,614	85,369									
Solyc10g081110	RING finger superfamily protein		C:GO:0005774; C:G(	C:vacuolar membrane; C:integral component of membrane; F:lig			IPR001841 (PFAM); IPR013083 (G3D	9,658	6,937	3,815	3,463	4,070									
Solyc10g081120	alpha-L-arabinofuranosidase		P:GO:0046373; F:G(	P:L-arabinose meta	EC:3.2.1.55	Non-reducing end alp	IPR013780 (G3DSA:2.60.40.GENE3D	48,464	53,407	59,599	71,039	79,917									
Solyc10g081130	Proteasome subunit alpha type (AHRD V3.3 *** K4D300_SOLLC)		F:GO:0004298; P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR000426 (PFAM); IPR001353 (PFA	43,587	48,314	68,076	66,533	62,605									
Solyc10g081140	LOW QUALITY:Protein kinase family protein (AHRD V3.3 *** Q9SLM4_ARATH)						G3DSA:1.10.510.10 (GENE3D): mobic	8,334	7,074	10,515	13,361	9,714									
Solyc10g081150	serine carboxypeptidase-like 43 (AHRD V3.3 --* AT2G12480.2)							72,981	103,034	79,071	77,474	74,525									
Solyc10g081160	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** B9HDR3_POPTR)		F:GO:0005524; P:G(	F:ATP binding; P:ubiquitin-dependent protein catabolic process;			IPR000608 (PFAM); IPR016135 (G3D	20,253	17,815	12,974	14,241	13,533									
Solyc10g081170	Calmodulin 2	CaM2	F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	365,063	916,227	365,577	461,182	478,704	1,350	0,002					up		
Solyc10g081180	RNA-binding protein (AHRD V3.3 *-* Q941H9_TOBAC)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	81,922	95,024	97,773	94,004	98,815									
Solyc10g081190	leucine-rich repeat protein		F:GO:0005515	F:protein binding			IPR001611 (PFAM); IPR013210 (PFA	469,952	514,550	576,263	629,499	581,951									
Solyc10g081200	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7L2Q0_MEDTR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	62,236	40,437	31,687	34,359	31,417									
Solyc10g081210	Nucleic acid-binding, OB-fold (AHRD V3.3 *** A0A103YMS1_CYNCS)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D			IPR013970 (PFAM); G3DSA:2.40.50.1	1,233	1,387	0,713	0,723	0,684									
Solyc10g081220	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9S4X8_RICCO)		C:GO:0005737; C:G(	C:cytoplasm; C:integral component of membrane			IPR001623 (PRINTS); IPR001623 (PF	7,554	6,984	11,912	10,982	11,293									
Solyc10g081240	GrpE protein homolog (AHRD V3.3 *** K4D311_SOLLC)		F:GO:0000774; P:G(	F:adenyl-nucleotide exchange factor activity; P:protein folding; I			IPR000740 (PRINTS); IPR000740 (PF	28,988	42,603	102,324	88,752	102,094	0,583	0,015					up		
Solyc10g081250	DNA polymerase (AHRD V3.3 *** K4D312_SOLLC)		F:GO:0000166; F:G(	F:nucleotide bindinc	EC:2.7.7.7	DNA-directed DNA pc	IPR006172 (PRINTS); IPR025687 (PF	23,263	20,146	16,312	14,674	15,396									
Solyc10g081260	Protein DETOXIFICATION (AHRD V3.3 *** K4D313_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); IPR002528 (TIGF	57,664	53,669	183,142	215,723	214,285									
Solyc10g081270	ELMO domain-containing protein A (AHRD V3.3 *** W9SFL1_9ROSA)						IPR006816 (PFAM); mobidb-lite (MOB	14,764	13,744	21,129	22,824	20,750									
Solyc10g081280	KHG/KDPG aldolase (AHRD V3.3 *** A0A061FSD4_THECC)		F:GO:0016829	F:lyase activity			IPR013785 (G3DSA:3.20.20.GENE3D	3,049	3,456	3,916	3,733	4,102									

Solyc10g081290	Splicing factor 3B subunit 1 (AHRD V3.3 *-* A0A0B2QRZ9_GLYSO)		P:GO:0000245; F:G(	P:spliceosomal complex assembly; F:mRNA binding			IPR011989 (G3DSA:1.25.10.GENE3D	1,487	1,790	2,354	3,057	2,355									
Solyc10g081300	Metacaspase 9 (AHRD V3.3 *** M4Y069_CAPAN),Pfam:PF00656						PF00656 (PFAM); G3DSA:3.40.50.12(	0,815	1,253	3,380	3,945	4,199									
Solyc10g081310	Histidine triad nucleotide binding protein (AHRD V3.3 *** A0A0K9Q2X0_ZOSMR)		F:GO:0003824	F:catalytic activity			IPR001310 (PRINTS); IPR036265 (G3	324,962	268,263	168,831	117,707	156,691					-0,518	0,002			down
Solyc10g081320	LOW QUALITY:R2R3MYB transcription factor 69	R2R3MYB69	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	5,134	29,880	0,399	0,604	0,537	2,565	0,000					up		
Solyc10g081330	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G41060.3)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	76,550	79,987	65,827	59,859	62,176									
Solyc10g081340	LOW QUALITY:Phytochrome kinase substrate 4, putative (AHRD V3.3 *** A0A061F5H7_THECC)		P:GO:0009638	P:phototropism			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,176	0,022	0,174	0,047									
Solyc10g081350	BZIP transcription factor (AHRD V3.3 *** Q32WR6_MALDO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc			IPR004827 (PFAM bZIP	10,626	10,086	13,007	11,879	12,381									
Solyc10g081360	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT3G03773.1)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:protein folding; F:chaperone binding; P:(			IPR008978 (G3DSA:2.60.40.GENE3D	14,305	13,108	18,915	15,628	15,711									
Solyc10g081370	small nuclear ribonucleoprotein F (AHRD V3.3 *** AT4G30220.1)		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:spliceosomal complex; C:sı			G3DSA:2.30.30.100 (GENE3D); IPR0(	43,707	45,019	51,194	47,557	48,060									
Solyc10g081380	DnaJ/Hsp40 cysteine-rich domain protein, putative (AHRD V3.3 *** G7L1K2_MEDTR)						PTHR15852:SF15 (PANTHER); PTHR	9,237	12,111	27,557	30,258	28,165									
Solyc10g081390	LOW QUALITY:transmembrane protein (AHRD V3.3 -** AT3G47510.1)							0,021	0,039	0,075	0,120	0,071									
Solyc10g081410	Plant cadmium resistance protein (AHRD V3.3 *** A0A072UD93_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR006461 (PFAM); IPR006461 (TIGF	0,142	0,137	0,075	0,122	0,186									
Solyc10g081420	Protein kinase (AHRD V3.3 *** Q2HVC0_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001245 (PFAM); IPR032675 (G3D	4,606	3,560	3,329	4,175	4,369									
Solyc10g081430	exostosin family protein (AHRD V3.3 *** AT3G45400.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM); IPR004263 (PAN	1,799	1,381	1,259	1,973	1,318									
Solyc10g081440	NADH-cytochrome b5 reductase (AHRD V3.3 *** K4D331_SOLLC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR001709 (PRINTS); IPR001834 (PF	67,681	71,321	139,610	143,492	134,730									
Solyc10g081450	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G17780.2)		C:GO:0016021	C:integral component of membrane			IPR000073 (PFAM); IPR029058 (G3D	1,184	0,962	1,246	1,314	1,501									
Solyc10g081460	Cationic amino acid transporter, putative (AHRD V3.3 *** B9SI71_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR002293 (PFAM); IPR029485 (PFA	109,755	72,079	147,506	157,886	137,762	-0,580	0,023					down		
Solyc10g081470	lutescent-2	l2	F:GO:0004222; P:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR008915 (PFAM); mobidb-lite (MOB	14,700	19,380	26,260	28,933	30,969									
Solyc10g081480	maltase-glucoamylase, intestinal protein (AHRD V3.3 *** AT5G37480.2)		C:GO:0016021	C:integral component of membrane			PTHR36396 (PANTHER)	102,106	67,275	102,763	75,910	84,963	-0,575	0,034			-0,434	0,005	down		down
Solyc10g081500	LOW QUALITY:Ankyrin repeat-containing protein (AHRD V3.3 *** A0A103YI11_CYNCS)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS); IPR002110 (PF	0,199	0,179	0,170	0,092	0,187									
Solyc10g081510	ethylene-responsive methionine synthase	er69	F:GO:0003871; F:G(	F:5-methyltetrahydr	EC:2.1.1.14	5-methyltetrahydropt(	IPR006276 (PIRSF); IPR002629 (PFA	983,234	1189,277	894,156	950,571	890,933									
Solyc10g081520	Blue copper protein (AHRD V3.3 *** A0A0M4FTF3_9SOLA)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM); IPR008972 (G3D	0,000	0,000	0,122	0,022	0,024									
Solyc10g081530	V-type proton ATPase subunit d2 (AHRD V3.3 *** VA0D2_ARATH)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR035067 (G3DSA:1.20.1690.GENE3	174,688	172,903	347,367	348,229	311,060									
Solyc10g081540	diphthamide synthesis DPH2 family protein (AHRD V3.3 *** AT3G59630.2)		P:GO:0017183	P:peptidyl-diphthamide biosynthetic process from peptidyl-histid			G3DSA:3.40.50.11860 (GENE3D); G3	14,160	14,650	20,615	19,118	17,703									
Solyc10g081550	Cytochrome P450, putative (AHRD V3.3 *** B9SYM5_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS); IPR002401 (PF	0,019	0,000	0,000	0,000	0,024									
Solyc10g081560	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		C:GO:0016021; F:G(	C:integral component of membrane; F:oxidoreductase activity; F			IPR002347 (PRINTS); IPR002347 (PF	0,000	0,041	0,025	0,000	0,000									
Solyc10g081570	Marmande		F:GO:0016874	F:ligase activity			mobidb-lite (MOBIDB_LITE); mobidb-lit	224,625	498,596	141,350	152,216	135,241									
Solyc10g081580	Syntaxin (AHRD V3.3 *** A0F0A7_NICBE)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			G3DSA:1.20.58.70 (GENE3D); IPR00(	154,162	121,618	101,081	108,973	89,524									
Solyc10g081590	Protein-lysine N-methyltransferase PGSC0003DMG400028129 (AHRD V3.3 *** M1CQ04_SOLTU)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	12,561	11,872	10,462	8,735	8,928									
Solyc10g081600	Rhomboid family protein (AHRD V3.3 *** B9H9X7_POPTR)		F:GO:0004252; F:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	G3DSA:1.10.8.10 (GENE3D); IPR015(	24,882	23,814	34,008	32,612	30,039									
Solyc10g081610	Ubiquitin carboxyl-terminal hydrolase 12 (AHRD V3.3 *** UBP12_ARATH)		F:GO:0005515; P:G(	F:protein binding; P	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR024729 (PFAM); G3DSA:3.90.70.1	156,433	140,146	187,931	178,893	180,702									
Solyc10g081620	myosin-binding protein (Protein of unknown function%2C DUF593) (AHRD V3.3 *** AT5G06560.1)		C:GO:0016021	C:integral component of membrane			IPR007656 (PFAM); PTHR31422:SF0	24,473	21,732	31,013	28,204	27,080									
Solyc10g081630	F-box protein (AHRD V3.3 *** A0A0B2SFJ8_GLYSO)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); G3DSA:2.60.120.	18,125	19,006	18,301	17,133	16,738									
Solyc10g081640	Calcium-dependent protein kinase (AHRD V3.3 *** H6UM43_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR002048 (PFAM); G3DSA:1.10.238.	0,175	0,210	0,022	0,120	0,023									
Solyc10g081650	carotenoid isomerase	CRTISO	P:GO:0016117; F:G(	P:carotenoid biosynthetic process; F:oxidoreductase activity; F			IPR036188 (G3DSA:3.50.50.GENE3D	26,153	35,560	139,454	152,583	144,789									
Solyc10g081660	sucrose phosphatase AF493563		F:GO:0000287; P:G(	F:magnesium ion bi	EC:3.1.3.23; EC:3.1.	Sugar-phosphatase;	G3DSA:3.10.450.50 (GENE3D); G3DS	31,595	39,395	38,628	40,979	41,714									
Solyc10g081680	LOW QUALITY:trehalose-6-phosphate synthase (AHRD V3.3 --* AT1G78580.4)							3,020	3,315	1,305	2,014	1,669									
Solyc10g081700	ATP synthase subunit b, chloroplastic (AHRD V3.3 --* ATPF_PIPCE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,769	2,412	0,540	0,116	0,282									
Solyc10g081710	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G15790.4)		F:GO:0016874	F:ligase activity			IPR001841 (PFAM); IPR013083 (G3D	38,230	35,364	46,082	52,020	46,815									
Solyc10g081720	fasciclin superfamily protein		C:GO:0016021	C:integral component of membrane			IPR036378 (G3DSA:2.30.180.GENE3I	215,810	150,124	117,675	148,974	127,651									
Solyc10g081730	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT2G35880.3)						IPR027329 (PFAM); mobidb-lite (MOB	94,300	50,413	23,585	22,655	23,893	-0,874	0,014					down		
Solyc10g081740	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9RL17_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:3.30.200.20 (GENE3D); G3DS	0,243	1,008	0,214	0,336	0,283									
Solyc10g081750	Mal d 1-associated protein (AHRD V3.3 *** Q6X182_MALDO)		C:GO:0005634	C:nucleus			mobidb-lite (MOBIDB_LITE); mobidb-lit	34,896	29,690	70,861	64,945	66,660									
Solyc10g081770	polyketide cyclase/dehydrase/lipid transport superfamily protein (AHRD V3.3 *** AT5G06440.3)		F:GO:0008289	F:lipid binding			IPR023393 (G3DSA:3.30.530.GENE3I	6,506	5,252	3,999	3,487	4,131									
Solyc10g081790	RING/U-box superfamily protein (AHRD V3.3 *** AT5G06490.1)		C:GO:0016021	C:integral component of membrane			IPR001841 (PFAM); IPR013083 (G3D	0,478	0,766	0,137	0,382	0,166									
Solyc10g081800	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein (AHRD V3.3 *** AT3		P:GO:0032366	P:intracellular sterol transport			IPR003172 (PFAM); G3DSA:2.60.40.7	0,257	0,225	0,000	0,101	0,000									
Solyc10g081810	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein (AHRD V3.3 *-* AT3		P:GO:0032366	P:intracellular sterol transport			G3DSA:2.60.40.770 (GENE3D); IPR0(	0,176	0,941	0,000	0,025	0,141									
Solyc10g081820	Expp1 protein (AHRD V3.3 *** Q2HPL4_SOLTU)		P:GO:0002098; C:G(	P:tRNA wobble uridine modification; C:nucleus; C:cytosol; P:pe(			PTHR21454 (PANTHER); PTHR21454	29,301	26,164	19,801	19,291	19,143									
Solyc10g081830	Replication protein A subunit (AHRD V3.3 *** A0A1D1Z493_9ARAE)		F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:DNA replication; P:DNA repair; P:D			G3DSA:2.40.50.140 (GENE3D); IPR0:	10,504	11,984	3,946	3,174	3,976									
Solyc10g081840	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			IPR001289 (PRIN NF-YA	0,371	0,401	0,261	0,122	0,259									
Solyc10g081850	Syntaxin, putative (AHRD V3.3 *** B9SDJ9_RICCO)		C:GO:0016020; P:G(	C:membrane; P:vesicle-mediated transport			IPR006011 (PFAM); G3DSA:1.20.58.7	8,505	14,223	3,904	3,995	3,750									
Solyc10g081860	ankyrin repeat family protein (AHRD V3.3 --* AT4G05040.7)							0,119	0,205	0,097	0,073	0,095									
Solyc10g081870	Digalactosyldiacylglycerol synthase 1 (AHRD V3.3 *-* W8SVK3_TOBAC)		C:GO:0009707; P:G(	C:chloroplast outer membrane; P:galactolipid biosynthetic proce			PTHR12526:SF532 (PANTHER); PTHF	5,156	4,973	4,827	3,605	3,628									
Solyc10g081880	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JSG8_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM); IPR002885 (PFA	8,878	6,921	6,096	7,415	6,055									
Solyc10g081900	Digalactosyldiacylglycerol synthase 1 (AHRD V3.3 *** W8SVK3_TOBAC)		C:GO:0009707; P:G(	C:chloroplast outer membrane; P:galactolipid biosynthetic proce			G3DSA:3.40.50.2000 (GENE3D); IPR(	60,248	62,211	117,589	110,983	115,357									
Solyc10g081910	Receptor-kinase-like protein (AHRD V3.3 *** A0A072U3D4_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	19,104	11,483	5,962	4,764	6,090	-0,705	0,034					down		
Solyc10g081920	Coatomer subunit beta (AHRD V3.3 *** M1CQJ9_SOLTU)		F:GO:0005198; P:G(	F:structural molecule activity; P:intracellular protein transport; P			IPR011710 (PFAM); IPR016460 (PIRS	167,759	165,074	152,782	156,694	142,605									
Solyc10g081940	Exocyst complex component 7 (AHRD V3.3 *** A0A151RD29_CAJCA)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis			IPR004140 (PFAM); mobidb-lite (MOB	6,615	5,195	1,575	2,115	1,698									
Solyc10g081950	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 --* AT2G27260.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,241	0,259	0,197	0,022	0,141									
Solyc10g081955	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G52470.1)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM); PTHR31415 (PAI	266,805	127,513	20,684	9,446	16,793	-1,037	0,002			-1,127	0,000	down		down
Solyc10g081970	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G35980.1)		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM); PTHR31415 (PAI	0,603	0,790	0,529	2,024	0,896					1,909	0,000			up
Solyc10g081980	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family, putative (AHRD V3.3 *** A0A06		C:GO:0009506; C:G(	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM); PTHR31415:SF4	38,447	17,309	18,415	67,318	33,280	-1,128	0,002	0,849	0,011	1,868	0,000	down	up	up
Solyc10g082000	Double Clp-N motif P-loop nucleoside triphosphate hydrolase superfamily protein (AHRD V3.3 *** A0A072VJI		P:GO:0019538	P:protein metabolic process			G3DSA:3.40.50.300 (GENE3D); IPR0:	0,172	0,449	0,000	0,000	0,000									
Solyc10g082020	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** I0IUQ3_SOLLC)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D); IPR0(	0,138	0,253	0,122	0,241	0,308									
Solyc10g082030	2-Cys peroxiredoxin 1		P:GO:0045454; F:G(	P:cell redox homeo:	EC:1.11.1.15	Peroxiredoxin	IPR000866 (PFAM); G3DSA:3.40.30.1	61,812	123,717	58,561	62,664	85,598	1,029	0,000	0,544	0,000			up	up	
Solyc10g082050	ovate family protein 21	OFP21	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (TIGRFAM); IPR006458 (F	0,218	0,367	0,000	0,000	0,000									
Solyc10g082055	Beige/BEACH and WD40 domain-containing protein (AHRD V3.3 --* AT4G02660.3)							0,314	0,292	0,022	0,025	0,096									
Solyc10g082065	Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *-* A0A061EH36_T		F:GO:0003723	F:RNA binding			IPR002075 (PFAM); G3DSA:3.10.450.	1,129	0,928	0,047	0,120	0,117									
Solyc10g083060	Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (AHRD V3.3 *-* A0A061EH36_T		F:GO:0003723	F:RNA binding			G3DSA:3.10.450.50 (GENE3D); IPR0(	0,021	0,000	0,000	0,000	0,000									
Solyc10g083110	4-hydroxy-tetrahydrodipicolinate synthase (AHRD V3.3 *** K4D398_SOLLC)		F:GO:0008840; P:G(	F:4-hydroxy-tetrahy	EC:4.3.3.7	4-hydroxy-tetrahydro	IPR002220 (PRINTS); IPR002220 (PF	88,045	71,279	40,356	34,603	34,751									
Solyc10g083120	Ubiquitin-conjugating enzyme, E2 (AHRD V3.3 *** A0A103XCT0_CYNCS)		F:GO:0004839; C:G(	F:ubiquitin activatin	EC:6.2.1.45	E1 ubiquitin-activatin	IPR016135 (G3DSA:3.10.110.GENE3I	59,338	60,022	97,382	96,167	84,998									
Solyc10g083140	Gb:AAF02129.1, putative (AHRD V3.3 *** A0A061GVZ4_THECC)						mobidb-lite (MOBIDB_LITE); PTHR331	0,452	0,398	0,516	0,597	0,612									
Solyc10g083150	DWNN domain, A CCHC-type zinc finger protein (AHRD V3.3 *** G7JHR9_MEDTR)		F:GO:0008270	F:zinc ion binding			IPR014891 (PFAM); G3DSA:4.10.60.1	75,577	80,261	91,240	82,786	89,492									
Solyc10g083160	TLD-domain containing nucleolar protein (AHRD V3.3 *** AT5G06260.1)		F:GO:0005509	F:calcium ion binding			IPR006571 (PFAM); G3DSA:1.10.238.	41,194	35,599	44,086	42,018	41,229									
Solyc10g083165	40S ribosomal protein S17 (AHRD V3.3 *** RS17_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001210 (PFAM); IPR036401 (G3D	94,849	83,471	50,983	47,694	46,110									
Solyc10g083170	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561						IPR002347 (PRINTS); IPR002347 (PF	0,000	0,000	0,000	0,000	0,047									
Solyc10g083180	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	2,732	2,206	1,627	1,335	1,581									
Solyc10g083190	Plant/F24K9-26 protein (AHRD V3.3 *** A0A072UED0_MEDTR)		C:GO:0005886	C:plasma membrane			mobidb-lite (MOBIDB_LITE); mobidb-lit	30,291	28,709	12,398	10,964	11,786									
Solyc10g083200	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein (AHRD V3.3 *** AT4G312		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; P:cellular calcium ion homeo			IPR035967 (G3DSA:1.10.10.GENE3D	24,806	21,920	33,130	30,451	32,090									
Solyc10g083210	B3 domain-containing protein family (AHRD V3.3 *** A0A151U3H1_CAJCA)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	3,725	5,424	1,698	1,640	2,934									
Solyc10g083220	embryo defective 2735 (AHRD V3.3 *** AT5G06240.1)						mobidb-lite (MOBIDB_LITE); PTHR360	11,026	11,983	7,279	7,226	6,806									
Solyc10g083230	F-box family protein (AHRD V3.3 *** B9NEF0_POPTR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); PTH	4,799	6,050	19,147	16,743	15,015									
Solyc10g083240	RNA binding protein, putative (AHRD V3.3 *** B9SX10_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM); IPR012677 (G3D	25,319	27,652	34,280	35,549	33,285									
Solyc10g083250	CASP-like protein (AHRD V3.3 *** K4D3B2_SOLLC)		C:GO:0005886; P:G(	C:plasma membrane; P:cell-cell junction assembly; C:integral cc			IPR006702 (PFAM); IPR006459 (TIGF	0,000	0,021	0,000	0,022	0,000									
Solyc10g083260	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *-* AT3G15040.1)						IPR007608 (PFAM); mobidb-lite (MOB	4,627	4,133	5,506	3,424	4,003					-0,683	0,036			down
Solyc10g083270	alpha/beta hydrolase domain-containing protein 11-like (ABHD11)		F:GO:0005524; C:G(	F:ATP binding; C:mitochondrion; F:hydrolase activity			IPR000073 (PFAM); IPR029058 (G3D	19,384	14,717	27,250	21,067	22,830									
Solyc10g083280	40S ribosomal protein S14-2		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001971 (PIRSF); IPR001971 (PFA	94,911	107,935	97,241	86,609	86,321									
Solyc10g083290	symbol=Lin6	IN6	F:GO:0004564; P:G(	F:beta-fructofurano:	EC:3.2.1.26	Beta-fructofuranosid:	G3DSA:2.60.120.560 (GENE3D); IPR(	0,178	1,321	1,120	2,765	5,464			2,271	0,001				up	
Solyc10g083300	cell-wall invertase	lin8	F:GO:0004564; P:G(	F:beta-fructofurano:	EC:3.2.1.26	Beta-fructofuranosid:	G3DSA:2.60.120.560 (GENE3D); IPR(	0,116	1,948	0,000	0,000	0,023									
Solyc10g083310	Kinesin-related protein (AHRD V3.3 *** A0A0B0NF68_GOSAR)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (PF	2,504	2,020	0,361	0,141	0,212									
Solyc10g083330	LOW QUALITY:At2g36220/F2H17.17 (AHRD V3.3 *** Q9SJN3_ARATH)						mobidb-lite (MOBIDB_LITE); mobidb-lit	10,351	11,394	0,855	1,069	1,172									
Solyc10g083335	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 --* AT4G04340.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,101	0,043	0,122	0,022	0,094									
Solyc10g083340	Myb family transcription factor APL (AHRD V3.3 *** A0A0B2R6R9_GLYSO)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	2,727	2,230	0,607	0,806	0,918									
Solyc10g083350	SOUL heme-binding family protein (AHRD V3.3 *** AT3G10130.1)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:plastoglobule; F:heme binc			IPR011256 (G3DSA:3.20.80.GENE3D	7,160	9,177	11,261	11,643	14,808									
Solyc10g083360	Calmodulin binding protein, putative (AHRD V3.3 *** B9T5N0_RICCO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	52,598	86,937	32,567	70,510	45,548	0,750	0,011			1,115	0,000	up		up
Solyc10g083380	BZIP transcription factor family protein (AHRD V3.3 *-* B9MTQ4_POPTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans(			PTHR22952 (PANTHER); PTHR22952	31,876	35,553	31,559	47,111	35,878					0,582	0,000			up
Solyc10g083390	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM); G3DSA:3.40.50.1	0,000	0,000	0,000	0,000	0,023									
Solyc10g083400	Cytochrome P450, putative (AHRD V3.3 *** B9T5M5_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR001128 (PRINTS); IPR002401 (PF	1,631	1,734	48,961	52,304	30,285									
Solyc10g083410	LOW QUALITY:Peptidoglycan-binding LysM domain protein (AHRD V3.3 *** A0A072VJR4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR036779 (G3DSA:3.10.350.GENE3I	0,021	0,000	0,000	0,000	0,000									
Solyc10g083420	Inosine-uridine preferring nucleoside hydrolase, putative (AHRD V3.3 *** B9SRU5_RICCO)		C:GO:0005829; P:G(	C:cytosol; P:purine	EC:3.2.2.1	Purine nucleosidase	IPR001910 (PFAM); IPR036452 (G3D	0,042	0,000	0,025	0,000	0,024									
Solyc10g083430	Inosine-uridine preferring nucleoside hydrolase (AHRD V3.3 *-* G7L609_MEDTR)		C:GO:0005829; P:G(	C:cytosol; P:purine	EC:3.2.2.1	Purine nucleosidase	IPR001910 (PFAM); IPR036452 (G3D	0,021	0,000	0,022	0,000	0,000									
Solyc10g083450	NAC domain protein (AHRD V3.3 *** A0JBY8_9ASPA)	NAC088	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,080	0,194	0,165	0,168	0,117									
Solyc10g083460	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** V5PZR5_9CARY)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			IPR035896 (G3DSA:4.10.1110.GENE:	7,753	8,298	12,459	12,473	13,436									
Solyc10g083470	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding			IPR019956 (PRINTS); G3DSA:3.90.17	17,987	17,578	20,413	21,755	19,912									
Solyc10g083480	F-box family protein (AHRD V3.3 *** B9HQ03_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	30,778	26,033	31,553	34,096	30,831									
Solyc10g083490	Cell division protein ftsZ, putative (AHRD V3.3 *** B9SRX2_RICCO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR003008 (PRINTS); IPR037103 (G3	27,176	33,946	37,026	32,215	39,843									
Solyc10g083500	Protein kinase family protein (AHRD V3.3 *-* Q9LZS4_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); mobidb-lite (MOB	38,505	29,208	15,271	14,960	16,062									
Solyc10g083510	Growth-regulating factor (AHRD V3.3 *** A0A072U430_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-ten			IPR014977 (PFAM GRF	0,262	0,426	0,000	0,075	0,000									
Solyc10g083520	RAB6-interacting golgin (DUF662) (AHRD V3.3 *** AT2G27740.1)						IPR007033 (PFAM); mobidb-lite (MOB	36,617	28,760	14,515	12,720	12,388									
Solyc10g083530	Phosphatidylinositol N-acetylglucosaminlytransferase subunit P-like protein (AHRD V3.3 --* AT2G39435.6)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,640	0,433	0,812	1,977	0,755					1,261	0,006			up
Solyc10g083540	Threonine dehydratase (AHRD V3.3 *** K4D3E1_SOLLC)		F:GO:0004794; P:G(	F:L-threonine amm(	EC:4.3.1.19	Threonine ammonia-l	IPR038110 (G3DSA:3.40.1020.GENE:	0,040	0,064	0,097	0,022	0,000									
Solyc10g083550	Glutamate-ammonia ligase-like protein (AHRD V3.3 *** Q9SC91_MEDTR)		F:GO:0004356; P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetas(	G3DSA:3.30.590.10 (GENE3D); IPR0:	0,000	0,000	0,000	0,025	0,000									
Solyc10g083560	Dehydration responsive element binding transcription factor (AHRD V3.3 *** W6FFV1_9ROSA)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PFAM ERF	0,000	0,000	0,022	0,000	0,000									
Solyc10g083563	Trihelix transcription factor GT-2-like protein (AHRD V3.3 *-* A0A0B0PED7_GOSAR)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			G3DSA:1.10.10.60 (GENE3D); mobidb	0,353	0,173	0,140	0,045	0,047									
Solyc10g083567	Trihelix transcription factor GT-2 (AHRD V3.3 *-* A0A0B2SLE3_GLYSO)						PF13837 (PFAM); G3DSA:1.10.10.60	0,316	0,172	0,072	0,022	0,023									
Solyc10g083570	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4D3E4_SOLLC)		F:GO:0004332; P:G(	F:fructose-bisphosp	EC:4.1.2.13	Fructose-bisphospha	IPR013785 (G3DSA:3.20.20.GENE3D	227,208	223,677	454,621	449,988	402,060									
Solyc10g083580	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)		C:GO:0005576; F:G(	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM); IPR009438 (PAN	56,158	34,341	196,234	183,674	153,354									
Solyc10g083590	Pre-mRNA cleavage complex 2 protein Pcf11 (AHRD V3.3 *** W9R453_9ROSA)		F:GO:0003676	F:nucleic acid binding			IPR008942 (G3DSA:1.25.40.GENE3D	32,178	29,493	36,177	34,284	32,130									
Solyc10g083600	Brix domain-containing protein (AHRD V3.3 *** H9A0F8_NICBE)		P:GO:0000027; P:G(	P:ribosomal large subunit assembly; P:maturation of LSU-rRNA:			IPR007109 (PFAM); mobidb-lite (MOB	8,308	8,399	9,603	8,621	7,977									
Solyc10g083610	ethylene-inducible CTR1-like protein kinase	CTR1	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS); G3DSA:1.10.51	41,837	53,540	75,336	91,422	75,252									
Solyc10g083620	Unknown protein (AHRD V3.3)							0,021	0,018	0,000	0,025	0,000									
Solyc10g083630	DNA demethylase 2	DML2	F:GO:0003824; P:G(	F:catalytic activity; P:base-excision repair			IPR028924 (PFAM); IPR023170 (G3D	259,226	187,646	1566,626	1912,709	1447,676									
Solyc10g083640	Zinc finger transcription factor 64	C3H64	P:GO:0000398; F:G(	P:mRNA splicing, via spliceosome; F:RNA binding; F:metal ion b			IPR009145 (PRINTS); IPR000504 (PF	153,795	158,869	199,428	188,140	180,939									
Solyc10g083650	Peroxiredoxin, putative (AHRD V3.3 *** B9SRG0_RICCO)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:cell redox homeostasis			IPR013740 (PFAM); G3DSA:3.40.30.1	67,348	95,910	777,606	729,336	733,628									
Solyc10g083670	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans			IPR029044 (G3DSA:3.90.550.GENE3I	65,111	36,430	0,915	0,832	0,302	-0,808	0,037					down		
Solyc10g083675	Glucomannan 4-beta-mannosyltransferase 9 (AHRD V3.3 *** A0A0B2NZ07_GLYSO)		C:GO:0016021; F:G(	C:integral compone	EC:2.4.1.32	Glucomannan 4-beta	IPR001173 (PFAM); IPR029044 (G3D	16,894	10,016	0,136	0,201	0,094									
Solyc10g083690	Cytochrome P450 (AHRD V3.3 *** Q8H0I7_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS); IPR001128 (PF	0,948	2,083	27,708	35,540	35,607									
Solyc10g083700	Cytochrome P450 (AHRD V3.3 *** Q8H0I7_PETHY)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS); IPR001128 (PF	1,375	4,031	4,999	5,820	8,130	1,564	0,001	0,699	0,014			up	up	
Solyc10g083710	3-deoxy-D-manno-octulosonic-acid transferase (AHRD V3.3 *** A0A151U3D0_CAJCA)		F:GO:0016740	F:transferase activity			IPR007507 (PFAM); IPR038107 (G3D	1,584	1,419	7,445	9,996	6,692									
Solyc10g083720	Pyruvate kinase family protein (AHRD V3.3 *** AT3G52990.1)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:2.7.1.4	Pyruvate kinase	IPR001697 (PRINTS); IPR036918 (G3	62,318	58,060	780,021	824,487	677,726									
Solyc10g083740	60S ribosomal protein L24 (AHRD V3.3 *** RL24_PRUAV)		P:GO:0000027; F:G(	P:ribosomal large subunit assembly; F:RNA binding; F:structural			IPR038630 (G3DSA:2.30.170.GENE3I	21,257	28,213	12,011	9,433	9,858									
Solyc10g083760	chloroplast threonine deaminase 1 precursor		F:GO:0004794; P:G(	F:L-threonine amm(	EC:4.3.1.19	Threonine ammonia-l	IPR001926 (PFAM); G3DSA:3.40.50.1	398,177	248,501	186,660	157,939	175,918	-0,652	0,016					down		
Solyc10g083790	CYP97C11	CYP97C1	C:GO:0000813; P:G(	C:ESCRT I complex; P:endosome transport via multivesicular bo			IPR029012 (G3DSA:1.10.287.GENE3I	21,817	22,003	26,449	25,688	25,515									
Solyc10g083795	Cytochrome P450, putative (AHRD V3.3 *** B9S0A8_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d(			IPR002401 (PRINTS); IPR001128 (PF	7,974	11,182	4,325	5,719	7,526			0,788	0,023				up	
Solyc10g083800	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *** A0A072VVJ3_MEDTR)		F:GO:0000977; F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR019787 (PFAM); G3DSA:3.40.630	49,377	41,975	44,199	46,069	44,954									
Solyc10g083820	Pectinesterase (AHRD V3.3 *** A0A068V420_COFCA)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3I	0,429	0,480	0,554	0,311	0,561									
Solyc10g083830	Glutamate-ammonia ligase-like protein (AHRD V3.3 *** A0A072VKI5_MEDTR)		F:GO:0004356; P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetas(	IPR036651 (G3DSA:3.10.20.GENE3D	25,954	25,947	34,306	39,143	39,806									
Solyc10g083850	Glutamate-ammonia ligase-like protein (AHRD V3.3 *** A0A072VKI5_MEDTR)		F:GO:0004356; P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetas(	G3DSA:3.30.590.10 (GENE3D); IPR0(	0,000	0,000	0,000	0,000	0,023									
Solyc10g083860	Glycosyltransferase (AHRD V3.3 *** A0A061EUB6_THECC)		F:GO:0005515; F:G(	F:protein binding; F:transferase activity, transferring hexosyl grc			IPR002110 (PFAM); IPR002213 (PFA	20,351	9,512	4,958	3,166	3,381	-1,068	0,002					down		
Solyc10g083870	Ankyrin repeat family protein (AHRD V3.3 *** AT3G09890.1)		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	1,246	0,803	1,384	1,203	1,018									
Solyc10g083880	tonoplast intrinsic protein 1.3	TIP1.3	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR000425 (PF	0,019	0,096	0,600	2,965	1,648					2,281	0,000			up

Solyc10g083890	Carbonic anhydrase, putative (AHRD V3.3 *** B9S0D9_RICCO)		F:GO:0004089; F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR036398 (G3DSA:3.10.200.GENE3I	0,000	0,018	0,000	0,000	0,000									
Solyc10g083900	R2R3MYB transcription factor 27	R2R3MYB27	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,000	0,036	0,025	0,025	0,024									
Solyc10g083910	BnaC04g08430D protein (AHRD V3.3 *** A0A078H5Q1_BRANA)		C:GO:0009941	C:chloroplast envelope			PTHR36737 (PANTHER)	13,466	17,895	18,859	17,290	17,761									
Solyc10g083920	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9IFU5_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR002554 (PFAM): IPR011989 (G3D	25,156	20,668	26,651	29,683	28,115									
Solyc10g083930	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4D3H9_SOLLC)		P:GO:0000413; F:G(	P:protein peptidyl-pı	EC:5.2.1.8	Peptidylprolyl isomer:	IPR002130 (PRINTS): IPR024936 (PII	12,778	11,513	18,600	18,385	17,196									
Solyc10g083940	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9NWX1_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR010658 (PFAM): G3DSA:1.20.125(	1,358	2,804	31,439	45,621	29,799					0,541	0,002			up
Solyc10g083950	LOW QUALITY:Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** A0A0K9NWX1_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			G3DSA:1.20.1250.20 (GENE3D): IPR(	3,056	2,694	3,792	3,641	3,881									
Solyc10g083960	Phosphoadenosine phosphosulfate reductase family protein (AHRD V3.3 *** G7L3W8_MEDTR)		F:GO:0003824	F:catalytic activity			IPR036425 (G3DSA:3.40.980.GENE3I	7,559	8,068	5,832	5,988	8,279									
Solyc10g083970	S-adenosylmethionine synthase (AHRD V3.3 *** A0A0V0IPC3_SOLCH)		F:GO:0004478; F:G(	F:methionine adeno	EC:2.5.1.6	Methionine adenosyl	IPR022628 (PFAM): IPR002133 (TIGF	489,679	789,327	146,918	148,651	166,970	0,714	0,046					up		
Solyc10g083980	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *-* B9GL08_POPTR)		F:GO:0046872; F:G(	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR027443 (G3DSA:2.60.120.GENE3I	0,000	0,041	0,000	0,000	0,000									
Solyc10g083990	D-tagatose-1,6-bisphosphate aldolase subunit (AHRD V3.3 *** AT2G36895.1)						PTHR36739 (PANTHER)	4,826	6,438	17,018	17,095	15,672									
Solyc10g084000	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT2G36950.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	23,971	20,798	7,423	14,132	10,963					0,926	0,026			up
Solyc10g084020	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061EU13_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374 (PAN	0,162	0,000	0,000	0,000	0,000									
Solyc10g084023	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G28085.1)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31374:SF1!	0,040	0,000	0,000	0,000	0,000									
Solyc10g084040	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic (AHRD V3.3 *** TL15B_ARATH)						PTHR35514:SF1 (PANTHER): PTHR3!	15,557	26,221	54,841	61,896	72,618	0,780	0,002	0,403	0,021			up	up	
Solyc10g084045	Transcription initiation factor TFIID subunit 8 (AHRD V3.3 --* A0A151S2X5_CAJCA)		F:GO:0003743; C:G(	F:translation initiation factor activity; C:transcription factor TFIII			mobidb-lite (MOBIDB_LITE)	1,655	1,575	2,199	1,977	2,143									
Solyc10g084050	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)		F:GO:0005524; F:G(	F:ATP binding; F:hydrolase activity			IPR005938 (TIGRFAM): G3DSA:3.10.:	126,283	143,742	306,283	343,131	294,591									
Solyc10g084060	cysteine-rich TM module stress tolerance protein (AHRD V3.3 *** AT5G04080.1)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			IPR028144 (PFAM): mobidb-lite (MOB	0,960	1,171	0,729	1,189	1,084									
Solyc10g084070	LOW QUALITY:Endoglucanase (AHRD V3.3 --* A0A022RID5_ERYGU)						G3DSA:3.10.20.90 (GENE3D): cd017(	1,880	2,648	16,908	17,269	14,526									
Solyc10g084080	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061F037_THECC)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	1,884	1,672	2,970	2,529	2,075									
Solyc10g084085	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G41540.1)							0,890	0,607	0,884	1,024	1,225									
Solyc10g084090	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061F037_THECC)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFAI	3,013	2,413	3,674	3,351	3,182									
Solyc10g084095	Kinase-like protein (AHRD V3.3 --* A8BLL9_PRUAV)							0,260	0,162	0,246	0,316	0,259									
Solyc10g084100	RING/U-box superfamily protein (AHRD V3.3 *** AT3G09770.1)		F:GO:0016874	F:ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	6,167	6,850	9,988	8,617	9,007									
Solyc10g084110	Kinase family protein (AHRD V3.3 *** B9NAB5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	0,000	0,021	0,000	0,022	0,023									
Solyc10g084120	plasma membrane intrinsic protein 2.5	PIP2.5	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR000425 (PF	0,375	0,307	0,072	0,073	0,046									
Solyc10g084140	Ferrochelatase (AHRD V3.3 *** K4D3K0_SOLLC)	FC/GUN6	F:GO:0004325; P:G(	F:ferrochelatase ac	EC:4.99.1.1	Protoporphyrin ferroc	G3DSA:3.40.50.1400 (GENE3D): IPR(	85,959	73,808	120,657	120,986	116,598									
Solyc10g084150	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** I0IUQ2_SOLLC)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): IPR0:	0,021	0,124	0,143	0,072	0,095									
Solyc10g084160	Small RNA degrading nuclease (AHRD V3.3 *** A0A072VF22_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR013520 (PFAM): IPR036397 (G3D	25,463	29,377	28,249	27,902	26,040									
Solyc10g084170	BAG family molecular chaperone regulator 5 (AHRD V3.3 *-* W9QTU5_9ROSA)		F:GO:0051087	F:chaperone binding			IPR003103 (PFAM): IPR036533 (G3D	10,639	9,080	7,277	8,549	7,534									
Solyc10g084180	Zinc finger family protein (AHRD V3.3 *** S8C619_9LAMI)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	28,753	31,782	7,062	7,012	10,454									
Solyc10g084200	Peroxidase (AHRD V3.3 *** K4D3K6_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,000	0,037	0,000	0,000	0,000									
Solyc10g084210	Syntaxin, putative (AHRD V3.3 *** B9S0N2_RICCO)		F:GO:0000149; F:G(	F:SNARE binding; F:SNAP receptor activity; C:endoplasmic reti			IPR000727 (PFAM): G3DSA:1.20.5.11	53,419	54,216	66,227	61,680	58,409									
Solyc10g084220	FAR1-related sequence 7 (AHRD V3.3 *** AT3G06250.3)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:zinc ion binding			IPR007527 (PFAN FAR1	1,965	1,328	3,027	3,118	2,595									
Solyc10g084230	DUF1685 family protein (AHRD V3.3 *** G7LJH7_MEDTR)		F:GO:0004527; P:G(	F:exonuclease activity; P:nucleic acid phosphodiester bond hyd			IPR012881 (PFAM): mobidb-lite (MOB	0,082	0,199	0,096	0,319	0,257									
Solyc10g084240	Peroxidase (AHRD V3.3 *** K4D3L0_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,038	0,021	0,025	0,000	0,000									
Solyc10g084250	clade VIII lectin receptor kinase		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	23,158	21,521	4,596	3,871	4,499									
Solyc10g084260	Cell number regulator 8 (AHRD V3.3 *** A0A0B2P442_GLYSO)						IPR006461 (PFAM): mobidb-lite (MOB	15,704	16,377	18,967	17,335	16,023									
Solyc10g084265	transmembrane protein (AHRD V3.3 --* AT5G03120.2)							0,000	0,000	0,022	0,000	0,000									
Solyc10g084270	Importin subunit alpha (AHRD V3.3 *** K4D3L3_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; C:cytoplasm; P:protein import into			IPR011989 (G3DSA:1.25.10.GENE3D	29,848	26,131	25,853	24,737	24,717									
Solyc10g084280	SUN-like protein 29	SUN29	F:GO:0005515	F:protein binding			IPR000048 (PFAM): mobidb-lite (MOB	71,801	71,621	20,206	18,494	23,982									
Solyc10g084290	Interactor of constitutive active ROPs 3-like protein (AHRD V3.3 *** A0A0B0N2C1_GOSAR)		F:GO:0051219	F:phosphoprotein binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,925	2,142	0,090	0,000	0,163									
Solyc10g084300	LOW QUALITY:DnaJ like protein (AHRD V3.3 *** Q9FEW7_SOLLC)		P:GO:0006457; F:G(	P:protein folding; F:unfolded protein binding			G3DSA:2.20.25.170 (GENE3D): IPR0(	6,339	5,044	11,169	12,078	10,509									
Solyc10g084310	Ribosomal protein S12 (AHRD V3.3 *** A0A059LPB2_9CHLO)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos			IPR006032 (PIRSF): G3DSA:2.40.50.:	188,165	184,671	113,185	103,794	104,586									
Solyc10g084320	Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)		F:GO:0004252; P:G(	F:serine-type endoı	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	11,601	12,371	4,279	4,226	2,899									
Solyc10g084325	Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)		F:GO:0004252; P:G(	F:serine-type endoı	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR010259 (PF	16,989	32,193	22,169	20,747	21,891	0,948	0,003					up		
Solyc10g084340	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VME8_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN AP2	2,800	2,352	0,577	0,727	0,800									
Solyc10g084350	60S ribosomal L4 (AHRD V3.3 *** A0A0B0NGW3_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002136 (PFAM): IPR023574 (G3D	130,616	143,664	150,789	126,549	129,631									
Solyc10g084370	MYB transcription factor (AHRD V3.3 *** B5TV64_CAMSI)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB_related	21,505	14,841	10,560	12,237	12,905									
Solyc10g084380	WRKY transcription factor 44	WRKY44	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAN WRKY	2,017	4,743	0,165	0,364	0,773									
Solyc10g084390	Protein kinase-like protein (AHRD V3.3 *** Q6TKQ5_VITAE)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	0,019	0,021	0,000	0,000	0,000									
Solyc10g084400	Glutathione S-transferase family protein (AHRD V3.3 *** AT5G02790.1)	GSTL3	F:GO:0005515	F:protein binding			G3DSA:3.40.30.10 (GENE3D): PF134	58,166	67,110	243,587	265,110	321,367									
Solyc10g084410	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G12620.2)		F:GO:0004722; P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	0,058	0,059	0,025	0,072	0,023									
Solyc10g084420	30S ribosomal protein S4, chloroplastic (AHRD V3.3 --* RR4_ANTOD)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,593	0,378	0,049	0,050	0,023									
Solyc10g084430	RING/U-box superfamily protein (AHRD V3.3 *** AT5G02750.1)		C:GO:0009501; P:G(	C:amyloplast; P:gravitropism; P:protein ubiquitination; F:ligase a			IPR013083 (G3DSA:3.30.40.GENE3D	0,288	0,226	0,000	0,025	0,000									
Solyc10g084440	Dirigent protein (AHRD V3.3 *-* D7LW00_ARALL)						G3DSA:2.30.30.140 (GENE3D): PTHF	5,257	3,013	5,730	5,603	5,171									
Solyc10g084500	LOW QUALITY:valine-tRNA ligase (AHRD V3.3 *** AT3G53490.1)		C:GO:0016021	C:integral component of membrane			PTHR33780:SF3 (PANTHER): PTHR3:	0,000	0,021	0,025	0,000	0,000									
Solyc10g084510	cullin 1 (AHRD V3.3 --* AT4G02570.4)						PTHR35304 (PANTHER)	2,145	1,706	1,232	1,071	0,847									
Solyc10g084520	RNAse THREE-like protein 3 (AHRD V3.3 --* AT5G45150.1)							4,261	3,997	8,725	7,270	6,201									
Solyc10g084530	Lung seven transmembrane receptor family protein (AHRD V3.3 *-* AT5G18520.1)		C:GO:0016021	C:integral component of membrane			PTHR21229:SF47 (PANTHER): IPR00	31,819	27,030	50,365	50,293	44,369									
Solyc10g084540	Phosphatidate phosphatase LPIN2-like protein (AHRD V3.3 *-* A0A0B2P3Z9_GLYSO)						IPR013209 (PFAM): IPR007651 (PFAI	3,917	2,200	11,997	12,265	9,716									
Solyc10g084557	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT5G63010.1)							0,000	0,000	0,051	0,025	0,000									
Solyc10g084560	Ankyrin repeat family protein (AHRD V3.3 *** AT3G09550.3)		F:GO:0004252; F:G(	F:serine-type endoı	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	6,030	5,287	8,922	3,829	7,669					-1,220	0,000			down
Solyc10g084600	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)						IPR006476 (PFAM): IPR006476 (TIGF	0,501	0,199	19,766	21,880	2,880			-2,778	0,000				down	
Solyc10g084610	60S ribosomal protein L23a (AHRD V3.3 *** RL23A_DAUCA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR019985 (TIGRFAM): IPR005633 (F	7,105	9,891	7,727	8,035	7,276									
Solyc10g084620	AT3g53630/F4P12_330 (AHRD V3.3 *** Q8VXU5_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,592	18,234	26,897	23,175	24,114									
Solyc10g084630	RNA-binding family protein (AHRD V3.3 *** A0A061ET74_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D	0,180	0,122	0,237	0,099	0,116									
Solyc10g084650	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 ***		F:GO:0046872	F:metal ion binding			IPR032308 (PFAM): IPR013083 (G3D	78,421	73,093	97,103	103,928	101,063									
Solyc10g084660	Actin depolymerizing factor, putative (AHRD V3.3 *** B9T4D2_RICCO)		F:GO:0003779; C:G(	F:actin binding; C:actin cytoskeleton; P:actin filament depolymeı			IPR002108 (PFAM): IPR029006 (G3D	8,837	8,412	3,611	2,163	3,374									
Solyc10g084670	Eukaryotic translation initiation factor 3 subunit A (AHRD V3.3 *** K4D3Q1_SOLLC)		C:GO:0005852	C:eukaryotic translation initiation factor 3 complex			G3DSA:4.10.860.10 (GENE3D): IPR0(	10,856	12,541	4,423	4,942	4,987									
Solyc10g084680	Sulfate transporter, putative (AHRD V3.3 *** A0A061GW43_THECC)		F:GO:0015098; P:G(	F:molybdate ion transmembrane transporter activity; P:molybda			IPR031563 (PFAM): IPR030161 (PTH	3,478	4,108	2,651	1,401	1,999					-0,913	0,027			down
Solyc10g084690	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *** A0A0K9Q1P3_ZOSMR)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR038508 (G3	22,343	25,718	15,322	11,811	13,998									
Solyc10g084700	30S ribosomal S18 (AHRD V3.3 *** A0A0B0MLA2_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001648 (PRINTS): IPR001648 (TI(	16,155	17,788	23,071	19,966	21,121									
Solyc10g084720	LOW QUALITY:Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein (AHRD V		F:GO:0005515; C:G(	F:protein binding; C:plasma membrane; C:integral component of			PF13515 (PFAM): PTHR30509 (PANT	0,000	0,041	0,000	0,000	0,000									
Solyc10g084730	Transducin/WD40 repeat-like superfamily protein, putative (AHRD V3.3 *-* A0A061ER69_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,057	0,000	0,000	0,000									
Solyc10g084740	rRNA-processing protein UTP23 like (AHRD V3.3 *-* A0A0B2NPV2_GLYSO)		P:GO:0009793; C:G(	P:embryo development ending in seed dormancy; C:small-subur			mobidb-lite (MOBIDB_LITE): mobidb-lit	11,180	10,290	10,610	9,853	10,532									
Solyc10g084745	rRNA-processing protein UTP23, putative (AHRD V3.3 *-* B9SW27_RICCO)		C:GO:0032040	C:small-subunit processome			G3DSA:3.40.50.1010 (GENE3D): PTH	4,188	3,038	4,292	4,249	4,051									
Solyc10g084750	TRM32-like protein (DUF3741) (AHRD V3.3 *** AT5G02390.3)						IPR025486 (PFAM): IPR022212 (PFAI	0,019	0,000	0,022	0,025	0,048									
Solyc10g084760	E3 ubiquitin-protein ligase (AHRD V3.3 *** W9SG42_9ROSA)		F:GO:0008270; F:G(	F:zinc ion binding; F:ubiquitin protein ligase activity; P:ubiquitin-(			IPR003126 (PFAM): G3DSA:2.10.110	249,514	190,857	282,339	325,110	317,610									
Solyc10g084770	Protein kinase (AHRD V3.3 *** A3RI54_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): G3DS	22,780	32,270	5,680	7,912	7,989									
Solyc10g084800	Oxysterol-binding protein (AHRD V3.3 *** Q6ST25_SOLTU)		C:GO:0005829; F:G(	C:cytosol; F:sterol transporter activity; P:sterol transport; C:meı			G3DSA:1.20.120.1290 (GENE3D): G3	35,669	49,920	38,640	41,936	39,934									
Solyc10g084810	S-acyltransferase (AHRD V3.3 *** M1ARM4_SOLTU)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR002696 (PFAM): IPR002696 (TIGF	2,148	2,085	0,834	1,404	1,271									
Solyc10g084820	S-acyltransferase (AHRD V3.3 *** K4D3R6_SOLLC)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883:SF2	1,687	1,555	1,888	1,816	1,833									
Solyc10g084830	Amino acid transporter family protein (AHRD V3.3 *** B9IFW4_POPTR)		C:GO:0016021	C:integral component of membrane			IPR013057 (PFAM): mobidb-lite (MOB	3,649	4,711	1,082	1,084	1,551									
Solyc10g084840	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072TZL3_MEDTR)						IPR001938 (PRINTS): IPR037176 (G3	0,233	0,354	0,049	0,022	0,047									
Solyc10g084850	glucose-induced degradation-like protein (AHRD V3.3 *** AT2G37680.2)		C:GO:0005773; P:G(	C:vacuole; P:protein targeting to vacuole; P:protein catabolic pr			IPR018618 (PFAM): IPR018618 (PAN	17,078	19,706	16,596	15,996	18,182									
Solyc10g084860	Clade XI lectin receptor kinase (AHRD V3.3 *** K4D3S0_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	0,582	0,623	0,412	0,344	0,378									
Solyc10g084880	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 137 (AHRD V3.3 *** Q9FQZ2_TOBAC)						IPR007700 (PFAM): IPR021864 (PFAI	70,492	24,512	26,930	77,112	32,242	-1,499	0,000			1,520	0,000	down		up
Solyc10g084890	Glycosyltransferase (AHRD V3.3 *** K4D3V7_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,021	0,043	0,900	1,801	1,291									
Solyc10g084920	PRA1 family protein (AHRD V3.3 *** M1ARP7_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): PTHR12859 (PAN	10,605	7,828	12,475	11,514	11,375									
Solyc10g084930	Kinase family protein (AHRD V3.3 *** B9HC64_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000615 (PIRSF): G3DSA:1.10.!	25,000	24,095	46,299	48,616	43,699									
Solyc10g084940	Major facilitator superfamily protein (AHRD V3.3 *-* AT2G37900.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			G3DSA:1.20.1250.20 (GENE3D): PTH	0,335	2,046	0,648	0,124	0,236	2,584	0,000					up		
Solyc10g084950	Major facilitator superfamily protein (AHRD V3.3 *** AT2G37900.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): G3DSA:1.20.125(	0,802	0,832	0,123	0,189	0,094									
Solyc10g084960	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GSTU51	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	7,886	12,151	5,166	5,893	7,209									
Solyc10g084970	WAS/WASL-interacting protein family member 2, putative isoform 1 (AHRD V3.3 *** A0A061FLH8_THECC)						mobidb-lite (MOBIDB_LITE): PTHR333	26,656	27,975	4,241	6,180	6,263									
Solyc10g084980	Copper transporter, putative (AHRD V3.3 *** A0A061ER83_THECC)		F:GO:0005375; C:G(	F:copper ion transmembrane transporter activity; C:integral con			IPR007274 (PFAM): PTHR12483:SF7(	0,242	0,171	0,000	0,000	0,000									
Solyc10g084990	Phosphatidylinositol:ceramide inositolphosphotransferase (AHRD V3.3 *** IPCS_ORYSI)		C:GO:0005802; C:G(	C:trans-Golgi netwc	EC:2.7.8.3; EC:2.7.8	Ceramide cholinepho	IPR025749 (PFAM): PTHR21290 (PAN	8,689	9,073	3,098	2,286	4,202									
Solyc10g085000	Kinase family protein (AHRD V3.3 *** B9IG10_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR011990 (G3DSA:1.25.40.GENE3D	61,649	78,219	12,715	12,492	15,766									
Solyc10g085010	PAR1 protein (AHRD V3.3 *** A0A061EYI9_THECC)						IPR009489 (PFAM): PTHR33649:SF4	35,779	60,355	17,712	37,480	34,471			0,957	0,007	1,081	0,000		up	up
Solyc10g085020	Tubulin beta chain (AHRD V3.3 *** M1ARQ6_SOLTU)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR002453 (PRINTS): IPR000217 (PF	311,847	353,769	95,043	72,555	96,504									
Solyc10g085030	SOUL heme-binding family protein (AHRD V3.3 *** AT2G37970.1)		F:GO:0020037	F:heme binding			IPR006917 (PFAM): IPR011256 (G3D	25,741	90,649	3,023	3,607	11,892	1,836	0,002	1,966	0,000			up	up	
Solyc10g085040	SOUL heme-binding family protein (AHRD V3.3 *** AT2G37970.1)		F:GO:0020037	F:heme binding			IPR006917 (PFAM): IPR011256 (G3D	1,070	0,513	4,419	7,788	5,548									
Solyc10g085050	O-fucosyltransferase family protein (AHRD V3.3 *** AT2G37980.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	3,992	2,477	9,610	7,155	7,419									
Solyc10g085060	Defective in exine formation protein (AHRD V3.3 *** G7JLW6_MEDTR)		F:GO:0005515	F:protein binding			PF13517 (PFAM): IPR015943 (G3DS/	26,070	23,510	48,017	49,723	43,947									
Solyc10g085070	UPF0503 protein, chloroplastic (AHRD V3.3 *** A0A199UN58_ANACO)		C:GO:0005886	C:plasma membrane			IPR008004 (PFAM): mobidb-lite (MOB	7,037	7,106	1,028	0,850	1,005									
Solyc10g085075	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT1G62910.1)							0,099	0,000	0,022	0,050	0,024									
Solyc10g085080	8-amino-7-oxononanoate synthase (AHRD V3.3 *** AT3G09050.1)		C:GO:0016021	C:integral component of membrane			PTHR35731 (PANTHER)	1,354	2,250	0,565	0,942	0,798									
Solyc10g085090	Laccase (AHRD V3.3 *** P93366_TOBAC)		F:GO:0005507; P:G(	F:copper ion bindin	EC:1.1.3; EC:1.1.3.2	Acting on diphenols a	IPR011706 (PFAM): IPR001117 (PFAI	1,784	1,588	0,143	0,047	0,189									
Solyc10g085100	sulfoquinovosyldiacylglycerol 2 (AHRD V3.3 *** AT5G01220.1)		P:GO:0009247; C:G(	P:glycolipid biosynthetic process; C:chloroplast envelope; P:sul			G3DSA:3.40.50.2000 (GENE3D): G3D	5,063	5,604	5,752	5,154	7,312									
Solyc10g085120	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001611 (PFAM): G3DSA:1.10.510.	0,203	0,309	0,000	0,022	0,047									
Solyc10g085130	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01520.1)		C:GO:0005829; P:G(	C:cytosol; P:ubiquitin-dependent protein catabolic process; P:re			PF13920 (PFAM): IPR013083 (G3DS/	4,048	2,537	9,518	10,336	7,259									
Solyc10g085140	Alkyl transferase (AHRD V3.3 *-* K7X479_SOLLC)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR036424 (G3DSA:3.40.1180.GENE:	1,839	2,817	13,628	17,834	17,247									
Solyc10g085150	cis-prenyltransferase 4		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth			IPR001441 (TIGRFAM): IPR001441 (F	3,133	5,948	3,332	3,659	3,467	0,946	0,030					up		
Solyc10g085160	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G01470.6)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			IPR019410 (PFAM): G3DSA:3.40.50.1	24,336	20,968	25,969	24,667	24,480									
Solyc10g085180	PHD finger alfin-like protein (AHRD V3.3 *** A0A072UGM4_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:histone binding			IPR013083 (G3DSA:3.30.40.GENE3D	9,016	9,322	15,384	17,386	15,292									
Solyc10g085190	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G11180.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc10g085200	Acyl-coenzyme A oxidase 4 (AHRD V3.3 *** W9RND6_9ROSA)		F:GO:0016627; F:G(	F:oxidoreductase activity, acting on the CH-CH group of donors			IPR013786 (PFAM): IPR006091 (PFAI	32,829	30,294	46,083	50,983	52,524									
Solyc10g085210	transcription factor-like protein (AHRD V3.3 *** AT1G58330.1)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindiı			IPR025422 (PFAM): PTHR22952:SF1(	0,259	1,142	0,547	1,092	0,989									
Solyc10g085215	UvrABC system C protein (AHRD V3.3 *** AT5G01350.1)						PTHR34966:SF3 (PANTHER): PTHR3(	32,559	29,984	49,900	48,634	50,840									
Solyc10g085220	Mitochondrial carrier protein, expressed (AHRD V3.3 *** Q10MX0_ORYSJ)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpc			IPR002067 (PRINTS): IPR023395 (G3	2,209	2,243	1,899	2,142	2,261									
Solyc10g085225	Heparanase-like protein 3 (AHRD V3.3 *** HPSE3_ARATH)		C:GO:0016020; F:G(	C:membrane; F:hydrolase activity, acting on glycosyl bonds			G3DSA:3.20.20.80 (GENE3D): IPR00!	12,821	12,407	7,643	5,138	8,345									
Solyc10g085230	ripening-related mRNA 1b	ert1b	F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	10,699	10,040	1097,938	1013,128	1075,957									
Solyc10g085240	Glycosyltransferase (AHRD V3.3 *** K4D3V8_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,038	0,116	2,649	1,027	2,197					-1,348	0,012			down
Solyc10g085255	NADH-ubiquinone oxidoreductase chain 2 (AHRD V3.3 --* NU2M_CHLRE)							0,102	0,060	0,191	0,166	0,188									
Solyc10g085270	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* A0A193D437_9POAL)							0,082	0,225	0,162	0,367	0,494									
Solyc10g085280	Glycosyltransferase (AHRD V3.3 *** K4D3W2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	9,482	6,379	10,598	9,531	14,230									
Solyc10g085285	Chalcone and stilbene synthase family protein (AHRD V3.3 --* AT4G00040.1)							0,084	0,184	6,868	7,414	6,124									
Solyc10g085290	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** A0A0B2PCD3_GLYSO)		F:GO:0051087	F:chaperone binding			IPR000626 (PFAM): IPR003103 (PFAI	24,347	25,589	24,903	28,282	24,923									
Solyc10g085300	uncharacterized protein						IPR036758 (G3DSA:2.30.240.GENE3I	28,997	40,477	26,546	27,414	28,989									
Solyc10g085310	Abscisic acid receptor (AHRD V3.3 *** G7KT83_MEDTR)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm			IPR023393 (G3DSA:3.30.530.GENE3I	5,081	10,203	1,114	0,451	0,936	1,028	0,002					up		
Solyc10g085320	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR026057 (PFAM): IPR025846 (PFAI	27,396	25,678	19,879	17,662	20,118									
Solyc10g085330	Protein DETOXIFICATION (AHRD V3.3 *-* A0A103YLD3_CYNCS)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM): mobidb-lite (MOB	3,114	3,191	4,076	4,355	4,996									
Solyc10g085335	Protein DETOXIFICATION (AHRD V3.3 *** B9SL10_RICCO)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (TIGRFAM): IPR002528 (F	0,220	0,143	0,074	0,120	0,187									
Solyc10g085350	Macrophage migration inhibitory factor (AHRD V3.3 *** A0A103YL90_CYNCS)						IPR014347 (G3DSA:3.30.429.GENE3I	0,659	1,327	0,109	0,098	0,210									
Solyc10g085360	Cell-wall invertase (AHRD V3.3 *** Q8LRN9_SOLLC)		F:GO:0004564; P:G(	F:beta-fructofurano:	EC:3.2.1.26	Beta-fructofuranosid:	IPR013148 (PFAM): IPR023296 (G3D	0,057	0,041	0,068	0,000	0,023									
Solyc10g085380	Short-chain dehydrogenase/reductase family protein (AHRD V3.3 *** B9HD90_POPTR),Pfam:PF13561		F:GO:0004316; P:G(	F:3-oxoacyl-[acyl-ca	EC:2.3.1.85; EC:1.1.	Fatty-acid synthase;	IPR002347 (PRINTS): IPR002347 (PF	0,294	0,465	0,000	0,000	0,024									
Solyc10g085400	D-alanine-D-alanine ligase family (AHRD V3.3 *** AT3G08840.2)		F:GO:0005524; F:G(	F:ATP binding; F:D-	EC:6.3.2.4	D-alanine--D-alanine	G3DSA:3.40.50.20 (GENE3D): G3DS/	60,494	50,457	18,623	11,767	17,962					-0,660	0,010			down
Solyc10g085410	Cactus-binding carboxy-terminal, cactin protein (AHRD V3.3 *** A0A072U2X1_MEDTR)		F:GO:0005515	F:protein binding			IPR018816 (PFAM): IPR019134 (PFAI	37,878	44,877	38,379	34,343	35,261									
Solyc10g085420	DNA polymerase epsilon catalytic subunit B (AHRD V3.3 --* DPOE2_ARATH)							0,100	0,195	0,090	0,099	0,072									
Solyc10g085430	LURP-one-like protein (AHRD V3.3 *-* G7KW17_MEDTR)		P:GO:0006629	P:lipid metabolic process			IPR007612 (PFAM): IPR007856 (PFAI	307,202	526,745	121,696	120,183	129,222									
Solyc10g085440	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* G4XMX4_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.310.80 (GENE3D)	0,828	0,851	0,938	1,228	0,801									

Solyc10g085450	Non-specific serine/threonine protein kinase (AHRD V3.3 *** G4XMX4_SOLLC)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR004041 (PFAM): G3DSA:3.30.310	26,356	24,269	24,894	24,588	24,832									
Solyc10g085460	Nbs-lrr resistance protein, putative (AHRD V3.3 *** A0A061FEU3_THECC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	46,420	43,462	19,288	21,581	25,499									
Solyc10g085480	60S ribosomal protein L24 (AHRD V3.3 *** RL24_PRUAV)		P:GO:0000027: F:G(	P:ribosomal large subunit assembly: F:RNA binding: F:structural			G3DSA:3.30.160.440 (GENE3D): IPR(	148,008	160,577	172,304	147,442	159,387									
Solyc10g085490	F-box protein PP2-A13 (AHRD V3.3 *** A0A072U2Z8_MEDTR)						IPR025886 (PFAM): PTHR31960:SF7	9,365	5,793	9,520	8,516	7,927									
Solyc10g085495	F-box PP2-A15-like protein (AHRD V3.3 *-* A0A0B0P567_GOSAR)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): mob	5,415	3,211	4,917	3,776	4,061									
Solyc10g085500	Cytochrome P450, putative (AHRD V3.3 *** B9SRM6_RICCO)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	19,277	15,802	0,093	0,145	0,116									
Solyc10g085530	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR003137 (PF	0,119	0,402	0,000	0,000	0,000									
Solyc10g085540	Subtilisin-like protease (AHRD V3.3 *** A0A151SNY0_CAJCA)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR037045 (G3	4,013	10,490	0,000	0,000	0,000									
Solyc10g085550	Enolase (AHRD V3.3 *-* ENO_SOLLC)		C:GO:0000015: F:G(	C:phosphopyruvate	EC:4.2.1.11	Phosphopyruvate hy	IPR000941 (PRINTS): IPR020811 (PF	10,485	13,372	21,105	22,197	21,755									
Solyc10g085555	Enolase (AHRD V3.3 *** AT2G36530.1)		C:GO:0000015: F:G(	C:phosphopyruvate	EC:4.2.1.11	Phosphopyruvate hy	IPR000941 (PRINTS): IPR036849 (G3	21,681	30,082	46,398	49,241	46,418									
Solyc10g085560	Histone deacetylase HDT1 (AHRD V3.3 *** HDT1_SOLCH)		F:GO:0003676	F:nucleic acid binding			PF12874 (PFAM): C2H2	44,287	44,988	34,387	32,185	33,221									
Solyc10g085570	CTR1-like protein kinase-4	CTR4	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PRINTS): PF14381 (PFAI	11,795	10,134	15,007	15,982	14,958									
Solyc10g085580	putative embryo sac development arrest 7		F:GO:0005515: C:G(	F:protein binding; C:nucleus			IPR012580 (PFAM): IPR015943 (G3D	33,219	32,008	41,976	41,298	38,600									
Solyc10g085590	Ubiquitin-conjugating enzyme/RWD-like protein (AHRD V3.3 *** AT3G12400.1)		P:GO:0006464: P:G(	P:cellular protein modification process; P:protein transport			IPR008883 (PFAM): IPR016135 (G3D	211,354	106,095	96,875	248,201	143,382	-0,972	0,027			1,359	0,000	down		up
Solyc10g085600	BTB/POZ domain-containing protein FBL11 (AHRD V3.3 *** A0A0B2QG81_GLYSO)		F:GO:0005515	F:protein binding			IPR011705 (PFAM): G3DSA:3.30.710	14,154	9,669	10,839	15,976	13,004					0,557	0,027			up
Solyc10g085610	Calmodulin binding protein, putative (AHRD V3.3 *** B9T5N0_RICCO)		F:GO:0005515	F:protein binding			mobidb-lite (MOBIDB_LITE): PTHR312	0,332	0,422	0,462	0,144	0,285									
Solyc10g085620	Myb family transcription factor APL (AHRD V3.3 *** A0A0B2R6R9_GLYSO)		F:GO:0003677	F:DNA binding			IPR025756 (PFAM G2-like	5,933	5,322	5,051	8,241	7,384					0,711	0,004			up
Solyc10g085630	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A0K9Q5H5_ZOSMR)		F:GO:0003860	F:3-hydroxyisobutyı	EC:3.1.2.4	3-hydroxyisobutyryl-(	G3DSA:3.90.226.40 (GENE3D): IPR0:	18,600	19,090	22,401	21,265	21,355									
Solyc10g085650	Cell-wall invertase (AHRD V3.3 *** Q8LRN9_SOLLC)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			IPR023296 (G3DSA:2.115.10.GENE3	0,060	0,082	0,171	0,269	0,140									
Solyc10g085660	F-box family protein (AHRD V3.3 *** AT1G08710.1)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): PTH	10,334	8,246	6,948	7,395	6,708									
Solyc10g085665	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561		F:GO:0016491: F:G(	F:oxidoreductase activity: F:androstan-3-alpha,17-beta-diol deh			IPR002347 (PRINTS): G3DSA:3.40.5(	0,078	0,083	0,051	0,022	0,023									
Solyc10g085670	MAP kinase kinase kinase 79	MAPKKK79	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200	0,903	0,796	0,025	0,000	0,117									
Solyc10g085680	Protein kinase superfamily protein (AHRD V3.3 *** AT5G01920.2)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	8,970	10,545	15,148	15,588	19,927									
Solyc10g085690	PRC-barrel-like protein (AHRD V3.3 *** A0A103XQI6_CYNCS)						mobidb-lite (MOBIDB_LITE): mobidb-lit	10,973	10,004	20,910	19,364	21,636									
Solyc10g085710	MACPF domain protein (AHRD V3.3 *** G7ILM1_MEDTR)						IPR020864 (PFAM): PTHR33199 (PAI	28,440	36,033	35,230	33,255	34,684									
Solyc10g085715	MACPF domain protein (AHRD V3.3 *-* G7ILM1_MEDTR)						IPR020864 (PFAM): PTHR33199:SF5	9,273	10,687	11,328	12,413	9,966									
Solyc10g085720	Kinase family protein (AHRD V3.3 *** B9MYL8_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200	54,398	46,242	23,958	27,963	31,246									
Solyc10g085730	Exostosin-like protein (AHRD V3.3 *** A0A103Y622_CYNCS)		P:GO:0006486: F:G(	P:protein glycosylation: F:transferase activity, transferring glyco			IPR040911 (PFAM): PTHR11062:SF6	0,019	0,000	0,025	0,000	0,000									
Solyc10g085740	GDSL esterase/lipase (AHRD V3.3 *** W9R8E1_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR036514 (G3DSA:3.40.50.GENE3D	6,998	3,427	0,099	0,201	0,000									
Solyc10g085750	Polyadenylate-binding protein (AHRD V3.3 *** K4D409_SOLLC)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	3,475	3,583	3,884	3,328	5,622									
Solyc10g085790	RNA helicase DEAD34	DEAD34	F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): G3DS	87,232	75,377	128,188	117,341	114,033									
Solyc10g085800	PLATZ transcription factor family protein (AHRD V3.3 *** G7IA73_MEDTR)		F:GO:0008270	F:zinc ion binding			G3DSA:3.30.40.200 (GENE3D): IPR0(	1,022	0,767	5,863	7,441	3,344			-0,806	0,014				down	
Solyc10g085810	Vacuolar protein-sorting-associated protein 37 homolog 2 (AHRD V3.3 *** VP372_ARATH)		C:GO:0000813: P:G(	C:ESCRT I complex: P:endosome transport via multivesicular bo			IPR009851 (PFAM): mobidb-lite (MOB	0,000	0,000	0,098	0,285	0,165									
Solyc10g085820	DnaJ subfamily C member 28 (AHRD V3.3 *** A0A0B0MTA2_GOSAR)						IPR018961 (PFAM): mobidb-lite (MOB	20,243	12,765	30,861	22,845	25,965	-0,638	0,031					down		
Solyc10g085830	Caffeic acid O-methyltransferase (AHRD V3.3 *** A0A072VA70_MEDTR)		F:GO:0008171	F:O-methyltransferase activity			IPR036388 (G3DSA:1.10.10.GENE3D	34,334	48,948	243,206	223,981	246,121									
Solyc10g085850	LOW QUALITY:S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61360.1)							6,808	9,079	5,924	4,616	4,346									
Solyc10g085860	Glycosyltransferase (AHRD V3.3 *** K4D420_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,295	0,530	0,022	0,075	0,047									
Solyc10g085870	Glycosyltransferase (AHRD V3.3 *** M1BFM3_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,726	1,262	5,101	5,306	5,598									
Solyc10g085880	Glycosyltransferase (AHRD V3.3 *** K4DF51_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	104,067	147,233	5525,469	5845,885	4880,380									
Solyc10g085890	poly(ADP-ribose) glycohydrolase 2 (AHRD V3.3 --* AT2G31865.3)							9,500	12,079	446,286	594,879	419,590									
Solyc10g085900	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT2G37400.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	10,562	7,663	109,000	131,572	110,838									
Solyc10g085910	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G02600.2)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	27,413	32,031	18,897	20,040	25,313									
Solyc10g085920	UDP-glucuronate decarboxylase protein 1 (AHRD V3.3 *** N0A9W0_POPTO)		C:GO:0005768: C:G(	C:endosome: C:trar	EC:4.1.1.35	UDP-glucuronate dec	G3DSA:3.40.50.720 (GENE3D): G3DS	2,234	2,561	1,932	1,828	2,027									
Solyc10g085930	YCF20-like protein (DUF565) (AHRD V3.3 *** AT3G56830.8)		C:GO:0016021	C:integral component of membrane			IPR007572 (PFAM): PTHR33787:SF3	6,165	5,517	9,710	8,987	8,570									
Solyc10g085950	aluminum sensitive 3 (AHRD V3.3 *** AT2G37330.1)		F:GO:0005460: C:G(	F:UDP-glucose transmembrane transporter activity: C:integral c			IPR005226 (TIGRFAM): IPR005226 (F	1,665	2,611	1,047	1,692	1,551									
Solyc10g085960	Pathogenesis-related protein 1 (AHRD V3.3 *-* A0A199VSB9_ANACO)		C:GO:0005615	C:extracellular space			IPR001283 (PRINTS): IPR035940 (G3	1,594	2,240	3,038	1,718	1,934									
Solyc10g085970	SAP domain-containing ribonucleoprotein (AHRD V3.3 *** A0A0B0P934_GOSAR)		C:GO:0005634: P:G(	C:nucleus; P:poly(A)+ mRNA export from nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	120,137	111,800	153,750	145,760	141,563									
Solyc10g085980	integral membrane TerC family protein (AHRD V3.3 *** AT5G12130.1)		C:GO:0016021	C:integral component of membrane			IPR005496 (PFAM): IPR022369 (TIGF	7,961	8,315	7,052	6,142	8,338									
Solyc10g085985	SCD6 protein-like protein (AHRD V3.3 --* AT4G19360.2)							0,040	0,099	0,022	0,072	0,046									
Solyc10g085990	Protein kinase-like protein (AHRD V3.3 *** Q6TKQ5_VITAE)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	31,261	27,790	25,443	24,546	24,727									
Solyc10g086000	Pseudo-response regulator (AHRD V3.3 *-* X5I0R0_IPONI)		P:GO:0000160	P:phosphorelay signal transduction system			G3DSA:3.40.50.2300 (GENE3D): IPR(	35,413	38,410	38,349	40,143	42,281									
Solyc10g086010	60S ribosomal L4 (AHRD V3.3 *** A0A0B0NGW3_GOSAR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR002136 (PFAM): IPR025755 (PFA	105,203	124,709	124,089	102,408	113,180									
Solyc10g086020	interactor of constitutive active ROPs 3		F:GO:0003735: P:G(	F:structural constituent of ribosome: P:translation: C:small ribos			IPR005680 (TIGRFAM): G3DSA:2.40.!	220,908	244,424	160,979	153,003	153,247									
Solyc10g086025	DNA-binding protein S1FA, putative (AHRD V3.3 --* B9SGP8_RICCO)		F:GO:0003677: C:G(	F:DNA binding: C:nucleus: P:regulation of transcription, DNA-templated: C:membrane: C:integral compo				34,510	37,623	46,851	48,384	42,743									
Solyc10g086030	Interactor of constitutive active ROPs 2, chloroplastic-like protein (AHRD V3.3 *** A0A0B0PSX8_GOSAR)		F:GO:0051219	F:phosphoprotein binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	10,852	11,774	2,550	2,918	4,627									
Solyc10g086040	Mitochondrial import inner membrane translocase subunit TIM14 (AHRD V3.3 *** B6SI13_MAIZE)		C:GO:0001405: F:G(	C:PAM complex, Tim23 associated import motor: F:ATPase acti			IPR036869 (G3DSA:1.10.287.GENE3I	10,719	13,609	27,442	29,182	25,988									
Solyc10g086060	SUN-like protein 30	SUN30	F:GO:0005515	F:protein binding			IPR000048 (PFAM): mobidb-lite (MOB	58,901	61,631	23,844	20,322	30,114									
Solyc10g086070	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G53390.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): mobidb-lite (MOB	22,456	23,471	38,751	40,117	38,936									
Solyc10g086080	RING/U-box superfamily protein (AHRD V3.3 *** AT3G09770.1)		F:GO:0016874	F:ligase activity			PF13920 (PFAM): IPR013083 (G3DS/	0,000	0,057	0,000	0,000	0,000									
Solyc10g086100	Proteinase inhibitor (AHRD V3.3 *** A0A0R4WSF0_TOBAC)		F:GO:0004867: P:G(	F:serine-type endopeptidase inhibitor activity: P:response to wo			IPR000864 (PRINTS): G3DSA:3.30.1(	0,236	0,384	0,428	0,413	0,588									
Solyc10g086110	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *** AT5G03230.1)						IPR007608 (PFAM): mobidb-lite (MOB	0,321	0,209	0,000	0,000	0,000									
Solyc10g086120	CASP-like protein (AHRD V3.3 *** K4D446_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021:SF1	9,597	6,542	6,706	5,994	7,140									
Solyc10g086125	Ubiquitin family protein (AHRD V3.3 *-* AT4G02890.4)		F:GO:0005515	F:protein binding			IPR019956 (PRINTS): G3DSA:3.10.2(	0,313	0,267	0,280	0,169	0,117									
Solyc10g086137	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT5G03250.1)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0(	0,156	0,177	0,050	0,000	0,000									
Solyc10g086150	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G37220.1)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D	33,385	68,686	41,329	31,683	58,134	1,068	0,000					up		
Solyc10g086160	LOW QUALITY:Threonine dehydratase (AHRD V3.3 *-* M1BHK0_SOLTU)		P:GO:0009082: F:G(	P:branched-chain amino acid biosynthetic process: F:lyase acti			IPR001721 (PFAM): G3DSA:3.40.50.1	0,000	0,018	0,000	0,000	0,024									
Solyc10g086170	amidase 1 (AHRD V3.3 *** AT1G08980.1)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR036928 (G3DSA:3.90.1300.GENE	6,950	8,948	8,713	10,636	13,710			0,645	0,022				up	
Solyc10g086180	Phenylalanine ammonia-lyase (AHRD V3.3 *** PAL2_TOBAC)	PAL	C:GO:0005737: P:G(	C:cytoplasm: P:L-phenylalanine catabolic process: F:ammonia-l			IPR023144 (G3DSA:1.10.274.GENE3I	7,599	11,644	75,061	93,343	73,669									
Solyc10g086190	Adenosine kinase, putative (AHRD V3.3 *** B9T0A9_RICCO)		F:GO:0004001: P:G(	F:adenosine kinase	EC:2.7.1.2	Adenosine kinase	IPR001805 (PRINTS): G3DSA:3.30.11	63,301	65,052	11,539	9,745	11,551									
Solyc10g086210	Translin family protein (AHRD V3.3 *** AT2G37020.3)		F:GO:0003697: F:G(	F:single-stranded DNA binding: F:RNA binding: P:RNA metabolic			IPR016069 (G3DSA:1.20.58.GENE3D	16,633	16,521	10,520	7,156	8,773					-0,555	0,033			down
Solyc10g086220	12-oxophytodienoate reductase	opr	F:GO:0010181: F:G(	F:FMN binding: F:oxidoreductase activity: P:oxidation-reduction			IPR013785 (G3DSA:3.20.20.GENE3D	22,232	18,417	7,025	7,564	11,260									
Solyc10g086240	Glycosyltransferase (AHRD V3.3 *** V4SWV8_9ROSI)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	1,289	1,636	0,744	0,481	0,618									
Solyc10g086250	R2R3MYB transcription factor 75	R2R3MYB75	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,077	1,671	0,090	0,022	0,282	4,265	0,000					up		
Solyc10g086280	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT5G03380.1)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D): IPR0(	253,167	102,290	17,306	47,542	38,122	-1,285	0,003	1,136	0,002	1,457	0,000	down	up	up
Solyc10g086290	R2R3MYB transcription factor 114	R2R3MYB114	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,063	0,083	0,212	0,147	0,306									
Solyc10g086320	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 *** A0A072VJC1_MEDTR)		F:GO:0005524: F:G(	F:ATP binding: F:1-	EC:2.7.1.68	1-phosphatidylinosito	IPR017163 (PIRSF): IPR027483 (G3D	10,749	8,489	2,319	1,651	1,295									
Solyc10g086335	Kinesin-related protein (AHRD V3.3 *** A0A0B0NAJ1_GOSAR)		F:GO:0003777: F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	0,341	0,511	0,443	0,345	0,234									
Solyc10g086350	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G59840.1)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	12,140	10,547	11,660	11,131	10,565									
Solyc10g086360	BRI1-KD interacting protein (AHRD V3.3 *** T2DLB0_PHAVU)						mobidb-lite (MOBIDB_LITE): mobidb-lit	68,737	63,956	76,558	75,326	76,644									
Solyc10g086370	GAI-like protein 1 (AHRD V3.3 *** A1YWN9_9ROSI)	GRAS	F:GO:0003712: C:G(	F:transcription coregulator activity; C:nucleus			IPR005202 (PFAM GRAS	0,489	0,547	0,362	0,703	0,609									
Solyc10g086380	GAI-like protein 1 (AHRD V3.3 *** A1YWN9_9ROSI)	GRAS	F:GO:0003712: C:G(	F:transcription coregulator activity; C:nucleus			IPR005202 (PFAM GRAS	2,251	8,537	0,461	0,679	1,105	1,939	0,011					up		
Solyc10g086390	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G02540.1)						IPR002347 (PRINTS): IPR002347 (PF	0,255	0,304	0,198	0,654	0,000									
Solyc10g086400	RNA-binding family protein (AHRD V3.3 *** A0A061ET42_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR025715 (PFA	198,371	186,562	128,575	115,671	114,741									
Solyc10g086410	LEHSC270_hsc-2heat shock protein cognate 70	hsc70	F:GO:0005524: C:G(	F:ATP binding: C:cy	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS): IPR029047 (G3	284,048	254,726	90,580	83,929	82,681									
Solyc10g086420	LOW QUALITY:HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT2G37570.1)		P:GO:0042538	P:hyperosmotic salinity response			IPR008978 (G3DSA:2.60.40.GENE3D	40,651	52,382	42,455	39,700	39,260									
Solyc10g086430	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7L3F0_MEDTR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	0,378	0,486	0,197	0,142	0,235									
Solyc10g086440	Dof zinc finger protein (AHRD V3.3 *** W9S882_9ROSA)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	1,330	1,459	1,364	1,382	1,532									
Solyc10g086450	LOW QUALITY:cyclin-dependent protein kinase inhibitor (AHRD V3.3 --* AT5G04470.1)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc10g086460	Actin (AHRD V3.3 *** ACT1_TOBAC)		F:GO:0005524	F:ATP binding			IPR004000 (PRINTS): G3DSA:3.30.42	0,019	0,120	0,000	0,051	0,023									
Solyc10g086470	Aldolase-type TIM barrel family protein (AHRD V3.3 --* AT3G14420.6)		C:GO:0016021	C:integral component of membrane			PTHR36006 (PANTHER): PTHR36006	2,756	2,903	3,114	2,167	3,219									
Solyc10g086480	Pectinacetylesterase family protein (AHRD V3.3 *** AT3G09410.1)		F:GO:0016787	F:hydrolase activity			IPR004963 (PFAM): IPR004963 (PAN	5,130	4,791	1,779	2,547	2,118									
Solyc10g086490	Protein phosphatase 2c, putative (AHRD V3.3 *** B9T262_RICCO)		F:GO:0004722: P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threo	IPR001932 (PFAM): IPR036457 (G3D	1,066	1,389	1,181	1,726	2,131									
Solyc10g086500	steroid 5 alpha reductase DET2	det2.1	F:GO:0003865: P:G(	F:3-oxo-5-alpha-ste	EC:1.3.99.5	3-oxo-5-alpha-steroi	G3DSA:1.20.120.1630 (GENE3D): IPI	2,627	5,622	2,717	2,530	2,464	1,124	0,012					up		
Solyc10g086510	Mitochondrial import inner membrane translocase subunit Tim9 (AHRD V3.3 *** TIM9_ORYSJ)		C:GO:0042719: C:G(	C:mitochondrial intermembrane space protein transporter compl			IPR035427 (G3DSA:1.10.287.GENE3I	24,336	24,876	32,597	35,039	32,732									
Solyc10g086520	expansin 6	EXPA6	C:GO:0005576: P:G(	C:extracellular region; P:plant-type cell wall organization			IPR007118 (PRINTS): IPR002963 (PF	41,572	46,094	10,351	16,283	16,468			0,667	0,026	0,654	0,035		up	up
Solyc10g086530	GRAS family transcription factor (AHRD V3.3 *** A0A072U0I2_MEDTR)	GRAS	F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR005202 (PFAM GRAS	0,379	0,431	0,147	0,123	0,306									
Solyc10g086535	Pyruvate, phosphate dikinase, chloroplastic (AHRD V3.3 --* PPDK_FLATR)							0,021	0,019	0,025	0,047	0,070									
Solyc10g086540	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** A0A0K9PCT4_ZOSMR)		F:GO:0004222: F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	G3DSA:3.40.50.300 (GENE3D): IPR0(	15,177	13,857	17,189	17,089	16,384									
Solyc10g086550	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** G7JUV4_MEDTR)		F:GO:0004222: F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	IPR005936 (TIGRFAM): G3DSA:3.40.	56,755	59,133	117,180	119,175	110,316									
Solyc10g086560	Far-red elongated hypocotyl 1, putative isoform 1 (AHRD V3.3 *** A0A061ES27_THECC)		P:GO:0009639	P:response to red or far red light			IPR037766 (PANTHER)	37,491	35,475	41,913	46,195	41,450									
Solyc10g086565	S-acyltransferase (AHRD V3.3 *** A0A0V0I2F0_SOLCH)		C:GO:0005783: C:G(	C:endoplasmic retic	EC:2.3.1.225	Protein S-acyltransfe	IPR001594 (PFAM): PTHR22883:SF2	2,465	1,599	1,421	2,028	1,671									
Solyc10g086570	Chaperone DnaJ (AHRD V3.3 *** A0A0B0NPS3_GOSAR)		C:GO:0009535: C:G(	C:chloroplast thylakoid membrane: C:integral component of men			PTHR36389 (PANTHER)	1,171	3,066	0,741	2,138	3,706	1,398	0,008	2,293	0,000	1,507	0,001	up	up	up
Solyc10g086580	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *** V9IMY5_NICAT)		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): G3DS	376,850	673,783	150,926	170,168	360,380	0,866	0,016	1,252	0,000			up	up	
Solyc10g086600	Subtilisin-like protease (AHRD V3.3 *-* W9RLB7_9ROSA)		F:GO:0004252: P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR000209 (PFAM): IPR010259 (PFA	0,058	0,061	0,000	0,025	0,000									
Solyc10g086610	LOW QUALITY:Plant self-incompatibility protein S1 family (AHRD V3.3 *** AT5G12060.1)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			IPR010264 (PFAM): IPR010264 (PAN	0,038	0,039	0,000	0,000	0,000									
Solyc10g086620	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	14,593	16,426	1,023	1,564	1,105									
Solyc10g086630	LOW QUALITY:Legume-specific protein (AHRD V3.3 *** S5VRI2_9FABA)						PTHR34670:SF3 (PANTHER): PTHR3-	0,340	0,098	0,050	0,050	0,024									
Solyc10g086640	BEL1-like homeodomain protein (AHRD V3.3 *** G7L5K2_MEDTR)		F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			G3DSA:1.10.10.6(TALE	1,574	2,392	0,359	0,165	0,282									
Solyc10g086650	LOW QUALITY:glyoxal oxidase-related protein (AHRD V3.3 *** AT3G53950.1)		C:GO:0016021	C:integral component of membrane			IPR015202 (PFAM): IPR013783 (G3D	25,920	23,551	18,682	20,660	25,869									
Solyc10g086660	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9T764_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.2010 (GENE3D): G3E	24,565	19,463	63,824	66,963	90,323									
Solyc10g086680	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	Hsp27.1	P:GO:0006457: P:G(	P:protein folding: P:response to heat: P:response to salt stress:			IPR002068 (PFAM): IPR008978 (G3D	0,708	2,047	1,562	1,282	1,058	1,548	0,040					up		
Solyc10g086690	Phosphatidylinositol:ceramide inositolphosphotransferase (AHRD V3.3 *** IPCS_ORYSI)		C:GO:0005802: C:G(	C:trans-Golgi netwc	EC:2.7.8.3: EC:2.7.8	Ceramide cholinepho	IPR025749 (PFAM): PTHR21290 (PAI	13,909	28,522	20,742	26,446	24,680									
Solyc10g086700	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EYJ3_THECC)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	4,242	4,833	3,656	4,088	4,446									
Solyc10g086710	PAR1-like protein (AHRD V3.3 *** A0A103XQ58_CYNCS)						IPR009489 (PFAM): IPR009489 (PAN	1,213	2,458	2,833	7,685	5,045			0,825	0,025	1,435	0,000		up	up
Solyc10g086720	Fructose-1,6-bisphosphatase, putative (AHRD V3.3 *** B9SPG7_RICCO)		P:GO:0005975: F:G(	P:carbohydrate met	EC:3.1.3.23: EC:3.1.	Sugar-phosphatase:	IPR028343 (PRINTS): G3DSA:3.40.1!	0,517	0,913	0,171	0,148	0,071									
Solyc10g086730	Fructose-1,6-bisphosphatase (AHRD V3.3 *** W9S5L8_9ROSA)		P:GO:0005975: F:G(	P:carbohydrate met	EC:3.1.3.23: EC:3.1.	Sugar-phosphatase:	IPR028343 (PRINTS): IPR028343 (PII	97,781	96,158	35,880	35,951	60,929			0,760	0,000				up	
Solyc10g086740	LOW QUALITY:DNA double-strand break repair rad50 ATPase, putative isoform 1 (AHRD V3.3 *** A0A061EYI5_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,101	0,079	0,212	0,117	0,423									
Solyc10g086750	LOW QUALITY:DNA double-strand break repair rad50 ATPase, putative isoform 2 (AHRD V3.3 *-* A0A061EQL2_THECC)						PTHR35117 (PANTHER)	0,000	0,000	0,000	0,000	0,024									
Solyc10g086760	Tubulin beta chain (AHRD V3.3 *** A0A103XQ61_CYNCS)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	IPR002453 (PRINTS): IPR000217 (PF	68,843	75,758	18,111	16,302	19,337									
Solyc10g086770	Ataxin-3 like (AHRD V3.3 *** A0A0B2QXG6_GLYSO)		F:GO:0004843: P:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	PR01233 (PRINTS): G3DSA:3.90.70.4	0,040	0,021	0,000	0,025	0,047									
Solyc10g086780	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G20400.1)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	9,409	10,530	12,819	12,200	12,553									
Solyc10g087010	Cytochrome P450 (AHRD V3.3 *** A0A103XWG4_CYNCS)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	48,409	57,282	34,631	28,954	45,262									
Solyc10g087013	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	0,077	0,609	0,071	0,267	0,070									
Solyc11g005000	Keratinocytes-associated protein 2 (AHRD V3.3 *** B6SJ34_MAIZE)		C:GO:0016021	C:integral component of membrane			IPR018614 (PFAM): IPR018614 (PAN	41,392	42,137	34,236	28,499	31,096									
Solyc11g005010	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT2G30710.1)		F:GO:0005096: C:G(	F:GTPase activator activity: C:cell: P:intracellular protein transp			IPR000195 (PFAM): G3DSA:1.10.8.27	16,151	17,431	19,068	21,462	17,923									
Solyc11g005015	Protein translocase subunit SecA (AHRD V3.3 *-* K4D4B5_SOLLC)		F:GO:0005524: P:G(	F:ATP binding: P:protein targeting: C:membrane: P:protein impo			G3DSA:1.10.3060.10 (GENE3D): IPR(	35,802	37,441	42,123	43,019	43,335									
Solyc11g005020	Protein translocase subunit SecA (AHRD V3.3 *** K4D4B5_SOLLC)		F:GO:0005524: P:G(	F:ATP binding: P:protein targeting: C:membrane: P:protein impo			IPR000185 (PRINTS): IPR011130 (PF	28,434	24,878	29,375	30,319	31,155									
Solyc11g005030	Protein translocase subunit SecA (AHRD V3.3 *** V4KTM1_EUTSA)		F:GO:0004672: F:G(	F:protein kinase activity: F:protein binding: F:ATP binding: P:pro			IPR027370 (PFAM): IPR015943 (G3D	27,956	26,843	31,502	35,221	30,951									
Solyc11g005050	Mitochondrial ATP synthase 6 kDa subunit (AHRD V3.3 *** A0A0K9PE24_ZOSMR)		C:GO:0016021	C:integral component of membrane			PTHR34565 (PANTHER)	56,610	58,038	68,323	61,536	65,261									
Solyc11g005060	NADH:ubiquinone oxidoreductase intermediate-associated protein 30 (AHRD V3.3 *** AT1G17350.5)		P:GO:0032981	P:mitochondrial respiratory chain complex I assembly			IPR013857 (PFAM): PTHR13194:SF1:	25,382	24,503	34,495	35,387	31,941									
Solyc11g005070	amino acid transporter 3	aap3	P:GO:0003333: C:G(	P:amino acid transmembrane transport: C:plasma membrane: F			IPR013057 (PFAM): PTHR22950 (PAI	0,835	1,760	1,184	1,573	1,273									
Solyc11g005090	cyclin A1	cyca1	C:GO:0005634	C:nucleus			G3DSA:1.10.472.10 (GENE3D): IPR0(	2,914	2,658	1,308	1,344	1,254									
Solyc11g005100	NAD kinase 2 (AHRD V3.3 *-* AT1G21640.1)		F:GO:0003951: P:G(	F:NAD+ kinase acti	EC:2.7.1.23	NAD(+) kinase	IPR017437 (G3DSA:2.60.200.GENE3I	0,377	0,122	0,025	0,025	0,023									
Solyc11g005110	MADS-box transcription factor (AHRD V3.3 *-* G7IA45_MEDTR)		F:GO:0003700: F:G(	F:DNA-binding transcription factor activity: F:protein binding: C:i			G3DSA:2.20.70.10 (GENE3D): IPR00:	40,858	37,546	56,684	54,378	52,549									
Solyc11g005130	Wound-responsive family protein (AHRD V3.3 *** B9H7J2_POPTR)						IPR014840 (PFAM): mobidb-lite (MOB	27,967	27,415	32,140	33,021	30,293									
Solyc11g005140	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RM09_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	25,984	31,583	25,814	24,417	23,304									
Solyc11g005150	entensin X55687		F:GO:0005515	F:protein binding			PR01217 (PRINTS): IPR032675 (G3D	74,269	55,081	18,377	30,051	28,351									
Solyc11g005160	F-box family protein (AHRD V3.3 *** B9MX84_POPTR)		F:GO:0005515	F:protein binding			IPR005174 (PFAM): PTHR13710:SF8	0,000	0,018	0,000	0,000	0,000									
Solyc11g005170	RNA-binding 39 (AHRD V3.3 *** A0A0B0PR36_GOSAR)		F:GO:0003723: C:G(	F:RNA binding; C:nucleus; P:mRNA processing			IPR012677 (G3DSA:3.30.70.GENE3D	222,953	211,616	281,151	266,429	264,383									
Solyc11g005180	LOW QUALITY:Protein SENSITIVITY TO RED LIGHT REDUCED 1 (AHRD V3.3 *-* SRR1_ARATH)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.1.3: EC:3.1.26:	Acting on ester bond:	IPR012942 (PFAM): IPR002156 (PFA	0,136	0,244	0,604	1,544	0,259									
Solyc11g005190	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G23730.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	3,277	3,675	11,188	30,464	10,464					1,452	0,000			up

Solyc11g005200	Prolyl 4-hydroxylase subunit alpha-1 (AHRD V3.3 *** A0A0B2RW69_GLYSO)	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	G3DSA:2.60.120.620 (GENE3D); IPRI	21,399	21,394	47,102	57,091	42,923									
Solyc11g005210	LOW QUALITY:B3 domain-containing protein (AHRD V3.3 *-* A0A0B2RZ88_GLYSO)			IPR005508 (PFAM); PTHR31541 (PAN	0,000	0,000	0,025	0,123	0,000									
Solyc11g005220	AP-1 complex subunit sigma-1 (AHRD V3.3 *** AP1S1_ARATH)	P:GO:0015031	P:protein transport	IPR016635 (PIRSF); IPR022775 (PFA	93,480	90,235	75,440	71,759	70,164									
Solyc11g005230	LOW QUALITY:Protein SENSITIVITY TO RED LIGHT REDUCED 1 (AHRD V3.3 *** SRR1_ARATH)	F:GO:0003676; F:G(	F:nucleic acid bindi; EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR036397 (G3DSA:3.30.420 GENE3	0,163	0,325	0,074	0,025	0,047									
Solyc11g005240	LOW QUALITY:Sensitivity to red light reduced 1 (AHRD V3.3 *-* A0A061F8P0_THECC)	F:GO:0003676; F:G(	F:nucleic acid bindi; EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR036397 (G3DSA:3.30.420 GENE3	0,247	0,924	0,361	0,249	0,373									
Solyc11g005250	SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein (AHRD V3.3 *** /	F:GO:0005515; F:G(	F:protein binding; F:ATP binding; F:zinc ion binding	IPR038718 (G3DSA:3.40.50 GENE3D	102,166	79,551	151,347	158,763	138,698									
Solyc11g005260	Sensitivity to red light reduced 1-like protein (AHRD V3.3 *** A0A0B0PCL2_GOSAR)			IPR012942 (PFAM); PTHR28626 SF3	6,433	6,841	8,188	8,026	7,687									
Solyc11g005270	LOW QUALITY:Glutaredoxin family protein (AHRD V3.3 *** AT5G13810.1)	F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	G3DSA:3.40.30.10 (GENE3D); IPR02	0,078	0,204	0,047	0,047	0,024									
Solyc11g005280	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40 GENE3D	0,525	0,327	0,144	0,122	0,071									
Solyc11g005290	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	C:GO:0016021	C:integral component of membrane	IPR001841 (PFAM); IPR013083 (G3D	0,102	0,252	0,000	0,000	0,000									
Solyc11g005300	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40 GENE3D	1,389	0,875	0,090	0,022	0,024									
Solyc11g005310	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	C:GO:0016021	C:integral component of membrane	IPR001841 (PFAM); IPR013083 (G3D	0,235	0,117	0,099	0,000	0,023									
Solyc11g005320	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40 GENE3D	0,603	0,402	0,165	0,022	0,023									
Solyc11g005330	Actin (AHRD V3.3 *** ACT_GOSHI) ACT2	F:GO:0005524	F:ATP binding	IPR004000 (PRINTS); G3DSA:3.30.42	833,989	817,146	657,972	602,186	606,813									
Solyc11g005340	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT5G09820.2)			IPR006843 (PFAM); PTHR31906 SF4	0,243	0,305	0,074	0,000	0,023									
Solyc11g005350	WAT1-related protein (AHRD V3.3 *** K4D4E8_SOLLC)	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); mobidb-lite (MOB	4,130	3,935	5,126	2,169	3,020					-1,239	0,009			down
Solyc11g005360	BolA protein (AHRD V3.3 *** A0A103YGA6_CYNCS)	C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:response to oxidative stress; P:respons	IPR002634 (PIRSF); G3DSA:3.30.300	18,029	18,582	54,429	49,788	52,088									
Solyc11g005370	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT1G76860.1)	P:GO:0000398; P:G(	P:mRNA splicing, via spliceosome; P:nuclear-transcribed mRNA	G3DSA:2.30.30.100 (GENE3D); IPR0	21,880	25,627	25,405	23,828	23,898									
Solyc11g005380	Trihelix transcription factor GT-2 (AHRD V3.3 *** W9RGP4_9ROSA)	F:GO:0003700; F:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	G3DSA:1.10.10.60; Trihelix	82,116	96,731	107,612	138,129	127,294									
Solyc11g005390	Transmembrane protein, putative (AHRD V3.3 *** G7JAX0_MEDTR)	C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane	PTHR36363 (PANTHER)	1,769	1,390	0,336	0,552	0,472									
Solyc11g005400	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XK28_CYNCS)			IPR036869 (G3DSA:1.10.287 GENE3	5,450	6,382	9,857	11,223	9,791									
Solyc11g005410	WAT1-related protein (AHRD V3.3 *** K4D4F4_SOLLC)	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); PTHR31218 SF7	0,255	0,200	0,000	0,000	0,000									
Solyc11g005420	NF-180 (AHRD V3.3 --* B6TUT1_MAIZE)	F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,142	0,216	0,025	0,073	0,188									
Solyc11g005430	WAT1-related protein (AHRD V3.3 *** K4D4F6_SOLLC)	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM); PTHR31218 SF1	0,000	0,021	0,000	0,000	0,000									
Solyc11g005440	Endonuclease or glycosyl hydrolase, putative isoform 1 (AHRD V3.3 *** A0A061DIG3_THECC)	C:GO:0005777; P:G(	C:peroxisome; P:regulation of gene expression	IPR025605 (PFAM); IPR021139 (PFA	7,665	6,621	7,460	6,263	5,825									
Solyc11g005450	Transcription elongation factor (TFIIS) family protein (AHRD V3.3 *** AT5G09850.5)	C:GO:0005634	C:nucleus	IPR017923 (PFAM); IPR035441 (G3D	132,409	116,911	102,727	91,898	99,115									
Solyc11g005460	ENTH/VHS/GAT family protein (AHRD V3.3 *** AT5G63640.2)	C:GO:0005622; P:G(	C:intracellular; P:intracellular protein transport	IPR008942 (G3DSA:1.25.40 GENE3D	17,912	20,695	13,359	12,070	14,077									
Solyc11g005480	Citrate binding protein (AHRD V3.3 *** Q8H9C1_SOLTU)			IPR014895 (PFAM); G3DSA:2.60.120	0,718	1,672	16,614	10,752	8,413									
Solyc11g005490	LOW QUALITY:Fasciclin-like arabinogalactan family protein (AHRD V3.3 *-* AT1G15190.1)			IPR000782 (PFAM); IPR036378 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc11g005520	Agenet-like domain-containing protein (AHRD V3.3 *-* A0A118K161_CYNCS)	F:GO:0003682	F:chromatin binding	IPR008395 (PFAM); mobidb-lite (MOB	1,169	0,704	0,025	0,025	0,000									
Solyc11g005530	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative (AHRD V3.3 *-* A0A(	F:GO:0003682	F:chromatin binding	IPR008395 (PFAM); mobidb-lite (MOB	1,160	0,781	0,000	0,000	0,000									
Solyc11g005550	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G64730.1)	F:GO:0005515	F:protein binding	IPR020472 (PRINTS); IPR001680 (PF	13,895	10,437	18,239	17,576	17,426									
Solyc11g005560	Cellulose synthase (AHRD V3.3 *** M0ZXJ5_SOLTU)	C:GO:0016020; F:G(	C:membrane; F:cell; EC:2.4.1.12 Cellulose synthase (U	IPR029044 (G3DSA:3.90.550 GENE3	12,032	14,714	32,178	41,976	32,328									
Solyc11g005570	axoneme-associated protein MST101(2) protein (AHRD V3.3 *** AT2G44820.2)	P:GO:0000462; C:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSU	IPR027973 (PFAM); mobidb-lite (MOB	20,376	19,020	27,614	26,962	24,209									
Solyc11g005580	S-adenosyl-methyltransferase mraw, putative (AHRD V3.3 *** B9S2X8_RICCO)	F:GO:0008168	F:methyltransferase activity	IPR023397 (G3DSA:1.10.150 GENE3	7,836	7,767	9,423	8,597	9,212									
Solyc11g005590	SKIP5-like protein skip5	F:GO:0005515	F:protein binding	G3DSA:1.20.1280.50 (GENE3D); IPRI	7,934	7,032	9,737	10,289	9,170									
Solyc11g005600	Translation initiation factor eIF-2B protein (AHRD V3.3 *** G7JWC0_MEDTR)	P:GO:0044237	P:cellular metabolic process	G3DSA:3.40.50.10470 (GENE3D); IPF	32,019	29,779	51,686	51,636	47,139									
Solyc11g005605	Proteasome subunit alpha type-1-B (AHRD V3.3 --* PSA1B_ARATH)				0,042	0,000	0,047	0,123	0,046									
Solyc11g005610	LOW QUALITY:GRAS family transcription factor (AHRD V3.3 *** G7LD66_MEDTR) GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM) GRAS	0,059	0,193	0,069	0,169	0,095									
Solyc11g005620	acetylglutamate kinase	F:GO:0003991; C:G(	F:acetylglutamate k; EC:2.7.2.8 Acetylglutamate kinas	IPR001057 (PRINTS); IPR004662 (TI(	24,590	29,452	25,334	23,921	27,202									
Solyc11g005640	Polyubiquitin (AHRD V3.3 *-* UBI2P_PETCR)	F:GO:0005515	F:protein binding	IPR000626 (PFAM); G3DSA:3.10.20.9	27,475	28,704	37,436	40,493	42,900									
Solyc11g005650	Ubiquitin family protein (AHRD V3.3 *-* AT4G02890.4)	F:GO:0005515	F:protein binding	IPR019956 (PRINTS); IPR000626 (PF	11,527	11,015	15,099	17,361	16,830									
Solyc11g005660	Kinase family protein (AHRD V3.3 *** U5FF83_POPTR)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); PIRSF000654 (P	17,752	15,653	22,153	29,317	26,479					0,405	0,033			up
Solyc11g005670	POLYUBIQUITIN 1	F:GO:0005515	F:protein binding	IPR019956 (PRINTS); IPR000626 (PF	1162,308	594,063	559,229	1303,193	825,275	-0,943	0,001	0,559	0,021	1,223	0,000	down	up	up
Solyc11g005680	Ribosomal protein S13 (AHRD V3.3 *** A0A103XPA4_CYNCS)	F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR027437 (G3DSA:4.10.910 GENE3	481,239	512,592	294,885	293,192	298,479									
Solyc11g005690	TONSOKU protein (AHRD V3.3 *** Q4W7J1_TOBAC)	F:GO:0005515	F:protein binding	PF13424 (PFAM); IPR011990 (G3DS/	12,048	9,764	3,438	3,028	3,101									
Solyc11g005700	U-box domain-containing family protein (AHRD V3.3 *** B9HEI4_POPTR)	F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR013083 (G3DSA:3.30.40 GENE3D	9,762	13,333	8,312	6,589	8,174									
Solyc11g005710	Transducin/WD-like repeat-protein (AHRD V3.3 *** A0A0C3Y5Y4_MEDTR)	F:GO:0005515	F:protein binding	IPR020472 (PRINTS); IPR001680 (PF	2,580	1,555	0,738	0,611	0,894									
Solyc11g005720	LOW QUALITY:VQ motif-containing family protein (AHRD V3.3 *** B9H7P8_POPTR)	C:GO:0005634; P:G(	C:nucleus; P:defense response signaling pathway, resistance g	IPR008889 (PFAM); mobidb-lite (MOB	21,511	12,290	12,866	19,521	11,537	-0,783	0,047			0,605	0,027	down		up
Solyc11g005730	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9R8G9_9ROSA)	F:GO:0005515	F:protein binding	IPR019787 (PFAM); G3DSA:2.170.27	8,471	10,627	17,223	14,902	14,579									
Solyc11g005740	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7JB00_MEDTR)	F:GO:0046872	F:metal ion binding	IPR013083 (G3DSA:3.30.40 GENE3D	2,131	2,576	2,074	1,436	1,789									
Solyc11g005750	Pectinesterase (AHRD V3.3 *** K4D4I8_SOLLC)	F:GO:0004857; F:G(	F:enzyme inhibitor a; EC:3.1.1.11; EC:3.1.1. Pectinesterase; Carb	IPR006501 (PFAM); IPR012334 (G3D	0,763	1,274	0,777	0,952	0,867									
Solyc11g005760	Hexosyltransferase (AHRD V3.3 *** K4D4I9_SOLLC)	C:GO:0005794; P:G(	C:Golgi apparatus; ; EC:2.4.1.17 Glucuronosyltransfer	IPR029044 (G3DSA:3.90.550 GENE3	9,480	11,806	1,599	1,226	2,340									
Solyc11g005770	pectinesterase family protein	F:GO:0004857; F:G(	F:enzyme inhibitor a; EC:3.1.1.11; EC:3.1. Pectinesterase; Carb	IPR000070 (PFAM); IPR006501 (TIG	13,426	23,553	8,808	5,858	8,569	0,838	0,004			-0,580	0,042	up		down
Solyc11g005780	bHLH transcription factor158	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat	IPR036638 (G3DS bHLH	0,019	0,000	0,000	0,000	0,000									
Solyc11g005790	Trichome birefringence-like 7 (AHRD V3.3 *** A0A061DKB6_THECC)	C:GO:0016021	C:integral component of membrane	IPR025846 (PFAM); IPR026057 (PFA	4,510	3,650	1,787	1,426	1,816									
Solyc11g005800	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G64630.2)	F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10 GENE3	4,590	4,463	1,631	1,381	1,388									
Solyc11g005810	intracellular protein transporter (AHRD V3.3 *** AT4G27620.2)	C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	26,553	29,507	47,761	42,786	46,451									
Solyc11g005820	Pectinesterase inhibitor (AHRD V3.3 *** A0A103Y9H8_CYNCS)	F:GO:0004857	F:enzyme inhibitor activity	IPR006501 (PFAM); IPR006501 (TIGF	0,801	1,192	0,143	0,025	0,093									
Solyc11g005830	Cysteine desulfurase (AHRD V3.3 *** A0A0K9Q199_ZOSMR)	F:GO:0003824	F:catalytic activity	IPR015422 (G3DSA:3.90.1150 GENE	0,021	0,039	0,000	0,000	0,000									
Solyc11g005840	Cysteine desulfurase (AHRD V3.3 *** A0A0K9Q199_ZOSMR)	F:GO:0003824	F:catalytic activity	IPR000192 (PFAM); IPR015421 (G3D	0,021	0,597	0,151	0,196	0,047									
Solyc11g005860	Cysteine desulfurase (AHRD V3.3 *** A0A0K9Q199_ZOSMR)	F:GO:0003824	F:catalytic activity	IPR015422 (G3DSA:3.90.1150 GENE	0,159	0,617	0,512	0,219	0,282									
Solyc11g005870	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G64600.1)	C:GO:0005634; C:G(	C:nucleus; C:cytoplasm; P:fucose metabolic process; C:integral	IPR024709 (PIRSF); IPR019378 (PFA	6,544	4,469	6,435	7,044	6,447									
Solyc11g005880	NADH-ubiquinone oxidoreductase-like protein (AHRD V3.3 *** AT3G62790.1)	C:GO:0005747; P:G(	C:mitochondrial respiratory chain complex I; P:mitochondrial res	IPR019342 (PFAM); mobidb-lite (MOB	38,366	37,580	58,206	51,206	51,899									
Solyc11g005900	Guanylate kinase (AHRD V3.3 *** A0A103Y9I8_CYNCS)	F:GO:0004385; P:G(	F:guanylate kinase; EC:2.7.4.8; EC:2.7.4 Nucleoside-phosphat	IPR017665 (TIGRFAM); IPR008145 (F	10,504	10,521	13,794	14,851	12,761									
Solyc11g005910	Phosphatidylinositol 4-kinase family protein (AHRD V3.3 *** B9HEK1_POPTR)	F:GO:0016301; P:G(	F:kinase activity; P:phosphatidylinositol phosphorylation; P:phos	G3DSA:3.30.1010.10 (GENE3D); IPR	79,425	65,891	85,160	97,560	90,084									
Solyc11g005915	Maturase K (AHRD V3.3 --* MATK_HUPLU)				6,398	8,276	9,000	8,420	8,490									
Solyc11g005920	NAC domain protein, (AHRD V3.3 *-* A0A061FNG1_THECC) NAC089	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	77,851	106,588	107,863	102,581	92,656									
Solyc11g005930	Coiled-coil domain-containing protein 18, putative isoform 2 (AHRD V3.3 *** A0A061DJK4_THECC)			PTHR34808 (PANTHER); PTHR34808	0,021	0,021	0,118	0,194	0,164									
Solyc11g005933	Nucleotide-sugar transporter family protein (AHRD V3.3 --* AT4G32390.1)				1,728	1,867	1,979	1,755	1,577									
Solyc11g005937	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 --* GAPN_MAIZE)				0,394	0,476	0,433	0,292	0,494									
Solyc11g005940	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9H052_POPTR)	F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR011990 ((	8,884	8,727	8,802	10,175	8,760									
Solyc11g005950	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A061DRF8_THECC)	F:GO:0005515	F:protein binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	17,683	15,132	14,365	11,861	15,202									
Solyc11g005960	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YER7_CYNCS)	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (TIGRFAM); IPR011990 ((	1,073	0,881	1,411	1,249	1,036									
Solyc11g005970	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JUV1_CYNCS)	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40 GENE3D	0,343	0,657	0,380	0,535	0,377									
Solyc11g005980	callose synthase 5 (AHRD V3.3 *-* AT2G13680.1)	C:GO:0000148; F:G(	C:1,3-beta-D-glucan; EC:2.4.1.34 1,3-beta-glucan synth	IPR039431 (PFAM); IPR026899 (PFA	0,000	0,041	0,025	0,000	0,000									
Solyc11g005985	Callose synthase (AHRD V3.3 *** A0A103XJY7_CYNCS)	C:GO:0000148; F:G(	C:1,3-beta-D-glucan; EC:2.4.1.34 1,3-beta-glucan synth	IPR003440 (PFAM); PTHR12741 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc11g005990	Transcriptional corepressor SEUSS-like protein (AHRD V3.3 *-* A0A0B0MD44_GOSAR)	P:GO:0000122; F:G(	P:negative regulation of transcription by RNA polymerase II; F:F	IPR029005 (PFAM); mobidb-lite (MOB	2,729	2,646	0,573	0,525	0,400									
Solyc11g006000	MAP kinase kinase kinase 80 MAPKKKa	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D); IPR0	118,807	155,953	143,927	169,372	156,293									
Solyc11g006010	DNA cross-link repair family protein (AHRD V3.3 *** B9HER4_POPTR)	F:GO:0004527; F:G(	F:exonuclease activity; F:ligase activity; P:nucleic acid phospho	G3DSA:3.40.50.12650 (GENE3D); IPF	0,949	0,642	0,360	0,464	0,281									
Solyc11g006020	NADH dehydrogenase-like complex O (AHRD V3.3 *** A0A0F7GYD5_9ROSI)	C:GO:0005886; F:G(	C:plasma membrane; F:oxidoreductase activity, acting on NAD(	IPR020905 (PFAM); mobidb-lite (MOB	5,250	19,989	0,886	1,375	5,251	1,952	0,000	2,546	0,000			up	up	
Solyc11g006030	U-box domain-containing family protein (AHRD V3.3 *** U5FLQ4_POPTR)	F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR011989 (G3DSA:1.25.10 GENE3D	0,060	0,838	0,072	0,000	0,071									
Solyc11g006040	Receptor protein kinase, putative (AHRD V3.3 *** B9T5F6_RICCO)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); IPR032675 (G3D	3,934	3,497	1,035	2,475	2,588			1,310	0,003	1,251	0,004		up	up
Solyc11g006060	Rubisco accumulation factor 1.1, chloroplastic (AHRD V3.3 *** RAF1_ARATH)	C:GO:0009507	C:chloroplast	IPR040858 (PFAM); IPR041358 (PFA	46,869	66,161	121,371	99,547	125,932									
Solyc11g006070	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** M1CSR8_SOLTU)	P:GO:0000413; F:G(	P:protein peptidyl-p; EC:5.2.1.8 Peptidylprolyl isomer	IPR002130 (PFAM); IPR002130 (PRIN	41,453	46,702	36,412	28,580	33,250									
Solyc11g006080	Myosin type-2 heavy chain 2 (AHRD V3.3 *** A0A1D1Z5G2_9ARAE)			mobidb-lite (MOBIDB_LITE); mobidb-lit	22,404	18,788	14,410	12,529	13,820									
Solyc11g006090	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A0K9PN07_ZOSMR)	F:GO:0003680	F:AT DNA binding	IPR014476 (PIRSF); IPR005175 (PFA	0,121	0,165	0,025	0,000	0,046									
Solyc11g006100	Glycosyltransferase (AHRD V3.3 *** K4D4M3_SOLLC)	F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR	0,019	0,000	0,000	0,000	0,000									
Solyc11g006115	Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)	F:GO:0005488; P:G(	F:binding; P:signal transduction; C:membrane; F:kinase activity;	PTHR43719 (PANTHER); PTHR43719	0,470	0,543	0,381	0,320	0,615									
Solyc11g006130	Methyltransferase (AHRD V3.3 *** F1DGA0_COFAR),Pfam:PF13489	F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	IPR029063 (G3DSA:3.40.50 GENE3	6,161	5,550	15,486	12,655	12,398									
Solyc11g006140	LOW QUALITY:Chaperone DnaJ-domain protein (AHRD V3.3 *-* G7JV72_MEDTR)			IPR036869 (G3DSA:1.10.287 GENE3	2,568	2,208	0,638	0,961	0,845									
Solyc11g006145	Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)	F:GO:0000155; F:G(	F:phosphorelay ser; EC:2.7.13.3 Histidine kinase		0,201	0,313	0,118	0,172	0,093									
Solyc11g006150	Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)	F:GO:0000155; F:G(	F:phosphorelay ser; EC:2.7.13.3 Histidine kinase		0,335	0,316	0,124	0,339	0,306									
Solyc11g006160	Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)	P:GO:0009987; P:G(	P:cellular process; P:response to stimulus	PTHR43719 (PANTHER); PTHR43719	0,361	0,132	0,137	0,148	0,233									
Solyc11g006170	DnaJ domain-containing protein (AHRD V3.3 *-* A0A118K6N5_CYNCS)			IPR036869 (G3DSA:1.10.287 GENE3	19,366	15,974	18,161	14,836	15,283									
Solyc11g006180	ethylene receptor homolog (ETR5) ETR5	F:GO:0000155; P:G(	F:phosphorelay ser; EC:2.7.13.3 Histidine kinase	G3DSA:3.40.50.2300 (GENE3D); IPR	12,616	9,795	17,920	18,489	15,493									
Solyc11g006190	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A061F8Z8_THECC)	F:GO:0003680	F:AT DNA binding	G3DSA:3.30.1330.80 (GENE3D); IPR	18,188	19,895	27,781	28,863	30,398									
Solyc11g006200	Homeodomain-like transcriptional regulator (AHRD V3.3 *** AT4G12750.1)	F:GO:0000976; F:G(	F:transcription regulatory region sequence-specific DNA bindin	IPR018501 (PFAM); IPR028941 (PFA	22,422	18,185	21,951	23,825	22,827									
Solyc11g006210	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 --* AT4G22120.6)				0,258	0,379	0,258	0,386	0,236									
Solyc11g006220	Myosin XI, putative (AHRD V3.3 *** B9S7I4_RICCO)	F:GO:0003774; F:G(	F:motor activity; F:; EC:3.6.1.15 Nucleoside-triphosph	IPR001609 (PRINTS); IPR002710 (PF	1,607	1,195	0,984	0,917	0,942									
Solyc11g006230	GRF1-interacting factor-like protein (AHRD V3.3 *** G7I6V2_MEDTR)	F:GO:0003713	F:transcription coactivator activity	IPR007726 (PFAM); mobidb-lite (MOB	19,295	37,521	0,093	0,119	0,023									
Solyc11g006240	LOW QUALITY:CTP synthase (AHRD V3.3 --* K4AXL0_SOLLC)			PTHR33592:SF1 (PANTHER); PTHR3:	0,019	0,019	0,000	0,000	0,000									
Solyc11g006245	zinc finger (C2H2 type) family protein (AHRD V3.3 *** AT4G12240.1)	F:GO:0003676	F:nucleic acid binding	PTHR35744:SF2 (PANTHER); PTHR3:	11,214	12,048	13,090	11,507	13,866									
Solyc11g006250	GDSL-motif lipase/hydrolase family protein 2 GDSL2	F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50 GENE3D	225,989	212,267	0,121	0,098	0,000									
Solyc11g006270	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** A0A072UJC1_MEDTR)	P:GO:0006629; F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t	IPR001104 (PFAM); IPR039357 (PAN	5,370	4,212	13,948	24,006	14,087					0,785	0,000			up
Solyc11g006290	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** AT5G16010.1)	P:GO:0006629; F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t	IPR001104 (PFAM); PTHR10556:SF3	0,587	0,562	1,284	1,493	1,788									
Solyc11g006300	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** AT5G16010.1)	P:GO:0006629; F:G(	P:lipid metabolic process; F:oxidoreductase activity, acting on t	IPR001104 (PFAM); PTHR10556:SF3	1,863	1,435	2,093	2,006	3,869									
Solyc11g006310	Gamete expressed protein 1, putative (AHRD V3.3 *** A0A061EBI0_THECC)	C:GO:0005886; P:G(	C:plasma membrane; P:embryo sac development; P:pollen devel	PTHR33538:SF2 (PANTHER); IPR04	0,040	0,021	0,099	0,072	0,023									
Solyc11g006320	Ubiquitin carboxyl-terminal hydrolase 12 (AHRD V3.3 *** UBP12_ARATH)	F:GO:0005515; P:G(	F:protein binding; P; EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:2.60.210.10 (GENE3D); IPR0	83,641	77,025	118,492	120,744	118,954									
Solyc11g006340	Phosphoribosylaminoimidazole carboxylase (AHRD V3.3 *** Q9AXD0_TOBAC)	F:GO:0004638; F:G(	F:phosphoribosylam; EC:4.1.1.21 Phosphoribosylamino	IPR005875 (TIGRFAM); IPR000031 (F	19,771	19,901	37,794	35,508	38,991									
Solyc11g006350	aspatate carbamoyltransferase	F:GO:0004070; P:G(	F:aspartate carbam; EC:2.1.3.2 Aspartate carbamoyl	IPR006130 (PRINTS); IPR002082 (PF	16,855	17,446	15,337	12,770	12,572									
Solyc11g006360	LOW QUALITY:TPR1 (AHRD V3.3 *-* F2XF89_SOYBN)	F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40 GENE3D	39,840	30,099	49,899	52,298	51,013									
Solyc11g006370	Calcium dependent protein kinase (AHRD V3.3 *** Q93XJ0_SOLTU)	F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	IPR000719 (PFAM); IPR002048 (PFA	55,984	49,225	86,693	98,227	80,059									
Solyc11g006380	Pentatricopeptide repeat-containing family protein	F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR011990 ((	12,883	14,120	17,313	17,605	17,721									
Solyc11g006390	Nuclear pore complex protein Nup136b (AHRD V3.3 *** W6JLY3_NICBE)	C:GO:0005635; P:G(	C:nuclear envelope; P:poly(A)+ mRNA export from nucleus; P:n	mobidb-lite (MOBIDB_LITE); mobidb-lit	87,877	66,888	52,279	50,126	52,015									
Solyc11g006400	Mitochondrial glycoprotein family protein, putative (AHRD V3.3 *** A0A061G4T0_THECC)	C:GO:0005759	C:mitochondrial matrix	IPR036561 (G3DSA:3.10.280 GENE3	14,860	15,721	21,406	20,254	22,035									
Solyc11g006410	EEIG1/EHBP1 N-terminal domain-containing protein (AHRD V3.3 *** A0A103YZW1_CYNCS)			IPR019448 (PFAM); mobidb-lite (MOB	1,342	1,524	2,109	1,623	1,996									
Solyc11g006420	Cytosolic 5-nucleotidase (AHRD V3.3 *** A0A059Q189_9POAL)	F:GO:0000287; C:G(	F:magnesium ion bi; EC:3.1.3.5; EC:3.1.3 5'-nucleotidase; Nucl	G3DSA:1.10.150.340 (GENE3D); IPR	3,637	3,932	1,498	0,884	1,599									
Solyc11g006430	LOW QUALITY:Glutaredoxin family protein, putative (AHRD V3.3 *** A0A061FWX9_THECC)	F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a	G3DSA:3.40.30.10 (GENE3D); IPR02	0,078	0,039	0,000	0,000	0,000									
Solyc11g006450	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FQW5_THECC)	C:GO:0016021	C:integral component of membrane	IPR001841 (PFAM); IPR013083 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc11g006460	DnaJ-like protein (AHRD V3.3 *-* Q9M7M2_SOLLC)	F:GO:0005524; C:G(	F:ATP binding; C:cytosol; P:protein folding; P:response to heat;	mobidb-lite (MOBIDB_LITE); PTHR438	760,930	690,692	473,447	448,489	435,646									
Solyc11g006465	DnaJ-like protein (AHRD V3.3 *-* Q9M7M2_SOLLC)	F:GO:0005524; C:G(	F:ATP binding; C:cytosol; P:protein folding; P:response to heat;	IPR001623 (PRINTS); IPR036869 (G3	759,743	634,851	444,063	456,348	427,603									
Solyc11g006470	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT5G22070.1)	F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane	IPR003406 (PFAM); PTHR31042 SF4	40,557	28,348	39,411	39,393	37,938									
Solyc11g006480	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHU8_9ROSA)	F:GO:0003676; P:G(	F:nucleic acid binding; P:nucleobase-containing compound meta	IPR036397 (G3DSA:3.30.420 GENE3	0,061	0,142	0,386	0,420	0,472									
Solyc11g006490	Basic-leucine zipper (bZIP) transcription factor family protein (AHRD V3.3 *** AT2G42380.2)	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transc	mobidb-lite (MOBIDB_LITE); mobidb-lit	1,120	1,030	0,166	0,561	0,213									
Solyc11g006500	Charged multivesicular body protein 5 (AHRD V3.3 *** W9R7A4_9ROSA)	P:GO:0007034	P:vacuolar transport	IPR005024 (PFAM); mobidb-lite (MOB	7,463	5,533	6,636	8,023	6,808									
Solyc11g006510	Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *** AT5G04830.2)			PTHR34213 (PANTHER); IPR032710	5,459	6,631	12,654	11,846	13,905									
Solyc11g006520	Disease resistance protein (AHRD V3.3 *** A0A103Y7R3_CYNCS)	F:GO:0043531	F:ADP binding	PR00364 (PRINTS); G3DSA:3.40.50.3	9,025	7,792	10,560	11,931	13,189									
Solyc11g006530	Disease resistance protein (AHRD V3.3 *** A0A103Y7R3_CYNCS)	F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	0,141	0,083	0,050	0,022	0,047									
Solyc11g006540	FAD-dependent pyridine nucleotide-disulphide oxidoreductase (AHRD V1 **-- D3M425_9ACTO)	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	PR00368 (PRINTS); G3DSA:3.50.50.1	53,174	83,816	15,245	22,701	22,321									
Solyc11g006550	urate oxidase	F:GO:0004846; C:G(	F:urate oxidase act; EC:1.7.3.3 Factor independent u	IPR002042 (PRINTS); IPR002042 (PF	95,800	87,238	123,366	106,024	114,936									
Solyc11g006560	Glycosyltransferase, putative (AHRD V3.3 *** B9RSB3_RICCO)	C:GO:0016021	C:integral component of membrane	G3DSA:3.40.50.2000 (GENE3D); IPR	4,170	2,707	2,941	3,342	3,377									
Solyc11g006570	Myo-inositol oxygenase (AHRD V3.3 *** C6K2L2_SOLLC)	F:GO:0005506; C:G(	F:iron ion binding; C; EC:1.13.99.1 Inositol oxygenase	IPR007828 (PFAM); IPR007828 (PAN	0,311	0,260	0,197	0,189	0,210									
Solyc11g006580	Nudix hydrolase (AHRD V3.3 *** A0A061FQV2_THECC)	F:GO:0016787	F:hydrolase activity	IPR020476 (PRINTS); IPR000086 (PF	9,209	9,436	6,210	5,265	6,373									
Solyc11g006590	Cytochrome P450, putative (AHRD V3.3 *** B9R857_RICCO)	F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR002401 (PRINTS); IPR001128 (PF	2,779	2,861	0,190	0,194	0,424									
Solyc11g006620	exocyst subunit exo70 family protein A1 (AHRD V3.3 *** AT5G03540.1)	C:GO:0000145; P:G(	C:exocyst; P:exocytosis	IPR004140 (PFAM); mobidb-lite (MOB	36,149	34,662	64,777	68,146	60,785									
Solyc11g006630	Disease resistance protein (AHRD V3.3 *** A0A103Y7R3_CYNCS)	F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	7,924	8,853	2,313	2,652	5,089			1,122	0,040				up	
Solyc11g006635	Disease resistance protein (AHRD V3.3 --* A0A118JWS7_CYNCS)	F:GO:0043531	F:ADP binding		0,744	1,337	0,243	0,244	0,468									
Solyc11g006640	Disease resistance protein (AHRD V3.3 *** A0A103Y7R3_CYNCS)	F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR032675 (G3D	5,152	4,486	2,066	2,562	2,811									
Solyc11g006650	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHR	P:GO:0019538	P:protein metabolic process	G3DSA:3.40.50.300 (GENE3D); IPR0:	0,662	0,529	0,000	0,050	0,047									
Solyc11g006660	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *** ERF1X_ARATH)	F:GO:0003747; C:G(	F:translation release factor activity; C:cytoplasm; P:translationa	G3DSA:3.30.420.60 (GENE3D); IPR0:	70,940	68,890	73,200	65,096	66,639									

Solyc11g006670	ovate family protein 29	OFP29	P:GO:0045892	P:negative regulation of transcription, DNA-templated	IPR006458 (PFAM): IPR006458 (TIGF	6,456	3,360	0,571	0,455	0,353									
Solyc11g006675	Photosystem II reaction center protein H (AHRD V3.3 *-* A0A172W736_9SOLA)		C:GO:0009523; P:G(	C:photosystem II; P:photosynthesis; F:phosphate ion binding; P	IPR001056 (PFAM): IPR036863 (G3D	0,019	0,101	0,025	0,075	0,116									
Solyc11g006680	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RPX5_RICCO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding	IPR002885 (PFAM): IPR011990 (G3D	22,383	22,855	28,472	25,949	29,444									
Solyc11g006690	40S ribosomal protein S17 (AHRD V3.3 *** RS17_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR036401 (G3DSA:1.10.60.GENE3D	181,619	196,790	157,504	137,785	146,785									
Solyc11g006700	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SG91_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR002885 (PFAM): IPR002885 (TIGF	1,552	2,181	2,272	1,846	1,814									
Solyc11g006710	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RPW6_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen	IPR002293 (PIRSF): IPR002293 (PFA	3,968	6,577	0,925	1,250	1,106									
Solyc11g006720	MYB-like transcription factor family protein (AHRD V3.3 *** G7ZYT0_MEDTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(MYB	11,851	19,508	25,714	28,926	23,801	0,743	0,044					up		
Solyc11g006730	Germin-like protein 1 (AHRD V3.3 *** B9HVV6_POPTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS): IPR014710 (G3	0,038	0,021	0,050	0,049	0,047									
Solyc11g006735	F-box protein PP2 (AHRD V3.3 *-* A0A059PC27_CICAR)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): G3DSA:1.20.128	1,307	1,867	0,714	0,583	0,564									
Solyc11g006740	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)		F:GO:0005515	F:protein binding	IPR025886 (PFAM): G3DSA:1.20.128	16,318	25,299	17,108	16,455	22,233	0,659	0,038					up		
Solyc11g006750	F1F0-ATPase inhibitor protein (AHRD V3.3 *** AT5G04750.1)		C:GO:0005747; C:G(	C:mitochondrial respiratory chain complex I; C:integral compone	mobidb-lite (MOBIDB_LITE): mobidb-lit	37,594	44,791	186,769	165,328	207,442									
Solyc11g006760	Multiple myeloma tumor-associated 2 (AHRD V3.3 *** A0A0B0P407_GOSAR)		F:GO:0005515	F:protein binding	IPR019315 (PFAM): mobidb-lite (MOB	17,126	19,335	21,410	22,005	19,780									
Solyc11g006770	AMMECR1 family (AHRD V3.3 *** AT2G38710.4)		C:GO:0005829; P:G(	C:cytosol; P:response to salt stress	IPR023473 (TIGRFAM): IPR002733 (F	30,731	33,186	61,295	69,517	58,588									
Solyc11g006780	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9RPU0_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo	IPR001388 (PRINTS): IPR010908 (PF	50,157	47,842	70,224	74,678	68,114									
Solyc11g006820	Small nuclear ribonucleoprotein family protein (AHRD V3.3 *** AT3G11500.2)		P:GO:0000387; C:G(	P:spliceosomal snRNP assembly; C:spliceosomal complex	PIRSF037188 (PIRSF): G3DSA:2.30.3	27,761	30,562	41,178	40,677	38,236									
Solyc11g006830	hemerythrin HHE cation-binding domain protein (AHRD V3.3 *** AT3G54290.1)				IPR012312 (PFAM): G3DSA:1.20.120	3,682	2,147	2,585	3,561	3,354									
Solyc11g006860	Ribonuclease (AHRD V3.3 *** K4D4U7_SOLLC)		F:GO:0003723; F:G(	F:RNA binding; F:RI EC:3.1.3; EC:3.1.26; Acting on ester bond:	IPR036397 (G3DSA:3.30.420.GENE3	10,453	9,961	9,273	8,711	9,702									
Solyc11g006870	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT5G19570.1)		C:GO:0016021	C:integral component of membrane	IPR018908 (PFAM): IPR018908 (PAN	3,869	3,455	7,444	5,513	6,238									
Solyc11g006880	jagunal-like protein (AHRD V3.3 *** AT5G51510.1)		C:GO:0005789; P:G(	C:endoplasmic reticulum membrane; P:endoplasmic reticulum or	IPR009787 (PFAM): PTHR20955:SF1	31,663	38,410	33,085	34,175	33,447									
Solyc11g006890	sterol 4-alpha-methyl-oxidase 2-2 (AHRD V3.3 --* AT2G29390.3)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane		3,939	2,625	0,875	1,238	1,104									
Solyc11g006900	LOW QUALITY:Calcium/calmodulin protein kinase (AHRD V3.3 *-* Q84ZT8_TOBAC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	4,529	6,204	9,517	8,948	8,029									
Solyc11g006910	Ferredoxin family protein (AHRD V3.3 *** B9MYW6_POPTR)		F:GO:0009055; P:G(	F:electron transfer activity; P:electron transport chain; F:2 iron,	IPR010241 (TIGRFAM): IPR012675 ((	0,076	0,318	6,328	11,500	5,232					0,870	0,001			up
Solyc11g006920	Iron-sulfur cluster assembly protein IscA (AHRD V3.3 *** I3T186_MEDTR)		F:GO:0005198; F:G(	F:structural molecule activity; F:iron-sulfur cluster binding; P:pro	IPR035903 (G3DSA:2.60.300.GENE3	6,588	5,325	9,291	9,177	7,658									
Solyc11g006930	4'-phosphopantetheinyl transferase family protein (AHRD V3.3 *** A0A072VJ15_MEDTR)		F:GO:0000287; F:G(	F:magnesium ion bi EC:2.7.8.7 Holo-[acyl-carrier-prc	IPR037143 (G3DSA:3.90.470.GENE3	5,098	5,198	1,358	2,435	1,833									
Solyc11g006940	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061ETI9_THECC)		P:GO:0000387; F:G(	P:spliceosomal snRNP assembly; F:protein binding; C:spliceosc	G3DSA:2.30.30.100 (GENE3D): IPR0(	4,474	5,288	4,910	4,670	3,962									
Solyc11g006950	Defensin-like family protein (AHRD V3.3 *** B9IP38_POPTR)		P:GO:0006952	P:defense response	IPR008176 (PRINTS): PF00304 (PFAI	0,799	0,557	0,143	0,069	0,048									
Solyc11g006960	Serine/arginine repetitive matrix protein 2 isoform 1 (AHRD V3.3 *** A0A061GKH0_THECC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	149,832	190,573	143,125	121,460	148,698									
Solyc11g006970	ACT domain-containing protein		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast stroma	PTHR31096:SF41 (PANTHER): IPR04	490,123	440,784	253,484	250,394	302,602									
Solyc11g006980	Germin family 1 protein (AHRD V3.3 *** A0A072VRM6_MEDTR)		F:GO:0030145; F:G(	F:manganese ion binding; F:nutrient reservoir activity	IPR001929 (PRINTS): IPR006045 (PF	0,233	0,271	0,046	0,022	0,000									
Solyc11g006990	Trichome birefringence-like 36 (AHRD V3.3 *** A0A061FQB5_THECC)		C:GO:0005794; F:G(	C:Golgi apparatus; F:O-acetyltransferase activity	IPR026057 (PFAM): IPR025846 (PFAI	36,834	41,862	245,751	241,110	236,868									
Solyc11g007000	Cytochrome c oxidase assembly protein COX15 (AHRD V3.3 *** COX15_ARATH)		P:GO:0006784; C:G(	P:heme a biosynthetic process; C:integral component of membr	IPR003780 (PFAM): PTHR23289:SF2	8,454	8,659	11,461	11,107	13,620									
Solyc11g007010	Proline-, glutamic acid-and leucine-rich protein 1 (AHRD V3.3 *** A0A0B2R520_GLYSO)		P:GO:0006364	P:rRNA processing	IPR012583 (PFAM): mobidb-lite (MOB	14,780	14,431	14,089	13,691	12,655									
Solyc11g007020	mevalonate disphosphate decarboxylase	mdc	F:GO:0004163; F:G(	F:diphosphomevalo EC:4.1.1.33 Diphosphomevalonat	IPR006204 (PFAM): IPR029765 (TIGF	40,247	44,214	85,348	82,073	83,065									
Solyc11g007030	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)				IPR029058 (G3DSA:3.40.50.GENE3D	0,063	0,592	0,022	0,100	0,328									
Solyc11g007040	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)				IPR000073 (PFAM): IPR029058 (G3D	7,899	8,811	26,930	29,554	26,405									
Solyc11g007050	LOW QUALITY:Serine protease inhibitor, potato inhibitor I-type family protein (AHRD V3.3 *** AT3G46860.1		F:GO:0004867; P:G(	F:serine-type endopeptidase inhibitor activity; P:response to wc	G3DSA:3.30.10.10 (GENE3D): IPR0(	0,366	0,612	0,000	0,000	0,000									
Solyc11g007060	40S ribosomal protein S27 (AHRD V3.3 *-* AT5G47940.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	51,807	32,672	55,960	52,568	47,473	-0,637	0,006					down		
Solyc11g007070	mitochondrial substrate carrier family protein		F:GO:0022857	F:transmembrane transporter activity	IPR023395 (G3DSA:1.50.40.GENE3D	14,829	13,599	28,643	27,147	25,648									
Solyc11g007080	Protein YIPF (AHRD V3.3 *** K4D4W9_SOLLC)		C:GO:0016020	C:membrane	IPR006977 (PFAM): mobidb-lite (MOB	18,651	20,300	24,226	23,557	19,711									
Solyc11g007090	Aspartyl aminopeptidase (AHRD V3.3 *** W9QGP4_9ROSA)		F:GO:0004177; P:G(	F:aminopeptidase a EC:3.4.11 Acting on peptide bor	IPR001948 (PRINTS): IPR001948 (PF	16,354	21,011	26,594	24,357	28,894									
Solyc11g007100	Protein LITTLE ZIPPER 4 (AHRD V3.3 *** A0A199VL62_ANACO)				mobidb-lite (MOBIDB_LITE): IPR0393	0,075	0,000	0,000	0,000	0,000									
Solyc11g007110	Single-stranded nucleic acid-binding protein R3H (AHRD V3.3 *** G7I367_MEDTR)		F:GO:0003676	F:nucleic acid binding	IPR001374 (PFAM): IPR024771 (PFAI	60,538	69,642	109,209	107,988	100,780									
Solyc11g007120	NifU-like protein 4 (AHRD V3.3 *** W9QGE4_9ROSA)		F:GO:0005506; P:G(	F:iron ion binding; P:iron-sulfur cluster assembly; F:iron-sulfur cl	IPR001075 (PFAM): IPR034904 (G3D	21,379	22,522	45,780	42,043	40,133									
Solyc11g007130	Hippocampus abundant transcript-like protein 1 (AHRD V3.3 *** W9QGN7_9ROSA)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM): G3DSA:1.20.125	35,532	15,851	42,853	40,379	33,691	-1,135	0,000					down		
Solyc11g007140	Hippocampus abundant transcript-like protein 1 (AHRD V3.3 *-* W9QGN7_9ROSA)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM): G3DSA:1.20.125	2,916	2,122	3,671	4,611	4,544									
Solyc11g007150	LOW QUALITY:Unknown protein (AHRD V3.3)					0,000	0,000	0,000	0,048	0,000									
Solyc11g007160	RNA binding protein, putative (AHRD V3.3 *** B9SG63_RICCO)		F:GO:0003676; P:G(	F:nucleic acid binding; P:cytidine to uridine editing	IPR000504 (PFAM): IPR012677 (G3D	6,041	6,617	2,233	1,987	2,868									
Solyc11g007170	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** A0A0J8ECK3_BETVU)		F:GO:0005524	F:ATP binding	IPR041569 (PFAM): IPR007330 (PFAI	121,147	122,088	184,037	175,761	165,560									
Solyc11g007180	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RXW1_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,000	0,000	0,000	0,050	0,000									
Solyc11g007190	ARM repeat superfamily protein (AHRD V3.3 --* AT3G03970.6)					0,042	0,122	0,287	0,218	0,281									
Solyc11g007200	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G27690.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding	IPR006121 (PFAM): G3DSA:3.30.70.1	7,588	15,287	55,495	78,047	67,409	1,036	0,008					up		
Solyc11g007230	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YE45_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (TIGF	1,958	2,436	1,815	2,013	2,656									
Solyc11g007250	Protein kinase like protein (AHRD V3.3 *** Q0WN21_ARATH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	0,932	1,790	0,000	0,000	0,000									
Solyc11g007270	Alkaline/neutral invertase (AHRD V3.3 *** A0A0X8AZR5_CAMSI)		F:GO:0033926	F:glycopeptide alph EC:3.2.1.97 Endo-alpha-N-acetylc	IPR024746 (PFAM): IPR012341 (G3D	39,749	44,956	50,992	55,908	59,827									
Solyc11g007280	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG48	F:GO:0005524; C:G(	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR029481 (PFAM): IPR013525 (PFAI	0,000	0,019	0,000	0,000	0,000									
Solyc11g007300	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG50	F:GO:0005524; C:G(	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR029481 (PFAM): IPR003439 (PFAI	0,000	0,039	0,000	0,000	0,000									
Solyc11g007310	Suppressor of gene silencing 3, putative (AHRD V3.3 *** A0A061FQZ7_THECC)		P:GO:0031047	P:gene silencing by RNA	IPR005380 (PFAM): IPR038588 (G3D	15,056	15,413	9,041	9,201	8,858									
Solyc11g007320	Galactose oxidase/kelch repeat protein (AHRD V3.3 *** A0A072VN65_MEDTR)		F:GO:0005515	F:protein binding	IPR015915 (G3DSA:2.120.10.GENE3	45,634	40,780	55,664	48,535	51,882									
Solyc11g007330	RAB6-interacting golgin (DUF662) (AHRD V3.3 *** AT2G27740.1)				IPR007033 (PFAM): mobidb-lite (MOB	0,297	0,468	0,051	0,000	0,070									
Solyc11g007340	Plant tudor-like RNA-binding protein (AHRD V3.3 *** A0A072UR05_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR005491 (PFAM): IPR008395 (PFAI	15,297	13,104	21,069	17,922	17,723									
Solyc11g007360	F-box family protein (AHRD V3.3 *-* D7L2W6_ARALL)		F:GO:0016740; F:G(	F:transferase activity; F:transferase activity, transferring glycos	IPR013187 (PFAM): IPR017451 (TIGF	3,959	3,346	3,629	4,857	3,911									
Solyc11g007380	Glycosyltransferase (AHRD V3.3 *** B6EWZ4_LYCBA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	0,000	0,000	0,000	0,025	0,023									
Solyc11g007390	Glycosyltransferase (AHRD V3.3 *** K4BWC0_SOLLC)		F:GO:0008194; F:G(	F:UDP-glycosyltransferase activity; F:transferase activity, trans	G3DSA:3.40.50.2000 (GENE3D): PTH	0,117	0,170	1,202	2,354	1,961									
Solyc11g007400	LOW QUALITY:Receptor-like protein kinase (AHRD V3.3 *-* Q9M576_ORYSA)				G3DSA:1.10.510.10 (GENE3D): PTHF	0,836	3,199	1,361	0,878	1,297	1,953	0,000					up		
Solyc11g007410	Receptor-like protein kinase (AHRD V3.3 *-* A0A061EYK6_THECC)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR33138:SF7	0,420	1,792	0,274	0,803	1,110									
Solyc11g007420	LOW QUALITY:Receptor-like protein kinase (AHRD V3.3 *-* Q9M576_ORYSA)				G3DSA:1.10.510.10 (GENE3D): PTHF	0,101	1,360	0,147	0,457	0,832									
Solyc11g007430	Receptor-like protein kinase (AHRD V3.3 *-* A0A061EYK6_THECC)		F:GO:0030247	F:polysaccharide binding	IPR025287 (PFAM): PTHR33138:SF7	0,140	0,920	0,166	0,092	0,739									
Solyc11g007460	Glycosyltransferase (AHRD V3.3 *** K4D507_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	0,140	0,213	0,050	0,119	0,118									
Solyc11g007470	Glycosyltransferase (AHRD V3.3 *** K4D508_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): IPR(	0,080	0,095	0,100	0,096	0,047									
Solyc11g007480	Glycosyltransferase (AHRD V3.3 *** K4D509_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	0,000	0,000	0,025	0,000	0,000									
Solyc11g007485	ribosomal protein S10 (AHRD V3.3 --* AT3G22300.1)					0,243	0,096	0,122	0,117	0,142									
Solyc11g007490	Glycosyltransferase (AHRD V3.3 *** K4D510_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	1,324	1,418	1,210	1,307	1,507									
Solyc11g007500	Glycosyltransferase (AHRD V3.3 *** M1BPV9_SOLTU)		F:GO:0008194; C:G(	F:UDP-glycosyltransferase activity; C:integral component of me	G3DSA:3.40.50.2000 (GENE3D): PTH	0,656	1,134	0,573	0,455	0,638									
Solyc11g007510	Mediator of RNA polymerase II transcription subunit 12 (AHRD V3.3 *** A0A0B0MWN8_GOSAR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	16,069	39,573	5,502	4,828	7,046	1,326	0,000					up		
Solyc11g007520	LOW QUALITY:Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (AHRD V3.3 --* MCCA_SOYBN)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,018	0,000	0,000	0,023									
Solyc11g007530	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DVK5_THECC)		C:GO:0016021	C:integral component of membrane	IPR001841 (PFAM): IPR013083 (G3D	0,755	1,275	0,147	0,142	0,166									
Solyc11g007540	cytochrome P450 77 A20		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR001128 (PRINTS): IPR002401 (PF	63,861	44,749	0,025	0,099	0,047									
Solyc11g007550	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation	G3DSA:3.40.50.150 (GENE3D): PTHF	1,728	1,497	1,505	1,138	1,153									
Solyc11g007560	Seed maturation protein PM36 (AHRD V3.3 *** A0A151ST20_CAJCA)		C:GO:0005829	C:cytosol	IPR004305 (PFAM): IPR016084 (G3D	0,156	0,398	0,173	0,379	0,000									
Solyc11g007570	Seed maturation PM36 (AHRD V3.3 *** A0A0B0PRT0_GOSAR)		C:GO:0005829	C:cytosol	IPR026285 (PIRSF): IPR004305 (PFA	1,315	1,936	0,853	0,856	0,962									
Solyc11g007580	DNA demethylase 3	DML3	F:GO:0003824; P:G(	F:catalytic activity; P:base-excision repair	IPR023170 (G3DSA:1.10.1670.GENE	77,271	76,043	76,177	79,739	81,130									
Solyc11g007590	OTU domain-containing protein (AHRD V3.3 *** A0A0B2NUV7_GLYSO)		F:GO:0004843; P:G(	F:thiol-dependent ul EC:3.4.19.12 Ubiquitinyl hydrolase	IPR003323 (PFAM): G3DSA:3.90.70.8	29,173	31,511	62,003	59,538	60,540									
Solyc11g007600	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans	IPR029044 (G3DSA:3.90.550.GENE3	0,118	0,163	0,000	0,000	0,000									
Solyc11g007610	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9SY26_RICCO)		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): IPR0	6,125	7,017	2,593	3,043	2,865									
Solyc11g007620	F-box family protein (AHRD V3.3 *** D7L723_ARALL)		F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,117	0,047	0,095	0,000									
Solyc11g007635	Protein kinase superfamily protein (AHRD V3.3 --* AT1G09600.1)					0,084	0,161	0,000	0,000	0,000									
Solyc11g007640	Mitotic checkpoint protein BUB3 (AHRD V3.3 *-* A0A0B2PGT6_GLYSO)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	1,311	1,955	0,116	0,069	0,118									
Solyc11g007650	F-box protein interaction domain protein (AHRD V3.3 *-* G7KDE0_MEDTR)				PTHR44293 (PANTHER)	0,021	0,000	0,122	0,050	0,000									
Solyc11g007660	type-1 restriction enzyme mjaxp r protein (DUF668) (AHRD V3.3 *** AT5G04550.2)				IPR021864 (PFAM): IPR007700 (PFAI	65,165	69,960	15,441	25,882	33,398			1,109	0,000	0,744	0,011		up	up
Solyc11g007670	Myotubularin-related protein 2 (AHRD V3.3 *** A0A0B2NUW1_GLYSO)		F:GO:0004725; P:G(	F:protein tyrosine p EC:3.1.3.16; EC:3.1. Protein-serine/threor	IPR011993 (G3DSA:2.30.29.GENE3D	33,490	26,183	35,130	31,976	32,796									
Solyc11g007680	Chloroplast outer envelope 24 kD protein (Omp24) (AHRD V3.3 *** Q41375_SPIOL)		C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR363	18,142	19,237	51,461	54,807	62,666									
Solyc11g007690	Pyruvate kinase (AHRD V3.3 *** K4D530_SOLLC)		F:GO:0000287; F:G(	F:magnesium ion bi EC:2.7.1.4 Pyruvate kinase	IPR001697 (PRINTS): IPR040442 (G3	63,169	45,333	28,756	32,096	32,330									
Solyc11g007700	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *** A0A097PS73_S(		F:GO:0004482	F:mRNA (guanine-N EC:2.1.1.56 mRNA (guanine-N(7)-	G3DSA:3.40.50.150 (GENE3D): IPR0(	13,699	11,799	15,489	13,886	14,139									
Solyc11g007710	3-oxoacyl-[acyl-carrier-protein] synthase-like protein (AHRD V3.3 *** Q9LZ73_ARATH)				IPR007402 (PFAM): IPR011197 (PIRS	6,485	7,367	8,508	6,615	7,713									
Solyc11g007720	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4D53		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR023213 (G3DSA:3.30.559.GENE3	69,493	63,282	109,162	103,364	96,851									
Solyc11g007730	Bark storage protein A (AHRD V3.3 *** W9SCI4_9ROSA)		F:GO:0003824; P:G(	F:catalytic activity; P:nucleoside metabolic process	IPR000845 (PFAM): PTHR21234 (PAN	0,585	0,805	0,259	0,144	0,399									
Solyc11g007740	Ribosome recycling factor (AHRD V3.3 *** AT3G01800.1)		P:GO:0006412	P:translation	G3DSA:3.30.1360.40 (GENE3D): IPR(	10,539	10,558	11,584	12,140	11,851									
Solyc11g007750	Nef-associated 1 (AHRD V3.3 *** A0A0B0P2J8_GOSAR)		C:GO:0016021; F:G(	C:integral compone EC:2.1.1.55 tRNA (adenine-N(6)-)	IPR023370 (PFAM): IPR036414 (G3D	0,402	0,631	0,377	0,503	0,400									
Solyc11g007760	3-phosphoinositide-dependent protein kinase-1	pdk1	F:GO:0004674; F:G(	F:protein serine/thr EC:2.7.11 Transferring phospho	G3DSA:3.30.200.20 (GENE3D): IPR0(	13,887	15,692	22,283	28,353	25,426									
Solyc11g007770	Exostosin-2 (AHRD V3.3 *** A0A0B2S0C1_GLYSO)		P:GO:0006486; C:G(	P:protein glycosylation; C:integral component of membrane; F:tr	IPR015338 (PFAM): IPR023296 (G3D	7,684	10,778	65,791	60,777	51,326									
Solyc11g007780	SEC12-like protein 1 (AHRD V3.3 *** A0A0B2S0C4_GLYSO)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	27,406	24,841	63,731	60,719	55,532									
Solyc11g007800	Ribonucleases P/MRP protein subunit POP1, putative (AHRD V3.3 *** A0A061DRG1_THECC)		C:GO:0000172; P:G(	C:ribonuclease MRP complex; P:tRNA 5'-leader removal; C:nucl	IPR012590 (PFAM): IPR039182 (PAN	9,032	9,230	9,485	9,075	8,320									
Solyc11g007803	Ribonucleases P/MRP protein subunit POP1, putative (AHRD V3.3 *-* A0A061DRG1_THECC)		C:GO:0000172; P:G(	C:ribonuclease MRP complex; P:tRNA 5'-leader removal; C:nucl	IPR039182 (PANTHER)	1,748	1,312	1,334	1,238	1,319									
Solyc11g007807	Ribonucleases P/MRP protein subunit POP1 (AHRD V3.3 *-* A0A0B2R1D7_GLYSO)		C:GO:0000172; P:G(	C:ribonuclease MRP complex; P:tRNA 5'-leader removal; C:nucl	IPR009723 (PFAM): mobidb-lite (MOB	3,262	2,818	2,934	2,841	2,919									
Solyc11g007810	RNA polymerase II, Rpb4, core protein (AHRD V3.3 *** AT5G62950.7)		F:GO:0000166; F:G(	F:nucleotide binding; F:catalytic activity; C:RNA polymerase III (	IPR005574 (PFAM): IPR038324 (G3D	7,733	8,351	6,546	6,881	7,319									
Solyc11g007820	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 ***		F:GO:0008168; F:G(	F:methyltransferase activity; F:transferase activity; P:methylatic	G3DSA:3.40.50.150 (GENE3D): PTHF	0,121	0,078	0,196	0,487	0,707									
Solyc11g007830	protein tyrosine phosphatase	ptpkis1	P:GO:0005982; P:G(	P:starch metabolic EC:3.1.3.16 Protein-serine/threor	IPR000340 (PFAM): IPR029021 (G3D	73,975	81,213	95,085	89,569	97,952									
Solyc11g007840	Glycosyl transferase, family 1 (AHRD V3.3 *** A0A124SG25_CYNCS)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.50.2000 (GENE3D): IPR(	19,178	20,334	11,821	12,319	12,466									
Solyc11g007850	DNA binding protein (AHRD V3.3 *-* AT3G52170.4)				mobidb-lite (MOBIDB_LITE): mobidb-lit	34,115	36,116	95,000	91,743	93,074									
Solyc11g007860	LOW QUALITY:Cyclin-dependent protein kinase inhibitor Siamese (AHRD V3.3 *** M4M6N3_GOSAR)		P:GO:0032875	P:regulation of DNA endoreduplication	PTHR33142:SF13 (PANTHER): IPR04	6,110	5,945	7,472	8,022	6,527									
Solyc11g007870	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 --* AT5G02220.1)		P:GO:0032875	P:regulation of DNA endoreduplication	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,143	0,174	0,000	0,050	0,000									
Solyc11g007880	LOW QUALITY:cyclin-dependent kinase inhibitor (AHRD V3.3 --* AT1G10690.1)		P:GO:0032875	P:regulation of DNA endoreduplication	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,363	0,154	0,000	0,000	0,000									
Solyc11g007890	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT2G36690.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	PR00682 (PRINTS): IPR027443 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc11g007900	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT2G36690.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3	67,263	41,996	33,976	29,470	30,587									
Solyc11g007910	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FPQ4_THECC)				IPR013083 (G3DSA:3.30.40.GENE3D	48,470	46,709	46,255	42,053	43,629									
Solyc11g007920	Histone H2B (AHRD V3.3 *** K4D553_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000558 (PRINTS): IPR007125 (PF	93,068	80,004	117,428	89,462	88,793									
Solyc11g007930	Histone H2B (AHRD V3.3 *** K4D554_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000558 (PRINTS): IPR007125 (PF	2,576	3,186	12,643	10,586	9,797									
Solyc11g007940	RNA-binding protein Nova-1 (AHRD V3.3 *** A0A151T0U1_CAJCA)		F:GO:0003723	F:RNA binding	IPR004088 (PFAM): IPR036612 (G3D	11,456	16,802	19,841	16,509	22,361									
Solyc11g007960	Acyl-CoA-binding domain-containing protein 4 (AHRD V3.3 *** A0A151T0U9_CAJCA)		F:GO:0005515	F:protein binding	IPR006652 (PFAM): IPR015915 (G3D	89,477	87,406	50,536	45,672	48,315									
Solyc11g007980	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR002401 (PRINTS): IPR001128 (PF	0,061	0,000	0,273	0,317	1,999									
Solyc11g007990	chloroplast malate dehydrogenase (mdh)	mdh	P:GO:0005975; P:G(	P:carbohydrate met EC:1.1.1.82 Malate dehydrogenas	G3DSA:3.40.50.720 (GENE3D): IPR0	167,665	216,567	169,912	209,314	320,390			0,912	0,000				up	
Solyc11g008000	NAC domain protein, (AHRD V3.3 *** A0A061FNG1_THECC)	NAC090	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	58,106	72,274	98,777	91,923	84,727									
Solyc11g008010	NAC domain protein, (AHRD V3.3 *** A0A061FQ99_THECC)	NAC091	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS NAC	73,842	68,051	123,407	104,036	114,473									
Solyc11g008020	GTP-binding family protein (AHRD V3.3 *** A9P9Z6_POPTR)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): IPR005225 (TIGF	4,878	5,001	9,075	7,446	7,653									
Solyc11g008030	Monocopper oxidase-like protein SKU5 (AHRD V3.3 *** A0A0B2NUZ0_GLYSO)		F:GO:0003924; F:G(	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFAI	0,019	0,021	0,000	0,000	0,000									
Solyc11g008040	Pullulanase, putative (AHRD V3.3 *** B9T3G1_RICCO)		P:GO:0005975; F:G(	P:carbohydrate met EC:3.2.1.41 Pullulanase	G3DSA:2.60.40.1130 (GENE3D): IPR(	13,098	13,702	5,731	6,225	7,262									
Solyc11g008070	LOW QUALITY:Hyccin (AHRD V3.3 *** A0A118JWG4_CYNCS)		C:GO:0005886; P:G(	C:plasma membrane; P:phosphatidylinositol phosphorylation; P:	IPR018619 (PFAM): mobidb-lite (MOB	0,155	0,157	0,071	0,047	0,000									
Solyc11g008080	DUF1635 family protein (AHRD V3.3 *** A0A072VZ15_MEDTR)				IPR012862 (PFAM): PTHR33431:SF3	1,143	0,866	0,165	0,045	0,072									
Solyc11g008090	Shugoshin, C-terminal (AHRD V3.3 *** A0A103YD26_CYNCS)		C:GO:0000775; C:G(	C:chromosome, centromeric region; C:nucleus; P:meiotic chrom	IPR011515 (PFAM): mobidb-lite (MOB	12,479	10,305	6,014	5,433	6,948									
Solyc11g008100	Ubiquitin-conjugating enzyme, E2 (AHRD V3.3 --* A0A103YHB1_CYNCS)				mobidb-lite (MOBIDB_LITE)	3,801	4,745	3,406	2,306	2,514									
Solyc11g008103	translocase subunit seca (AHRD V3.3 *-* AT1G13390.2)				PTHR33384 (PANTHER): PTHR33384	3,162	3,041	2,198	2,789	2,377									
Solyc11g008120	nuclear pore complex protein-like protein (AHRD V3.3 *-* AT5G05680.1)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:ribosomal sma	IPR037700 (PANTHER)	15,565	14,086	17,966	18,311	16,846									
Solyc11g008130	nuclear pore complex protein-like protein (AHRD V3.3 *-* AT5G05680.1)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:ribosomal sma	IPR037700 (PANTHER)	16,756	16,724	19,093	20,108	20,057									
Solyc11g008140	Pectate lyase (AHRD V3.3 *** K4D575_SOLLC)		C:GO:0016021; F:G(	C:integral compone EC:4.2.2.2 Pectate lyase	IPR018082 (PRINTS): IPR002022 (PF	9,007	6,689	0,327	0,453	0,399									
Solyc11g008150	Transcription elongation factor SPT5 (AHRD V3.3 *-* A9SZZ9_PHYPA)		P:GO:0006357; P:G(	P:regulation of transcription by RNA polymerase II; P:regulation	IPR036735 (G3DSA:3.30.70.GENE3D	233,022	178,195	160,485	142,334	160,125									
Solyc11g008200	LOW QUALITY:Major facilitator superfamily protein (AHRD V3.3 *** AT2G39210.1)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D): IPR(	0,000	0,000	0,000	0,000	0,023									
Solyc11g008210	Glycine-rich RNA-binding family protein (AHRD V3.3 *** B9HUL0_POPTR)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding	IPR012677 (G3DSA:3.30.70.GENE3D	14,758	14,897	15,083	11,773	13,237									
Solyc11g008215	Mitochondrial ribosomal protein L37 (AHRD V3.3 --* AT5G14290.1)					3,508	3,785	4,576	4,165	4,201									
Solyc11g008220	Glycine-rich RNA-binding protein, putative (AHRD V3.3 *-* B9T555_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	2,609	1,759	2,043	2,642	2,143									
Solyc11g008240	SLF-interacting SKP1-like protein 3 (AHRD V3.3 *** K4D584_SOLLC)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process	IPR016073 (PFAM): IPR016072 (PFAI	0,019	0,000	0,022	0,000	0,000									
Solyc11g008250	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT3G10420.2)		F:GO:0005524	F:ATP binding	IPR003959 (PFAM): G3DSA:3.40.50.3	11,160	10,120	19,391	19,875	22,918									

Solyc11g008260	Papain family cysteine protease (AHRD V3.3 *** AT3G54940.2)		P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR013201 (PF	11,778	15,074	7,429	11,174	4,311									
Solyc11g008270	DUF4050 family protein (AHRD V3.3 *** A0A072VNV4_MEDTR)				IPR025124 (PFAM): PTHR33373:SF2	7,902	7,637	5,764	8,303	6,482					0,530	0,049			up
Solyc11g008280	Carboxypeptidase (AHRD V3.3 *** K4D588_SOLLC)		F:GO:0004185; P:GO	F:serine-type carbo EC:3.4.21; EC:3.4.16 Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	42,856	50,448	36,865	47,570	46,413									
Solyc11g008290	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT4G20030.1)		F:GO:0003676; F:GO	F:nucleic acid binding; F:zinc ion binding	IPR012677 (G3DSA:3.30.70.GENE3D	12,554	12,700	18,028	15,791	15,955									
Solyc11g008300	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *-* S1RTT0_THECC)		F:GO:0005515	F:protein binding	IPR001810 (PFAM): G3DSA:1.20.128	0,078	0,078	0,025	0,025	0,095									
Solyc11g008310	MEF2BNB-like protein (AHRD V3.3 *** AT2G39170.1)				IPR019320 (PFAM): mobidb-lite (MOB	23,420	23,839	43,257	46,194	43,265									
Solyc11g008320	Lysine-specific histone demethylase 1-like protein (AHRD V3.3 *** A0A0B0PVB3_GOSAR)		F:GO:0003677; F:GO	F:DNA binding; F:protein binding; F:oxidoreductase activity; P:o	IPR036188 (G3DSA:3.50.50.GENE3D	23,816	24,524	33,743	32,122	31,393									
Solyc11g008340	Exocyst complex component Sec8 family protein (AHRD V3.3 *** U5G1P5_POPTR)		C:GO:0000145; P:GO	C:exocyst; P:vesicle docking involved in exocytosis; P:vesicle t	IPR007191 (PFAM): mobidb-lite (MOB	83,951	68,729	95,359	99,093	97,122									
Solyc11g008350	Kinesin-like protein (AHRD V3.3 *** A0A0B0P6I8_GOSAR)		F:GO:0003777; F:GO	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR000225 (PF	17,741	18,958	58,482	76,803	53,818									
Solyc11g008360	pseudouridine synthase family protein (AHRD V3.3 *** AT2G39140.1)		P:GO:0001522; F:GO	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine syn	G3DSA:3.30.70.1560 (GENE3D): IPR0	28,840	37,464	99,782	91,207	96,618									
Solyc11g008380	Glycerol-3-phosphate dehydrogenase (AHRD V3.3 *** K4D598_SOLLC)		F:GO:0004368; P:GO	F:glycerol-3-phosph EC:1.1.5.3 Glycerol-3-phosphate	IPR000447 (PRINTS): G3DSA:3.30.9.	7,825	8,258	28,320	37,257	29,059					0,399	0,050			up
Solyc11g008390	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PZF9_ZOSMR)		F:GO:0004842; F:GO	F:ubiquitin-protein transferase activity; F:protein binding; P:cell	IPR013083 (G3DSA:3.30.40.GENE3D	40,648	50,015	47,649	46,968	43,238									
Solyc11g008410	SolycHsfl3		P:GO:0006355; F:GO	P:regulation of transcription, DNA-templated; F:sequence-specif	mobidb-lite (MOBIDB_LITE): PTHR100	0,019	0,041	0,000	0,000	0,000									
Solyc11g008420	SKP1-like protein (AHRD V3.3 *** A0A0K0PT05_NICBE)		P:GO:0006511	P:ubiquitin-dependent protein catabolic process	IPR016897 (PIRSF): IPR016073 (PFA	5,698	4,773	8,064	7,272	6,891									
Solyc11g008430	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT3G54840.1)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	37,579	41,480	59,446	62,822	55,551									
Solyc11g008440	Amino acid transporter family protein (AHRD V3.3 *** B9HLH9_POPTR)		P:GO:0003333; C:GO	P:amino acid transmembrane transport; C:vacuolar membrane;	IPR013057 (PFAM): mobidb-lite (MOB	12,370	11,384	78,758	108,342	79,973									
Solyc11g008450	Thioredoxin (AHRD V3.3 *** A0A103YCX9_CYNCS)		P:GO:0006662; F:GO	P:glycerol ether metabolic process; F:protein disulfide oxidoredu	IPR013766 (PFAM): G3DSA:3.40.30.1	3,236	3,476	8,238	8,835	7,787									
Solyc11g008460	U4/U6.U5 tri-snRNP-associated 1 (AHRD V3.3 *-* A0A0B0PND3_GOSAR)		P:GO:0000398	P:mRNA splicing, via spliceosome	IPR005011 (PFAM): mobidb-lite (MOB	53,677	45,845	54,995	46,321	44,157									
Solyc11g008470	U4/U6.U5 tri-snRNP-associated protein 1 (AHRD V3.3 *** A0A0B2S142_GLYSO)		P:GO:0000398	P:mRNA splicing, via spliceosome	IPR005011 (PFAM): mobidb-lite (MOB	68,999	64,412	74,205	64,304	64,549									
Solyc11g008480	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** AT3G05410.2)		F:GO:0005509; C:GO	F:calcium ion binding; C:photosystem II oxygen evolving comple	IPR002683 (PFAM): IPR016123 (G3D	0,877	2,124	0,050	0,409	1,007									
Solyc11g008490	Pumilio-like protein (AHRD V3.3 *** A0A0B0PW20_GOSAR)		F:GO:0003723	F:RNA binding	IPR011989 (G3DSA:1.25.10.GENE3D	0,000	0,018	0,000	0,000	0,000									
Solyc11g008500	Actin, putative (AHRD V3.3 *** B9RVQ0_RICCO)		C:GO:0005634; P:GO	C:nucleus; P:chromatin organization; P:developmental process	IPR004000 (PRINTS): G3DSA:3.90.64	10,726	10,322	10,014	9,430	9,576									
Solyc11g008510	60S ribosomal protein L38 (AHRD V3.3 *** RL38_SOLLC)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation	IPR038464 (G3DSA:3.30.720.GENE3	137,137	151,879	77,658	72,660	74,924									
Solyc11g008520	Dicer-like 2c	DCL2c	F:GO:0004525; F:GO	F:ribonuclease III a EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR005034 (PFAM): G3DSA:3.40.50.3	0,307	0,291	0,000	0,045	0,046									
Solyc11g008530	Dicer-like 2d	DCL2d	F:GO:0004525; F:GO	F:ribonuclease III a EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR005034 (PFAM): IPR001650 (PFA	30,861	48,730	7,144	10,685	10,403									
Solyc11g008540	Dicer-like 2b	DCL2b	F:GO:0003676; F:GO	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR001650 (PFAM): IPR036389 (G3D	216,015	511,326	27,206	24,016	30,348	1,267	0,000					up		
Solyc11g008550	Lecithin:cholesterol acyltransferase family protein (AHRD V3.3 *** G7KSE0_MEDTR)		P:GO:0006629; F:GO	P:lipid metabolic process; F:O-acyltransferase activity	IPR003386 (PFAM): IPR029058 (G3D	13,190	11,421	23,952	27,547	26,022									
Solyc11g008560	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A0K9PVT8_ZOSMR)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN AP2	0,042	0,059	0,000	0,000	0,000									
Solyc11g008570	Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** A0A061EY73_THECC)		F:GO:0016787	F:hydrolase activity	IPR004843 (PFAM): IPR029052 (G3D	18,893	15,918	23,631	20,853	20,383									
Solyc11g008580	RING/U-box superfamily protein (AHRD V3.3 *** AT1G05890.1)		F:GO:0004842; P:GO	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (PFAM): G3DSA:2.20.28.1	82,312	71,429	115,757	103,177	111,595									
Solyc11g008590	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT4G35335.1)		C:GO:0000139; F:GO	C:Golgi membrane; F:pyrimidine nucleotide-sugar transmembran	TIGR00803 (TIGRFAM): IPR007271 (I	13,632	10,199	10,706	9,513	9,589									
Solyc11g008600	LOW QUALITY:cotton fiber protein (AHRD V3.3 *** AT5G57510.1)				IPR008480 (PFAM): PTHR33098 (PAN	0,140	0,144	0,194	0,850	0,590									
Solyc11g008610	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT2G43240.1)		C:GO:0000139; F:GO	C:Golgi membrane; F:pyrimidine nucleotide-sugar transmembran	IPR007271 (PIRSF): IPR007271 (PFA	6,487	6,111	4,068	4,241	3,676									
Solyc11g008620	Phosphoglycolate phosphatase (AHRD V3.3 *** A0A0V0I1W8_SOLCH)		F:GO:0016791	F:phosphatase activity	IPR006357 (TIGRFAM): IPR006357 (I	32,095	61,144	26,708	29,585	49,965	0,957	0,000	0,900	0,000			up	up	
Solyc11g008630	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT1G65450.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	IPR003480 (PFAM): IPR023213 (G3D	50,816	38,258	2,378	1,905	1,358									
Solyc11g008640	Flowering locus T (AHRD V3.3 *** D5LM18_PETHY)		F:GO:0008429; P:GO	F:phosphatidylethanolamine binding; P:regulation of flower deve	IPR008914 (PFAM): IPR036610 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc11g008670	Chromatin assembly factor 1, subunit A, putative (AHRD V3.3 *** B9RM13_RICCO)		P:GO:0000724; C:GO	P:double-strand break repair via homologous recombination; C:n	IPR022043 (PFAM): mobidb-lite (MOB	18,482	14,154	8,066	5,345	7,066									
Solyc11g008680	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A060IKL1_NICBE)		P:GO:0006631; F:GO	P:fatty acid metabo EC:1.14.19.2; EC:1. Stearoyl-[acyl-carrier	IPR012348 (G3DSA:1.10.620.GENE3	21,434	19,066	87,039	67,880	74,132									
Solyc11g008700	RNA binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT5G16260.1)		P:GO:0000398; F:GO	P:mRNA splicing, via spliceosome; F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	30,706	27,743	40,680	37,619	37,587									
Solyc11g008710	Ribosomal protein S5 family protein (AHRD V3.3 *** A0A061F6Z5_THECC)		F:GO:0003723; F:GO	F:RNA binding; F:structural constituent of ribosome; C:ribosome	IPR014721 (G3DSA:3.30.230.GENE3	24,539	22,840	34,487	33,774	31,321									
Solyc11g008720	Beta-glucosidase (AHRD V3.3 *** K4D5D2_SOLLC)		F:GO:0008422; P:GO	F:beta-glucosidase EC:3.2.1.21 Beta-glucosidase	IPR001360 (PRINTS): G3DSA:3.20.2	0,440	0,907	44,851	112,749	37,026					1,336	0,000			up
Solyc11g008730	U11/U12 small nuclear ribonucleoprotein 25 kDa (AHRD V3.3 *** A0A0B0PJE8_GOSAR)		P:GO:0000398; F:GO	P:mRNA splicing, via spliceosome; F:protein binding; C:U12-typ	G3DSA:3.10.20.90 (GENE3D): IPR04	13,713	12,523	19,080	17,499	16,684									
Solyc11g008740	Sister chromatid cohesion 1 protein 3 (AHRD V3.3 *** W9SSS4_9ROSA)		F:GO:0005515; P:GO	F:protein binding; P:sister chromatid cohesion; C:cohesin comp	IPR006909 (PFAM): IPR023093 (G3D	90,325	72,965	94,083	102,864	92,888									
Solyc11g008750	LOW QUALITY:Branched-chain-amino-acid aminotransferase (AHRD V3.3 --* A3C731_ORYSJ)				mobidb-lite (MOBIDB_LITE): PTHR341	0,117	0,162	0,046	0,292	0,142									
Solyc11g008760	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** A0A061DRT6_THECC)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	4,915	2,828	17,812	24,628	13,940									
Solyc11g008770	LETM1 and EF-hand domain-containing protein 1 (AHRD V3.3 *** A0A061EI71_THECC)		F:GO:0005509; F:GO	F:calcium ion binding; F:ribosome binding	IPR011685 (PFAM): G3DSA:1.10.238	46,116	46,106	64,353	66,098	69,168									
Solyc11g008775	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 --* R0I7Q4_9BRAS)					0,077	0,123	0,071	0,173	0,069									
Solyc11g008780	Acetolactate synthase small subunit (AHRD V3.3 *** A0A151UBY0_CAJCA)		F:GO:0003984; P:GO	F:acetolactate synt EC:2.2.1.6 Acetolactate synthas	IPR004789 (TIGRFAM): G3DSA:3.30.	9,057	10,335	5,185	4,459	5,345									
Solyc11g008790	Protein arv1 like (AHRD V3.3 *-* A0A0B2RER2_GLYSO)		C:GO:0005794; P:GO	C:Golgi apparatus; P:sphingolipid metabolic process; C:integral	IPR007290 (PFAM)	1,742	1,408	1,481	1,186	1,437									
Solyc11g008800	Type II inositol 5-phosphatase, putative (AHRD V3.3 *** B9RM01_RICCO)		F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	64,305	77,588	87,333	97,648	88,033									
Solyc11g008810	Beta-hexosaminidase (AHRD V3.3 *** M1BC44_SOLTU)		F:GO:0004563; P:GO	F:beta-N-acetylhex EC:3.2.1.52 Beta-N-acetylhexosa	IPR025705 (PRINTS): IPR025705 (PI	26,854	23,267	0,607	0,669	0,797									
Solyc11g008820	Endoglucanase (AHRD V3.3 *** A0A0V0II53_SOLCH)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	30,587	34,494	8,463	9,745	12,854			0,594	0,049				up	
Solyc11g008830	Asymmetric leaves 2 (AHRD V3.3 *** A7L4B2_CARPA)		P:GO:0003002	P:regionalization	IPR004883 (PFAM LBD	0,096	0,041	0,044	0,000	0,047									
Solyc11g008840	ATP-binding protein, putative (AHRD V3.3 *-* A0A072V076_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,018	0,000	0,025	0,000									
Solyc11g008850	Protease Do-like 10 (AHRD V3.3 *** W9SEX8_9ROSA)		F:GO:0004252; F:GO	F:serine-type endo EC:3.4.21 Acting on peptide bor	IPR001940 (PRINTS): G3DSA:2.40.10	19,886	17,102	12,327	9,323	10,036									
Solyc11g008870	Methylenetetrahydrofolate reductase (AHRD V3.3 *** K4D5E7_SOLLC)		F:GO:0004489; P:GO	F:methylenetetrahy EC:1.5.1.2 Methylenetetrahydrol	G3DSA:3.20.20.220 (GENE3D): IPR0	182,925	172,793	101,618	99,028	95,778									
Solyc11g008880	ROP-interactive CRIB motif protein (AHRD V3.3 *** Q2HW10_MEDTR)		P:GO:0009860; P:GO	P:pollen tube growth; P:cellulose microfibril organization; C:apic	IPR000095 (PFAM): PTHR23177 (PAN	0,371	0,398	0,119	0,240	0,117									
Solyc11g008890	GDT1-like protein (AHRD V3.3 *** A2Q167_MEDTR)		C:GO:0005794; C:GO	C:Golgi apparatus; C:integral component of membrane	IPR001727 (PFAM): IPR001727 (PAN	75,200	74,191	60,878	59,286	55,089									
Solyc11g008900	Zinc finger transcription factor 65	C3H65	F:GO:0046872	F:metal ion binding	G3DSA:2.30.30.11 C3H	63,667	60,642	83,421	84,074	75,653									
Solyc11g008910	ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** AT1G65295.1)				PTHR33786:SF2 (PANTHER): PTHR3	5,178	3,057	10,207	9,120	7,804									
Solyc11g008930	lysine ketoglutarate reductase trans-splicing-like protein, putative (DUF707) (AHRD V3.3 *** AT4G18530.3)				IPR007877 (PFAM): mobidb-lite (MOB	0,019	0,116	0,000	0,000	0,024									
Solyc11g008940	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K217_CYNCS)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	4,592	6,017	9,884	10,584	9,892									
Solyc11g008960	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9P3X9_ZOSMR)		F:GO:0004672; F:GO	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001611 (PFAM): IPR032675 (G3D	16,487	13,371	58,877	76,793	51,458									
Solyc11g008970	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y632_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFA	4,641	3,647	5,854	6,091	5,374									
Solyc11g008980	Protein TIC 20-II, chloroplastic (AHRD V3.3 *** TI202_ARATH)		C:GO:0005739; C:GO	C:mitochondrion; C:chloroplast inner membrane; C:integral com	IPR005691 (PFAM): PTHR33510:SF1	17,680	23,659	30,736	26,707	35,230									
Solyc11g008990	Membrane-associated 30 kDa, chloroplastic (AHRD V3.3 *** A0A0B0PBX1_GOSAR)				IPR007157 (PFAM): mobidb-lite (MOB	40,159	55,963	95,583	100,629	107,088	0,506	0,043					up		
Solyc11g009000	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G09430.1)		C:GO:0005886; F:GO	C:plasma membrane; F:hydrolase activity	IPR000073 (PRINTS): IPR000073 (PF	12,000	8,484	70,110	74,775	61,543									
Solyc11g009010	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* AT4G39955.1)		F:GO:0016787	F:hydrolase activity	IPR000073 (PRINTS): IPR029058 (G3D	10,704	8,706	66,502	74,304	62,175									
Solyc11g009020	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein (AHRD V3.3 *** AT4G39970.1)		F:GO:0016787	F:hydrolase activity	IPR006439 (PRINTS): IPR041492 (PF	2,061	7,284	0,707	0,746	2,445	1,846	0,000	1,750	0,000			up	up	
Solyc11g009030	LOW QUALITY:glycine-rich protein (AHRD V3.3 *** AT4G10330.1)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR342	1,538	1,382	1,195	1,092	1,269									
Solyc11g009040	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *** AT5G10310.2),Pfam:PF17181		P:GO:0010374	P:stomatal complex development	PF17181 (PFAM): mobidb-lite (MOBID	0,021	0,018	0,000	0,000	0,000									
Solyc11g009050	F-box protein (AHRD V3.3 *** M4MFP9_CUCSA)				G3DSA:1.20.1280.50 (GENE3D): IPR0	26,458	20,504	19,726	15,524	17,819									
Solyc11g009060	ATP synthase subunit B (AHRD V3.3 *** AT5G10320.5)				PTHR35754 (PANTHER)	8,984	7,227	13,818	13,657	11,952									
Solyc11g009070	transmembrane protein (AHRD V3.3 *** AT5G65250.1)		C:GO:0009941; C:GO	C:chloroplast envelope; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	9,731	9,373	14,130	11,896	12,476									
Solyc11g009080	DAHP synthase 1 precursor	DAHPS1	F:GO:0003849; P:GO	F:3-deoxy-7-phosph EC:2.5.1.54 3-deoxy-7-phosphohe	IPR002480 (PFAM): IPR013785 (G3D	555,062	422,292	497,382	451,176	475,127									
Solyc11g009090	Polyadenylate-binding 2 (AHRD V3.3 *** A0A0B0MLP3_GOSAR)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	68,519	67,612	66,341	60,957	63,824									
Solyc11g009100	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	ABCG25	F:GO:0005524; C:GO	F:ATP binding; C:m EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	0,000	0,043	0,025	0,025	0,000									
Solyc11g010100	Ras-related protein Rab11D (AHRD V3.3 *** RB11D_TOBAC)		F:GO:0003924; F:GO	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	34,517	39,508	23,702	23,674	26,276									
Solyc11g010105	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-* AT2G22400.1)		F:GO:0008168	F:methyltransferase activity	G3DSA:3.40.50.150 (GENE3D): mobid	14,729	12,682	8,790	9,007	8,012									
Solyc11g010110	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT2G22400.1)		F:GO:0016428	F:tRNA (cytosine-5-)-methyltransferase activity	IPR023270 (PRINTS): IPR023267 (PF	38,887	37,434	23,016	22,122	24,149									
Solyc11g010120	Peroxidase (AHRD V3.3 *** K4D5H3_SOLLC)		F:GO:0004601; P:GO	F:peroxidase activi EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	18,457	20,536	1,257	1,266	1,995									
Solyc11g010130	Protein kinase (AHRD V3.3 *** Q40264_MESCR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): G3DSA:3.30.200	0,078	0,018	0,050	0,050	0,046									
Solyc11g010170	LanC-like protein 2 (AHRD V3.3 *** A0A0B0NZR1_GOSAR)		F:GO:0003824	F:catalytic activity	IPR007822 (PRINTS): IPR020464 (PF	34,320	37,848	32,796	28,876	41,145									
Solyc11g010180	Mitochondrial ribosomal protein L37 (AHRD V3.3 *** AT5G14290.1)		C:GO:0005840	C:ribosome	IPR013870 (PFAM): IPR013870 (PAN	0,267	0,326	0,457	0,410	0,516									
Solyc11g010190	Prohibitin (AHRD V3.3 *** O04361_TOBAC)		C:GO:0016020	C:membrane	IPR000163 (PRINTS): IPR001107 (PF	79,052	84,980	140,738	112,125	121,704									
Solyc11g010200	14-3-3 family protein AF079104		F:GO:0019904	F:protein domain specific binding	IPR000308 (PRINTS): IPR023410 (PF	64,799	77,970	17,052	14,615	18,407									
Solyc11g010210	WEB family protein, chloroplastic (AHRD V3.3 *-* A0A199V6Z9_ANACO)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,893	1,919	0,667	0,723	0,610	1,124	0,048					up		
Solyc11g010220	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118I7L5_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,036	1,816	0,289	0,383	0,259									
Solyc11g010230	Histone H3 (AHRD V3.3 *** K7VSQ3_MAIZE)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS): IPR007125 (PF	0,080	0,085	0,193	0,147	0,213									
Solyc11g010240	Histone H3 (AHRD V3.3 *-* K7VSQ3_MAIZE)		C:GO:0000786; F:GO	C:nucleosome; F:DNA binding; F:transcription corepressor activ	IPR000164 (PRINTS): IPR009072 (G3	31,775	23,580	29,868	35,265	28,803									
Solyc11g010250	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 75 (AHRD V3.3 *** Q9FQY9_TOBAC)				PTHR34046 (PANTHER): PTHR34046	16,416	24,389	7,604	6,818	9,588									
Solyc11g010260	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XU85_CYNCS)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,565	1,811	1,566	1,856	1,389									
Solyc11g010270	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072TTL6_MEDTR)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans	IPR000047 (PRIN HD-ZIP	140,043	129,843	60,713	39,356	60,988					-0,623	0,007			down
Solyc11g010290	2-oxoglutarate/malate translocator, chloroplastic (AHRD V3.3 *** A0A1D1ZLG4_9ARAE)		F:GO:0005215; P:GO	F:transporter activity; P:sodium ion transport; C:membrane; P:tr	IPR030676 (PIRSF): IPR001898 (PFA	0,221	0,223	0,025	0,073	0,071									
Solyc11g010300	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase (AHRD V3.3 *** Q6A4W9_MALDO)		F:GO:0003935; F:GO	F:GTP cyclohydrola EC:3.5.4.25; EC:4.1. GTP cyclohydrolase	IPR000422 (TIGRFAM): IPR000422 (I	17,115	18,170	35,402	32,209	32,927									
Solyc11g010310	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9S9D0_RICCO)		F:GO:0003723; F:GO	F:RNA binding; F:he EC:3.6.1.15 Nucleoside-triphosph	G3DSA:3.40.50.300 (GENE3D): IPR0	41,872	31,449	105,632	109,512	90,504									
Solyc11g010330	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E293_THECC)		C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40.GENE3D	71,670	85,489	78,541	85,484	87,937									
Solyc11g010340	bHLH transcription factor 069	bHLH069	F:GO:0046983	F:protein dimerization activity	IPR011598 (PFAM bHLH	0,232	1,029	0,000	0,000	0,000									
Solyc11g010350	Glucan 1,3-beta-glucosidase (AHRD V3.3 *** A0A151U914_CAJCA)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001547 (PFAM): G3DSA:2.80.10.5	5,239	5,429	3,162	2,575	3,545									
Solyc11g010360	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G65340.1)				IPR006460 (PFAM): IPR006460 (TIGF	0,021	0,000	0,000	0,000	0,000									
Solyc11g010370	ENTH/ANTH/VHS superfamily protein, putative (AHRD V3.3 *** A0A061DPV2_THECC)		F:GO:0005543	F:phospholipid binding	IPR011417 (PFAM): IPR008942 (G3D	11,212	13,326	7,979	6,127	7,935									
Solyc11g010380	Protein DETOXIFICATION (AHRD V3.3 *** K4D5J9_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transpo	IPR002528 (TIGRFAM): IPR002528 (I	29,829	28,098	26,676	35,599	34,320					0,417	0,045			up
Solyc11g010390	LOW QUALITY:Arabinogalactan-protein (AHRD V3.3 -** Q40380_NICAL)				PR01217 (PRINTS): mobidb-lite (MOB	23,681	19,393	5,677	10,550	9,277			0,705	0,019	0,893	0,002		up	up
Solyc11g010400	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G24530.1)		F:GO:0016491; P:GO	F:oxidoreductase activity; P:oxidation-reduction process	IPR027443 (G3DSA:2.60.120.GENE3	0,000	0,000	0,000	0,000	0,023									
Solyc11g010420	Dihydrofolate reductase-like protein (AHRD V3.3 *** G7JXR7_MEDTR)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm	IPR029058 (G3DSA:3.40.50.GENE3D	7,065	6,036	7,635	7,591	7,849									
Solyc11g010430	Dihydrofolate reductase-like protein (AHRD V3.3 *** G7JXR7_MEDTR)		C:GO:0005634; C:GO	C:nucleus; C:cytoplasm	IPR005645 (PFAM): IPR029058 (G3D	13,978	12,879	17,769	16,401	19,669									
Solyc11g010440	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)				IPR011993 (G3DSA:2.30.29.GENE3D	47,094	39,155	19,998	14,440	19,682									
Solyc11g010450	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** K4D5K6_SOLLC)		F:GO:0003872; F:GO	F:6-phosphofructok EC:2.7.1.11 6-phosphofructokinas	IPR022953 (PRINTS): IPR000023 (PF	79,140	52,567	247,765	245,979	250,482	-0,563	0,035					down		
Solyc11g010460	cyclinD4_1	CycD4_1	C:GO:0005634	C:nucleus	G3DSA:1.10.472.10 (GENE3D): IPR0	0,652	0,811	0,124	0,073	0,117									
Solyc11g010470	14-3-3 protein 1		F:GO:0019904	F:protein domain specific binding	IPR000308 (PRINTS): IPR023410 (PF	163,147	208,474	133,734	133,384	142,936									
Solyc11g010480	Protein curvature thylakoid chloroplastic-like (AHRD V3.3 *-* A0A061SMW2_9CHLO)		C:GO:0009579	C:thylakoid	IPR025564 (PFAM): mobidb-lite (MOB	31,280	45,141	52,172	56,525	61,982									
Solyc11g010490	pesticidal crystal cry8Ba protein (AHRD V3.3 *** AT4G24610.1)		C:GO:0005886	C:plasma membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	62,343	63,190	69,008	80,866	72,250									
Solyc11g010500	Mitochondrial carrier protein (AHRD V3.3 *** A0A0K9PSM6_ZOSMR)		P:GO:0006839; F:GO	P:mitochondrial transport; F:transmembrane transporter activity	IPR002030 (PRINTS): IPR018108 (PF	358,686	415,110	140,264	174,335	184,946									
Solyc11g010510	IMPACT family member in pol 5'region (AHRD V3.3 *** A0A0B0MZ52_GOSAR)				IPR001498 (PFAM): IPR036956 (G3D	9,413	9,635	24,341	24,626	25,454									
Solyc11g010520	evolutionarily conserved C-terminal region 5 (AHRD V3.3 --* AT3G13060.4)				IPR010800 (PFAM): PTHR37389:SF3	0,339	3,224	4,256	11,647	2,628									
Solyc11g010530	29 kDa ribonucleoprotein B, chloroplastic (AHRD V3.3 --* ROC2_NICSY)				IPR010800 (PFAM): mobidb-lite (MOB	0,019	0,000	2,497	0,594	3,609					-2,061	0,000			down
Solyc11g010540	LOW QUALITY:Chaperone DnaJ-domain protein (AHRD V3.3 *** A0A072TTF8_MEDTR)				IPR036869 (G3DSA:1.10.287.GENE3	0,040	0,000	0,234	0,025	0,142									
Solyc11g010550	GPI ethanolamine phosphate transferase (AHRD V3.3 *** G7JXN2_MEDTR)		P:GO:0006506; F:GO	P:GPI anchor biosynthetic process; F:mannose-ethanolamine p	IPR002591 (PFAM): IPR017849 (G3D	14,627	10,880	16,393	21,121	19,055									
Solyc11g010560	Kinesin-like protein KCA1 (AHRD V3.3 *** A0A199VSQ9_ANACO)		F:GO:0003777; F:GO	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS): IPR036961 (G3	135,343	129,626	67,280	61,767	77,057									
Solyc11g010570	jointless		F:GO:0000977; F:GO	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRIN MIKC_MADS	1,170	0,964	0,263	0,431	0,613									
Solyc11g010590	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase (AHRD V3.3 *** A0A068TZ66_COFCA)		C:GO:0005789; P:GO	C:endoplasmic retic EC:4.2.1.134 Very-long-chain (3R)	IPR007482 (PFAM): IPR007482 (PAN	0,735	0,673	0,448	0,388	0,330									
Solyc11g010600	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G65470.1)		P:GO:0006004; F:GO	P:fucose metabolic process; F:transferase activity, transferring	IPR024709 (PIRSF): IPR019378 (PFA	529,669	444,658	103,170	103,149	105,023									
Solyc11g010610	Mechanosensitive ion channel-like protein (AHRD V3.3 *** G7JWE5_MEDTR)		C:GO:0016020; P:GO	C:membrane; P:transmembrane transport	IPR006685 (PFAM): mobidb-lite (MOB	46,808	49,860	51,172	54,683	52,228									
Solyc11g010620	Basic helix loop helix protein, putative (AHRD V3.3 *** A0A072TTF3_MEDTR)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,113	0,196	0,000	0,025	0,000									
Solyc11g010625	Ribosomal RNA small subunit methyltransferase A (AHRD V3.3 *** A0A0B0NTG7_GOSAR)				PTHR34464 (PANTHER): PTHR34464	10,253	18,536	17,815	19,819	13,449	0,882	0,043					up		
Solyc11g010630	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** AT2G22560.1)		F:GO:0003779	F:actin binding	IPR011684 (PFAM): mobidb-lite (MOB	0,572	0,232	3,694	6,067	3,344					0,724	0,032			up
Solyc11g010650	nicotinamidase 1 (AHRD V3.3 *** AT2G22570.1)		F:GO:0003824	F:catalytic activity	IPR036380 (G3DSA:3.40.50.GENE3D	2,517	1,706	2,749	2,652	2,887									
Solyc11g010660	protein SGT1		C:GO:0005634	C:nucleus	IPR010770 (PFAM): mobidb-lite (MOB	73,432	64,821	94,152	90,872	97,232									
Solyc11g010670	LOW QUALITY:SGNH hydrolase-type esterase superfamily protein isoform 1 (AHRD V3.3 --* A0A061GDU5_THECC)					23,764	20,722	2,989	7,242	4,991					1,273	0,001			up
Solyc11g010680	V-type proton ATPase subunit a (AHRD V3.3 --* Q8GUB1_MESCR)				mobidb-lite (MOBIDB_LITE)	12,165	11,986	17,881	15,259	15,219									
Solyc11g010690	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *-* A0A072TRH3_MEDTR)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmem	IPR006043 (PFAM): mobidb-lite (MOB	16,441	11,285	2,849	2,845	3,328									
Solyc11g010700	Kinase family protein (AHRD V3.3 *** D7MTZ0_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): G3DSA:1.10.510	7,442	6,284	5,417	5,083	6,106									
Solyc11g010710	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7JWC7_MEDTR)		F:GO:0003677; F:GO	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN AP2	3,785	4,063	26,500	40,109	22,694					0,604	0,010			up
Solyc11g010720	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G65520.1)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	6,382	6,321	10,172	9,049	8,154									
Solyc11g010730	Protein kinase family protein (AHRD V3.3 *** F4KI00_ARATH)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): G3DSA:3.30.200	5,854	4,257	10,960	13,473	13,573									
Solyc11g010740	Glycosyltransferase (AHRD V3.3 *** K4D5N3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): IPR0	0,037	0,165	0,050	0,000	0,000									
Solyc11g010750	Glycosyltransferase (AHRD V3.3 *-* K4D5N3_SOLLC)		C:GO:0016021; C:GO	C:integral component of membrane; C:intracellular membrane-bo	G3DSA:3.40.50.2000 (GENE3D): PTH	0,021	0,062	0,075	0,022	0,046									
Solyc11g010760	Glycosyltransferase (AHRD V3.3 *** K4D5N3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	1,837	2,534	0,853	1,585	1,290									
Solyc11g010780	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	1,803	2,253	0,370	0,616	0,492									
Solyc11g010790	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	IPR002213 (PFAM): G3DSA:3.40.50.2	10,637	4,886	0,144	0,457	0,328	-1,095	0,002					down		
Solyc11g010810	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	32,808	26,305	1,809	1,366	2,696									

Solyc11g010840	RNA-binding KH domain protein (AHRD V3.3 *** G7JV44_MEDTR)		F:GO:0003723	F:RNA binding			IPR036612 (G3DSA:3.30.1370.GENE	32,871	27,997	46,073	41,168	38,406									
Solyc11g010850	1-deoxy-D-xylulose 5-phosphate synthase (AHRD V3.3 *** B6E973_STERE)	DXS2	F:GO:0008661; P:G	F:1-deoxy-D-xylulos	EC:2.2.1.7	1-deoxy-D-xylulose-5	IPR005477 (PFAM): IPR005477 (TIGF	3,774	2,153	1,445	0,888	1,076									
Solyc11g010860	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G74620.1)		F:GO:0008270; F:G	F:zinc ion binding; F:ligase activity; F:metal ion binding			IPR001841 (PFAM): IPR013083 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc11g010870	chromatin remodeling factor CHD3 (PICKLE) (AHRD V3.3 --* AT2G25170.4)							10,745	8,610	6,160	6,958	5,980									
Solyc11g010880	global transcription factor group E4 (AHRD V3.3 --* AT1G06230.4)		F:GO:0005388; P:G	F:calcium-transporting ATPase activity; P:calcium ion transmem			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,214	0,162	0,071	0,067	0,142									
Solyc11g010895	Exostosin family protein (AHRD V3.3 *** AT4G38040.1)		P:GO:0006486; F:G	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): PTHR11062:SF6	15,202	13,288	10,435	8,131	9,573									
Solyc11g010900	tRNA/rRNA methyltransferase family protein (AHRD V3.3 *** D7M9L1_ARALL)		F:GO:0003723; P:G	F:RNA binding; P:RNA processing; F:RNA methyltransferase ac			IPR029064 (G3DSA:3.30.1330.GENE	1,058	2,113	1,032	1,257	2,304			1,145	0,010				up	
Solyc11g010910	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT4G29860.1)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	3,884	4,450	5,088	4,440	4,957									
Solyc11g010915	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G29860.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	3,924	4,218	5,706	5,782	5,931									
Solyc11g010920	Kinesin-like protein (AHRD V3.3 *** A0A061DHI4_THECC)		F:GO:0003777; F:G	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	3,738	3,361	0,549	0,536	0,560									
Solyc11g010930	HVA22-like protein (AHRD V3.3 *** M1BBW7_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004345 (PFAM): mobidb-lite (MOB	5,233	4,590	4,935	5,535	3,895									
Solyc11g010940	Dof zinc finger protein (AHRD V3.3 *** W9T134_9ROSA)		F:GO:0003677; P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	0,974	0,806	0,025	0,098	0,000									
Solyc11g010950	Elongator complex 4 (AHRD V3.3 *** A0A0B0P040_GOSAR)		P:GO:0002098; C:G	P:tRNA wobble uridine modification; C:Elongator holoenzyme co			IPR008728 (PFAM): G3DSA:3.40.50.3	17,221	16,039	23,992	22,499	21,786									
Solyc11g010960	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9T7R7_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): G3DSA:3.40.50.7	16,718	11,010	0,094	0,050	0,094									
Solyc11g010990	Alcohol dehydrogenase, C-terminal (AHRD V3.3 *** A0A103YGD7_CYNCS)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): IPR0	0,040	0,039	0,000	0,000	0,047									
Solyc11g011000	Cysteine-rich repeat secretory protein 60 (AHRD V3.3 *** A0A061EEI8_THECC)		C:GO:0009506; C:G	C:plasmodesma; C:integral component of membrane			IPR002902 (PFAM): IPR038408 (G3D	0,877	0,665	0,046	0,025	0,023									
Solyc11g011010	LOW QUALITY:B-cell receptor-associated-like protein (AHRD V3.3 *** AT5G17190.1)		C:GO:0005783; P:G	C:endoplasmic reticulum; P:intracellular protein transport; C:inte			PTHR12701:SF12 (PANTHER): IPR00	14,859	14,709	4,813	4,011	4,846									
Solyc11g011020	Ovary receptor kinase 11 (AHRD V3.3 *** S4WG09_SOLCH)		F:GO:0004672; F:G	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR000719 (PFAM): IPR013210 (PFA	35,634	22,316	9,770	10,811	10,924									
Solyc11g011030	Pto-responsive gene 1		C:GO:0005634; P:G	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (PFAM): IPR018467 (PFA	0,466	2,506	0,125	0,073	0,191	2,408	0,000					up		
Solyc11g011040	ADP-ribosylation factor, putative (AHRD V3.3 *** B9SYE9_RICCO)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS): G3DSA:3.40.50	27,906	30,174	25,301	24,450	23,433									
Solyc11g011050	R2R3MYB transcription factor 43	R2R3MYB43/THM16	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	1,616	0,449	0,497	0,721	0,750									
Solyc11g011060	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT5G17680.1)		F:GO:0005515; P:G	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	47,785	39,551	36,344	52,752	45,558					0,537	0,011			up
Solyc11g011070	Sensory neuron membrane protein 2 (AHRD V3.3 *-* A0A1D1XJW9_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	11,666	14,172	8,345	7,364	10,705									
Solyc11g011080	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		F:GO:0005515; P:G	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	20,478	32,030	11,919	13,659	15,564									
Solyc11g011085	Ubiquitin carboxyl-terminal hydrolase-related protein (AHRD V3.3 --* AT1G65130.5)		F:GO:0016787	F:hydrolase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,503	4,522	8,643	8,904	5,227									
Solyc11g011100	LOW QUALITY:FAF-like protein (DUF3049) (AHRD V3.3 --* AT5G22090.2)		C:GO:0016020; C:G	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,938	1,391	0,320	0,375	0,516									
Solyc11g011110	GDSL esterase/lipase (AHRD V3.3 *** W9S179_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	0,175	0,081	0,652	1,026	0,731									
Solyc11g011120	Calmodulin-binding heat-shock protein (AHRD V3.3 *** Q41251_TOBAC)		P:GO:0016042	P:lipid catabolic process			IPR029058 (G3DSA:3.40.50.GENE3D	35,567	36,454	36,725	45,905	36,426									
Solyc11g011130	RNA-binding family protein (AHRD V3.3 *** A0A061ET42_THECC)		F:GO:0003676	F:nucleic acid binding			IPR025715 (PFAM): IPR000504 (PFA	51,803	113,446	70,899	71,564	76,225	1,157	0,000					up		
Solyc11g011140	Ribosomal protein L23 family protein (AHRD V3.3 *** Q38HS8_SOLTU)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR013025 (PFAM): IPR012677 (G3D	20,270	24,849	23,155	22,876	23,012									
Solyc11g011150	DNA repair protein xp-C / rad4, putative (AHRD V3.3 *** B9T0Z6_RICCO)		F:GO:0003684; C:G	F:damaged DNA binding; C:nucleus; P:nucleotide-excision repai			IPR018328 (PFAM): IPR002931 (PFA	14,893	11,202	18,037	18,809	16,662									
Solyc11g011160	HMG-Y-related A (AHRD V3.3 *** A0A0B0M969_GOSAR)		C:GO:0000786; F:G	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem			IPR000116 (PRINTS): IPR017956 (PF	2,320	2,562	3,207	4,425	4,017									
Solyc11g011170	Senescence-associated protein (AHRD V3.3 *** Q9AXU3_IPOBA)		C:GO:0009507; P:G	C:chloroplast; P:leaf senescence; P:cellular response to oxidati			mobidb-lite (MOBIDB_LITE): PTHR367	36,920	34,402	50,930	53,757	56,870									
Solyc11g011180	Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *** G7JP58_MEDTR)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	1,778	6,619	1,272	1,767	1,923									
Solyc11g011190	LOW QUALITY:Exostosin-like protein (AHRD V3.3 *** A0A118K5Z5_CYNCS)		P:GO:0006486; F:G	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): PTHR11062:SF1	29,202	27,076	9,690	10,947	9,990									
Solyc11g011200	Post-GPI attachment-like factor-protein (AHRD V3.3 *** A0A072UAB4_MEDTR)		C:GO:0000139; P:G	C:Golgi membrane; P:GPI anchor biosynthetic process; C:integ			IPR007217 (PFAM): PTHR13148:SF5	21,088	20,996	36,153	36,878	33,922									
Solyc11g011210	Gibberellin-regulated family protein (AHRD V3.3 *** AT1G74670.1)		C:GO:0005576; C:G	C:extracellular region; C:integral component of membrane			IPR003854 (PFAM): PTHR23201 (PAN	2,380	4,136	113,478	186,666	93,977									
Solyc11g011220	Transmembrane protein (AHRD V3.3 *** A0A0B0N9X1_GOSAR)		C:GO:0005634; C:G	C:nucleus; C:vacuolar membrane; C:endoplasmic reticulum; C:C			IPR019308 (PFAM): mobidb-lite (MOB	150,466	131,209	137,243	116,271	119,068									
Solyc11g011250	dehydroascorbate reductase 2	DHAR5	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	29,957	43,212	45,311	47,393	56,298	0,556	0,029					up		
Solyc11g011260	GAI	GRAS	F:GO:0003712; C:G	F:transcription coregulator activity; C:nucleus			IPR038088 (G3DS GRAS	66,731	67,524	49,092	43,086	44,117									
Solyc11g011285	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09890.4)		F:GO:0003824; P:G	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR010325 (PFAM): IPR029411 (PFA	0,042	0,019	0,000	0,000	0,000									
Solyc11g011300	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT2G22620.3)		F:GO:0003824; P:G	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR029411 (PFAM): IPR029413 (PFA	5,381	5,923	37,677	52,005	37,173									
Solyc11g011310	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT2G22620.2)		F:GO:0003824; P:G	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR029413 (PFAM): IPR010325 (PFA	1,161	1,354	0,271	0,124	0,024									
Solyc11g011330	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9T7R7_RICCO)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.40.50.720 (GENE3D): IPR0	0,079	1,164	0,119	0,337	0,563									
Solyc11g011340	cultivar Rio Grande ELI3	eli3	P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): IPR0	0,119	0,584	0,716	1,024	1,339									
Solyc11g011350	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		F:GO:0005515; P:G	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR000157 (PFA	1,061	0,885	0,407	1,062	0,756									
Solyc11g011360	Nudix hydrolase-like protein (AHRD V3.3 *** G7J9C3_MEDTR)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D): IPR00	0,042	0,237	0,000	0,000	0,000									
Solyc11g011370	Condensin complex subunit 3 (AHRD V3.3 *** A0A0B0N462_GOSAR)		C:GO:0000796; P:G	C:condensin complex; P:mitotic chromosome condensation			IPR011989 (G3DSA:1.25.10.GENE3D	5,743	4,957	1,840	1,051	1,080									
Solyc11g011380	glutamine synthetase	gs1	F:GO:0004356; P:G	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetase	IPR008147 (PFAM): IPR036651 (G3D	17,533	17,409	57,749	75,042	52,795					0,381	0,047			up
Solyc11g011390	Glutamine synthetase (AHRD V3.3 *-* GLNA_NICPL)		F:GO:0004356; F:G	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetase	IPR011990 (G3DSA:1.25.40.GENE3D	26,960	24,541	40,576	36,241	35,320									
Solyc11g011400	Linoleate 9S-lipoxygenase (AHRD V3.3 --* LOXB_PHAVU)							11,270	8,424	17,650	10,664	11,524			-0,615	0,036	-0,721	0,023		down	down
Solyc11g011410	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** U5FHA0_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	12,348	9,339	12,471	11,404	11,058									
Solyc11g011420	Peptidyl-prolyl cis-trans isomerase PASTICCINO1 (AHRD V3.3 *** A0A0B2Q6Q1_GLYSO)		F:GO:0005515; P:G	F:protein binding; P:cell differentiation; P:very long-chain fatty a			G3DSA:3.10.50.40 (GENE3D): G3DS	55,941	53,967	84,256	73,686	77,643									
Solyc11g011430	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:G	F:ATP binding; C:chloroplast			IPR008543 (PFAM): IPR008543 (PAN	0,000	0,000	0,000	0,000	0,023									
Solyc11g011440	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G66180.1)		F:GO:0004190; P:G	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS): IPR032799 (PF	42,180	31,652	47,414	28,124	25,219			-0,913	0,001	-0,753	0,009		down	down
Solyc11g011450	Centromere protein V (AHRD V3.3 *** W9RKQ0_9ROSA)		F:GO:0016846	F:carbon-sulfur lyase activity			IPR006913 (PFAM): G3DSA:2.170.15	2,357	2,293	4,877	5,118	3,983									
Solyc11g011460	ATP-dependent RNA helicase (AHRD V3.3 *** AT5G39840.1)		F:GO:0016817	F:hydrolase activity, acting on acid anhydrides			G3DSA:3.40.50.300 (GENE3D): G3DS	11,711	11,133	12,294	12,563	12,259									
Solyc11g011470	NADH-ubiquinone dehydrogenase (AHRD V3.3 *** AT5G37510.1)		F:GO:0009055; F:G	F:electron transfer activity; F:oxidoreductase activity, acting on			IPR006656 (PFAM): G3DSA:3.40.50.7	245,556	211,423	324,891	276,992	300,136									
Solyc11g011480	Nicastrin-related family protein (AHRD V3.3 *** B9H3E1_POPTR)		C:GO:0016021; P:G	C:integral component of membrane; P:protein processing			IPR008710 (PFAM): IPR041084 (PFA	36,936	35,461	57,116	59,807	58,720									
Solyc11g011490	Zinc finger protein 830 family (AHRD V3.3 *** A0A151S1W8_CAJCA)		F:GO:0003676; C:G	F:nucleic acid binding; C:spliceosomal complex; F:zinc ion bindi			PF12874 (PFAM): mobidb-lite (MOBID	18,323	17,741	17,036	16,997	18,090									
Solyc11g011504	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** A0A072TU20_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,712	0,561	0,233	0,116	0,094									
Solyc11g011506	uridine kinase-like 5 (AHRD V3.3 --* AT3G27440.3)							0,570	0,276	0,192	0,166	0,212									
Solyc11g011508	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)						IPR032675 (G3DSA:3.80.10.GENE3D	2,058	2,085	1,168	1,398	1,320									
Solyc11g011510	LOW QUALITY:OSBP(oxysterol binding protein)-related protein 1D (AHRD V3.3 --* AT1G13170.2)							0,196	0,195	0,143	0,025	0,095									
Solyc11g011530	F-box family protein (AHRD V3.3 --* B9HWR1_POPTR)							0,706	0,380	0,507	0,795	0,471									
Solyc11g011535	D-arabinono-1,4-lactone oxidase family protein (AHRD V3.3 --* AT1G32300.1)							3,613	2,918	3,598	3,307	3,632									
Solyc11g011540	F-box/RNI/FBD-like domain protein (AHRD V3.3 *** A0A072TJJ6_MEDTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	7,592	7,292	6,573	7,447	7,249									
Solyc11g011542	F-box family protein (AHRD V3.3 --* D7KQH0_ARALL)						mobidb-lite (MOBIDB_LITE): PTHR444	4,238	3,877	4,805	5,488	4,404									
Solyc11g011544	zinc finger FYVE domain protein, putative (DUF1666) (AHRD V3.3 --* AT1G69610.3)							0,555	0,301	0,335	0,435	0,354									
Solyc11g011546	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): IPR032675 (G3D	4,764	3,860	3,484	3,540	3,061									
Solyc11g011548	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	5,594	5,666	4,226	3,887	3,973									
Solyc11g011570	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		F:GO:0008270; C:G	F:zinc ion binding; C:endomembrane system; P:protein ubiquitin			IPR013083 (G3DSA:3.30.40.GENE3D	0,248	0,202	0,047	0,073	0,000									
Solyc11g011580	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)						IPR011993 (G3DSA:2.30.29.GENE3D	1,925	1,620	1,166	1,535	1,298									
Solyc11g011590	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)						IPR011993 (G3DSA:2.30.29.GENE3D	1,353	1,414	0,381	0,764	0,566									
Solyc11g011600	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** AT5G23350.1)						IPR011993 (G3DSA:2.30.29.GENE3D	0,377	0,318	0,051	0,047	0,070									
Solyc11g011605	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175:SF2	2,932	5,764	9,827	11,289	10,399									
Solyc11g011610	UPF0678 fatty acid-binding protein-like protein family (AHRD V3.3 *** A0A151RPZ2_CAJCA)						IPR012674 (G3DSA:2.40.128.GENE3	36,045	47,422	61,392	67,047	58,640									
Solyc11g011615	LOW QUALITY:SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): mobidb-lite (MOB	0,082	0,060	0,279	0,249	0,280									
Solyc11g011620	UPF0678 fatty acid-binding protein-like protein (AHRD V3.3 *** A0A0B2QJ30_GLYSO)						IPR014878 (PFAM): IPR012674 (G3D	2,789	3,933	3,454	3,271	3,730									
Solyc11g011630	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31175:SF2	0,927	0,476	0,270	0,257	0,237									
Solyc11g011650	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT2G21210.2)		P:GO:0009733	P:response to auxin			IPR003676 (PFAM): PTHR31929 (PAN	0,021	0,000	0,025	0,048	0,023									
Solyc11g011740	Ethylene-responsive transcription factor (AHRD V3.3 *** F2Y9E9_COFAR)		F:GO:0003677; F:G	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,077	0,118	0,000	0,000	0,047									
Solyc11g011750	Ethylene-responsive transcription factor (AHRD V3.3 *** F1DGA5_COFAR)		F:GO:0003677; F:G	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,021	0,000	0,151	0,022	0,023									
Solyc11g011760	NAD(P)H-quinone oxidoreductase subunit 6, chloroplastic (AHRD V3.3 --* R4PTT2_UTRGI)		C:GO:0005783; C:G	C:endoplasmic reticulum; C:integral component of membrane			PTHR35508 (PANTHER)	116,515	86,420	57,537	48,162	50,721									
Solyc11g011770	Myb family transcription factor-like protein (AHRD V3.3 *** A0A0K9Q0J8_ZOSMR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6 G2-like	7,743	3,594	6,428	7,472	6,688	-1,080	0,002					down		
Solyc11g011780	Nonsense-mediated mRNA decay NMD3 family protein (AHRD V3.3 *** B9H0C6_POPTR)		F:GO:0043023	F:ribosomal large subunit binding			IPR007064 (PFAM): IPR039768 (PAN	0,082	0,054	0,022	0,076	0,024									
Solyc11g011790	Importin-5 (AHRD V3.3 *-* A0A0B2PAL2_GLYSO)		P:GO:0006606	P:protein import into nucleus			IPR011989 (G3DSA:1.25.10.GENE3D	0,240	0,138	0,171	0,461	0,307									
Solyc11g011800	Importin-5 (AHRD V3.3 *** A0A1D1XN17_9ARAE)		F:GO:0005515; P:G	F:protein binding; P:protein import into nucleus			IPR000357 (PFAM): IPR041653 (PFA	1,268	0,949	1,586	1,958	1,844									
Solyc11g011820	Oxidoreductase, putative (AHRD V3.3 *** B9T5L5_RICCO)		F:GO:0016491	F:oxidoreductase activity			G3DSA:3.30.360.10 (GENE3D): G3DS	0,077	0,104	0,172	0,072	0,211									
Solyc11g011840	Oxidoreductase, putative (AHRD V3.3 *** B9T5L5_RICCO)		F:GO:0016491	F:oxidoreductase activity			IPR000683 (PFAM): G3DSA:3.40.50.7	8,352	7,273	14,521	15,364	18,137									
Solyc11g011850	glycosyltransferase	pglcat8	F:GO:0015018; C:G	F:galactosylgalacto	EC:2.4.1.17; EC:2.4.	Glucuronosyltransfer	IPR029044 (G3DSA:3.90.550.GENE3	56,211	47,485	60,698	69,532	63,880									
Solyc11g011860	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151RGT3_CAJCA)		F:GO:0005515; F:G	F:protein binding; F:zinc ion binding			IPR032867 (PFAM): IPR002885 (PFA	1,653	2,451	6,377	5,319	6,347									
Solyc11g011870	Receptor-like protein kinase (AHRD V3.3 *** C6ZS18_SOYBN)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): IPR000719 (F	0,402	0,527	0,438	0,468	0,497									
Solyc11g011873	Protein phosphatase 2C family protein (AHRD V3.3 --* AT5G57050.2)							1,477	2,614	1,012	0,732	0,919									
Solyc11g011875	Protein kinase (AHRD V3.3 *-* A9CM11_IPONI)		F:GO:0004674; C:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	G3DSA:3.30.200.20 (GENE3D): PTHR	0,589	0,706	0,616	0,756	0,942									
Solyc11g011877	Cysteine-rich RLK (Receptor-like kinase) protein (AHRD V3.3 *-* G7J7V4_MEDTR)		F:GO:0004674; F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR002902 (PFAM): IPR038408 (G3D	0,059	0,077	0,096	0,246	0,142									
Solyc11g011880	Protein kinase (AHRD V3.3 *** A9CM11_IPONI)		F:GO:0004672; F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR038408 (G3DSA:3.30.430.GENE3	4,661	5,615	4,493	5,151	6,877									
Solyc11g011890	Zinc finger protein, putative (AHRD V3.3 *** B9T5L7_RICCO)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	3,954	4,234	0,319	0,098	0,282									
Solyc11g011910	Transmembrane 9 superfamily member (AHRD V3.3 *** K4D5Z6_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): IPR004240 (PAN	116,878	103,917	118,498	128,827	113,154									
Solyc11g011920	Glutamate decarboxylase (AHRD V3.3 *** B1Q3F1_SOLLC)		F:GO:0004351; P:G	F:glutamate decarb	EC:4.1.1.15	Glutamate decarboxy	IPR010107 (TIGRFAM): IPR015421 (G	332,458	339,329	57,578	50,889	64,770									
Solyc11g011930	Isocitrate dehydrogenase [NADP] (AHRD V3.3 *** K4D5Z8_SOLLC)		F:GO:0004450; P:G	F:isocitrate dehydr	EC:1.1.1.42	Isocitrate dehydroge	IPR024084 (PFAM): G3DSA:3.40.718	60,259	57,312	244,401	230,534	210,053									
Solyc11g011940	Homeobox-leucine zipper family protein (AHRD V3.3 *-* B9N3B2_POPTR)		F:GO:0003677; F:G	F:DNA binding; F:lipid binding			IPR002913 (PFAM HD-ZIP	0,384	0,806	0,140	0,662	0,490									
Solyc11g011960	UDP-GLUCOSE PYROPHOSPHORYLASE 1 (AHRD V3.3 *** AT3G03250.1)		F:GO:0003983; P:G	F:UTP:glucose-1-ph	EC:2.7.7.64; EC:2.7.	UTP-monosaccharide	IPR029044 (G3DSA:3.90.550.GENE3	727,465	658,928	273,641	234,941	260,419									
Solyc11g011970	Tyrosine-protein phosphatase (AHRD V3.3 *** R9Q9C6_FRAVE)		F:GO:0016791	F:phosphatase activity			IPR020428 (PRINTS): IPR029021 (G3	42,871	32,835	35,246	33,723	30,832									
Solyc11g011980	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G32950.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	4,831	4,375	2,610	2,316	4,662			0,834	0,012				up	
Solyc11g011990	plastid terminal oxidase	ptox	F:GO:0009916; P:G	F:alternative oxidas	EC:1.1.3	Acting on diphenols a	IPR002680 (PFAM): IPR038659 (G3D	22,105	27,990	125,409	117,078	117,952									
Solyc11g012000	extracellular ligand-gated ion channel protein (DUF3537) (AHRD V3.3 *** AT3G20300.1)		C:GO:0016021	C:integral component of membrane			IPR021924 (PFAM): IPR021924 (PAN	8,306	5,261	12,262	10,685	10,303									
Solyc11g012020	EH domain-containing protein 1 (AHRD V3.3 *** A0A1D1YR31_9ARAE)		F:GO:0005509; F:G	F:calcium ion binding; F:protein binding; F:GTP binding			IPR040990 (PFAM): IPR022812 (PFA	0,819	1,250	0,093	0,099	0,212									
Solyc11g012030	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** A0A072USM3_MEDTR)		F:GO:0004553; P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (PFAM): G3DSA:3.20.20.8	0,021	0,019	0,000	0,000	0,000									
Solyc11g012040	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *** AT4G22290.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	9,871	5,993	0,268	0,075	0,399									
Solyc11g012050	MAP kinase kinase kinase 81	MAPKKK81	F:GO:0004674; F:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR001245 (PRINTS): IPR001245 (PF	1,279	1,007	0,509	0,547	0,355									
Solyc11g012060	Protein F12F1.11-, putative (AHRD V3.3 *** Q2HVF3_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	6,451	5,209	3,406	3,453	3,669									
Solyc11g012070	Acyl-protein thioesterase, putative (AHRD V3.3 *** G7JKH0_MEDTR)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	11,875	14,612	7,641	8,507	11,126									
Solyc11g012080	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4D613_SOLLC)		C:GO:0005743; P:G	C:mitochondrial inner membrane; P:mitochondrial pyruvate trans			IPR005336 (PFAM): PTHR14154 (PAN	34,282	34,500	63,734	68,058	61,973									
Solyc11g012090	Autophagy-related protein 9 (AHRD V3.3 *** A0A1D1ZI98_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,247	2,623	2,434	1,960	1,975									
Solyc11g012100	Phosphoribosylglycinamide formyltransferase (AHRD V3.3 *** W9SAR2_9ROSA)		F:GO:0004644; P:G	F:phosphoribosylgly	EC:2.1.2.2	Phosphoribosylglycin	G3DSA:3.40.50.170 (GENE3D): IPR0	9,290	10,006	12,762	13,451	12,397									
Solyc11g012110	60S ribosomal protein L6 (AHRD V3.3 *** RL6_MESCR)		F:GO:0003735; C:G	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000915 (PFAM): IPR014722 (G3D	177,853	190,793	135,737	129,280	126,785									
Solyc11g012120	DUF506 family protein (AHRD V3.3 *** G7JKH5_MEDTR)		C:GO:0009522; P:G	C:photosystem I; P:photosynthesis; C:integral component of me			IPR006502 (PFAM): IPR006502 (TIGF	0,075	0,043	0,047	0,094	0,023									
Solyc11g012130	Blue copper protein (AHRD V3.3 *** A0A0B2RLQ3_GLYSO)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	0,260	0,326	0,050	0,050	0,024									
Solyc11g012140	Isoleucyl-tRNA synthetase family protein (AHRD V3.3 *** B9HH75_POPTR)		F:GO:0000049; F:G	F:tRNA binding; F:a	EC:6.1.1.5; EC:3.1.1	Isoleucine--tRNA liga	IPR002301 (PRINTS): IPR002301 (TI	280,049	237,739	213,581	199,605	220,044									
Solyc11g012150	Transcription initiation factor IIF alpha subunit family protein (AHRD V3.3 *** B9HCF8_POPTR)		F:GO:0003677; C:G	F:DNA binding; C:nucleus; P:transcription initiation from RNA po			IPR013083 (G3DSA:3.30.40.GENE3D	53,578	50,232	132,833	128,300	120,821									
Solyc11g012160	fumarylacetoacetase (AHRD V3.3 *** AT1G12050.1)		F:GO:0004334; P:G	F:fumarylacetoacet	EC:3.7.1.2	Fumarylacetoacetase	IPR011234 (PFAM): IPR005959 (TIGF	131,457	104,418	290,871	289,736	292,295									
Solyc11g012180	Acyl carrier protein (AHRD V3.3 *** K4D623_SOLLC)		P:GO:0006633	P:fatty acid biosynthetic process			IPR003231 (TIGRFAM): IPR036736 (G	5,190	6,728	6,752	6,203	7,230									
Solyc11g012190	Mannan endo-1,4-beta-mannosidase 1 (AHRD V3.3 *** MAN1_ORYSJ)		F:GO:0004553; P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	11,813	12,599	3,502	2,643	4,257									
Solyc11g012195	DNA-directed RNA polymerase (AHRD V3.3 *** G7KSV3_MEDTR)		P:GO:0006351; F:G	P:transcription, DNA-templated; F:protein dimerization activity			IPR009025 (PFAM): IPR036603 (G3D	0,587	0,613	0,361	0,409	0,635									
Solyc11g012200	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55340.1)		F:GO:0008374	F:O-acyltransferase activity			IPR017088 (PIRSF): IPR032805 (PFA	0,176	0,201	0,000	0,000	0,000									
Solyc11g012220	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55340.1)		F:GO:0008374	F:O-acyltransferase activity			IPR032805 (PFAM): IPR017088 (PIRS	0,000	0,105	0,000	0,022	0,023									
Solyc11g012230	QWRF motif protein (DUF566) (AHRD V3.3 --* AT2G20815.4)							0,000	0,083	0,047	0,000	0,023									
Solyc11g012240	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55350.1)		F:GO:0008374	F:O-acyltransferase activity			IPR032805 (PFAM): IPR017088 (PIRS	0,061	0,158	0,099	0,050	0,142									
Solyc11g012250	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** Q2HT39_MEDTR)		F:GO:0008374	F:O-acyltransferase activity			IPR032805 (PFAM): IPR017088 (PIRS	0,000	0,039	0,000	0,000	0,024									
Solyc11g012260	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** Q2HT39_MEDTR)		F:GO:0008374; C:G	F:O-acyltransferase activity; C:integral component of membrane			IPR032805 (PFAM): PTHR31595:SF1	10,742	13,426	29,536	30,905	32,337									
Solyc11g012270	Rho GDP-dissociation inhibitor 1 (AHRD V3.3 *** A0A151S024_CAJCA)		F:GO:0005094; C:G	F:Rho GDP-dissociation inhibitor activity; C:cytoplasm			IPR000406 (PRINTS): IPR024792 (G3	7,343	7,501	2,717	2,626	3,291									
Solyc11g012280	Sulfate adenylyltransferase subunit 2 (AHRD V3.3 *** A0A061GG86_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR363	53,572	52,553	55,750	48,384	53,036									
Solyc11g012290	Upstream activation factor subunit spp27 (AHRD V3.3 *** W9QUP5_9ROSA)		F:GO:0005515	F:protein binding			IPR003121 (PFAM): IPR036885 (G3D	16,221	13,583	15,296	14,162	14,034									
Solyc11g012310	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT4G22370.2)		C:GO:0016021	C:integral component of membrane			PTHR33698:SF2 (PANTHER): PTHR3	0,040	0,059	2,040	0,716	2,537					-1,500	0,007			down
Solyc11g012320	SKP1-like 12 (AHRD V3.3 --* AT4G34470.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4824,420	4032,319	9496,528	8034,947	8196,056									
Solyc11g012330	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842	F:ubiquitin-protein transferase activity			G3DSA:3.90.1750.10 (GENE3D): G3D	0,037	0,000	0,025	0,000	0,000									
Solyc11g012360	Tonoplast dicarboxylate transporter (AHRD V3.3 *** K4D641_SOLLC)		F:GO:0005215; P:G	F:transporter activity; P:sodium ion transport; C:membrane; P:tr			IPR001898 (PFAM): IPR001898 (TIGF	2,213	2,991	16,207	10,761	14,380									
Solyc11g012370	LOW QUALITY:Cysteine proteinase inhibitor (AHRD V3.3 --* A0A075F939_TOBAC)		F:GO:0004869; P:G	F:cysteine-type endopeptidase inhibitor activity; P:proteolysis; I			G3DSA:3.10.450.10 (GENE3D): SSF5	3,200	4,958	0,000	0,000	0,000									
Solyc11g012375	LOW QUALITY:Cysteine proteinase inhibitor (AHRD V3.3 *** M1B0W4_SOLTU)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			G3DSA:3.10.450.10 (GENE3D): IPR0	0,000	0,018	0,000	0,000	0,000									
Solyc11g012400	Calcium-binding protein, putative (AHRD V3.3 *** B9T038_RICCO)		F:GO:0004674; P:G	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR011989 (G3DSA:1.25.10.GENE3D	51,689	51,623	64,754	68,196	62,173									

Solyc11g012410	myo-inositol monophosphatase 3	U39059	F:GO:0008934; P:G(	F:inositol monophos	EC:3.1.3.25	Inositol-phosphate ph	IPR000760 (PRINTS); IPR020552 (PF	35,097	35,986	115,199	108,912	103,198									
Solyc11g012420	Auxin induced-like protein (AHRD V3.3 *** A0A0K9NX81_ZOSMR)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR017214 (PIRSF); IPR005018 (PFA	0,000	0,036	0,000	0,070	0,024									
Solyc11g012440	LOW QUALITY:U-box domain-containing protein 4 (AHRD V3.3 *** W9R7F2_9ROSA)		F:GO:0005515	F:protein binding			IPR011989 (G3DSA:1.25.10.GENE3D	67,992	57,948	72,407	67,228	76,525									
Solyc11g012450	Inositol transporter 4	INT4	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); IPR003663 (TI(	29,034	33,804	25,172	30,167	37,620			0,575	0,007				up	
Solyc11g012455	Ornithine aminotransferase (AHRD V3.3 --* OAT_VIGAC)							8,158	5,105	6,099	6,378	6,171									
Solyc11g012460	RAB GTPase homolog A5A (AHRD V3.3 *** AT5G47520.1)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS); G3DSA:3.40.50.3	19,545	14,684	18,265	16,180	15,857									
Solyc11g012470	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	66,573	55,691	69,158	69,003	64,285									
Solyc11g012475	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K094_CYNCS)		F:GO:0004797; F:G(	F:thymidine kinase a	EC:2.7.1.145; EC:2.7	Deoxynucleoside kin	IPR011990 (G3DSA:1.25.40.GENE3D	3,720	4,034	6,876	6,085	7,143									
Solyc11g012480	Thymidine kinase (AHRD V3.3 *** K4D652_SOLLC)		F:GO:0004797; F:G(	F:thymidine kinase a	EC:2.7.1.145; EC:2.7	Deoxynucleoside kin	IPR001267 (PFAM); G3DSA:3.30.60.2	5,804	6,355	10,518	8,935	10,156									
Solyc11g012490	dynamin-like protein (AHRD V3.3 --* AT5G42080.4)							0,061	0,062	0,074	0,022	0,047									
Solyc11g012500	zinc finger CCCH domain protein (AHRD V3.3 *** AT4G16460.3)							0,021	0,690	0,171	0,050	0,048									
Solyc11g012510	GRAS1	GRAS1	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	118,215	115,577	22,916	24,974	34,243									
Solyc11g012520	LOW QUALITY:Interleukin-1 receptor-associated kinase 4 protein (AHRD V3.3 --* AT5G11360.3)						PTHR34570 (PANTHER); PTHR34570	0,202	0,101	0,047	0,000	0,023									
Solyc11g012530	Phosphoglycerate mutase-like family protein (AHRD V3.3 --* AT3G01310.3)							1,488	1,178	1,268	1,380	1,465									
Solyc11g012540	F-box family protein (AHRD V3.3 *** A0A061EN61_THECC)		F:GO:0005515	F:protein binding			IPR017451 (TIGRFAM); G3DSA:1.20.1	5,697	4,153	4,993	6,000	4,734									
Solyc11g012550	F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D); IPR(	9,639	10,065	8,585	8,718	9,112									
Solyc11g012560	F-box family protein (AHRD V3.3 *** A0A061EN61_THECC)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); G3DSA:1.20.128	0,616	0,534	0,679	0,381	0,543									
Solyc11g012563	Peptidyl-tRNA hydrolase II (PTH2) family protein (AHRD V3.3 --* G5DXA5_SILLA)							1,766	1,990	1,168	1,531	1,416									
Solyc11g012567	Protein kinase superfamily protein (AHRD V3.3 --* AT1G68690.4)							0,137	0,136	0,068	0,097	0,046									
Solyc11g012570	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XK68_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	1,777	2,113	1,179	1,079	1,320									
Solyc11g012580	Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 *** A0A061GP73_THECC)		C:GO:0016021	C:integral component of membrane			IPR012946 (PFAM); PTHR32227 (PAN	0,449	0,527	0,118	0,094	0,237									
Solyc11g012590	CASP-like protein (AHRD V3.3 *** M1B0Y6_SOLTU)		C:GO:0005783	C:endoplasmic reticulum			IPR010580 (PFAM); IPR006702 (PFA	0,253	0,313	0,046	0,047	0,164									
Solyc11g012610	structural maintenance of chromosomes protein (AHRD V3.3 *** AT4G17240.1)						mobidb-lite (MOBIDB_LITE); PTHR354	1,251	1,373	0,214	0,392	0,352									
Solyc11g012620	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative (AHRD V3.3 *-* A0A(		F:GO:0003682	F:chromatin binding			G3DSA:2.30.30.490 (GENE3D); PTHR	6,603	5,659	7,857	7,463	7,273									
Solyc11g012640	LOW QUALITY:Peroxiredoxin Q, chloroplastic (AHRD V3.3 *-* M8CFS7_AEGTA)		C:GO:0016021	C:integral component of membrane			IPR008470 (PFAM); PTHR36049 (PAN	0,456	1,394	0,526	0,333	0,821									
Solyc11g012650	Tapetum determinant 1 (AHRD V3.3 *** A0A061FZR9_THECC)		P:GO:0001709; C:G(	P:cell fate determination; C:membrane			IPR040361 (PANTHER); PTHR33184:	0,982	0,468	0,000	0,000	0,000									
Solyc11g012660	Microtubule-associated protein 70-5 (AHRD V3.3 *** A0A0B0MZW7_GOSAR)		P:GO:0007010; F:G(	P:cytoskeleton organization; F:microtubule binding			IPR009768 (PFAM); mobidb-lite (MOB	0,138	0,181	0,343	0,761	0,518									
Solyc11g012670	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JXR5_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	12,148	20,159	35,688	31,717	34,855	0,760	0,004					up		
Solyc11g012680	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT4G16380.1)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); mobic	14,022	13,043	3,453	4,086	5,769			0,733	0,024				up	
Solyc11g012690	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** I3STQ6_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM); G3DSA:3.30.70.1	0,654	0,576	0,196	0,390	0,332									
Solyc11g012700	oligopeptide transporter (AHRD V3.3 *** AT4G16370.1)		P:GO:0055085	P:transmembrane transport			IPR004813 (PFAM); IPR004813 (TIGF	148,546	169,131	291,430	282,932	277,304									
Solyc11g012705	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** AT5G47635.1)						PF01190 (PFAM); IPR039923 (PANTH	0,694	0,443	0,044	0,025	0,000									
Solyc11g012710	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** AT4G16360.1)		F:GO:0005515	F:protein binding			IPR032640 (PFAM); G3DSA:3.30.160.	7,495	5,010	8,121	7,890	8,162									
Solyc11g012720	Trihelix transcription factor GT-2 (AHRD V3.3 *** A0A0B2S925_GLYSO)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			G3DSA:1.10.10.60 Trihelix	7,846	6,753	11,655	8,878	8,548									
Solyc11g012730	Thioredoxin family protein (AHRD V3.3 *** Q9LSU4_ARATH)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D); IPR01:	37,145	35,284	28,721	26,038	25,932									
Solyc11g012740	Regulation of nuclear pre-mRNA domain-containing protein 1B (AHRD V3.3 *** A0A0B2S634_GLYSO)						IPR008942 (G3DSA:1.25.40.GENE3D	17,061	14,008	18,768	16,894	17,938									
Solyc11g012745	Fe superoxide dismutase 2 (AHRD V3.3 --* AT5G51100.4)						mobidb-lite (MOBIDB_LITE)	0,059	0,019	0,025	0,000	0,048									
Solyc11g012760	tRNA (guanine(9)-N1)-methyltransferase-like protein (AHRD V3.3 *** AT5G47680.1)		F:GO:0008168	F:methyltransferase activity			IPR038459 (G3DSA:3.40.1280.GENE:	12,857	13,387	16,117	13,223	13,578									
Solyc11g012770	Sister chromatid cohesion PDS5 B (AHRD V3.3 *** A0A0B0N9Z2_GOSAR)		P:GO:0007064	P:mitotic sister chromatid cohesion			G3DSA:2.30.30.140 (GENE3D); mobic	133,453	104,961	146,719	154,825	149,545									
Solyc11g012780	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G47710.4)						IPR000008 (PRINTS); IPR035892 (G3	14,109	22,658	22,551	24,355	24,928									
Solyc11g012785	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *-* AT5G55860.1)		C:GO:0005829; P:G(	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac			IPR008545 (PFAM); mobidb-lite (MOB	0,000	0,075	0,022	0,025	0,000									
Solyc11g012790	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G55840.1)						IPR036865 (G3DSA:3.40.525.GENE3I	15,844	14,936	7,933	8,143	8,083									
Solyc11g012810	Bromo-adjacent-like (BAH) domain protein (AHRD V3.3 *** G7J2X9_MEDTR)		F:GO:0003682	F:chromatin binding			IPR001025 (PFAM); G3DSA:2.30.30.4	23,070	18,869	19,002	17,999	18,807									
Solyc11g012813	ARM repeat superfamily protein (AHRD V3.3 --* AT5G27970.5)							0,040	0,059	0,025	0,022	0,000									
Solyc11g012820	Replication factor C subunit (AHRD V3.3 *** A0A0K9NM53_ZOSMR)		F:GO:0003677; F:G(	F:DNA binding; F:ATP binding; P:DNA replication			IPR000641 (PRINTS); IPR013748 (PF	21,124	20,297	24,178	22,723	23,798									
Solyc11g012830	F-box family protein (AHRD V3.3 *** D7KKU2_ARALL)		C:GO:0005634; C:G(	C:nucleus; C:mitochondrion; P:regulation of translation; P:respo			PTHR12874:SF9 (PANTHER); PTHR12	51,835	46,025	68,793	67,621	64,550									
Solyc11g012850	Chlorophyllide a oxygenase (AHRD V3.3 *** W9SD87_9ROSA)	CAO	F:GO:0010277; F:G(	F:chlorophyllide a o	EC:1.13.12; EC:1.14	Acting on single donc	IPR017941 (PFAM); IPR013626 (PFA	25,584	26,506	35,719	39,443	39,937									
Solyc11g012860	coiled-coil protein	fpp					IPR008587 (PFAM); mobidb-lite (MOB	57,853	42,975	10,195	7,208	10,255									
Solyc11g012870	lysM domain-containing protein						IPR018392 (PFAM); IPR036779 (G3D	18,818	16,541	10,663	11,631	9,758									
Solyc11g012880	EamA-like transporter family protein (AHRD V3.3 *** AT1G77610.1)		F:GO:0005459; F:G(	F:UDP-galactose transmembrane transporter activity; F:UDP-gl			IPR004853 (PFAM); mobidb-lite (MOB	0,500	0,348	0,025	0,000	0,023									
Solyc11g012890	Auxin efflux carrier component (AHRD V3.3 --* A0A075IGY3_9SPER)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane			PTHR38355 (PANTHER)	9,259	9,955	18,078	18,462	17,816									
Solyc11g012900	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT4G08320.1)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	43,429	45,858	56,155	53,894	51,364									
Solyc11g012905	Small glutamine-rich tetratricopeptide repeat-containing beta (AHRD V3.3 *-* A0A0B0N1L7_GOSAR)		P:GO:0006620; C:G(	P:posttranslational protein targeting to endoplasmic reticulum m			G3DSA:1.20.5.420 (GENE3D); IPR03:	9,119	7,886	10,687	11,423	11,551									
Solyc11g012910	Gamma-glutamylcyclotransferase (AHRD V3.3 *** K4D695_SOLLC)		F:GO:0003839; P:G(	F:gamma-glutamylc	EC:4.3.2.9	Gamma-glutamylcycl	G3DSA:3.10.490.10 (GENE3D); IPR0(	23,417	29,019	35,985	32,944	39,359									
Solyc11g012920	translation initiation factor (AHRD V3.3 *** AT1G44780.2)						IPR019098 (PFAM); mobidb-lite (MOB	26,325	25,389	29,732	31,890	29,852									
Solyc11g012930	WAT1-related protein (AHRD V3.3 *** K4D697_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM); PTHR31218:SF1:	11,320	15,376	15,569	26,614	24,835			0,667	0,002	0,775	0,002		up	up
Solyc11g012940	Glutaredoxin-like protein (AHRD V3.3 *** K4D698_SOLLC)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR008554 (PFAM); G3DSA:3.40.30.1	3,951	5,716	6,354	6,155	6,431									
Solyc11g012950	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FP05_THECC)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	0,733	2,096	0,602	0,902	0,800	1,525	0,009					up		
Solyc11g012970	Aminoacylase-1 (AHRD V3.3 *** M0ZK11_SOLTU)		F:GO:0004046; C:G(	F:aminoacylase act	EC:3.5.1.14	N-acyl-aliphatic-L-am	IPR010159 (TIGRFAM); PIRSF036696	68,855	56,131	98,351	91,366	94,448									
Solyc11g012980	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A0K9P1G2_ZOSMR)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN1 ERF	10,329	0,698	0,785	6,915	3,497	-3,847	0,000	2,109	0,000	3,083	0,000	down	up	up
Solyc11g012990	LOW QUALITY:Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT4G33905.		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM); PTHR11266:SF1:	0,019	0,000	0,000	0,000	0,000									
Solyc11g013000	Transmembrane emp24 domain-containing protein 10, putative (AHRD V3.3 *** B9RJ70_RICCO)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:endoplasmic reticulum-G			IPR009038 (PFAM); PTHR22811:SF7(	21,933	26,220	46,738	48,990	44,313									
Solyc11g013010	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 *** B9H7C8_POPTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:kinase activity; P:phosph			IPR003409 (PFAM); G3DSA:2.20.110.	13,266	8,719	10,612	7,489	9,536									
Solyc11g013020	histone-lysine N-methyltransferase (AHRD V3.3 *** AT4G08240.2)		F:GO:0008168; F:G(	F:methyltransferase activity; F:transferase activity; P:methylatio			mobidb-lite (MOBIDB_LITE); PTHR372	26,731	21,456	30,234	25,644	26,700									
Solyc11g013030	DIS3-like exonuclease 2 (AHRD V3.3 *** K4D6A7_SOLLC)		F:GO:0000175; F:G(	F:3'-5'-exoribonucle	EC:3.1.13; EC:3.1.15	Acting on ester bonds	IPR041505 (PFAM); G3DSA:2.40.50.6	35,953	40,465	39,631	41,584	38,511									
Solyc11g013050	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151U161_CAJCA)						IPR019557 (PFAM); PTHR44194 (PAN	0,000	0,036	0,000	0,000	0,000									
Solyc11g013060	Inner membrane OXA1-like protein (AHRD V3.3 --* G7KQL5_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase acti			PTHR12428:SF22 (PANTHER); IPR00	2,962	2,847	5,864	6,628	6,537									
Solyc11g013065	Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain-containing protein (AHRD V3.3		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase acti			PTHR12428:SF22 (PANTHER); IPR00	0,868	0,816	1,985	2,582	1,987									
Solyc11g013080	ALBINO3-like protein 2 (AHRD V3.3 *-* W9SEX0_9ROSA)		F:GO:0005515	F:protein binding			IPR011990 (SUPERFAMILY)	5,590	4,842	9,661	10,454	8,993									
Solyc11g013083	Serine/threonine-protein kinase (AHRD V3.3 *** M0ZK20_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); IPR0(	0,279	0,301	0,184	0,117	0,283									
Solyc11g013087	co-factor for nitrate, reductase and xanthine dehydrogenase 7 (AHRD V3.3 --* AT4G10100.3)							0,019	0,000	0,022	0,096	0,094									
Solyc11g013090	Serine/threonine-protein kinase (AHRD V3.3 *-* M0ZK20_SOLTU)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR036950 (G3DSA:1.10.3810.GENE:	0,105	0,103	0,094	0,094	0,048									
Solyc11g013100	Glycine-rich protein (AHRD V3.3 *** R4L3H8_CANWI)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:Golgi apparatus; P:calciu			IPR024491 (PFAM); mobidb-lite (MOB	73,032	71,737	182,377	176,031	168,316									
Solyc11g013110	Flavonol synthase (AHRD V3.3 *** C0LUV3_SOLTU)	FLS	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS); IPR005123 (PFA	431,133	393,436	2342,566	2521,506	2776,973									
Solyc11g013120	Camphor resistance CrcB family protein (AHRD V3.3 *** B9GUE1_POPTR)		C:GO:0016021	C:integral component of membrane			IPR003691 (PFAM); mobidb-lite (MOB	34,947	24,450	29,798	35,601	32,508									
Solyc11g013130	cysteine-rich/transmembrane domain protein A (AHRD V3.3 --* AT2G33520.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	62,487	54,243	7,728	4,754	7,733					-0,699	0,033			down
Solyc11g013150	GRAS family transcription factor (AHRD V3.3 *** A0A061FHT3_THECC)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	9,469	5,342	4,968	3,294	3,815									
Solyc11g013155	Ribosomal protein S12 (AHRD V3.3 --* A0A059LPB2_9CHLO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.50.140 (GENE3D); IPR0(	0,274	0,174	0,288	0,220	0,236									
Solyc11g013170	Aminotransferase (AHRD V3.3 *** Q67UZ0_ORYSJ)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha			IPR015421 (G3DSA:3.40.640.GENE3I	49,331	68,128	89,795	89,783	89,688									
Solyc11g013180	Phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *** B9RJA3_RICCO)		F:GO:0005524; F:G(	F:ATP binding; F:1-p	EC:2.7.1.68	1-phosphatidylinosito	IPR017163 (PIRSF); IPR027484 (G3D	59,290	56,999	37,659	40,832	37,872									
Solyc11g013190	Oxysterol-binding family protein (AHRD V3.3 *** B9GUF2_POPTR)		C:GO:0005829; F:G(	C:cytosol; F:sterol transporter activity; P:sterol transport; C:mei			PF15413 (PFAM); G3DSA:2.40.160.1:	88,086	106,881	108,196	102,217	100,953									
Solyc11g013200	holocarboxylase synthetase 2 (AHRD V3.3 *** AT1G37150.2)		F:GO:0004077; P:G(	F:biotin-[acetyl-CoA	EC:6.3.4.15	Biotin--[biotin carbox	IPR003142 (PFAM); G3DSA:3.30.930.	6,132	7,887	5,876	6,188	5,855									
Solyc11g013210	Transposon protein, putative, Mutator sub-class (AHRD V3.3 --* Q2R3A0_ORYSJ)		F:GO:0005488	F:binding			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,019	0,039	0,000	0,000	0,000									
Solyc11g013220	C2H2-like zinc finger protein (AHRD V3.3 *** A0A061FHR6_THECC)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.90.228.10 (GENE3D); mobic	0,061	0,021	0,000	0,000	0,000									
Solyc11g013235	Serine/threonine-protein kinase mph1 (AHRD V3.3 *-* A0A0B0N0H8_GOSAR)		F:GO:0004712; P:G(	F:protein serine/thre	EC:2.7.12.1	Dual-specificity kinas	mobidb-lite (MOBIDB_LITE); PTHR229	1,031	1,397	0,211	0,265	0,424									
Solyc11g013240	Kinase family protein (AHRD V3.3 *-* D7KUM0_ARALL)		F:GO:0004712; F:G(	F:protein serine/thre	EC:2.7.12.1	Dual-specificity kinas	G3DSA:1.10.510.10 (GENE3D); IPR0(	0,439	0,890	0,195	0,145	0,281									
Solyc11g013260	Prohibitin (AHRD V3.3 *** O04361_TOBAC)		C:GO:0016020	C:membrane			IPR000163 (PRINTS); IPR001107 (PF	59,187	59,489	95,745	93,194	91,061									
Solyc11g013270	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G38131.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR024709 (PIRSF); IPR019378 (PFA	12,557	11,092	1,128	0,806	0,804									
Solyc11g013290	Protein PIR (AHRD V3.3 *** PIR_ARATH)						IPR008081 (PRINTS); IPR008081 (PII	0,000	0,000	0,000	0,000	0,023									
Solyc11g013293	Protein PIR (AHRD V3.3 *-* PIR_ARATH)						IPR008081 (PIRSF); IPR009828 (PFA	23,205	17,082	20,080	20,140	21,741									
Solyc11g013297	LOW QUALITY:BED zinc finger,hAT family dimerization domain (AHRD V3.3 --* A0A061G1J7_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); IPR012337 (SUP	0,000	0,000	0,000	0,000	0,023									
Solyc11g013300	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7K8X4_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR001938 (PRINTS); IPR037176 (G3	0,179	0,347	0,137	0,000	0,119									
Solyc11g013310	SILAX3		P:GO:0003333; F:G(	P:amino acid transmembrane transport; F:amino acid transmem			IPR013057 (PFAM); PTHR22950:SF3	22,531	19,857	19,334	24,183	21,780									
Solyc11g013320	Rhomboid-like protein (AHRD V3.3 *** K4D6D6_SOLLC)		F:GO:0004252; P:G(	F:serine-type endop	EC:3.4.21	Acting on peptide bor	IPR022764 (PFAM); IPR035952 (G3D	0,019	0,060	0,000	0,000	0,000									
Solyc11g013330	BPS1-like protein (AHRD V3.3 *** AT1G22030.1)						PTHR31509:SF42 (PANTHER); PTHR:	1,740	1,446	17,589	25,165	10,632									
Solyc11g013340	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G51630.5)						mobidb-lite (MOBIDB_LITE)	3,012	1,448	3,748	2,703	2,974									
Solyc11g013345	transmembrane protein (AHRD V3.3 *** AT1G36380.1)		C:GO:0016021	C:integral component of membrane			IPR031851 (PFAM); PTHR37192 (PAN	2,803	1,680	5,170	4,356	4,220									
Solyc11g013350	Breast cancer 1, early onset (ISS) (AHRD V3.3 --* K8FCY3_9CHLO)							0,592	0,270	0,773	1,176	0,754									
Solyc11g013360	Gibberellin 20 oxidase 2 (AHRD V3.3 *** W6AW87_9ERIC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS); IPR026992 (PFA	0,000	0,021	0,000	0,022	0,000									
Solyc11g013370	E3 ubiquitin-protein ligase BRE1-like 1 (AHRD V3.3 *** A0A0B0M5V2_GOSAR)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:histone monoubiquitin			IPR013083 (G3DSA:3.30.40.GENE3D	66,332	56,207	129,992	148,701	124,868									
Solyc11g013375	LOW QUALITY:Retrovirus-related Pol polyprotein LINE-1 (AHRD V3.3 --* A0A151TS47_CAJCA)		F:GO:0043167	F:ion binding			IPR025558 (PFAM); mobidb-lite (MOB	0,426	0,163	0,476	0,835	0,377									
Solyc11g013390	GrpE protein homolog (AHRD V3.3 *-* M1A828_SOLTU)		P:GO:0006457	P:protein folding			IPR009012 (G3DSA:2.30.22.GENE3D	1,836	1,526	2,125	2,159	1,813									
Solyc11g013393	GrpE protein homolog (AHRD V3.3 *** M1A828_SOLTU)		F:GO:0000774; P:G(	F:adenyl-nucleotide exchange factor activity; P:protein folding; I			IPR013805 (G3DSA:3.90.20.GENE3D	1,883	1,970	2,750	2,800	2,900									
Solyc11g013400	Bushy growth protein (AHRD V3.3 *** A0A097PLV6_9BRAS)		C:GO:0000228; P:G(	C:nuclear chromosome; P:chromatin remodeling			IPR006939 (PFAM); mobidb-lite (MOB	42,446	33,894	41,906	37,113	39,490									
Solyc11g013410	Bushy growth protein (AHRD V3.3 *-* A0A097PLT5_9MAGN)		C:GO:0000228; P:G(	C:nuclear chromosome; P:chromatin remodeling			IPR006939 (PFAM); IPR006939 (PAN	1,732	0,124	0,000	0,000	0,000									
Solyc11g013420	LOW QUALITY:F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT3G24580.1)							0,292	0,037	0,000	0,000	0,000									
Solyc11g013430	Bushy growth protein (AHRD V3.3 *** A0A097PLU4_ERYGU)		C:GO:0000228; P:G(	C:nuclear chromosome; P:chromatin remodeling			IPR006939 (PFAM); PTHR10019:SF5	4,476	0,353	0,000	0,000	0,000									
Solyc11g013440	Eukaryotic translation initiation factor 3 subunit F (AHRD V3.3 *** K4D6E8_SOLLC)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; C:eukar			IPR000555 (PFAM); IPR024969 (PFA	46,094	48,930	56,306	53,663	52,496									
Solyc11g013450	BnaA07g10860D protein (AHRD V3.3 *** A0A078EP73_BRANA)						IPR008004 (PFAM); PTHR35995 (PAN	0,122	0,079	0,000	0,000	0,000									
Solyc11g013460	dephospho-CoA kinase family (AHRD V3.3 *** AT2G27490.4)		F:GO:0004140; F:G(	F:dephospho-CoA k	EC:2.7.1.24	Dephospho-CoA kina	G3DSA:3.40.50.300 (GENE3D); IPR0(	11,746	10,592	28,292	27,334	24,349									
Solyc11g013467	NBS-LRR disease resistance-like protein (AHRD V3.3 *-* Q2LEF8_9ROSI)		P:GO:0007165; F:G(	P:signal transduction; F:ADP binding			IPR035897 (G3DSA:3.40.50.GENE3D	0,942	1,173	1,115	1,269	1,535									
Solyc11g013480	Auxin Response Factor 17	ARF17	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-ter			G3DSA:2.30.30.10 ARF	10,694	8,149	47,346	42,535	44,041									
Solyc11g013490	Hexosyltransferase (AHRD V3.3 *** K4D6F3_SOLLC)		P:GO:0006486; F:G(	P:protein glycosylation; F:galactosyltransferase activity; C:mem			G3DSA:3.90.550.50 (GENE3D); IPR0:	30,289	28,612	36,200	35,545	35,577									
Solyc11g013500	LOW QUALITY:Lysine-specific demethylase rbr-2 (AHRD V3.3 *** A0A0B0NCB7_GOSAR)		C:GO:0048046	C:apoplast			mobidb-lite (MOBIDB_LITE); PTHR363	1,776	2,501	6,625	6,406	6,430									
Solyc11g013520	Histone acetyltransferase (AHRD V3.3 *** K4D6F6_SOLLC)		F:GO:0004402; P:G(	F:histone acetyltrar	EC:2.3.1.5; EC:2.3.1	Arylamine N-acetyltra	G3DSA:2.30.30.140 (GENE3D); G3DS	45,017	33,122	44,132	40,819	42,926									
Solyc11g013530	Phd finger protein, putative (AHRD V3.3 *** B9RJB8_RICCO)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation; F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	72,256	61,310	87,193	83,854	82,291									
Solyc11g013550	transmembrane 50A-like protein (AHRD V3.3 *** AT1G36980.2)		C:GO:0005623; C:G(	C:cell; C:integral component of membrane; P:late endosome to			IPR007919 (PFAM); IPR007919 (PAN	9,957	9,526	10,515	11,151	10,182									
Solyc11g013650	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4DEU6_SOLLC)		F:GO:0005524	F:ATP binding			IPR015415 (PFAM); G3DSA:1.10.8.60	0,000	0,018	0,000	0,000	0,000									
Solyc11g013690	LOW QUALITY:Calcium-binding EF-hand (AHRD V3.3 *-* A0A103XBE8_CYNCS)		F:GO:0005509	F:calcium ion binding			IPR002048 (PROSITE_PROFILES); IF	0,019	0,000	0,000	0,000	0,000									
Solyc11g013730	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_NICOT)		F:GO:0000287	F:magnesium ion binding			G3DSA:2.40.50.140 (GENE3D); IPR0:	0,238	0,628	0,316	0,569	0,517									
Solyc11g013740	Guanylate-binding family protein (AHRD V3.3 *-* AT5G46070.1)		F:GO:0000166	F:nucleotide binding			G3DSA:3.40.50.300 (GENE3D); PTHF	0,078	0,260	0,025	0,249	0,118									
Solyc11g013750	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *** AT5G36930.4)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS); G3DSA:3.40.50.3	30,680	24,712	21,149	24,232	21,652									
Solyc11g013760	mediator of RNA polymerase II transcription subunit-like protein (AHRD V3.3 *** AT4G08510.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	30,805	29,086	37,130	40,753	37,712									
Solyc11g013770	Resistance gene-like (AHRD V3.3 --* Q93YA6_SOLTU)							9,335	9,260	7,019	7,463	7,896									
Solyc11g013780	LOW QUALITY:Photosystem II protein D1 (AHRD V3.3 *-* PSBA_POPDE)		P:GO:0009772; F:G(	P:photosynthetic electron transport in photosystem II; F:electro			IPR000484 (PFAM); IPR036854 (G3D	0,311	0,363	0,396	0,775	1,118									
Solyc11g013790	LOW QUALITY:Tim10/DDP family zinc finger protein (AHRD V3.3 --* AT2G29530.2)							0,077	0,000	0,000	0,000	0,047									
Solyc11g013810	Nitrate reductase (AHRD V3.3 *** K4D6I5_SOLLC)	NR-NADH1	P:GO:0006809; F:G(	P:nitric oxide biosyı	EC:1.7.1.3; EC:1.7.9	Nitrate reductase (NA	IPR008335 (PRINTS); IPR001834 (PF	98,868	94,941	139,288	139,490	149,010									
Solyc11g013820	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *-* A0A0B2NUT1_GLYSO)		F:GO:0005524; F:G(	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;			mobidb-lite (MOBIDB_LITE); mobidb-lit	16,379	11,210	14,221	17,777	16,849									
Solyc11g013830	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** W9QXB1_9ROSA)		F:GO:0005524; F:G(	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;			IPR002498 (PFAM); IPR027409 (G3D	86,746	67,163	88,902	110,226	95,503									
Solyc11g013840	Exostosin family protein (AHRD V3.3 *** AT1G34270.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR040911 (PFAM); IPR004263 (PAN	10,724	11,019	12,702	11,141	10,909									
Solyc11g013845	Exostosin family protein (AHRD V3.3 *-* AT1G34270.1)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc			IPR040911 (PFAM); IPR004263 (PAN	6,074	6,003	6,865	7,619	5,972									
Solyc11g013850	PyrD (AHRD V3.3 *** A0A0B0PQ95_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	5,773	5,512	6,282	5,403	5,945									
Solyc11g013880	Serine/threonine-protein kinase (AHRD V3.3 *** K4D6J2_SOLLC)		F:GO:0004674; F:G(	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR024171 (PIRSF); IPR036426 (G3D	35,179	35,747	44,267	45,129	42,401									
Solyc11g013890	F-box protein (AHRD V3.3 *** W9SM54_9ROSA)		F:GO:0005515	F:protein binding			IPR006527 (PFAM); IPR001810 (PFA	5,471	5,240	2,702	2,611	3,740									
Solyc11g013895	F-box protein interaction domain protein (AHRD V3.3 --* A0A072UU57_MEDTR)							0,141	0,182	0,071	0,048	0,024									
Solyc11g015890	F-box protein (AHRD V3.3 *** W9SM54_9ROSA)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR017451 (TIGF	2,356	2,949	0,402	0,912	0,870									
Solyc11g015897	F-box protein (AHRD V3.3 --* W9SM54_9ROSA)						PTHR31790 (PANTHER); PTHR31790	0,142	0,182	0,074	0,050	0,071									
Solyc11g015910	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGE9_ARATH)		C:GO:0016020; F:G(	C:membrane; F:kinase activity; P:phosphorylation			IPR032675 (G3DSA:3.80.10.GENE3D	0,019	0,000	0,000	0,025	0,000									
Solyc11g016930	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGE9_ARATH)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	3,478	4,782	0,572	0,700	1,288									
Solyc11g016940	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM); PTHR12570:SF2:	6,841	5,384	8,214	9,077	7,661									
Solyc11g016970	Protein DETOXIFICATION (AHRD V3.3 *** K4D6K1_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transp			IPR002528 (TIGRFAM); IPR002528 (F	1,125	0,997	1,806	2,642	2,329									

Solyc11g016980	Transcription initiation factor TFIID subunit 8 (AHRD V3.3 *-* A0A0B0P5F6_GOSAR)		F:GO:0046982	F:protein heterodimerization activity	PTHR37604 (PANTHER)	0,000	0,018	0,000	0,025	0,000									
Solyc11g016990	Protein tyrosine phosphatase (AHRD V3.3 *** Q6J2K7_PHAVU)		F:GO:0004725; P:G(	F:protein tyrosine p EC:3.1.3.16; EC:3.1. Protein-serine/threor	IPR000242 (PRINTS); IPR029021 (G3	23,744	22,284	25,631	25,337	24,890									
Solyc11g017000	DUF668 family protein (AHRD V3.3 *** A0A072VPK0_MEDTR)				IPR021864 (PFAM); IPR007700 (PFA	28,517	67,816	34,650	25,596	35,407	1,274	0,003					up		
Solyc11g017010	SISUT1	SUT1	C:GO:0005887; F:G(	C:integral component of plasma membrane; F:sucrose transmer	G3DSA:1.20.1250.20 (GENE3D); PF1	55,000	78,130	75,640	110,337	113,317			0,580	0,007	0,546	0,002		up	up
Solyc11g017030	LOW QUALITY:UDP-N-acetylglucosamine 1-carboxyvinyltransferase (AHRD V3.3 *-* W9S9V0_9ROSA)		F:GO:0016765	F:transferase activity, transferring alkyl or aryl (other than meth	IPR036968 (G3DSA:3.65.10.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc11g017035	S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61360.4)		F:GO:0003677	F:DNA binding	G3DSA:2.40.50.140 (GENE3D); IPR0	0,037	0,000	0,022	0,025	0,023									
Solyc11g017040	Ulp1 protease family protein (AHRD V3.3 *** B9GN40_POPTR)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR003653 (PFAM); G3DSA:3.40.395	43,311	38,132	51,635	52,773	52,627									
Solyc11g017050	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT2G44020.1)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR003690 (PFAM); IPR038538 (G3D	8,312	9,111	11,760	9,639	9,642									
Solyc11g017060	Maturase K (AHRD V3.3 --* Q5GIQ6_9MYRT)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity; F:cysteine-type peptidase a	mobidb-lite (MOBIDB_LITE); PTHR453	1,816	1,720	2,082	2,563	2,055									
Solyc11g017070	Eukaryotic translation initiation factor 3 subunit I (AHRD V3.3 *** K4D6L1_SOLLC)		F:GO:0003743; F:G(	F:translation initiation factor activity; F:protein binding; C:eukar	IPR020472 (PRINTS); IPR015943 (G3	66,621	82,837	96,878	90,725	87,368									
Solyc11g017090	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SA73_CAJCA)				IPR019557 (PFAM); PTHR44194 (PAN	0,021	0,021	0,025	0,000	0,000									
Solyc11g017100	LOW QUALITY:GRAS family transcription factor	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	IPR005202 (PFAM GRAS	0,000	0,000	0,051	0,022	0,000									
Solyc11g017130	PSL1 (AHRD V3.3 *** F5A7N4_9SOLN)		F:GO:0005515	F:protein binding	G3DSA:3.40.50.1010 (GENE3D); IPR(	0,514	0,555	0,262	0,323	0,352									
Solyc11g017140	Protein SENSITIVE TO PROTON RHIZOTOXICITY 1 (AHRD V3.3 *** W9QXR9_9ROSA)		F:GO:0003676	F:nucleic acid binding	G3DSA:3.30.160.6 C2H2	0,000	0,000	0,075	0,000	0,000									
Solyc11g017180	LOW QUALITY:RNA-directed DNA polymerase (Reverse transcriptase) (AHRD V3.3 --* A2Q4L4_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:membrane; C:integral component of membrane;	F:kinase activity; P:phosphorylation	0,000	0,039	0,000	0,051	0,000									
Solyc11g017190	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IYV3_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi EC:3.6.1.3; EC:3.6.3 Adenosinetriphospha	PR00119 (PRINTS); IPR023214 (G3D	23,601	22,877	33,970	35,587	32,976									
Solyc11g017200	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G22700.1)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	11,729	15,081	28,493	30,169	32,520									
Solyc11g017210	Transposon-like element Lyt2-2 DNA (AHRD V3.3 *-* D5MNY6_SOLLC)		P:GO:0006355	P:regulation of transcription, DNA-templated	IPR004330 (PFAM FAR1	0,037	0,021	0,022	0,000	0,000									
Solyc11g017230	5'-3' exonuclease family protein (AHRD V3.3 *** AT1G34380.2)		F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.7 DNA-directed DNA pc	G3DSA:3.40.50.1010 (GENE3D); IPR(	4,771	3,915	7,161	7,639	7,360									
Solyc11g017240	chorismate mutase	CM2	F:GO:0004106; P:G(	F:chorismate mutas EC:5.4.99.5 Chorismate mutase	IPR037039 (G3DSA:1.10.590.GENE3	3,858	4,681	9,102	11,687	9,190									
Solyc11g017250	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4D6M		F:GO:0016746	F:transferase activity, transferring acyl groups	IPR000089 (PFAM); G3DSA:2.40.50.1	36,575	49,756	97,028	106,580	104,514									
Solyc11g017270	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072VP05_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS); IPR032675 (G3D	59,511	194,202	21,043	25,509	37,830	1,727	0,003	0,843	0,001			up	up	
Solyc11g017280	Leucine-rich repeat receptor-like tyrosine-protein kinase (AHRD V3.3 *** W9QXS4_9ROSA)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	PR00019 (PRINTS); G3DSA:1.10.510	0,306	0,459	0,118	0,050	0,257									
Solyc11g017285	Cyclin-B2-1 (AHRD V3.3 --* CCB21_ORYSJ)					1,476	1,080	1,084	0,965	1,109									
Solyc11g017290	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JW06_CYNCS)		F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR002885 (I	1,846	1,755	1,150	1,617	1,226									
Solyc11g017300	COP9 signalosome complex subunit CSN5	JAB	F:GO:0005515	F:protein binding	IPR000555 (PFAM); IPR040961 (PFA	52,283	51,186	37,961	32,987	39,050									
Solyc11g017310	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *-* A0A061EFM5_THECC)		P:GO:0009451	P:RNA modification	PTHR24015:SF389 (PANTHER); PTHI	0,618	0,377	0,434	0,621	0,609									
Solyc11g017320	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A172CHJ1_POPTO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,278	0,449	0,333	0,288	0,379									
Solyc11g017325	Aldolase superfamily protein (AHRD V3.3 --* AT2G26800.5)					0,156	0,078	0,122	0,074	0,165									
Solyc11g017330	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *-* AT2G13600.1)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	2,625	1,844	2,049	2,043	1,838									
Solyc11g017335	F-box family protein (AHRD V3.3 *** B9HWR1_POPTR)		F:GO:0005515	F:protein binding	IPR001810 (PFAM); IPR032675 (G3D	1,383	1,357	0,570	0,464	0,564									
Solyc11g017340	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A172CHJ1_POPTO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	0,653	0,351	0,500	0,717	0,637									
Solyc11g017360	Myb family transcription factor (AHRD V3.3 *-* D7M1F0_ARALL)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(MYB_related	1,194	1,363	0,847	0,567	0,773									
Solyc11g017365	DEAD-box ATP-dependent RNA helicase 8 (AHRD V3.3 --* RH8_ORYSJ)					0,181	0,222	0,143	0,143	0,140									
Solyc11g017370	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A172CHJ1_POPTO)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,816	2,057	0,993	1,033	1,338									
Solyc11g017380	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes	IPR008521 (PFAM); mobidb-lite (MOB	2,183	2,160	3,287	3,891	3,241									
Solyc11g017390	LOW QUALITY:RNA-binding KH domain-containing protein (AHRD V3.3 --* AT5G46190.4)				mobidb-lite (MOBIDB_LITE); PTHR346	0,357	0,296	0,125	0,411	0,024									
Solyc11g017400	N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein (AHRD V3.3 *** AT3G58130.2)		F:GO:0000225; P:G(	F:N-acetylglucosar EC:3.5.1.89 N-acetylglucosamin	IPR024078 (G3DSA:3.40.50.GENE3D	2,129	1,907	3,252	2,979	3,147									
Solyc11g017420	transmembrane protein (DUF616) (AHRD V3.3 *** AT4G09630.2)		P:GO:0006672; C:G(	P:ceramide metabolic process; C:integral component of membr	IPR006852 (PFAM); mobidb-lite (MOB	32,104	28,213	18,777	18,494	17,771									
Solyc11g017430	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT4G09620.3)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN	IPR038538 (G3DSA:1.25.70.GENE3D	3,292	4,403	4,019	5,332	5,213									
Solyc11g017440	Gibberellin-regulated family protein (AHRD V3.3 *** AT1G22690.3)				IPR003854 (PFAM); PTHR23201:SF2	0,868	1,039	0,143	0,538	0,519									
Solyc11g017450	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** A5C9M8_VITVI)		F:GO:0004553; P:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucos	IPR000757 (PFAM); IPR016455 (PIRS	0,543	0,693	0,000	0,000	0,000									
Solyc11g017460	U-box domain-containing protein 13 (AHRD V3.3 *** W9R751_9ROSA)		F:GO:0005515	F:protein binding	IPR011989 (G3DSA:1.25.10.GENE3D	81,653	37,660	53,470	45,662	42,974	-1,088	0,000					down		
Solyc11g017470	NAC domain-containing protein, putative (AHRD V3.3 *** B9S2X2_RICCO)	NAC4	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM NAC	35,729	37,067	250,555	313,452	164,717			-0,608	0,001				down	
Solyc11g017478	CBS domain protein with a domain protein (DUF21) (AHRD V3.3 --* AT5G52790.4)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc11g018490	Beta-galactosidase (AHRD V3.3 *-* K4D6Q4_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS); IPR031330 (PF	0,272	0,252	1,529	3,240	2,164					1,075	0,002			up
Solyc11g018495	Beta-galactosidase (AHRD V3.3 *-* K4D6Q3_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:2.60.120.740 (GENE3D); IPR(	0,451	0,401	1,584	3,443	2,095					1,119	0,004			up
Solyc11g018500	Beta-galactosidase (AHRD V3.3 *** A0A022QYX4_ERYGU)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001944 (PRINTS); IPR041392 (PF	7,152	4,978	2,082	1,353	1,876									
Solyc11g018510	DNA glycosylase (AHRD V3.3 *** I0YSC3_COCSC)		F:GO:0003684; P:G(	F:damaged DNA bir EC:3.2.2.23 DNA-formamidopyrir	G3DSA:3.30.310.40 (GENE3D); IPR0	7,797	5,787	6,096	5,708	6,008									
Solyc11g018550	ascorbate peroxidase 6	APX6	F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS); IPR002207 (PF	22,305	36,325	17,074	12,105	23,504	0,732	0,011	0,460	0,029	-0,490	0,028	up	up	down
Solyc11g018555	LOW QUALITY:sterol 4-alpha-methyl-oxidase 2-2 (AHRD V3.3 --* AT2G29390.5)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR015410 (PFAM)	0,096	0,037	0,075	0,047	0,072									
Solyc11g018560	50S ribosomal protein L25, putative (AHRD V3.3 *** B9RCJ6_RICCO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR029751 (PFAM); IPR020057 (PFA	12,674	15,411	16,576	13,461	13,855									
Solyc11g018580	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0G2SJ82_SALMI)		F:GO:0003824	F:catalytic activity	G3DSA:3.40.50.12780 (GENE3D); IPI	118,942	112,148	111,680	114,787	125,434									
Solyc11g018590	LOW QUALITY:Subtilisin-like protease (AHRD V3.3 *** A0A0B2SQW1_GLYSO)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity	IPR037045 (G3DSA:3.30.70.GENE3D	1,908	2,082	3,230	3,515	2,856									
Solyc11g018600	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G51680.1).Pfam:PF13561		F:GO:0016616; P:G(	F:oxidoreductase activity, acting on the CH-OH group of donors	IPR002347 (PRINTS); IPR002347 (PF	0,255	0,060	0,047	0,363	0,306									
Solyc11g018610	Calcium-dependent protein kinase (AHRD V3.3 *** H6UM40_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F	PIRSF000654 (PIRSF); G3DSA:3.30.2	3,313	7,224	0,477	0,699	0,777	1,147	0,004					up		
Solyc11g018620	SNARE associated Golgi protein family (AHRD V3.3 *** AT4G09580.1)		C:GO:0016021	C:integral component of membrane	IPR032816 (PFAM); PTHR43220:SF3	3,704	2,756	4,568	5,061	4,969									
Solyc11g018660	NAC domain-containing protein, putative (AHRD V3.3 *** B9SLE9_RICCO)	NAC093	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR003441 (PFAM NAC	0,082	0,021	0,000	0,000	0,000									
Solyc11g018670	DNAJ heat shock N-terminal domain-containing protein (AHRD V3.3 *** AT1G65280.2)				IPR001623 (PRINTS); IPR036869 (G3	58,121	49,101	65,744	65,001	59,425									
Solyc11g018680	ABC transporter family protein (AHRD V3.3 *-* B9IQI5_POPTR)	ABCG66	C:GO:0016020	C:membrane	IPR013525 (PFAM); PTHR19241 (PAI	13,898	12,322	6,133	8,598	8,305									
Solyc11g018690	ABC transporter family protein (AHRD V3.3 *-* B9IQI5_POPTR)	ABCG63	F:GO:0005524; F:G(	F:ATP binding; F:AT EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR003439 (PFAM); G3DSA:3.40.50.3	15,795	13,495	6,709	9,015	8,812									
Solyc11g018700	Ycf15 protein (AHRD V3.3 *** A0A0C5C0V6_9SOLA)		C:GO:0009507	C:chloroplast	IPR019645 (PFAM)	0,019	0,043	0,000	0,025	0,046									
Solyc11g018710	LOW QUALITY:DUF688 family protein (AHRD V3.3 *** A0A072VNH4_MEDTR)				mobidb-lite (MOBIDB_LITE); mobidb-lit	1,871	1,758	0,144	0,337	0,119									
Solyc11g018740	Inner membrane OXA1-like protein (AHRD V3.3 *-* G7KQL5_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase acti	PTHR12428:SF22 (PANTHER); IPR00	8,145	8,201	10,354	10,931	11,144									
Solyc11g018743	Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain-containing protein (AHRD V3.3		C:GO:0016021; F:G(	C:integral component of membrane; F:membrane insertase acti	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,276	0,268	0,334	0,530	0,329									
Solyc11g018747	Inner membrane ALBINO3-like protein (AHRD V3.3 *** Q5SNL9_ORYSJ)		F:GO:0005515; C:G(	F:protein binding; C:integral component of membrane; F:membr	IPR011990 (G3DSA:1.25.40.GENE3D	4,631	5,314	7,830	7,165	6,942									
Solyc11g018750	transmembrane protein, putative (DUF707) (AHRD V3.3 --* AT1G13000.5)					1,674	1,029	0,804	0,910	0,918									
Solyc11g018770	CCA tRNA nucleotidyltransferase (AHRD V3.3 *** W9SEV9_9ROSA)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti	G3DSA:3.30.460.10 (GENE3D); G3DS	8,900	13,378	12,494	10,553	11,909									
Solyc11g018775	Peroxidase (AHRD V3.3 *** M1CN26_SOLTU)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,019	0,019	0,000	0,000	0,047									
Solyc11g018777	Peroxidase (AHRD V3.3 *** K4D6T3_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR002016 (PRINTS); IPR000823 (PF	0,363	3,318	0,582	0,533	1,287									
Solyc11g018800	Peroxidase (AHRD V3.3 *** K4D6T3_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,021	0,224	0,097	0,025	0,046									
Solyc11g018805	Peroxidase (AHRD V3.3 *** M1CN26_SOLTU)		F:GO:0004601; P:G(	F:peroxidase activil EC:1.11.1.7 Peroxidase	IPR000823 (PRINTS); IPR002016 (PF	0,000	0,021	0,000	0,000	0,000									
Solyc11g018810	CCA tRNA nucleotidyltransferase (AHRD V3.3 *-* W9SEV9_9ROSA)		F:GO:0003723; F:G(	F:RNA binding; F:tR EC:2.7.7.25; EC:2.7. Transferring phospho	PTHR13734 (PANTHER); PTHR13734	1,826	3,098	1,973	2,415	1,839									
Solyc11g018820	Polynucleotide adenylyltransferase family protein (AHRD V3.3 *** AT1G22660.5)		F:GO:0003723; P:G(	F:RNA binding; P:RNA processing; F:nucleotidyltransferase acti	G3DSA:3.30.460.10 (GENE3D); IPR0	0,099	0,114	0,100	0,073	0,165									
Solyc11g018837	WD-40 repeat family protein / beige-like protein (AHRD V3.3 --* AT2G45540.6)					0,057	0,021	0,025	0,000	0,000									
Solyc11g018850	Histone-lysine N-methyltransferase ASHR2 (AHRD V3.3 --* ASHR2_ARATH)					0,077	0,224	0,094	0,070	0,094									
Solyc11g019910	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** I3T947_MEDTR)		F:GO:0004857	F:enzyme inhibitor activity	IPR035513 (G3DSA:1.20.140.GENE3	3,800	5,316	0,409	0,466	0,514									
Solyc11g019920	Protein disulfide isomerase, putative (AHRD V3.3 *** B9T6K9_RICCO)		P:GO:0045454	P:cell redox homeostasis	PR00421 (PRINTS); G3DSA:3.40.30.1	5,895	6,112	8,935	9,675	8,359									
Solyc11g019930	RING/U-box superfamily protein (AHRD V3.3 *** AT1G35625.1)		C:GO:0000306; P:G(	C:extrinsic component of vacuolar membrane; P:ubiquitin-deper	G3DSA:3.50.30.30 (GENE3D); IPR00	17,474	12,527	22,961	26,005	21,588									
Solyc11g019940	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT4G36960.2)					0,000	0,000	0,000	0,072	0,023									
Solyc11g019950	Long chain base biosynthesis protein 1 (AHRD V3.3 *** LCB1_ARATH)		F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	IPR015421 (G3DSA:3.40.640.GENE3	19,876	17,668	37,083	38,023	32,550									
Solyc11g019960	Retrograde Golgi transport protein RGP1 (AHRD V3.3 *** A0A1D1XLL4_9ARAE)				IPR014752 (G3DSA:2.60.40.GENE3D	13,292	12,835	14,400	14,797	14,023									
Solyc11g019970	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT5G48040.1)				IPR021099 (PFAM); PTHR31476:SF6	9,311	9,501	10,609	11,672	10,141									
Solyc11g020003	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 --* AT1G62305.1)		F:GO:0008270	F:zinc ion binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,022	0,047	0,024									
Solyc11g020020	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SGZ7_CAJCA)				IPR019557 (PFAM); PTHR44194 (PAI	0,058	0,037	0,000	0,000	0,000									
Solyc11g020030	Lysine--tRNA ligase (AHRD V3.3 *-* A0A0V0IK21_SOLCH)		F:GO:0000049; F:G(	F:tRNA binding; F:l EC:6.1.1.6 Lysine--tRNA ligase	G3DSA:3.30.930.10 (GENE3D); PTHF	0,096	0,138	0,125	0,116	0,023									
Solyc11g020040	heat shock protein 70	hsp70	F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding	IPR013126 (PRINTS); IPR029047 (G3	120,180	75,561	641,732	468,206	614,458	-0,643	0,023					down		
Solyc11g020050	LOW QUALITY:Cytosolic Fe-S cluster assembly factor nar-1 (AHRD V3.3 -** A0A1D1Z971_9ARAE)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,838	0,626	0,388	0,340	0,472									
Solyc11g020060	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** A0A0B2QT46_GLYSO)		F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors	G3DSA:3.40.50.720 (GENE3D); G3DS	14,864	13,065	60,344	67,427	52,597									
Solyc11g020100	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS); IPR002182 (PFA	6,913	8,658	3,314	3,435	5,694									
Solyc11g020135	PCI domain-containing protein 2 (AHRD V3.3 *-* A0A0B2PGA1_GLYSO)		P:GO:0000973; F:G(	P:posttranscriptional tethering of RNA polymerase II gene DNA at	nuclear periphery; F:double-stranded	0,000	0,018	0,000	0,000	0,000									
Solyc11g020140	chromatin remodeling 38 (AHRD V3.3 --* AT3G42670.4)					0,000	0,000	0,100	0,022	0,000									
Solyc11g020157	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061FID3_THECC)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	PTHR23272:SF54 (PANTHER); PTHR	0,000	0,021	0,000	0,000	0,000									
Solyc11g020160	nuclear pore complex protein-like protein (AHRD V3.3 *-* AT5G05680.1)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:ribosomal sma	IPR019321 (PFAM); IPR037700 (PAN	0,116	0,217	0,212	0,221	0,164									
Solyc11g020180	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151U9T1_CAJCA)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:ribosomal sma	mobidb-lite (MOBIDB_LITE); mobidb-lit	24,507	22,101	27,808	30,908	30,639									
Solyc11g020210	CYCLIN D7-1 (AHRD V3.3 --* AT5G02110.2)					2,675	2,523	2,221	1,884	2,241									
Solyc11g020230	Cytokinin-regulated kinase 1 (AHRD V3.3 *** Q9FLK3_TOBAC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR009091 (G3DSA:2.130.10.GENE3	24,006	12,331	2,794	5,394	5,419	-0,937	0,001	0,956	0,016	0,954	0,016	down	up	up
Solyc11g020280	Receptor-like protein kinase HSL1 (AHRD V3.3 *** W9T2E3_9ROSA)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR000719 (PFAM); G3DSA:1.10.510	65,670	80,325	26,569	24,205	35,646									
Solyc11g020290	Phosphoenolpyruvate carboxylase (AHRD V3.3 *-* C9W981_ARAHY)		F:GO:0005515; P:G(	F:protein binding; P: EC:4.1.1.31; EC:4.1. Phosphoenolpyruvate	IPR015943 (G3DSA:2.130.10.GENE3	9,346	7,914	3,327	2,330	4,505									
Solyc11g020300	Protein TIC 40, chloroplastic (AHRD V3.3 *** TIC40_PEA)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:chloroplast organization; C	IPR041243 (PFAM); G3DSA:1.10.260	70,187	89,377	117,393	115,418	121,515									
Solyc11g020305	Photosystem I assembly protein Ycf4 (AHRD V3.3 --* YCF4_GOSHI)					0,042	0,021	0,000	0,000	0,000									
Solyc11g020320	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *** A0A072U6V5_MEDTR)		F:GO:0000981; F:G(	F:DNA-binding transcription factor activity, RNA polymerase II-s	IPR002100 (PRIN M-type_MADS	0,037	0,064	0,047	0,048	0,047									
Solyc11g020330	leer-sHSP small heat shock protein	Hsp21.5C	C:GO:0005783; P:G(	C:endoplasmic reticulum; P:protein folding; P:response to heat;	IPR008978 (G3DSA:2.60.40.GENE3D	132,893	96,016	1186,261	1027,311	1119,566									
Solyc11g020474	NBS-LRR resistance protein-like protein (AHRD V3.3 *-* A1Y9Q5_9SOLN)		F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,039	0,000	0,000	0,000									
Solyc11g020476	Disease resistance protein (AHRD V3.3 --* A0A103XRK3_CYNCS)		F:GO:0043531	F:ADP binding	G3DSA:3.40.50.300 (GENE3D)	0,000	0,000	0,000	0,025	0,000									
Solyc11g020478	Disease resistance protein (AHRD V3.3 *-* A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding	G3DSA:1.10.8.430 (GENE3D); IPR00	0,000	0,060	0,000	0,025	0,000									
Solyc11g020550	LOW QUALITY:Forkhead-associated (FHA) domain-containing protein (AHRD V3.3 --* AT3G54350.5)				mobidb-lite (MOBIDB_LITE)	0,141	0,196	0,150	0,022	0,023									
Solyc11g020555	Pentatricopeptide repeat-containing protein (AHRD V3.3 --* A0A103XBJ8_CYNCS)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane	IPR040338 (PANTHER)	0,000	0,018	0,000	0,000	0,023									
Solyc11g020590	Peptide chain release factor family protein (AHRD V3.3 *** B9N1R9_POPTR)		F:GO:0003747; P:G(	F:translation release factor activity; P:translational termination	IPR000352 (PFAM); G3DSA:3.30.160	12,165	11,477	19,290	20,207	18,764									
Solyc11g020610	cytosolic neutral/alkaline invertase D	NI4	F:GO:0033926	F:glycopeptide alph EC:3.2.1.97 Endo-alpha-N-acetyl	IPR024746 (PFAM); IPR012341 (G3D	8,889	9,086	7,403	7,182	7,193									
Solyc11g020660	LOW QUALITY:Mads box protein, putative (AHRD V3.3 *-* B9RKR2_RICCO)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity	IPR036879 (G3DS M-type_MADS	0,000	0,018	0,025	0,050	0,046									
Solyc11g020670	TCP transcription factor 12	TCP12			IPR017887 (PFAM TCP	34,474	37,197	39,261	48,388	39,450									
Solyc11g020690	LOW QUALITY:ubiquitin-specific protease 21 (AHRD V3.3 --* AT5G46740.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc11g020710	cytochrome C oxidase biogenesis Cmc1-like protein (AHRD V3.3 *** AT1G31175.2)					3,869	3,272	3,867	4,493	3,867									
Solyc11g020720	Alpha/beta-hydrolase superfamily protein (AHRD V3.3 *-* G7LIR3_MEDTR)		P:GO:0044255	P:cellular lipid metabolic process	PTHR12482:SF11 (PANTHER); PTHR	10,428	7,755	18,215	19,060	18,317									
Solyc11g020730	Dof-type zinc finger DNA-binding family protein (AHRD V3.3 --* AT3G61850.4)					6,279	4,283	8,935	9,252	9,182									
Solyc11g020760	DEAD/DEAH box RNA helicase family protein (AHRD V3.3 *-* AT1G35530.3)		F:GO:0003677; F:G(	F:DNA binding; F:A EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0(	1,493	1,185	0,739	0,952	1,342									
Solyc11g020770	DEAD/DEAH box RNA helicase family protein (AHRD V3.3 *** AT1G35530.4)		P:GO:0006281; F:G(	P:DNA repair; F:ATI EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0(	11,776	10,253	7,298	7,725	7,453									
Solyc11g020780	dCK/dGK-like deoxyribonucleoside kinase		C:GO:0005737; P:G(	C:cytoplasm; P:pho EC:2.7.1.145 Deoxynucleoside kin	IPR031314 (PFAM); mobidb-lite (MOB	32,043	34,357	40,953	37,860	39,611									
Solyc11g020810	FtsJ-like methyltransferase family protein (AHRD V3.3 *** AT4G25730.1)		C:GO:0005634; F:G(	C:nucleus; F:rRNA methyltransferase activity; P:rRNA methylati	IPR024576 (PFAM); IPR012920 (PFA	67,784	95,488	67,106	63,964	65,486									
Solyc11g020820	FtsJ-like methyltransferase family protein (AHRD V3.3 *** AT4G25730.1)		C:GO:0005634; F:G(	C:nucleus; F:rRNA methyltransferase activity; P:rRNA methylati	IPR002877 (PFAM); IPR024576 (PFA	18,449	23,868	17,606	16,460	18,418									
Solyc11g020830	30S ribosomal protein S7, chloroplastic (AHRD V3.3 *** RR7_TOBAC)		P:GO:0006412	P:translation	IPR036823 (G3DSA:1.10.455.GENE3	0,000	0,021	0,000	0,000	0,000									
Solyc11g020840	LOW QUALITY:SGF29 tudor-like domain-containing protein (AHRD V3.3 --* AT5G40550.3)					0,019	0,000	0,000	0,000	0,000									
Solyc11g020850	zein-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *** AT5G57830.1)				IPR007656 (PFAM); mobidb-lite (MOB	0,177	0,200	0,147	0,196	0,188									
Solyc11g020870	Metal-dependent protein hydrolase (AHRD V3.3 *** AT5G41970.1)		C:GO:0005634; C:G(	C:nucleus; C:mitochondrion; C:cytosol	IPR003226 (PFAM); IPR003226 (PAN	21,353	23,011	31,165	27,050	28,321									
Solyc11g020875	Ubiquitin-like-specific protease ESD4 (AHRD V3.3 --* A0A0B2P0Q4_GLYSO)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR003653 (PFAM); G3DSA:3.40.395	0,000	0,019	0,000	0,000	0,000									
Solyc11g020890	40S ribosomal S29-like protein (AHRD V3.3 *** A0A0B0MKW3_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR001209 (PFAM); G3DSA:4.10.830	32,936	40,539	34,554	31,816	30,138									
Solyc11g020910	2-isopropylmalate synthase (AHRD V3.3 *** A0A0B0NSJ4_GOSAR)				PTHR36786 (PANTHER)	11,999	11,312	13,240	13,517	13,986									
Solyc11g020930	LOW QUALITY:disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 --* AT1G51480.1)					0,117	0,064	0,172	0,099	0,093									
Solyc11g020950	BZIP family transcription factor family protein (AHRD V3.3 *** B9N898_POPTR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	G3DSA:1.20.5.17(bZIP	0,019	0,105	0,075	0,047	0,023									
Solyc11g020960	Proteinase inhibitor II (AHRD V3.3 *-* B3F0C1_TOBAC)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity	G3DSA:3.30.60.30 (GENE3D); IPR00	19,075	8,154	12,669	3,892	6,725			-0,916	0,001	-1,697	0,000		down	down
Solyc11g020990	Proteinase inhibitor II (AHRD V3.3 *** B3F0C1_TOBAC)		F:GO:0004867; F:G(	F:serine-type endopeptidase inhibitor activity; F:carboxy-lyase	G3DSA:3.30.60.30 (GENE3D); IPR01	0,038	0,061	0,000	0,000	0,000									
Solyc11g021010	Copia-like polyprotein/retrotransposon (AHRD V3.3 --* AT5G48050.1)		C:GO:0000943	C:retrotransposon nucleocapsid	IPR039537 (PANTHER); PTHR11439	0,040	0,000	0,000	0,025	0,000									
Solyc11g021020	Proteinase inhibitor II (AHRD V3.3 *-* B3F0C1_TOBAC)		F:GO:0004867	F:serine-type endopeptidase inhibitor activity	IPR003465 (PFAM); G3DSA:3.30.60.3	0,000	0,018	0,000	0,000	0,000									
Solyc11g021060	TOMARPIX_proteinase inhibitor		F:GO:0004867	F:serine-type endopeptidase inhibitor activity	G3DSA:3.30.60.30 (GENE3D); G3DSA	0,836	1,040	0,050	0,000	0,118									
Solyc11g021070	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR008543 (PFAM); IPR008543 (PAN	0,000	0,021	0,050	0,000	0,023									
Solyc11g021080	Protein Ycf2 (AHRD V3.3 *-* YCF2_VITVI)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR019645 (PFAM); IPR008543 (PAN	0,021	0,043	0,000	0,100	0,071									
Solyc11g021090	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* X2GCQ3_9ROSI)		P:GO:0008152; C:G(	P:metabolic process; C:plastid; C:membrane; F:oxidoreductase	IPR001750 (PFAM); PTHR22773 (PAI	0,040	0,059	0,044	0,101	0,070									
Solyc11g021100	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* A0A0F6NLZ2_VICSA)		F:GO:0008137; C:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or NA	DPH; NADH dehydrogenase; NADH:ub	0,081	0,037	0,072	0,125	0,047									
Solyc11g021110	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_ANACO)		F:GO:0008137; C:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR001750 (PFAM); PTHR45564 (PAN	0,063	0,126	0,050	0,050	0,166									
Solyc11g021120	NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_BRANA)		C:GO:0005886; F:G(	C:plasma membrane EC:1.6.99.5; EC:1.6. Acting on NADH or NA	DPH; NADH dehydrogenase; NADH:ub	0,000	0,082	0,022	0,072	0,120									

Solyc11g021130	30S ribosomal protein S7, chloroplastic (AHRD V3.3 *** RR7_TOBAC)		F:GO:0003735: P:G(	F:structural constituent of ribosome: P:translation: C:small ribos	IPR006032 (PRINTS): G3DSA:2.40.5(	1,328	2,343	1,294	1,801	1,745									
Solyc11g021140	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (AHRD V3.3 --'		C:GO:0005739: C:G(	C:mitochondrion; C:chloroplast		0,000	0,000	0,022	0,047	0,000									
Solyc11g021160	Ycf68 (AHRD V3.3 *-* A0A0F6NPP1_9POAL)		C:GO:0005576: C:G(	C:extracellular region: C:cell wall: C:chloroplast: F:hydrolase ac	PTHR34890 (PANTHER)	0,119	0,220	0,301	0,298	0,356									
Solyc11g021170	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT4G13330.6)		C:GO:0009507	C:chloroplast		7,236	19,312	6,056	22,965	18,101	1,436	0,047	1,580	0,000	1,930	0,000	up	up	up
Solyc11g021180	Ycf1 (AHRD V3.3 *-* A0A140G1X7_TOBAC)		C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM): IPR008896 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc11g021190	NADH dehydrogenase subunit (AHRD V3.3 *-* A9X6M6_9SOLA)		C:GO:0009507: C:G(	C:chloroplast: C:thylakoid: C:membrane: F:oxidoreductase activ	PR01434 (PRINTS): IPR001750 (PFA	0,000	0,078	0,000	0,022	0,070									
Solyc11g021210	Cytochrome c biogenesis protein CcsA (AHRD V3.3 *** CCSA_SOLLC)		P:GO:0017004: F:G(	P:cytochrome complex assembly; F:heme binding	IPR017562 (TIGRFAM): IPR002541 (F	0,061	0,142	0,050	0,050	0,071									
Solyc11g021220	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic (AHRD V3.3 *** K4D771_SOLLC)		F:GO:0008137: C:G(	F:NADH dehydroge EC:1.6.99.5: EC:1.6. Acting on NADH or N	IPR017896 (PFAM): IPR010226 (TIGF	0,000	0,064	0,000	0,000	0,000									
Solyc11g021230	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 *** NU1C_LACSA)		C:GO:0016020: P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM): PTHR11432:SF1:	0,138	0,432	0,171	0,197	0,209									
Solyc11g021240	Ycf1 (AHRD V3.3 *-* A0A0U1ZHZ0_9SOLN)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE): IPR0088!	0,019	0,085	0,169	0,075	0,163									
Solyc11g021260	Ycf1 (AHRD V3.3 *-* A0A0U1ZG15_SOLCE)		C:GO:0016021	C:integral component of membrane	IPR008896 (PANTHER): IPR008896 (I	0,037	0,061	0,025	0,150	0,047									
Solyc11g021270	Ycf1 (AHRD V3.3 *-* V5NDV5_9SOLN)		C:GO:0009706: P:G(	C:chloroplast inner membrane; P:protein transport; C:integral component of membrane		0,000	0,043	0,000	0,025	0,023									
Solyc11g021280	Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)		C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM): PTHR33163:SF1:	0,000	0,128	0,000	0,149	0,094									
Solyc11g021290	Ycf1 (AHRD V3.3 *-* A0A0U1ZK62_SOLHA)		C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM): mobidb-lite (MOB	0,094	0,021	0,074	0,150	0,024									
Solyc11g021300	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZG15_SOLCE)		C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM): IPR008896 (PAN	0,042	0,085	0,000	0,025	0,023									
Solyc11g021310	Ycf1 (AHRD V3.3 *-* A0A0U1ZKJ5_SOLPI)		C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM): mobidb-lite (MOB	0,000	0,169	0,025	0,097	0,116									
Solyc11g021360	Protease Do-like 7 (AHRD V3.3 --* DEGP7_ARATH)					0,843	5,453	0,262	0,823	2,364	2,714	0,000					up		
Solyc11g021365	Heat shock protein DnaJ, cysteine-rich domain-containing protein (AHRD V3.3 *-* A0A118JYI6_CYNCS)		F:GO:0046983	F:protein dimerization activity	IPR008906 (PFAM): PTHR15852:SF1:	2,950	8,211	0,630	0,681	1,972	1,500	0,000	1,634	0,001			up	up	
Solyc11g022380	Phosphoinositide phosphatase family protein (AHRD V3.3 *** AT1G22620.1)		F:GO:0042578	F:phosphoric ester hydrolase activity	IPR002013 (PFAM): mobidb-lite (MOB	46,249	39,266	60,813	54,789	54,504									
Solyc11g022385	Acid phosphatase/vanadium-dependent haloperoxidase (AHRD V3.3 --* G7IRI8_MEDTR)				mobidb-lite (MOBIDB_LITE)	0,138	0,096	0,151	0,069	0,024									
Solyc11g022390	CDK5 regulatory subunit-associated protein 1-like 1 (AHRD V3.3 *** A0A0B0P0K6_GOSAR)		P:GO:0006400: F:G(	P:tRNA modification: F:transferase activity: F:4 iron. 4 sulfur clu	IPR007197 (PFAM): IPR013848 (PFA	15,291	13,413	22,259	21,121	21,430									
Solyc11g022395	Polyphenol oxidase I, chloroplastic (AHRD V3.3 --* PPO1_IPOBA)					0,061	0,043	0,047	0,048	0,048									
Solyc11g022400	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT1G22610.1)		C:GO:0005829: C:G(	C:cytosol: C:plasmodesma: C:chloroplast: C:integral component	IPR035892 (G3DSA:2.60.40.GENE3D	17,154	13,100	11,016	9,268	10,643									
Solyc11g022430	Homeobox leucine zipper protein (AHRD V3.3 *-* A0A072UAM9_MEDTR)		F:GO:0008289	F:lipid binding	IPR002913 (PFAM): PTHR24326 (PAN	0,000	0,000	0,000	0,022	0,000									
Solyc11g022460	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT1G22610.1)		C:GO:0005829: C:G(	C:cytosol: C:plasmodesma: C:chloroplast: C:integral component	IPR035892 (G3DSA:2.60.40.GENE3D	88,579	56,792	144,329	162,763	111,325	-0,614	0,017					down		
Solyc11g022470	Myb family transcription factor family protein (AHRD V3.3 *** B9N3W8_POPTR)		F:GO:0003677	F:DNA binding	IPR025756 (PFAM G2-like	31,584	34,670	39,904	40,678	38,607									
Solyc11g022530	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 *** A0A072UTU9_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR025423 (PFAM): G3DSA:1.20.120	3,180	3,081	18,178	23,625	21,295									
Solyc11g022540	Transmembrane 9 superfamily member (AHRD V3.3 *** K4D7A1_SOLLC)		C:GO:0016021	C:integral component of membrane	IPR004240 (PFAM): IPR004240 (PAN	74,182	76,322	91,776	95,661	81,011									
Solyc11g022590	trypsin inhibitor-like protein precursor		F:GO:0004866	F:endopeptidase inhibitor activity	IPR002160 (PRINTS): G3DSA:2.80.1(	94,290	38,262	2,072	0,175	0,258	-1,272	0,005					down		
Solyc11g022600	Mitochondrial transcription termination factor-like (AHRD V3.3 *-* Q6Z8L0_ORYSJ)		F:GO:0003690: P:G(	F:double-stranded DNA binding: P:regulation of transcription. DN	IPR038538 (G3DSA:1.25.70.GENE3D	6,375	4,892	4,511	5,144	4,918									
Solyc11g022605	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic (AHRD V3.3 *-* NDHJ_NICTO)		F:GO:0008137: P:G(	F:NADH dehydroge EC:1.6.99.5: EC:1.6. Acting on NADH or N	IPR037232 (G3DSA:3.30.460.GENE3I	0,021	0,018	0,068	0,000	0,024									
Solyc11g022610	30S ribosomal protein S4, chloroplastic (AHRD V3.3 *-* RR4_SOLBU)		F:GO:0003735: P:G(	F:structural constituent of ribosome: P:translation: C:small ribos	G3DSA:1.10.1050.10 (GENE3D): IPR(	0,000	0,019	0,000	0,000	0,024									
Solyc11g027630	LOW QUALITY:glycosyl hydrolase 9A3 (AHRD V3.3 --* AT4G24260.1)					0,395	0,712	0,376	0,965	0,591									
Solyc11g027640	LOW QUALITY:phosphatidylinositol 4-OH kinase beta1 (AHRD V3.3 --* AT5G64070.2)					0,079	0,000	0,025	0,073	0,023									
Solyc11g027645	Ribosomal RNA small subunit methyltransferase B (AHRD V3.3 --* W9QFJ5_9ROSA)				mobidb-lite (MOBIDB_LITE): mobidb-lit	13,250	16,951	14,907	35,170	20,909					1,244	0,000			up
Solyc11g027660	LOW QUALITY:DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain-containing protein (AHRD V3.3 --* AT5G60410.6)				PTHR33047 (PANTHER): PTHR33047	0,877	0,971	0,932	2,599	1,506					1,483	0,001			up
Solyc11g027670	LOW QUALITY:Cytochrome P450 like_TBP (AHRD V3.3 *-* O04892_TOBAC)				mobidb-lite (MOBIDB_LITE): mobidb-lit	3,179	4,929	4,397	8,110	5,112									
Solyc11g027690	LOW QUALITY:Flavin-binding kelch domain F box protein (AHRD V3.3 --* A0A088AWQ7_SOYBN)		F:GO:0016740	F:transferase activity	mobidb-lite (MOBIDB_LITE): mobidb-lit	4,198	7,078	4,862	11,387	6,818					1,236	0,007			up
Solyc11g027710	WRKY DNA-binding protein 55 (AHRD V3.3 --* AT2G40740.3)				PTHR33187 (PANTHER): PTHR33187	1,736	2,360	2,447	4,900	2,937					1,002	0,026			up
Solyc11g027730	LOW QUALITY:Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT3G13340.3)					2,039	2,979	2,157	5,983	3,980					1,478	0,006			up
Solyc11g027760	LOW QUALITY:Cytochrome P450 like_TBP (AHRD V3.3 *-* O04892_TOBAC)				PTHR34141 (PANTHER): PTHR34141	8,888	10,380	8,305	21,109	11,243					1,352	0,000			up
Solyc11g027770	Senescence-associated protein (AHRD V3.3 *-* A0A072THZ1_MEDTR)				PTHR33047 (PANTHER)	3,883	4,941	4,056	7,984	5,564									
Solyc11g027773	60S ribosomal protein L29, putative (AHRD V3.3 --* B9RZN1_RICCO)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation	IPR002673 (PFAM): mobidb-lite (MOB	0,021	0,018	0,046	0,022	0,000									
Solyc11g027775	40S ribosomal protein S5 (AHRD V3.3 *-* RS5_NICPL)		P:GO:0006412	P:translation	IPR036823 (G3DSA:1.10.455.GENE3I	0,563	0,299	0,496	0,410	0,920									
Solyc11g027800	Sulfotransferase (AHRD V3.3 *** K4D7C3_SOLLC)		F:GO:0008146	F:sulfotransferase activity	G3DSA:3.40.50.300 (GENE3D): IPR(	0,510	0,267	0,000	0,000	0,000									
Solyc11g027810	RING finger protein (AHRD V3.3 *** A0A0B0PUN2_GOSAR)		F:GO:0046872: F:G(	F:metal ion binding; F:ubiquitin protein ligase activity	IPR018957 (PFAM): IPR013083 (G3D	4,342	4,844	5,027	4,564	4,621									
Solyc11g027830	ATP-dependent protease La (LON) domain protein (AHRD V3.3 *** AT1G35340.1)		C:GO:0009507	C:chloroplast	IPR003111 (PFAM): G3DSA:2.30.130	9,388	9,874	3,492	3,038	4,462									
Solyc11g027840	1,4-beta-D-glucanase (AHRD V3.3 *** B4FHX7_MAIZE)		F:GO:0016787	F:hydrolase activity	IPR002925 (PFAM): IPR029058 (G3D	1,145	1,916	0,184	0,441	0,778									
Solyc11g027860	LOW QUALITY:BTB-POZ and MATH domain 5 (AHRD V3.3 --* AT5G21010.1)					0,000	0,000	0,000	0,025	0,000									
Solyc11g027870	Mitochondrial inner membrane organizing system protein 1 (AHRD V3.3 *** A0A1D1ZLH1_9ARAE)		C:GO:0061617	C:MICOS complex	IPR007512 (PFAM): IPR007512 (PAN	40,237	39,446	78,089	67,224	69,175									
Solyc11g027880	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G72160.1)		C:GO:0009507: P:G(	C:chloroplast: P:cellular response to auxin stimulus: P:protein lo	PR00180 (PRINTS): IPR011074 (PFA	36,096	31,488	4,612	4,246	3,838									
Solyc11g027910	LOW QUALITY:protein arginine methyltransferase 4A (AHRD V3.3 --* AT5G49020.2)					0,019	0,018	0,000	0,000	0,000									
Solyc11g027920	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *-* A0A144KR40_MAIZE)		F:GO:0005524: C:G(	F:ATP binding; C:chloroplast thylakoid membrane	G3DSA:3.40.50.300 (GENE3D): PTHF	1,123	1,972	0,548	0,049	1,395									
Solyc11g027986	Heat shock protein DnaJ with tetratricopeptide repeat-containing protein (AHRD V3.3 --* AT5G12430.1)					2,494	2,851	1,826	1,871	1,785									
Solyc11g027988	armadillo repeat only 4 (AHRD V3.3 --* AT3G26600.2)					0,100	0,122	0,046	0,025	0,047									
Solyc11g028000	Class II aaRS and biotin synthetases superfamily protein (AHRD V3.3 --* AT3G62120.2)					0,124	0,096	0,162	0,171	0,211									
Solyc11g028010	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** A0A061FL24_THE		F:GO:0005525	F:GTP binding	G3DSA:3.40.50.300 (GENE3D): IPR(	84,679	88,347	142,356	136,095	130,144									
Solyc11g028020	Tomato AGAMOUS like 11	tagl11	F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRIN' MIKC_MADS	22,904	28,392	4,704	4,470	4,851									
Solyc11g028070	Defensin-like protein (AHRD V3.3 *** DEF_TOBAC)		P:GO:0006952	P:defense response	IPR008176 (PRINTS): IPR036574 (G:	4,134	5,371	0,046	0,025	0,000									
Solyc11g028080	Transmembrane protein, putative (AHRD V3.3 *** G7JN47_MEDTR)		C:GO:0016021	C:integral component of membrane	PTHR33780 (PANTHER): PTHR33780	14,458	12,738	15,439	13,385	12,348									
Solyc11g028090	Elongation factor 1-gamma (AHRD V3.3 *-* EF1G_PRUAV)	EF1By2	F:GO:0003746: F:G(	F:translation elongation factor activity: F:protein binding: P:trans	G3DSA:1.20.1050.10 (GENE3D): IPR(	0,116	0,099	0,025	0,050	0,047									
Solyc11g028100	Elongation factor 1-gamma 1 (AHRD V3.3 *** EF1G1_ORYSJ)	EF1By3	F:GO:0003746: F:G(	F:translation elongation factor activity: F:protein binding: P:trans	G3DSA:1.20.1050.10 (GENE3D): IPR(	404,606	371,353	183,412	148,116	178,745									
Solyc11g028140	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLBU)		F:GO:0005524: C:G(	F:ATP binding; C:chloroplast	IPR008543 (PFAM): mobidb-lite (MOB	0,000	0,039	0,000	0,025	0,000									
Solyc11g028150	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 --* A0A151UBC4		P:GO:0001172: F:G(	P:transcription. RNA-templated: F:RNA-directed 5'-3' RNA polym	IPR008686 (PFAM): IPR008686 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc11g028160	Cytochrome c biogenesis B (AHRD V3.3 *** A0A0C5ARM5_HYONI)		F:GO:0015232: P:G(	F:heme transporter activity: P:heme transport: C:membrane: P:(	IPR003544 (PANTHER)	0,019	0,000	0,000	0,000	0,000									
Solyc11g028175	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *** A0A061FD65_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity	IPR008906 (PFAM): IPR003656 (PFA	0,021	0,039	0,000	0,000	0,000									
Solyc11g028180	DNA replication helicase (AHRD V3.3 --* AT1G08840.4)				mobidb-lite (MOBIDB_LITE)	0,019	0,021	0,000	0,000	0,000									
Solyc11g028200	ELF4-like 4 (AHRD V3.3 *** AT1G17455.2)		P:GO:0042753	P:positive regulation of circadian rhythm	IPR009741 (PFAM): PTHR33469:SF1	0,254	0,172	0,241	0,198	0,236									
Solyc11g028206	Adenylate isopentenyltransferase (AHRD V3.3 *** F6KQG9_MALDO)				G3DSA:3.40.50.300 (GENE3D): G3DS	0,000	0,019	0,000	0,000	0,000									
Solyc11g028310	DNA topoisomerase 6 subunit B (AHRD V3.3 *-* A0A0V0IMM5_SOLCH)		F:GO:0003677: F:G(	F:DNA binding: F:DI EC:3.6.1.3: EC:5.99. Adenosinetriphospha	IPR036890 (G3DSA:3.30.565.GENE3I	0,667	0,561	0,444	0,625	0,495									
Solyc11g030380	Elongation factor 4 (AHRD V3.3 *** A0A0B0MG27_GOSAR)		C:GO:0016021	C:integral component of membrane	PTHR33874:SF3 (PANTHER): PTHR3:	0,040	0,104	0,025	0,000	0,000									
Solyc11g030390	Elongation factor 4 (AHRD V3.3 *** A0A0B0MG27_GOSAR)		C:GO:0016021	C:integral component of membrane	PTHR33874:SF3 (PANTHER): PTHR3:	33,148	28,879	42,811	39,727	37,050									
Solyc11g030475	Mannosyltransferase (AHRD V3.3 *-* K4AYT1_SOLLC)		C:GO:0005783: C:G(	C:endoplasmic reticulum: C:endoplasmic reticulum lumen: C:end	mobidb-lite (MOBIDB_LITE)	7,640	5,388	4,856	4,468	5,235									
Solyc11g030550	Cyclin family protein (AHRD V3.3 *-* AT5G06150.2)		P:GO:0031047	P:gene silencing by RNA	G3DSA:1.10.472.10 (GENE3D): IPR(	9,365	6,550	6,953	4,855	5,183									
Solyc11g030570	LOW QUALITY:NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 *-* NU4M_WHEAT)		F:GO:0008137: P:G(	F:NADH dehydroge EC:1.6.99.5: EC:1.6. Acting on NADH or N	IPR001750 (PFAM): IPR003918 (PAN	0,042	0,043	0,118	0,171	0,000									
Solyc11g030600	cytosine-5 DNA methyltransferase	smet	F:GO:0003682: F:G(	F:chromatin binding EC:2.1.1.37 DNA (cytosine-5-)-m	IPR001525 (PRINTS): G3DSA:2.30.3(	63,781	58,409	31,697	27,922	28,829									
Solyc11g030700	UPF0301 protein (AHRD V3.3 *-* A0A0B2SQH2_GLYSO)					1,570	1,303	2,806	2,750	2,028									
Solyc11g030710	UPF0301 protein (AHRD V3.3 *** A0A0B2QLB9_GLYSO)				G3DSA:3.40.1740.10 (GENE3D): IPR(	20,540	17,521	34,377	32,888	32,282									
Solyc11g030720	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TLD0_MEDTR)		P:GO:0055114	P:oxidation-reduction process	G3DSA:3.40.50.720 (GENE3D): IPR0	6,531	7,172	6,442	6,937	6,922									
Solyc11g030730	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity. acting on paired do	IPR001128 (PRINTS): IPR002401 (PF	3,012	5,671	0,721	1,408	2,117									
Solyc11g030865	transmembrane protein (AHRD V3.3 *-* AT2G07674.1)		C:GO:0016020	C:membrane	PTHR35289 (PANTHER): PD020792 (	0,042	0,021	0,000	0,000	0,000									
Solyc11g030910	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G02780.2)					0,059	0,079	0,174	0,075	0,142									
Solyc11g030957	Branched-chain-amino-acid aminotransferase (AHRD V3.3 --* M1A1M6_SOLTU)					0,040	0,041	0,000	0,025	0,000									
Solyc11g031950	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT4G09990.1)		P:GO:0045492	P:xylan biosynthetic process	IPR021148 (PFAM): IPR006514 (TIGF	0,413	0,424	0,047	0,025	0,071									
Solyc11g031960	Lipase, GDSL (AHRD V3.3 *** A0A103V493_CYNCS)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM): IPR036514 (G3D	0,000	0,019	0,000	0,000	0,000									
Solyc11g031970	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** A0A0B0P3R2_GOSAR)		C:GO:0016021	C:integral component of membrane	IPR018392 (PFAM): IPR036779 (G3D	1,202	1,770	3,776	4,500	4,720									
Solyc11g032050	GDSL esterase/lipase (AHRD V3.3 *** W9S0Q7_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	1,094	0,782	0,000	0,126	0,023									
Solyc11g032060	GDSL esterase/lipase (AHRD V3.3 *** W9S0Q7_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	1,347	2,505	0,410	0,985	0,491									
Solyc11g032090	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)		C:GO:0016021	C:integral component of membrane	PTHR33916 (PANTHER): PTHR33916	6,712	8,328	1,712	0,959	1,644									
Solyc11g032100	Tomato AGAMOUS 12	tagl12	F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I	IPR002100 (PRIN' MIKC_MADS	3,989	3,502	2,284	1,645	1,176									
Solyc11g032110	zinc ion binding/nucleic acid binding protein (AHRD V3.3 --* AT2G47090.3)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,000	0,000	0,000	0,000									
Solyc11g032120	Cyclin/Brf1-like TBP-binding protein (AHRD V3.3 --* AT2G01280.3)				mobidb-lite (MOBIDB_LITE)	0,021	0,018	0,000	0,000	0,000									
Solyc11g032130	FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 --* AT3G55520.3)				mobidb-lite (MOBIDB_LITE)	1,696	3,309	1,923	1,963	1,861									
Solyc11g032133	12-oxophytodienoate reductase-like protein (AHRD V3.3 *** G7K3S4_MEDTR)		F:GO:0010181: F:G(	F:FMN binding: F:oxidoreductase activity: P:oxidation-reduction	IPR001155 (PFAM): IPR013785 (G3D	14,421	22,292	18,382	17,338	18,420									
Solyc11g032190	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT2G14080.2)					1,770	1,809	1,355	1,771	1,763									
Solyc11g032200	Lipase (AHRD V3.3 *** K4D7Q5_SOLLC)		P:GO:0006629: F:G(	P:lipid metabolic process: F:hydrolase activity. acting on ester b	IPR025483 (PIRSF): IPR029058 (G3D	13,711	13,787	13,486	14,455	15,439									
Solyc11g032220	12-oxophytodienoate reductase-like protein (AHRD V3.3 *** G7K3S4_MEDTR)		F:GO:0010181: F:G(	F:FMN binding: F:oxidoreductase activity: P:oxidation-reduction	IPR001155 (PFAM): IPR013785 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc11g032230	12-oxophytodienoate reductase-like protein (AHRD V3.3 *** G7K3S2_MEDTR)		F:GO:0010181: F:G(	F:FMN binding: F:oxidoreductase activity: P:oxidation-reduction	IPR001155 (PFAM): IPR013785 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc11g032235	12-oxophytodienoate reductase-like protein (AHRD V3.3 *** G7K3S4_MEDTR)		F:GO:0010181: F:G(	F:FMN binding: F:oxidoreductase activity: P:oxidation-reduction	IPR001155 (PFAM): IPR013785 (G3D	0,019	0,000	0,000	0,000	0,000									
Solyc11g033260	Pseudouridine-5'-phosphate glycosidase (AHRD V3.3 *** A0A0B0NN49_GOSAR)		F:GO:0016798	F:hydrolase activity, acting on glycosyl bonds	IPR007342 (PFAM): IPR022830 (G3D	12,938	11,964	14,441	15,584	15,422									
Solyc11g033270	MAP kinase kinase kinase 82	MAPKKK82	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati	IPR001245 (PRINTS): G3DSA:1.10.51	223,094	163,868	155,416	149,267	160,745									
Solyc11g033280	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9S4I6_RICCO)		F:GO:0003676: F:G(	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): G3DS	97,924	107,195	119,580	108,835	106,323									
Solyc11g038340	LOW QUALITY:Nuclear control of ATP synthase 2 (AHRD V3.3 --* Q01GB1_OSTTA)					0,040	0,078	0,075	0,025	0,000									
Solyc11g038350	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT2G26790.2)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc11g039350	LOW QUALITY:mitochondrial editing factor 19 (AHRD V3.3 --* AT3G05240.1)					0,019	0,021	0,000	0,025	0,000									
Solyc11g039360	Cytochrome c biogenesis FC (AHRD V3.3 *** W0FFF8_HELAN)		C:GO:0005739: C:G(	C:mitochondrion; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,050	0,023									
Solyc11g039370	LOW QUALITY:Glycosyl hydrolase superfamily protein (AHRD V3.3 --* AT3G15800.1)					0,000	0,036	0,096	0,000	0,000									
Solyc11g039380	LOW QUALITY:TRICHOME BIREFRINGENCE-LIKE 9 (AHRD V3.3 --* AT5G06230.3)					0,019	0,000	0,000	0,025	0,000									
Solyc11g039480	LOW QUALITY:ATP-dependent zinc metalloprotease (AHRD V3.3 --* AT1G56180.1)					4,579	3,153	1,262	1,357	1,365									
Solyc11g039530	LOW QUALITY:30S ribosomal protein S3, chloroplastic (AHRD V3.3 *-* RR3_SOLTU)		F:GO:0003723	F:RNA binding	IPR015946 (G3DSA:3.30.300.GENE3I	0,042	0,041	0,000	0,126	0,117									
Solyc11g039550	LOW QUALITY:Unknown protein (AHRD V3.3)					0,098	0,021	0,068	0,000	0,024									
Solyc11g039590	PAS domain-containing protein tyrosine kinase family protein (AHRD V3.3 --* AT5G49470.2)					0,000	0,000	0,125	0,224	0,073									
Solyc11g039650	Dynamin (AHRD V3.3 *** A0A103XDG1_CYNCS)		F:GO:0003924: F:G(	F:GTPase activity: EC:3.6.1.15 Nucleoside-triphosph	IPR022812 (PRINTS): IPR003130 (PF	206,836	246,488	246,334	228,804	222,483									
Solyc11g039670	LOW QUALITY:transcription coactivator (AHRD V3.3 --* AT1G77320.3)					0,094	0,018	0,000	0,000	0,000									
Solyc11g039740	UPF0496 protein (AHRD V3.3 *** A0A0B2Q4B8_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR007749 (PFAM): mobidb-lite (MOB	38,061	20,229	17,104	25,050	17,587	-0,886	0,000			0,552	0,002	down		up
Solyc11g039750	MYB transcription factor (AHRD V3.3 *-* B9I4W4_POPTR)		F:GO:0003677	F:DNA binding	IPR001005 (PFAM MYB_related	0,019	0,021	0,000	0,000	0,000									
Solyc11g039830	Glycyl-tRNA synthetase family protein (AHRD V3.3 *** B9GMU1_POPTR)		F:GO:0004820: F:G(	F:glycine-tRNA ligas EC:6.1.1.14 Glycine--tRNA ligase	IPR002315 (PRINTS): G3DSA:3.30.9:	82,593	91,179	130,633	113,792	121,654									
Solyc11g039840	Cytochrome b-c1 complex subunit Rieske, mitochondrial (AHRD V3.3 *** UCRI_SOLTU)		F:GO:0008121: C:G(	F:ubiquinol-cytochr EC:1.1.2: EC:1.1.2.2 Acting on diphenols a	IPR005805 (PRINTS): IPR004192 (PF	562,152	569,805	938,194	943,068	950,345									
Solyc11g039860	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G77360.2)					13,188	31,242	10,140	35,224	29,701			1,549	0,000	1,804	0,001		up	up
Solyc11g039880	Nuclear pore complex protein Nup188a (AHRD V3.3 *** W6JJC0_NICBE)				PTHR31431 (PANTHER)	34,309	32,791	31,139	33,454	33,795									
Solyc11g039890	Nuclear pore complex protein Nup188a (AHRD V3.3 *-* W6JJC0_NICBE)		C:GO:0005643	C:nuclear pore	IPR021827 (PFAM): PTHR31431 (PAI	2,546	2,401	2,384	2,392	2,210									
Solyc11g039910	Mitochondrial import inner membrane translocase subunit Tim17-like protein (AHRD V3.3 *** A0A0B0N743_(		C:GO:0005744: F:G(	C:TIM23 mitochondrial import inner membrane translocase com	PF02466 (PFAM): mobidb-lite (MOBID	88,227	92,818	78,128	72,882	73,465									
Solyc11g039930	Dehydroascorbate reductase (AHRD V3.3 *-* Q1G0W3_SOLLC)	DHAR6	P:GO:0010731: F:G(	P:protein glutathion EC:1.8.5.1 Glutathione dehydroc	G3DSA:1.20.1050.10 (GENE3D): PTH	0,000	0,021	0,000	0,000	0,023									
Solyc11g039950	Ca(2+)-dependent nuclease family protein (AHRD V3.3 --* AT2G40410.2)					2,934	2,397	1,833	1,799	1,150									
Solyc11g039953	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT4G10110.1)		F:GO:0003676	F:nucleic acid binding	IPR012677 (G3DSA:3.30.70.GENE3D	17,555	24,691	16,878	21,034	22,280									
Solyc11g039960	peptidoglycan-binding LysM domain-containing protein (AHRD V3.3 *** AT5G08200.1)				IPR018392 (PFAM): IPR036779 (G3D	13,535	14,806	14,303	14,922	12,852									
Solyc11g039980	ATP synthase subunit alpha (AHRD V3.3 *** Q5M9V4_TOBAC)		F:GO:0005524: P:G(	F:ATP binding: P:ATP metabolic process: P:proton transmembra	IPR000194 (PFAM): IPR023366 (G3D	1,632	2,823	1,835	4,698	1,967									
Solyc11g039990	Protein plastid transcriptionally active 16, chloroplastic (AHRD V3.3 --* PTA16_ARATH)		C:GO:0005739: C:G(	C:mitochondrion; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,022	0,000	0,000									
Solyc11g040030	30S ribosomal protein S19, chloroplastic (AHRD V3.3 --* RR19_CALFG)					0,237	0,222	0,264	0,340	0,357									
Solyc11g040040	Phototropic-responsive NPH3 family protein (AHRD V3.3 *** AT3G19850.1)		F:GO:0005515	F:protein binding	G3DSA:3.30.710.10 (GENE3D): IPR0:	3,314	2,775	2,888	3,566	3,509									
Solyc11g040050	RNA binding protein, putative (AHRD V3.3 *** B9S3N2_RICCO)		F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM): IPR012677 (G3D	19,520	18,597	22,769	19,539	18,331									
Solyc11g040060	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199VXB2_ANACO)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	5,409	5,001	2,565	3,263	3,236									
Solyc11g040063	Ribosomal protein S3 (AHRD V3.3 *-* I3NTS2_9LAMI)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: C:mitochondrion: C:ribosome: P:translation: C:cyto		2,110	1,724	0,878	0,825	1,059									
Solyc11g040067	F-box/associated interaction domain protein (AHRD V3.3 --* AT1G53360.2)					0,902	0,810	1,062	0,727	0,683									
Solyc11g040105	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity	IPR008906 (PFAM): IPR025525 (PFA	3,575	3,920	3,745	2,884	2,921									
Solyc11g040110	cobalt ion-binding protein (AHRD V3.3 *** AT5G47870.1)		P:GO:0000724: F:G(	P:double-strand break repair via homologous recombination: F:I	mobidb-lite (MOBIDB_LITE): mobidb-lit	34,608	36,798	46,822	40,869	44,180									
Solyc11g040120	DNA helicase (AHRD V3.3 *** M0ZQ54_SOLTU)		F:GO:0003677: F:G(	F:DNA binding: F:ATP binding: C:nucleus: P:DNA replication initi	IPR008045 (PRINTS): IPR001208 (PF	58,931	53,703	82,292	73,713	77,402									
Solyc11g040130	TVP38/TMEM64 family membrane protein (AHRD V3.3 *** A0A0B0NAW3_GOSAR)		C:GO:0016021	C:integral component of membrane	IPR032816 (PFAM): mobidb-lite (MOB	11,667	11,003	28,555	33,494	25,239									
Solyc11g040140	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4D7Y8_SOLLC)		F:GO:0004553: C:G(	F:hydrolase activity EC:2.4.1.27 Xyloglucan:xyloglucc	IPR000757 (PFAM): IPR010713 (PFA	0,000	0,043	0,168	0,167	0,140									
Solyc11g040150	Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *** A0A0B0P2Z2_GOSAR)		C:GO:0016021: F:G(	C:integral component of membrane: F:transferase activity. trans	IPR012429 (PFAM): mobidb-lite (MOB	22,037	23,128	4,072	2,577	5,838									
Solyc11g040170	mRNA-capping enzyme (AHRD V3.3 *-* W9RTY7_9ROSA)		F:GO:0003910: F:G(	F:DNA ligase (ATP) EC:2.7.7.5: EC:3.1.3 mRNA guanylyltransf	IPR029021 (G3DSA:3.90.190.GENE3I	9,932	7,667	7,892	8,142	8,800									

Solyc11g040173	RING/U-box superfamily protein (AHRD V3.3 --* AT3G19910.2)				1,720	1,275	1,654	1,650	1,606									
Solyc11g040180	mRNA capping enzyme family protein (AHRD V3.3 *** AT3G09100.2)	F:GO:0003910; F:GC	F:DNA ligase (ATP) EC:2.7.7.5; EC:3.1.3 mRNA guanylyltransfe	IPR013846 (PFAM); IPR001339 (PFA	38,421	32,346	31,060	34,118	31,886									
Solyc11g040220	Ribosomal protein L37 (AHRD V3.3 *** A0A0V0HB71_SOLCH)	F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	IPR011331 (G3DSA:2.20.25.GENE3D	0,059	0,200	0,121	0,025	0,142									
Solyc11g040221	Peptidyl-prolyl cis-trans isomerase CYP18-2 (AHRD V3.3 --* CP18B_ARATH)				0,000	0,000	0,022	0,000	0,000									
Solyc11g040222	Cytochrome P450 (AHRD V3.3 *-* W9R369_9ROSA)	F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do	IPR001128 (PRINTS); IPR002401 (PF	5,797	5,001	3,990	4,231	4,452									
Solyc11g040224	Cytochrome P450 97B2, chloroplastic (AHRD V3.3 --* A0A199UIU7_ANACO)	F:GO:0004497; F:GC	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase activity, acting on paired donors, with i		0,956	0,807	0,824	0,927	0,870									
Solyc11g040260	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9STG7_RICCO)	F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR011990 (G3D	11,135	11,969	15,429	18,067	18,233									
Solyc11g040270	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G40910.6)				0,077	0,122	0,072	0,124	0,023									
Solyc11g040285	Ribosomal protein S10p/S20e family protein (AHRD V3.3 --* AT3G13120.3)				1,404	1,450	1,625	2,039	1,578									
Solyc11g040300	transmembrane protein (AHRD V3.3 *-* AT4G10080.1)	C:GO:0016021	C:integral component of membrane	PTHR33646:SF3 (PANTHER); PTHR3	0,639	1,133	1,303	0,848	1,103									
Solyc11g040330	Endo-1,4-beta-xylanase A (AHRD V3.3 *** W9QKK9_9ROSA)	F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D); IPR00	1,407	1,487	0,476	0,482	0,330									
Solyc11g040340	LEE14BDGL L.esculentum endo-1,4-beta-D-glucanase cel7	F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR012341 (G3DSA:1.50.10.GENE3D	2,253	2,962	0,143	0,000	0,024									
Solyc11g040370	Far upstream element-binding protein 2 (AHRD V3.3 *** A0A0B2RS73_GLYSO)	F:GO:0003723	F:RNA binding	IPR036612 (G3DSA:3.30.1370.GENE	139,677	153,344	174,603	169,365	170,392									
Solyc11g040380	Homoserine dehydrogenase (AHRD V3.3 *-* S8BUI7_9LAMI)	P:GO:0006520; P:GC	P:cellular amino acid metabolic process; P:oxidation-reduction p	IPR001342 (PFAM); G3DSA:3.40.50.7	6,332	7,100	11,870	13,177	11,986									
Solyc11g040390	Aspartokinase-homoserine dehydrogenase (AHRD V3.3 *** O65027_SOYBN)	F:GO:0004072; F:GC	F:aspartate kinase EC:1.1.1.3; EC:2.7.2 Homoserine dehydro	IPR001342 (PFAM); IPR001048 (PFA	51,400	54,927	89,722	87,645	91,032									
Solyc11g040410	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* A0A068EW35_SOLLC)	F:GO:0043531	F:ADP binding	PTHR23155 (PANTHER); PTHR23155	0,037	0,021	0,000	0,000	0,023									
Solyc11g042420	Cytochrome c (AHRD V3.3 *** CYC_SOLTU)	F:GO:0009055; F:GC	F:electron transfer activity; F:heme binding	IPR002327 (PRINTS); IPR009056 (PF	1,192	0,928	0,389	0,539	0,329									
Solyc11g042430	Protein phosphatase methylesterase 1 (AHRD V3.3 *** K4D815_SOLLC)	P:GO:0006482; F:GC	P:protein demethyla EC:3.1.1.1 Carboxylesterase	IPR000073 (PRINTS); IPR029058 (G3	17,180	14,562	18,968	16,343	15,825									
Solyc11g042440	LOW QUALITY:NF-X-like 1 (AHRD V3.3 --* AT1G10170.4)			mobidb-lite (MOBIDB_LITE); PTHR351	3,440	2,147	1,951	1,908	2,017									
Solyc11g042460	Non-lysosomal glucosylceramidase (AHRD V3.3 *** K4D818_SOLLC)	F:GO:0004348; P:GC	F:glucosylceramida EC:3.2.1.45 Glucosylceramidase	IPR014551 (PIRSF); IPR024462 (PFA	30,676	15,734	9,933	8,137	7,509									
Solyc11g042500	TUBULIN-FOLDING COFACTOR E family protein (AHRD V3.3 *** B9IQ98_POPTR)	F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	6,050	5,532	3,673	5,264	4,940									
Solyc11g042520	LOW QUALITY:Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 --* AT2G42930.1)				0,021	0,021	0,000	0,025	0,000									
Solyc11g042523	Tubulin-specific chaperone E (AHRD V3.3 *-* W9RLI1_9ROSA)	C:GO:0009507; P:GC	C:chloroplast; P:embryo development ending in seed dormancy	G3DSA:3.10.20.90 (GENE3D); PTHR1	4,433	3,972	2,844	3,618	3,382									
Solyc11g042560	Ethylene-responsive transcription factor ERF021 family (AHRD V3.3 *** A0A151SD08_CAJCA)	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	3,446	1,038	0,667	0,986	1,170	-1,709	0,009					down		
Solyc11g042580	Ethylene-responsive transcription factor ERF021 (AHRD V3.3 *** ERF21_ARATH)	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN ERF	0,302	0,172	0,172	0,146	0,189									
Solyc11g042610	Ribosomal protein S5/S7 (AHRD V3.3 *** A0A103XH68_CYNCS)	F:GO:0003735; P:GC	F:structural constituent of ribosome; P:translation; C:small ribos	IPR000235 (PIRSF); IPR036823 (G3D	46,708	56,134	42,985	36,685	36,138									
Solyc11g042620	Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *-* AT1G71480.2)	C:GO:0009535	C:chloroplast thylakoid membrane	G3DSA:3.10.450.50 (GENE3D); IPR0	20,417	19,104	45,763	39,365	46,894									
Solyc11g042630	DUF506 family protein (AHRD V3.3 *** G7K973_MEDTR)			IPR006502 (PFAM); IPR006502 (TIGF	1,065	1,605	0,050	0,000	0,023									
Solyc11g042640	Rieske domain containing protein (AHRD V3.3 *** B6U301_MAIZE)	F:GO:0008942; F:GC	F:nitrite reductase [EC:1.7.1.4 Nitrite reductase (NA	IPR012748 (PFAM); IPR036922 (G3D	30,170	40,050	31,831	29,183	45,707			0,519	0,001				up	
Solyc11g042710	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT2G24190.2)	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process	IPR002347 (PFAM); G3DSA:3.40.50.7	0,021	0,000	0,000	0,072	0,000									
Solyc11g042740	Eukaryotic initiation factor 4A-2 (AHRD V3.3 --* IF4A2_NICPL)				0,058	0,062	0,000	0,075	0,000									
Solyc11g042800	Late embryogenesis abundant protein (AHRD V3.3 *-* Q56ZD1_ARATH)	C:GO:0005829	C:cytosol	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,159	0,568	0,244	0,479	0,023									
Solyc11g042810	Hexosyltransferase (AHRD V3.3 *** K4D848_SOLLC)	P:GO:0006486; F:GC	P:protein glycosylation; F:galactosyltransferase activity; C:mem	IPR025298 (PFAM); G3DSA:3.90.550	0,059	0,194	0,000	0,000	0,000									
Solyc11g042820	Major facilitator superfamily protein (AHRD V3.3 *** AT1G59740.1)	C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmem	IPR000109 (PFAM); G3DSA:1.20.125	0,585	0,565	0,306	0,116	0,375									
Solyc11g042850	pfkB-like carbohydrate kinase family protein (AHRD V3.3 *** AT4G10260.1)	C:GO:0005829; P:GC	C:cytosol; P:fructos EC:2.7.1.4; EC:2.7.1 Fructokinase; Hexoki	IPR011611 (PFAM); IPR029056 (G3D	0,021	0,018	0,022	0,000	0,023									
Solyc11g042855	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151RUJ4_CAJCA)			IPR019557 (PFAM); PTHR44194 (PAI	0,056	0,036	0,000	0,000	0,000									
Solyc11g042870	60S ribosomal protein L7A-like (AHRD V3.3 *-* Q2VCI3_SOLTU)	P:GO:0000470; F:GC	P:maturation of LSU-rRNA; F:RNA binding; C:cytosolic large ribo	IPR038524 (G3DSA:3.30.1330.GENE	0,021	0,019	0,000	0,000	0,000									
Solyc11g042880	Late embryogenesis abundant protein (AHRD V3.3 *** A0A072UNH6_MEDTR)	C:GO:0016021	C:integral component of membrane	IPR004864 (PFAM); PTHR31852:SF8	0,349	0,362	0,000	0,000	0,000									
Solyc11g042883	60S ribosomal protein L7A-like (AHRD V3.3 *-* Q2VCI3_SOLTU)	C:GO:0005840; P:GC	C:ribosome; P:ribosome biogenesis	IPR038524 (G3DSA:3.30.1330.GENE	0,858	0,825	0,818	0,339	0,682									
Solyc11g042890	RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain-containing protein (	C:GO:0016021	C:integral component of membrane		0,040	0,000	0,000	0,000	0,000									
Solyc11g042920	Plasma membrane ATPase (AHRD V3.3 --* PMA1_WHEAT)	C:GO:0016020	C:membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,814	2,563	1,426	1,397	1,852									
Solyc11g042930	SKP1 (AHRD V3.3 *** Q68GS0_TOBAC)	P:GO:0006511	P:ubiquitin-dependent protein catabolic process	IPR016073 (PFAM); G3DSA:3.30.710	487,309	483,088	475,152	393,788	448,744									
Solyc11g042940	Xylulose kinase, putative (AHRD V3.3 *** B9RHB4_RICCO)	P:GO:0005975; F:GC	P:carbohydrate metabolic process; F:phosphotransferase activi	IPR018484 (PFAM); G3DSA:3.30.420	20,383	26,258	4,628	3,241	8,742									
Solyc11g042970	LOW QUALITY:Pentatricopeptide repeat-containing family protein (AHRD V3.3 *-* B9GWP3_POPTR)	F:GO:0005515	F:protein binding	IPR002885 (PFAM); IPR002885 (TIGF	0,000	0,000	0,000	0,000	0,024									
Solyc11g042990	Protein kinase family protein (AHRD V3.3 *** F4I313_ARATH)	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); G3DSA:1.10.510	91,167	76,619	101,865	102,685	101,723									
Solyc11g043010	Translocase of chloroplast 120 (AHRD V3.3 *-* W9QKE7_9ROSA)	F:GO:0005525	F:GTP binding	G3DSA:3.40.50.300 (GENE3D); IPR0	0,000	0,000	0,000	0,025	0,024									
Solyc11g043060	Disease resistance protein (AHRD V3.3 *-* A0A068EW43_SOLHA)	F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,199	0,073	0,000	0,000	0,000									
Solyc11g043070	Disease resistance protein (AHRD V3.3 *-* A0A068F1E3_SOLHA)	F:GO:0043531	F:ADP binding	PTHR23155:SF414 (PANTHER); PTHI	0,239	0,116	0,075	0,000	0,024									
Solyc11g043090	Disease resistance protein (AHRD V3.3 *-* A0A068EUA9_SOLLC)	F:GO:0043531	F:ADP binding	IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,000	0,000	0,000	0,024									
Solyc11g043110	GDSL esterase/lipase (AHRD V3.3 *** W9SHN8_9ROSA)	F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	36,727	23,914	0,639	1,552	0,047									
Solyc11g043115	Cytochrome c biogenesis protein CcsA (AHRD V3.3 --* CCSA_WELMI)				5,356	3,781	0,025	0,226	0,000									
Solyc11g043120	Phosphatidylinositol 4-kinase, putative (AHRD V3.3 *-* B9RZB3_RICCO)	F:GO:0016301; P:GC	F:kinase activity; P:phosphatidylinositol phosphorylation; P:pho	IPR001263 (PFAM); G3DSA:3.30.101	39,435	38,879	46,720	42,939	44,420									
Solyc11g043130	Phosphatidylinositol 4-kinase alpha-like protein (AHRD V3.3 *** A0A0B0N164_GOSAR)	P:GO:0046854; P:GC	P:phosphatidylinositol phosphorylation; P:phosphatidylinositol-m	PTHR10048:SF15 (PANTHER); IPR01	74,768	61,471	79,286	84,842	82,552									
Solyc11g043140	HAUS augmin-like complex subunit 6 (AHRD V3.3 --* A0A1D1Y0Z2_9ARAE)				0,021	0,019	0,000	0,000	0,000									
Solyc11g043150	Signal recognition particle receptor subunit beta (AHRD V3.3 *** W9RN76_9ROSA)	F:GO:0005525	F:GTP binding	IPR019009 (PFAM); G3DSA:3.40.50.3	40,210	38,191	32,899	32,471	30,681									
Solyc11g043155	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THECC)	F:GO:0003677	F:DNA binding	IPR025525 (PFAM); PTHR23272:SF5	3,566	3,581	3,973	3,078	3,195									
Solyc11g043170	Dynamin (AHRD V3.3 *-* A0A118K0T3_CYNCS)	F:GO:0005525	F:GTP binding	IPR022812 (PRINTS); IPR022812 (PF	17,001	16,263	21,488	18,767	21,874									
Solyc11g043180	LOW QUALITY:Sister-chromatide cohesion protein (AHRD V3.3 --* A0A072UEZ1_MEDTR)			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,025	0,000									
Solyc11g043190	Ribosomal protein L5 (AHRD V3.3 *-* Q70G83_SOLCO)	F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	PTHR11994:SF11 (PANTHER); IPR00	0,000	0,000	0,025	0,025	0,000									
Solyc11g043210	Dynamin, putative (AHRD V3.3 *** B9T3E4_RICCO)	F:GO:0003924; F:GC	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR022812 (PRINTS); IPR003130 (PF	70,493	71,675	85,787	89,330	90,565									
Solyc11g044230	costars family protein (AHRD V3.3 *** AT4G33640.2)	P:GO:0032970	P:regulation of actin filament-based process	IPR038095 (G3DSA:1.10.10.GENE3D	108,227	99,131	81,572	72,389	75,145									
Solyc11g044250	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NYY6_ZOSMR)	P:GO:0006813; F:GC	P:potassium ion transport; F:solute:proton antiporter activity; C:	IPR006153 (PFAM); IPR003148 (PFA	9,038	11,892	11,256	12,123	12,706									
Solyc11g044260	K(+) efflux antiporter (AHRD V3.3 *-* A0A0K9NYY6_ZOSMR)	P:GO:0006812; F:GC	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR006153 (PFAM); IPR038770 (G3D	4,267	4,256	3,936	5,864	5,434									
Solyc11g044270	Major facilitator superfamily protein (AHRD V3.3 *** AT2G22730.3)	C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM); G3DSA:1.20.125	20,690	14,913	30,283	34,978	31,281									
Solyc11g044310	Proline iminopeptidase (AHRD V3.3 *** K4D899_SOLLC)	F:GO:0004177; C:GC	F:aminopeptidase a EC:3.4.11 Acting on peptide bor	IPR000073 (PRINTS); IPR002410 (PF	29,002	31,787	26,737	26,225	27,873									
Solyc11g044320	Myb transcription factor (AHRD V3.3 *** A0A072VG04_MEDTR)	C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; P:nucleosome assem	IPR036388 (G3DS MYB_related	12,506	12,368	30,089	30,266	27,097									
Solyc11g044330	Zinc finger SWIM domain-containing protein 7 (AHRD V3.3 *** A0A151SYF3_CAJCA)	F:GO:0008270	F:zinc ion binding	PTHR28498 (PANTHER)	3,236	2,555	2,534	2,270	2,421									
Solyc11g044340	pre-mRNA-processing protein 40A (AHRD V3.3 *** AT1G44910.1)	F:GO:0005515; P:GC	F:protein binding; P:mRNA cis splicing, via spliceosome	G3DSA:2.20.70.10 (GENE3D); IPR03	20,266	18,929	15,620	15,729	16,458									
Solyc11g044360	mTERF family protein	F:GO:0003690; P:GC	F:double-stranded DNA binding; P:regulation of transcription, DI	IPR038538 (G3DSA:1.25.70.GENE3D	3,849	4,259	2,817	4,223	5,574			0,973	0,001				up	
Solyc11g044430	LOW QUALITY:PWWP domain-containing family protein (AHRD V3.3 *-* U5GDF3_POPTR)			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,025	0,046									
Solyc11g044450	DnaJ-like protein (AHRD V3.3 *** E9P1K1_MUSAC)	P:GO:0006457; F:GC	P:protein folding; F:unfolded protein binding	IPR001623 (PRINTS); IPR036869 (G3	4,854	5,040	0,359	0,262	0,281									
Solyc11g044455	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SUT9_CAJCA)			IPR019557 (PFAM); mobidb-lite (MOB	0,145	0,100	0,000	0,000	0,071									
Solyc11g044460	Receptor-like kinase (AHRD V3.3 *** G7J6J8_MEDTR)	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM); G3DSA:1.10.510	0,000	0,021	0,000	0,000	0,023									
Solyc11g044470	RNA binding protein, putative (AHRD V3.3 *** B9RW95_RICCO)	F:GO:0003676	F:nucleic acid binding	IPR000504 (PFAM); IPR012677 (G3D	47,903	61,418	20,580	25,943	23,638									
Solyc11g044480	Protein EFR3 like B (AHRD V3.3 *** A0A0B2R6R2_GLYSO)	P:GO:0072659	P:protein localization to plasma membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	76,746	63,513	87,469	90,664	89,474									
Solyc11g044510	B3 DNA binding domain-containing protein (AHRD V3.3 *** A0A103XMR5_CYNCS)	F:GO:0003677; C:GC	F:DNA binding; C:nucleus	IPR015300 (G3DSA:2.40.330.GENE3	13,211	13,142	12,422	12,562	13,414									
Solyc11g044530	Plastid-lipid associated protein PAP / fibrillin family protein (AHRD V3.3 *** AT3G26070.1)			IPR006843 (PFAM); PTHR31906:SF1	5,256	8,812	1,119	1,450	2,347			1,051	0,042				up	
Solyc11g044535	TBC1 domain family member 13 (AHRD V3.3 *-* A0A0B0MMD4_GOSAR)			IPR035969 (SUPERFAMILY)	3,767	4,202	4,030	3,698	3,772									
Solyc11g044540	Na+/H+ antiporter (AHRD V3.3 *** A0A072VQN5_MEDTR)	C:GO:0016021; P:GC	C:integral component of membrane; P:transmembrane transport	IPR004680 (PFAM); PTHR43269:SF2	48,619	51,199	76,027	74,577	84,090									
Solyc11g044560	ABA responsive transcription factor (AHRD V3.3 *** G5EM38_SOLLC)	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of trans	IPR004827 (PFAM bZIP	112,616	106,048	56,472	42,917	54,153					-0,394	0,029			down
Solyc11g044590	ubiquitin-specific protease 8 (AHRD V3.3 --* AT5G22030.1)	F:GO:0005488	F:binding	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,056	0,000	0,000	0,000	0,000									
Solyc11g044610	NAD(P)H-quinone oxidoreductase chain 4, chloroplastic (AHRD V3.3 --* NU4C_AGRST)			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,142	0,000	0,101	0,093									
Solyc11g044620	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 3, chloroplastic (AHRD V3.3 --* NU3C_ADICA)	C:GO:0009507	C:chloroplast	mobidb-lite (MOBIDB_LITE)	0,077	0,308	0,072	0,272	0,236									
Solyc11g044632	Ycf1 protein (AHRD V3.3 *-* ATCG01130.1)	C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM); IPR008896 (PAN	0,256	0,118	0,170	0,227	0,309									
Solyc11g044638	NADH dehydrogenase subunit (AHRD V3.3 *-* B7SRD9_9SOLA)	C:GO:0009507; C:GC	C:chloroplast; C:thylakoid; C:membrane; F:oxidoreductase activ	PR01434 (PRINTS); IPR001750 (PFA	0,075	0,043	0,051	0,124	0,000									
Solyc11g044650	Ycf68 protein (AHRD V3.3 *-* A0A0K0Q5V3_9CARY)	C:GO:0043231; C:GC	C:intracellular membrane-bounded organelle; C:cytoplasmic part	IPR022546 (PFAM); mobidb-lite (MOB	0,019	0,059	0,025	0,073	0,071									
Solyc11g044660	LOW QUALITY:beta glucosidase 43 (AHRD V3.3 --* AT3G18070.6)				0,019	0,000	0,000	0,025	0,000									
Solyc11g044680	Ycf1 (AHRD V3.3 *-* A0A140G1X7_TOBAC)	C:GO:0016021	C:integral component of membrane	IPR008896 (PFAM); mobidb-lite (MOB	0,019	0,000	0,000	0,025	0,000									
Solyc11g044740	Pollen specific LIM domain protein 1a (AHRD V3.3 *** Q9SNX4_TOBAC)	F:GO:0046872	F:metal ion binding	G3DSA:2.10.110.10 (GENE3D); IPR0	0,817	1,111	0,165	0,025	0,069									
Solyc11g044750	mtDNA-binding protein WHIRLY2-like	F:GO:0003697; P:GC	F:single-stranded DNA binding; P:regulation of transcription, DN	IPR013742 (PFAM Whirly	0,546	0,518	0,404	0,386	0,590									
Solyc11g044800	Protein trpH (AHRD V3.3 *** A0A151T262_CAJCA)	F:GO:0003824	F:catalytic activity	G3DSA:3.20.20.140 (GENE3D); IPR0	11,216	11,553	7,025	6,228	6,722									
Solyc11g044810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM); IPR027443 (G3D	0,040	0,000	0,000	0,000	0,000									
Solyc11g044840	Aspartate aminotransferase, putative (AHRD V3.3 *** B9T7N8_RICCO)	F:GO:0008483; P:GC	F:transaminase activity; P:biosynthetic process; F:pyridoxal pho	IPR015422 (G3DSA:3.90.1150.GENE	0,000	0,075	0,000	0,025	0,047									
Solyc11g044870	Armadillo repeat-containing protein, putative (AHRD V3.3 *** B9S778_RICCO)			IPR011989 (G3DSA:1.25.10.GENE3D	28,462	23,789	32,831	32,551	32,026									
Solyc11g044880	Kinesin-like protein (AHRD V3.3 *** V7AE44_PHAVU)	F:GO:0003777; F:GC	F:microtubule motor EC:3.6.1.15 Nucleoside-triphosph	IPR001752 (PRINTS); PF13920 (PFAI	79,971	62,306	41,995	45,829	45,175									
Solyc11g044900	Poly(A) RNA polymerase GLD2 (AHRD V3.3 *** A0A1D1YK78_9ARAE)			G3DSA:1.10.1410.10 (GENE3D); G3D	16,002	16,915	32,247	31,956	29,952									
Solyc11g044910	Beta-D-xylosidase family protein (AHRD V3.3 *** B9HWX2_POPTR)	F:GO:0004553; P:GC	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001764 (PRINTS); IPR013783 (G3	2,825	5,022	140,296	264,657	188,657			0,424	0,043	0,918	0,000		up	up
Solyc11g044940	Kinase family protein (AHRD V3.3 *** A0A0K9P5Z4_ZOSMR)	F:GO:0004672; F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	IPR001245 (PFAM); G3DSA:1.10.510	6,636	4,855	0,352	0,346	0,164									
Solyc11g044950	protein kinase family protein (AHRD V3.3 *-* AT3G59410.4)	C:GO:0005737	C:cytoplasm	IPR036621 (G3DSA:3.40.50.GENE3D	2,560	3,024	1,842	1,863	2,092									
Solyc11g044960	Protein kinase family protein GCN2 (AHRD V3.3 *-* A0A0N7AH70_TOBAC)	F:GO:0005515; F:GC	F:protein binding; F:ubiquitin protein ligase activity	IPR016135 (G3DSA:3.10.110.GENE3	2,962	2,367	1,838	2,204	2,352									
Solyc11g044965	protein kinase family protein (AHRD V3.3 *** AT3G59410.5)	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D); G3DS	8,233	8,087	4,943	5,590	5,750									
Solyc11g045030	cytoplasmic membrane protein	C:GO:0016021	C:integral component of membrane	IPR018639 (PFAM); PTHR35102 (PAI	5,848	5,590	1,551	0,979	1,221									
Solyc11g045035	Protein kinase family protein GCN2 (AHRD V3.3 --* A0A0N7AH70_TOBAC)	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,946	0,917	0,522	0,470	0,402									
Solyc11g045040	Glycerophosphodiester phosphodiesterase family protein (AHRD V3.3 *** A0A072USJ9_MEDTR)	P:GO:0006629; F:GC	P:lipid metabolic prc EC:3.1.4.46 Glycerophosphodiest	IPR030395 (PFAM); IPR017946 (G3D	6,554	5,193	7,436	7,603	7,855									
Solyc11g045100	tropomyosin (AHRD V3.3 *** AT1G33500.3)			PTHR38353 (PANTHER)	0,960	0,978	0,478	0,548	0,378									
Solyc11g045110	Sucrose-phosphate synthase family protein (AHRD V3.3 *** AT4G10120.3)	P:GO:0005985; F:GC	P:sucrose metaboli EC:2.4.1.14; EC:2.4. Sucrose-phosphate s	G3DSA:3.40.50.2000 (GENE3D); IPRI	12,541	10,680	6,545	7,047	8,398									
Solyc11g045120	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151R7Y9_CAJCA)	P:GO:0001731; F:GC	P:formation of translation preinitiation complex; F:translation init	IPR013103 (PFAM); IPR036974 (G3D	37,686	34,402	42,840	44,160	45,598									
Solyc11g045130	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT2G32070.1)	F:GO:0003676; F:GC	F:nucleic acid bindi EC:3.1.13; EC:3.1.1! Acting on ester bonds	IPR036397 (G3DSA:3.30.420.GENE3	96,180	119,560	90,858	99,826	91,665									
Solyc11g045140	LOW QUALITY:Vacuolar protein sorting-associated protein, putative (AHRD V3.3 *-* B9RXC4_RICCO)			IPR026854 (PFAM); IPR026847 (PAN	2,005	1,197	1,611	2,484	2,543									
Solyc11g045150	myosin XI D (AHRD V3.3 --* AT2G33240.8)	C:GO:0005739	C:mitochondrion	PTHR37773 (PANTHER)	4,148	3,812	6,602	9,979	9,138									
Solyc11g045160	vacuolar protein sorting-associated protein, putative (DUF1162) (AHRD V3.3 *** AT5G24740.4)			IPR031642 (PFAM); IPR031646 (PFA	35,541	23,442	32,585	45,358	39,300					0,477	0,038			up
Solyc11g045180	DEAD-box ATP-dependent RNA helicase (AHRD V3.3 *** A0A068BG41_COCNU)	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding	IPR011545 (PFAM); G3DSA:3.40.50.3	23,302	26,971	50,944	56,181	55,846									
Solyc11g045185	Vacuolar protein sorting-associated protein, putative (AHRD V3.3 *-* B9RXC4_RICCO)			IPR031645 (PFAM); PTHR16166:SF1	19,455	16,182	24,583	24,459	22,635									
Solyc11g045210	UPF0739 protein C1orf74 (AHRD V3.3 *** A0A1D1XLV4_9ARAE)			IPR027850 (PFAM); IPR027850 (PAN	10,898	11,917	13,409	16,402	14,597									
Solyc11g045220	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199V464_ANACO)	F:GO:0005515	F:protein binding	IPR002885 (TIGRFAM); IPR002885 (F	8,591	7,365	13,606	13,316	11,780									
Solyc11g045230	SPX (SYG1/Pho81/XPR1) domain-containing protein / zinc finger (C3HC4-type RING finger) protein-related (	F:GO:0016874; F:GC	F:ligase activity; F:metal ion binding	IPR013083 (G3DSA:3.30.40.GENE3D	0,180	0,158	0,025	0,050	0,047									
Solyc11g045240	Glutamate carboxypeptidase, putative (AHRD V3.3 *** A0A072U3L2_MEDTR)	F:GO:0004180; P:GC	F:carboxypeptidase activity; P:proteolysis; C:integral componer	G3DSA:3.40.630.10 (GENE3D); IPR0	27,219	25,404	11,606	11,031	13,047									
Solyc11g045260	Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_ZYGCR)	C:GO:0009521; P:GC	C:photosystem; P:photosynthetic electron transport chain; F:chl	IPR000932 (PFAM); PTHR33180:SF4	0,310	0,704	0,296	0,346	0,450									
Solyc11g045270	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *-* AT3G11890.7)	F:GO:0005515	F:protein binding	IPR001660 (PFAM); G3DSA:1.10.150	6,554	6,058	7,687	8,694	8,268									
Solyc11g045310	MADS box protein (AHRD V3.3 *** Q84KS1_TOBAC)	F:GO:0000981; F:GC	F:DNA-binding transcription factor activity, RNA polymerase II-s	IPR002100 (PRINTS); IPR036879 (G3	15,112	16,483	12,660	11,277	14,130									
Solyc11g045320	LOW QUALITY:Paired amphipathic helix protein Sin3 (AHRD V3.3 *-* A0A151TFV5_CAJCA)	F:GO:0003714; P:GC	F:transcription corepressor activity; P:regulation of transcriptior	G3DSA:1.20.1160.11 (GENE3D); IPRI	0,021	0,000	0,000	0,000	0,000									
Solyc11g045330	GPI-anchored protein (AHRD V3.3 *** AT2G30700.1)	C:GO:0005886	C:plasma membrane	PTHR33831:SF3 (PANTHER); IPR040	15,209	9,097	19,202	19,591	18,576	-0,711	0,036					down		
Solyc11g045333	Paired amphipathic helix protein Sin3 (AHRD V3.3 --* M8BTL4_AEGTA)	F:GO:0003714; C:GC	F:transcription corepressor activity; C:nucleus; P:regulation of transcription, DNA-templated; P:negative		0,056	0,021	0,000	0,000	0,000									
Solyc11g045350	Plant regulator RWP-RK family protein (AHRD V3.3 *** AT2G43500.9)	F:GO:0005515	F:protein binding	IPR003035 (PFAM Nin-like	46,564	35,624	59,004	59,365	56,161									
Solyc11g045390	D-lactate dehydrogenase, putative (AHRD V3.3 *** B9SDP2_RICCO)	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI	IPR016171 (G3DSA:1.10.45.GENE3D	17,446	17,428	22,202	23,413	23,893									
Solyc11g045410	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* A0A068EW38_SOLLC)	F:GO:0043531	F:ADP binding	PTHR23155:SF414 (PANTHER); PTHI	0,019	0,000	0,000	0,000	0,048									
Solyc11g045430	transmembrane protein (AHRD V3.3 *-* AT2G07674.1)	C:GO:0005739; C:GC	C:mitochondrion; C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,183	0,050	0,148	0,189									
Solyc11g045440	LOW QUALITY:delta(3), delta(2)-enoyl CoA isomerase 1 (AHRD V3.3 --* AT1G65520.1)	C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); PTHR331	0,301	0,245	0,392	0,396	0,469									
Solyc11g045450	B3 domain-containing protein family (AHRD V3.3 *-* A0A151RF19_CAJCA)	F:GO:0003677	F:DNA binding	IPR015300 (G3DS B3	1,268	0,519	0,000	0,000	0,000									
Solyc11g045460	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-* A0A061GZL6_THECC)	F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM); IPR029058 (G3D	0,000	0,039	0,075	0,025	0,165									
Solyc11g045465	Alpha/beta-Hydrolases superfamily protein, putative (AHRD V3.3 *-* A0A061EX94_THECC)	F:GO:0016787	F:hydrolase activity	IPR013094 (PFAM); IPR029058 (G3D	0,021	0,037	0,050	0,144	0,283									
Solyc11g045480	myosin-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *** AT5G06560.1)	C:GO:0016020	C:membrane	IPR007656 (PFAM); PTHR31422 (PAI	11,125	11,440	12,075	13,039	12,443									
Solyc11g045510	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT5G12920.8)	F:GO:0005515	F:protein binding	IPR015943 (G3DSA:2.130.10.GENE3	5,788	4,922	5,498	6,288	5,552									
Solyc11g045520	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE-like protein	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process	IPR005123 (PFAM); IPR027443 (G3D	0,059	0,092	0,000	0,000	0,000									
Solyc11g045523	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT5G12920.4)	C:GO:0016021	C:integral component of membrane		7,338	6,757	6,602	6,914	6,987									
Solyc11g045527	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *-* AT5G12920.1)	C:GO:0016020	C:membrane	PTHR22850 (PANTHER); PTHR22850	2,533	2,004	1,873	2,748	2,142									
Solyc11g045530	LOB domain-containing protein, putative (AHRD V3.3 *** B9RI26_RICCO)			IPR004883 (PFAM LBD	2,070	2,173	0,213	0,100	0,069									
Solyc11g045610	Protein kinase family protein (AHRD V3.3 *** Q9LQ29_ARATH)	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM); G3DSA:1.10.510	9,192	6,591	8,767	7,646	9,215									
Solyc11g045645	trithorax-like protein 2 (AHRD V3.3 --* AT1G05830.4)				0,000	0,000	0,000	0,000	0,024									
Solyc11g045670	S-acyltransferase (AHRD V3.3 *** A0A0V0ING6_SOLCH)	C:GO:0016021; F:GC	C:integral compone EC:2.3.1.225 Protein S-acyltransfe	IPR001594 (PFAM); PTHR22883:SF1	7,629	7,178	6,935	7,189	7,862									
Solyc11g045677	vesicle-associated protein 1-4 (AHRD V3.3 --* AT1G51270.9)			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,061	0,000	0,000	0,075	0,000									

Solyc11g050760	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 *-* NU1C_SOLLC)	C:GO:0016020; P:G(	C:membrane; P:oxidation-reduction process	IPR001694 (PFAM); PTHR11432:SF1	0,329	0,786	0,318	0,352	0,234									
Solyc11g050770	Photosystem II reaction center protein Z (AHRD V3.3 *** K4D8P0_SOLLC)	C:GO:0009539; P:G(	C:photosystem II reaction center; P:photosystem II stabilization	IPR002644 (PFAM); IPR036512 (G3D	0,058	0,162	0,025	0,149	0,117									
Solyc11g050810	LOW QUALITY:Cellulose synthase (AHRD V3.3 *-* K4BTR6_SOLLC)	C:GO:0016020; F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (U	IPR005150 (PFAM); PTHR13301:SF2	0,000	0,021	0,000	0,000	0,000									
Solyc11g050822	Histidine decarboxylase (AHRD V3.3 *-* DCHS_SOLLC)	F:GO:0016831; P:G(	F:carboxy-lyase activity; P:carboxylic acid metabolic process; F	IPR015421 (G3DSA:3.40.640.GENE3	0,000	0,000	0,025	0,072	0,000									
Solyc11g050880	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4D8Q1_SOLLC)	F:GO:0005509; F:G(	F:calcium ion bindin EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR015415 (PFAM); G3DSA:1.10.8.60	0,234	0,688	0,143	0,171	0,212									
Solyc11g050890	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT3G49650.1)			mobidb-lite (MOBIDB_LITE); mobidb-lit	1,625	1,408	1,291	2,111	1,929									
Solyc11g050930	Sulfotransferase (AHRD V3.3 *** K4D8Q6_SOLLC)	F:GO:0008146	F:sulfotransferase activity	IPR000863 (PFAM); G3DSA:3.40.50.3	1,252	0,853	0,000	0,000	0,000									
Solyc11g051035	pre-mRNA-splicing factor of RES complex protein (AHRD V3.3 --* AT1G31870.2)				0,239	0,247	0,000	0,000	0,072									
Solyc11g051060	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)	F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,057	0,103	0,050	0,047	0,000									
Solyc11g051090	Sulfotransferase (AHRD V3.3 *** K4D8S0_SOLLC)	F:GO:0008146	F:sulfotransferase activity	IPR000863 (PFAM); G3DSA:3.40.50.3	1,079	0,645	0,000	0,000	0,000									
Solyc11g051120	Lipase, GDSL (AHRD V3.3 *-* A0A124SDS7_CYNCS)	F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); PTHR22835:SF2	0,000	0,113	0,000	0,025	0,000									
Solyc11g051125	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 --* AT5G14550.2)			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,788	0,919	0,384	0,555	0,448									
Solyc11g051160	Patellin-like protein (AHRD V3.3 *** A0A072UTX7_MEDTR)			IPR011074 (PFAM); IPR036865 (G3D	235,941	153,522	529,891	528,913	501,402	-0,593	0,030					down		
Solyc11g051170	LOW QUALITY:ATP synthase subunit alpha, chloroplastic (AHRD V3.3 *-* ATPA_TOBAC)	F:GO:0005524	F:ATP binding	IPR000194 (PFAM); G3DSA:3.40.50.3	0,217	1,312	0,197	0,296	0,188									
Solyc11g051200	LOW QUALITY:Senescence-associated protein (AHRD V3.3 *-* A0A072THH1_MEDTR)			mobidb-lite (MOBIDB_LITE); mobidb-lit	4,919	7,247	5,728	13,520	7,301					1,246	0,006			up
Solyc11g056250	LOW QUALITY:glutamine-dependent asparagine synthase 1 (AHRD V3.3 --* AT3G47340.3)	C:GO:0005739	C:mitochondrion	PTHR34890 (PANTHER)	1,219	2,095	2,360	3,198	3,813									
Solyc11g056270	LOW QUALITY:Maturase (AHRD V3.3 *** O79414_SOLTU)	C:GO:0005739; P:G(	C:mitochondrion; P:mRNA processing	PTHR33642 (PANTHER); PTHR33642	0,373	0,793	0,464	0,766	0,610									
Solyc11g056280	LOW QUALITY:1,2-alpha-L-fucosidase (AHRD V3.3 --* AT4G34260.1)				0,000	0,000	0,025	0,000	0,000									
Solyc11g056290	LOW QUALITY:DNA-directed RNA polymerase (AHRD V3.3 --* B6VJT2_VITVI)	C:GO:0005739	C:mitochondrion		0,000	0,000	0,000	0,025	0,000									
Solyc11g056310	Ribosomal protein S13 (AHRD V3.3 *** A0A142I0Y0_NICSY)	F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome	G3DSA:1.10.8.50 (GENE3D); IPR027	0,061	0,248	0,097	0,320	0,188									
Solyc11g056320	LOW QUALITY:Photosystem II CP47 reaction center protein (AHRD V3.3 --* PSBB_SPIOL)	C:GO:0005739	C:mitochondrion	mobidb-lite (MOBIDB_LITE); mobidb-lit	1,017	2,225	0,980	2,202	0,847									
Solyc11g056330	cysteine-rich RLK (RECEPTOR-like protein kinase) 19 (AHRD V3.3 --* AT4G23270.3)	C:GO:0005739; C:G(	C:mitochondrion; C:membrane	mobidb-lite (MOBIDB_LITE); PTHR352	0,390	0,636	0,610	1,042	0,542									
Solyc11g056340	LOW QUALITY:Photosystem II protein D1 (AHRD V3.3 *-* PSBA_SOLNI)	P:GO:0009772; F:G(	P:photosynthetic electron transport in photosystem II; F:electro	IPR036854 (G3DSA:1.20.85.GENE3D	0,602	1,493	1,461	2,705	3,224			1,137	0,029				up	
Solyc11g056350	LOW QUALITY:RHOMBOID-like protein 4 (AHRD V3.3 --* AT3G53780.3)				0,000	0,019	0,000	0,000	0,000									
Solyc11g056360	Ribosomal protein S12 (AHRD V3.3 *** A0A0C5ARW5_HYONI)	F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:small ribos	IPR006032 (PRINTS); G3DSA:2.40.50	0,721	1,383	0,537	0,923	0,423									
Solyc11g056370	NADH-ubiquinone oxidoreductase chain 3 (AHRD V3.3 *** NU3M_SOLTU)	F:GO:0008137; P:G(	F:NADH dehydroge EC:1.6.99.5; EC:1.6. Acting on NADH or N	IPR000440 (PFAM); IPR038430 (G3D	0,040	0,329	0,000	0,226	0,070									
Solyc11g056380	LOW QUALITY:Protein transport protein sec23, putative (AHRD V3.3 *-* B9RN42_RICCO)	C:GO:0005783; C:G(	C:endoplasmic reticulum; C:ER to Golgi transport vesicle memb	IPR036465 (G3DSA:3.40.50.GENE3D	0,038	0,043	0,072	0,022	0,000									
Solyc11g056400	Ribosomal protein S3 (AHRD V3.3 *** A0A075VXF7_CAPAN)	F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:mitochon	PTHR35928 (PANTHER)	0,231	0,380	0,422	1,070	0,397									
Solyc11g056410	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* A0A0C5B2A3_HYONI)	F:GO:0004129; F:G(	F:cytochrome-c oxi EC:1.9.3.1 Cytochrome-c oxidas	PR01166 (PRINTS); IPR008972 (G3D	0,155	0,310	0,242	1,244	0,399									
Solyc11g056420	LOW QUALITY:Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 --* AT3G13800.4)				0,000	0,000	0,022	0,000	0,024									
Solyc11g056440	LOW QUALITY:ureide permease 2 (AHRD V3.3 --* AT2G03530.4)				0,019	0,021	0,075	0,048	0,093									
Solyc11g056450	ATP synthase subunit a (AHRD V3.3 *** ATP6_TOBAC)	F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP synthesis c	IPR000568 (PRINTS); IPR000568 (PF	0,019	0,000	0,000	0,000	0,000									
Solyc11g056460	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 --* A0A151RQY5_CAJCA)				0,000	0,021	0,000	0,000	0,000									
Solyc11g056500	LOW QUALITY:OR338 (AHRD V3.3 *-* R4IUB8_VICFA)	P:GO:0044237	P:cellular metabolic process	mobidb-lite (MOBIDB_LITE); mobidb-lit	0,082	0,225	0,437	0,314	0,163									
Solyc11g056510	LOW QUALITY:Ribonuclease H (AHRD V3.3 --* Q2HU20_MEDTR)	F:GO:0003676; F:G(	F:nucleic acid bindi EC:3.1.3; EC:3.1.26; Acting on ester bond	IPR002156 (PFAM); IPR036397 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc11g056520	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)	F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR008543 (PANTHER)	0,000	0,019	0,000	0,000	0,024									
Solyc11g056530	LOW QUALITY:RNA-directed DNA polymerase (Reverse transcriptase) (AHRD V3.3 --* Q1SKV6_MEDTR)				0,000	0,000	0,025	0,000	0,000									
Solyc11g056620	Cobyric acid synthase (AHRD V3.3 *** A0A1D1YI90_9ARAE)			PTHR33984 (PANTHER); PTHR33984	0,983	3,508	2,769	3,778	4,016									
Solyc11g056637	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G48120.1)			IPR019557 (PFAM); PTHR44194 (PAN	0,000	0,000	0,000	0,050	0,000									
Solyc11g056640	Inactive rhomboid 1 (AHRD V3.3 *** A0A0B0MQ80_GOSAR)			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,219	2,256	0,633	0,697	0,662									
Solyc11g056650	bHLH transcription factor 096	F:GO:0046983	F:protein dimerization activity	IPR011598 (PFAM bHLH	3,250	2,947	4,313	5,099	4,107									
Solyc11g056680	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *** A0A0K9PVU5_ZOSMR)	F:GO:0005515	F:protein binding	IPR032675 (G3DSA:3.80.10.GENE3D	213,356	81,883	32,030	16,069	21,115	-1,353	0,000					down		
Solyc11g061690	Charged multivesicular body protein 1 (AHRD V3.3 *-* A0A1D1YV61_9ARAE)	C:GO:0000815; C:G(	C:ESCRT III complex; C:multivesicular body; P:protein transport	PTHR10476:SF2 (PANTHER); PTHR1(	0,021	0,019	0,075	0,025	0,047									
Solyc11g061700	DUF1680 domain protein (AHRD V3.3 *** G7JCI1_MEDTR)	F:GO:0003824	F:catalytic activity	IPR012878 (PFAM); PTHR31151 (PAN	7,596	10,322	0,096	0,000	0,047									
Solyc11g061720	Kinase family protein (AHRD V3.3 *** D7KZX1_ARALL)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D); G3DS	7,309	7,080	2,229	2,119	2,590									
Solyc11g061750	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7JCJ4_MEDTR)	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN AP2	0,021	0,021	0,000	0,050	0,000									
Solyc11g061760	MSF1-like family protein (AHRD V3.3 *** AT5G13070.1)	C:GO:0005758	C:mitochondrial intermembrane space	IPR006797 (PFAM); PTHR11158:SF1	0,075	0,272	0,096	0,122	0,117									
Solyc11g061770	A20/AN1 zinc finger protein	F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding	IPR002653 (PFAM); IPR035896 (G3D	29,722	26,545	54,417	58,737	47,214									
Solyc11g061960	Kinase family protein (AHRD V3.3 *** D7KZX4_ARALL)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	PIRSF000654 (PIRSF); G3DSA:1.10.5	2,756	1,698	0,072	0,000	0,071									
Solyc11g061980	Glycosyltransferase (AHRD V3.3 *** K4D910_SOLLC)	F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); G3D	0,311	0,826	0,269	0,536	0,355									
Solyc11g062010	Chromatin structure-remodeling complex subunit snf21 (AHRD V3.3 *-* A0A0B2P221_GLYSO)	F:GO:0005524; F:G(	F:ATP binding; F:histone binding	IPR001650 (PFAM); IPR029295 (PFA	365,833	297,003	339,939	371,182	371,027									
Solyc11g062020	Zinc transporter ZTP29 (AHRD V3.3 *** ZTP29_ARATH)	C:GO:0016020; P:G(	C:membrane; P:metal ion transport; F:metal ion transmembrane	IPR003689 (PFAM); PTHR11040 (PAN	18,803	22,294	30,673	34,637	32,078									
Solyc11g062030	tRNA (met) cytidine acetyltransferase, putative (DUF616) (AHRD V3.3 --* AT1G53040.6)			PS51257 (PROSITE_PROFILES)	3,117	3,744	1,964	2,812	2,961									
Solyc11g062040	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_TOBAC)	F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR008543 (PFAM); IPR008543 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc11g062050	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)	F:GO:0005524; C:G(	F:ATP binding; C:chloroplast	IPR008543 (PANTHER)	0,000	0,043	0,000	0,149	0,023									
Solyc11g062060	Protein TRANSPARENT TESTA 1 (AHRD V3.3 *** A0A1D1ZJL0_9ARAE)	F:GO:0003676	F:nucleic acid binding	mobidb-lite (MOBII C2H2	1,858	2,805	3,709	4,724	2,030									
Solyc11g062070	Outer envelope protein 80, chloroplastic (AHRD V3.3 *-* OEP80_ARATH)	C:GO:0005739; P:G(	C:mitochondrion; P:chloroplast organization; C:chloroplast enve	G3DSA:3.10.20.310 (GENE3D); G3DS	37,977	45,243	48,793	46,729	49,578									
Solyc11g062110	LOW QUALITY:DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0A0RT77_9GENT)	F:GO:0003677; F:G(	F:DNA binding; F:DI EC:2.7.7.6 DNA-directed RNA polymerase		0,096	0,019	0,118	0,151	0,047									
Solyc11g062120	Copper-transporting atpase p-type, putative (AHRD V3.3 *** B9RIA4_RICCO)	F:GO:0005507; C:G(	F:copper ion binding; C:integral component of membrane; P:met	PR00942 (PRINTS); G3DSA:2.70.150	7,805	7,113	14,608	16,529	18,378									
Solyc11g062130	ADP/ATP translocator	C:GO:0005743; F:G(	C:mitochondrial inner membrane; F:transmembrane transporter	IPR002113 (PRINTS); IPR002067 (PF	1093,926	1171,784	877,763	841,368	859,687									
Solyc11g062190	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 *** ADT1_SOLTU)	C:GO:0005743; F:G(	C:mitochondrial inner membrane; F:transmembrane transporter	IPR002113 (PRINTS); IPR002067 (PF	722,760	787,415	545,759	492,565	509,755									
Solyc11g062195	RNase H family protein (AHRD V3.3 --* Q0KIQ6_SOLDE)	F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis		2,107	1,073	1,502	1,253	1,600									
Solyc11g062210	LOW QUALITY:RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT5G36670.3)	F:GO:0043565	F:sequence-specific DNA binding		0,019	0,018	0,000	0,000	0,000									
Solyc11g062220	Zinc finger CCCH domain-containing protein 44 (AHRD V3.3 *-* W9QRR2_9ROSA)	F:GO:0003677; F:G(	F:DNA binding; F:protein binding	IPR004343 (PFAM); IPR013083 (G3D	55,670	43,654	58,392	58,385	57,235									
Solyc11g062230	LOW QUALITY:F-box/associated interaction domain protein (AHRD V3.3 --* AT1G43005.1)				0,021	0,000	0,076	0,025	0,024									
Solyc11g062240	Zinc finger transcription factor 66 C3H66				55,465	50,176	66,225	59,643	59,418									
Solyc11g062260	E3 ubiquitin ligase BIG brother-like protein (AHRD V3.3 *** G7JDP3_MEDTR)	F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination;	PTHR14155 (PANTHER); PTHR14155	4,660	4,214	2,945	3,119	2,489									
Solyc11g062270	Signal recognition particle subunit SRP72 (AHRD V3.3 *** K4D938_SOLLC)	F:GO:0005515; P:G(	F:protein binding; P:SRP-dependent cotranslational protein targ	IPR013699 (PFAM); IPR031545 (PFA	42,507	37,776	49,608	51,501	47,923									
Solyc11g062280	Lactoylglutathione lyase/glyoxalase I family protein (AHRD V3.3 *** G7KAQ0_MEDTR)	F:GO:0016829; F:G(	F:lyase activity; F:dioxygenase activity; P:oxidation-reduction p	IPR029068 (G3DSA:3.10.180.GENE3	10,440	10,618	6,146	7,350	6,636									
Solyc11g062290	30S ribosomal protein S19, chloroplastic (AHRD V3.3 -** RR19_MARPO)				1,055	1,162	0,912	0,590	0,538									
Solyc11g062300	ARM repeat superfamily protein (AHRD V3.3 *-* AT2G26780.2)	F:GO:0032947; P:G(	F:protein-containing complex scaffold activity; P:proteasome as	IPR011989 (G3DSA:1.25.10.GENE3D	6,433	5,766	5,893	5,833	5,606									
Solyc11g062310	ARM repeat superfamily protein (AHRD V3.3 *** AT2G26780.2)	F:GO:0032947; P:G(	F:protein-containing complex scaffold activity; P:proteasome as	IPR024372 (PFAM); IPR011989 (G3D	26,788	20,045	23,807	26,876	23,473									
Solyc11g062320	Proteasome-associated ECM29-like protein (AHRD V3.3 *-* G7KCU1_MEDTR)	F:GO:0032947; P:G(	F:protein-containing complex scaffold activity; P:proteasome as	IPR024372 (PFAM); IPR024372 (PTH	6,208	5,253	5,209	7,415	6,501									
Solyc11g062350	Blue copper protein (AHRD V3.3 *** A0A199UNZ4_ANACO)	F:GO:0009055	F:electron transfer activity	IPR003245 (PFAM); IPR008972 (G3D	2,158	1,009	0,172	0,152	0,187									
Solyc11g062360	Transferring glycosyl group transferase, putative (AHRD V3.3 *** G7L963_MEDTR)	C:GO:0005768; C:G(	C:endosome; C:trans-Golgi network; C:integral component of m	PTHR33604:SF1 (PANTHER); PTHR3	8,729	6,141	7,379	7,739	7,007									
Solyc11g062390	ATP synthase subunit beta, chloroplastic (AHRD V3.3 --* ATPB_OENGL)	F:GO:0003779; P:G(	F:actin binding; P:actin filament organization; P:regulation of sto	IPR032009 (PFAM); IPR041144 (PFA	23,093	24,490	9,861	10,207	12,567									
Solyc11g062400	Protein kinase (AHRD V3.3 *** C6ZRQ9_SOYBN)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	PIRSF000654 (PIRSF); G3DSA:1.10.5	0,507	1,842	0,409	0,482	1,010	1,881	0,015					up		
Solyc11g062410	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IHL6_SOLCH)	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR004041 (PFAM); G3DSA:1.10.510	38,323	35,568	25,934	26,889	26,922									
Solyc11g062420	SCR (AHRD V3.3 -** A0A072TY38_MEDTR)	P:GO:0007165	P:signal transduction	IPR010682 (PANTHER)	0,019	0,172	0,000	0,000	0,000									
Solyc11g062430	COP9 signalosome complex subunit 2 (AHRD V3.3 *** W9QZI3_9ROSA)	C:GO:0008180	C:COP9 signalosome	IPR000717 (PFAM); G3DSA:1.25.40.5	38,029	31,346	42,740	40,233	41,152									
Solyc11g062440	L-ascorbate oxidase (AHRD V3.3 *** ASO_TOBAC)	F:GO:0005507; C:G(	F:copper ion binding; C:extracellular region; F:oxidoreductase a	IPR011706 (PFAM); IPR011707 (PFA	101,303	128,470	4,027	0,921	1,789			-1,172	0,007	-2,114	0,000		down	down
Solyc11g063440	50S ribosomal protein L20, chloroplastic (AHRD V3.3 *** Q06R42_9LAMI)	F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR005813 (PRINTS); IPR005813 (PF	0,000	0,021	0,025	0,000	0,000									
Solyc11g063480	LOW QUALITY:delta(3), delta(2)-enoyl CoA isomerase 1 (AHRD V3.3 --* AT1G65520.1)	C:GO:0005739	C:mitochondrion		0,021	0,021	0,025	0,000	0,000									
Solyc11g063490	LOW QUALITY:Glucose-6-phosphate isomerase, cytosolic 1 (AHRD V3.3 --* G6PI1_CLAFR)				0,000	0,000	0,025	0,000	0,000									
Solyc11g063500	LOW QUALITY:nitrite reductase 1 (AHRD V3.3 --* AT2G15620.1)			mobidb-lite (MOBIDB_LITE); mobidb-lit	2,732	3,170	3,216	5,501	3,255									
Solyc11g063510	LOW QUALITY:Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 --* AT4G28550.1)				0,330	0,385	0,693	0,736	0,710									
Solyc11g063520	sequence-specific DNA binding transcription factor ATNDX (AHRD V3.3 --* AT4G03090.5)	C:GO:0005739	C:mitochondrion	PTHR34890 (PANTHER)	2,256	2,661	3,333	5,653	3,962									
Solyc11g063530	Mitovirus RNA-dependent RNA polymerase (AHRD V3.3 *-* ATMG01110.1)	C:GO:0005739; C:G(	C:mitochondrion; C:membrane	IPR008686 (PFAM)	0,099	0,079	0,118	0,097	0,071									
Solyc11g063540	Photosystem II CP43 reaction center protein (AHRD V3.3 --* PSBC_AMBTC)	C:GO:0005739	C:mitochondrion	IPR008686 (PFAM); IPR008686 (PAN	0,037	0,062	0,094	0,022	0,070									
Solyc11g063580	LOW QUALITY:Photosystem II stability/assembly factor HCF136, chloroplastic (AHRD V3.3 --* P2SAF_ORYSJ)				0,000	0,018	0,000	0,000	0,000									
Solyc11g063590	cytochrome B/B6 protein (AHRD V3.3 --* AT2G07773.1)	C:GO:0005739; C:G(	C:mitochondrion; C:membrane; C:integral component of membra	PTHR30071:SF1 (PANTHER); PTHR3(	0,000	0,000	0,000	0,097	0,024									
Solyc11g063600	Cytochrome c oxidase subunit 1 (AHRD V3.3 *-* COX1_SOYBN)	F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;	IPR001848 (PRINTS); IPR036838 (G3	0,138	0,337	0,218	0,573	0,329									
Solyc11g063610	Cytochrome c oxidase subunit 1 (AHRD V3.3 *** A0A0C5ARM9_HYONI)	F:GO:0004129; P:G(	F:cytochrome-c oxi EC:1.9.3.1 Cytochrome-c oxidas	IPR000883 (PRINTS); IPR000883 (PF	0,201	0,456	0,386	0,967	0,591									
Solyc11g063620	Cytochrome c biogenesis FN (AHRD V3.3 *** A0A0C5ART5_HYONI)	F:GO:0015232; P:G(	F:heme transporter activity; P:heme transport; C:membrane; P:(	IPR003569 (PRINTS); IPR003567 (PF	0,019	0,000	0,000	0,025	0,000									
Solyc11g063630	Cytochrome c biogenesis FN (AHRD V3.3 *** A0A0C5ART5_HYONI)	F:GO:0015232; P:G(	F:heme transporter activity; P:heme transport; C:membrane; P:(	IPR003567 (PRINTS); IPR003569 (PF	0,021	0,000	0,000	0,000	0,000									
Solyc11g063640	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_OPUQU)	C:GO:0009522; C:G(	C:photosystem I; C:thylakoid; P:photosynthesis; C:integral comp	mobidb-lite (MOBIDB_LITE)	0,021	0,000	0,000	0,000	0,000									
Solyc11g064780	F-box/RNI-like superfamily protein, putative (AHRD V3.3 *** A0A061GGX0_THECC)	F:GO:0005515	F:protein binding	IPR001810 (PFAM); IPR032675 (G3D	0,021	0,039	0,046	0,069	0,000									
Solyc11g064785	LOW QUALITY:Reverse transcriptase (AHRD V3.3 *-* Q8H0R3_ELAGV)	F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity;	IPR000477 (PFAM); PTHR19446 (PAN	0,000	0,000	0,000	0,025	0,000									
Solyc11g064790	signal peptide peptidase (AHRD V3.3 *** AT2G03120.1)	F:GO:0004190; C:G(	F:aspartic-type end EC:3.4.23 Acting on peptide bor	IPR007369 (PFAM); IPR007369 (PAN	35,712	36,491	49,375	54,654	44,243									
Solyc11g064800	Lateral root primordium (LRP) protein-like protein (AHRD V3.3 *** AT5G12330.4)	F:GO:0003677; C:G(	F:DNA binding; C:nucleus; P:positive regulation of transcription,	PF05142 (PFAM); SRS	0,592	0,723	1,408	1,799	1,102									
Solyc11g064830	RING/U-box superfamily protein (AHRD V3.3 *** AT5G19430.6)			IPR013083 (G3DSA:3.30.40.GENE3D	33,967	36,871	44,790	42,470	41,573									
Solyc11g064835	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *-* AT2G23060.1)	F:GO:0016747	F:transferase activity, transferring acyl groups other than amino	PTHR43072:SF12 (PANTHER); PTHR	1,382	1,056	0,511	1,011	0,728									
Solyc11g064840	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** G7K355_MEDTR)			IPR000008 (PFAM); IPR035892 (G3D	0,222	0,114	0,000	0,025	0,000									
Solyc11g064850	Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *** AT5G13500.3)	C:GO:0016021	C:integral component of membrane	PTHR31485 (PANTHER); PTHR31485	45,002	35,671	102,670	100,480	96,744									
Solyc11g064880	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9NLF4_ZOSMR)	P:GO:0007165	P:signal transduction	IPR000198 (PFAM); IPR001849 (PFA	17,854	16,416	23,954	27,905	24,711									
Solyc11g064890	hypoxia-induced protein L31	F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro	G3DSA:3.30.200.20 (GENE3D); IPR0	121,829	118,323	110,861	109,964	103,045									
Solyc11g064920	Dihydropyrimidinase (AHRD V3.3 *** DPYS_ARATH)	C:GO:0005737; F:G(	C:cytoplasm; F:hydrolase activity, acting on carbon-nitrogen (bu	IPR011778 (TIGRFAM); IPR011059 ((	19,880	20,117	25,796	27,187	25,002									
Solyc11g064930	RPM1-interacting protein 4 (RIN4) family protein (AHRD V3.3 *-* AT5G19473.1)			IPR008700 (PFAM); mobidb-lite (MOB	0,057	0,021	0,025	0,072	0,048									
Solyc11g064940	LOW QUALITY:AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT5G38120.4)				0,000	0,000	0,000	0,000	0,023									
Solyc11g064950	BZIP transcription factor (AHRD V3.3 *** Q9SQK1_TOBAC)	P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir	IPR025422 (PFAM bZIP	14,647	24,134	16,553	17,801	18,824									
Solyc11g064953	BZIP transcription factor (AHRD V3.3 *-* Q9SQK1_TOBAC)	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	G3DSA:1.20.5.170 (GENE3D); IPR00	13,755	18,424	12,553	14,753	15,561									
Solyc11g064957	Vacuolar iron transporter like 4 (AHRD V3.3 --* A0A0B2NPW9_GLYSO)	F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ion transmembrane transporter activity; C:		6,456	3,771	3,111	3,226	2,659									
Solyc11g064960	Vacuolar iron transporter like 4 (AHRD V3.3 --* A0A0B2NPW9_GLYSO)	F:GO:0005381; F:G(	F:iron ion transmembrane transporter activity; F:manganese ion transmembrane transporter activity; C:		0,214	0,141	0,025	0,198	0,140									
Solyc11g064980	LOW QUALITY:Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1 (AHRD V3.3 --* A0A1D1YYA0_9ARAE)				0,019	0,037	0,000	0,025	0,000									
Solyc11g065000	F-box family protein (AHRD V3.3 *** B9HNI4_POPTR)	F:GO:0005515	F:protein binding	IPR001810 (PFAM); G3DSA:1.20.128	123,918	73,283	60,160	62,251	69,745	-0,731	0,002					down		
Solyc11g065010	LOW QUALITY:AR781, pheromone receptor-like protein (DUF1645) (AHRD V3.3 *-* AT2G26530.1)	C:GO:0005886	C:plasma membrane	IPR012442 (PFAM); mobidb-lite (MOB	0,000	0,000	0,000	0,025	0,000									
Solyc11g065020	GDP-mannose transporter, putative (AHRD V3.3 *-* B9SA23_RICCO)	C:GO:0016021	C:integral component of membrane	PTHR44371 (PANTHER)	2,735	3,116	1,668	1,451	1,787									
Solyc11g065030	GDP-mannose transporter (AHRD V3.3 *** M5VX95_PRUPE)	F:GO:0005458; C:G(	F:GDP-mannose transmembrane transporter activity; C:Golgi ar	PTHR44371 (PANTHER); PTHR44371	1,873	2,864	1,421	1,316	1,104									
Solyc11g065040	Methyltransferase family protein isoform 3 (AHRD V3.3 *** A0A061GZD7_THECC)	P:GO:0006479; F:G(	P:protein methylation; F:protein methyltransferase activity	G3DSA:3.40.50.150 (GENE3D); IPR0	3,271	3,707	3,333	3,707	3,572									
Solyc11g065070	Hydroxymethylglutaryl-CoA lyase (AHRD V3.3 *** W9QRW1_9ROSA)	F:GO:0004419; C:G(	F:hydroxymethylglut EC:4.1.3.4 Hydroxymethylglutary	IPR000891 (PFAM); IPR013785 (G3D	47,110	32,488	75,750	76,445	73,300									
Solyc11g065080	S2 self-incompatibility locus-linked pollen 3.2 protein (AHRD V3.3 *-* Q7XAE8_PETIN)			mobidb-lite (MOBIDB_LITE); PTHR353	8,728	8,183	7,970	6,479	6,326									
Solyc11g065090	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)	F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes	IPR008521 (PFAM); mobidb-lite (MOB	31,668	28,729	42,374	48,805	39,314									
Solyc11g065100	Mitochondria fission 1 protein (AHRD V3.3 *** A0A151RUY2_CAJCA)	P:GO:0000266; F:G(	P:mitochondrial fission; F:protein binding	IPR028058 (PFAM); IPR028061 (PFA	38,970	36,960	56,119	53,838	54,009									
Solyc11g065110	Homeobox leucine zipper protein (AHRD V3.3 *** G7K365_MEDTR)	F:GO:0003677	F:DNA binding	G3DSA:1.10.10.60 HB-other	28,601	27,756	37,868	38,512	35,970									
Solyc11g065120	Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 *** G7K368_MEDTR)	F:GO:0046872	F:metal ion binding	IPR000408 (PRINTS); IPR001849 (PF	14,108	9,999	14,008	14,544	14,236									
Solyc11g065125	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHI	F:GO:0046872	F:metal ion binding	IPR013591 (PFAM); IPR027988 (PFA	7,181	5,448	7,654	7,266	8,053									
Solyc11g065130	LOW QUALITY:tonoplast monosaccharide transporter2 (AHRD V3.3 --* AT4G35300.9)				0,000	0,021	0,025	0,000	0,000									
Solyc11g065135	Reactive oxygen species modulator 1 (AHRD V3.3 *-* A0A061FT24_THECC)	C:GO:0016021	C:integral component of membrane	IPR018450 (PFAM); PTHR28525:SF3	4,255	3,913	4,741	3,663	4,400									
Solyc11g065160	Nucleosome-remodeling factor subunit BPTF (AHRD V3.3 *** W9RR58_9ROSA)	F:GO:0046872	F:metal ion binding	IPR018501 (PFAM); IPR013083 (G3D	71,290	56,267	67,613	68,220	67,134									
Solyc11g065180	THUMP domain-containing protein (AHRD V3.3 *** AT5G12410.1)	F:GO:0003723; P:G(	F:RNA binding; P:tRNA modification	IPR004114 (PFAM); G3DSA:3.30.230	32,525	29,605	27,526	27,830	26,705									
Solyc11g065190	Ubiquitin-conjugating enzyme (AHRD V3.3 *** G7K9A0_MEDTR)	F:GO:0005524; C:G(	F:ATP binding; C:nucleus; P:protein ubiquitination; F:ligase activ	IPR000608 (PFAM); IPR016135 (G3D	1,252	1,488	0,327	0,315	0,281									
Solyc11g065193	interactor of constitutive active rops 1 (AHRD V3.3 --* AT1G17140.2)				0,541	0,699	0,769	0,728	0,709									
Solyc11g065195	Laminin subunit beta-1 (AHRD V3.3 *-* A0A0B0N352_GOSAR)			PTHR33144 (PANTHER); PTHR33144	1,839	1,986	1,826	2,338	1,385									
Solyc11g065197	Signal peptide peptidase-like 2 (AHRD V3.3 --* SIPL2_ORYSJ)				0,042	0,000	0,025	0,025	0,047									
Solyc11g065200	peroxin 10 (AHRD V3.3 --* AT2G26350.5)				0,078	0,134	0,140	0,259	0,024									
Solyc11g065210	Dbxref=InterPro:IPR001394,Pfam:PF00443	P:GO:0016579; F:G(	P:protein deubiquiti EC:3.4.19.12 Ubiquitinyl hydrolase	G3DSA:3.90.70.10 (GENE3D); IPR00	16,411	13,783	16,179	16,726	14,536									
Solyc11g065220	Phosphotransferase (AHRD V3.3 *** K4D9D5_SOLLC)	P:GO:0001678; F:G(	P:cellular glucose h EC:2.7.1.1 Hexokinase	PR00475 (PRINTS); G3DSA:3.30.420	9,503	8,474	2,096	2,242	2,790									
Solyc11g065240	Saccharopine dehydrogenase (AHRD V3.3 *** AT1G50450.1)	F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process	IPR005097 (PFAM); G3DSA:3.40.50.7	8,862	12,971	16,390	17,596	21,041									
Solyc11g065250	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061FB64_THECC)	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding	IPR011990 (G3DSA:1.25.40.GENE3D	1,387	0,845	0,755	1,193	1,338									
Solyc11g065255	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G51630.6)				0,616	0,535	0,562	0,211	0,494									
Solyc11g065260	DnaJ domain-containing protein (AHRD V3.3 *** A0A103XZS0_CYNCS)	F:GO:0005515	F:protein binding	IPR001623 (PRINTS); IPR036869 (G3	35,136	28,997	23,881	22,474	24,644									

Solyc11g065270	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial (AHRD V3.3 *** A0A1D1Z8R7_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,379	17,263	24,394	26,004	24,101									
Solyc11g065280	beta-1,3-glucanase	bga2	F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D); IPR00	5,644	6,117	0,000	0,000	0,000									
Solyc11g065310	Tubulin alpha chain (AHRD V3.3 --* TBA_PRUDU)							0,000	0,019	0,000	0,000	0,000									
Solyc11g065320	Zinc finger transcription factor 67	C3H67	F:GO:0003676; F:GO	F:nucleic acid binding; F:metal ion binding			IPR000571 (PFAM); IPR000504 (PFA	65,776	44,867	11,189	9,720	12,264									
Solyc11g065323	Mono-/di-acylglycerol lipase, N-terminal, Lipase, class 3 (AHRD V3.3 --* AT3G14075.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,141	0,158	0,025	0,025	0,000									
Solyc11g065340	Magnesium-chelatase subunit H (AHRD V3.3 *** A0A0B0N4Q7_GOSAR)	CHLH	F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	2,392	2,107	1,671	2,422	2,336									
Solyc11g065350	ABC transporter-related family protein (AHRD V3.3 *** B9GEU6_POPTR)	ABCG26	F:GO:0005524; C:GO	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); G3DSA:3.40.50.3	81,245	60,662	56,685	75,653	68,188					0,418	0,009			up
Solyc11g065360	ABC transporter G family member (AHRD V3.3 *** A0A0K9PC58_ZOSMR)	ABCG27	F:GO:0005524; C:GO	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR013525 (PFA	0,154	0,158	0,000	0,000	0,000									
Solyc11g065370	Set1/Ash2 histone methyltransferase complex subunit ASH2 (AHRD V3.3 *** A0A0B0NGF2_GOSAR)		F:GO:0005515; C:GO	F:protein binding; C:Set1C/COMPASS complex; P:histone H3-K			IPR003877 (PFAM); mobidb-lite (MOB	21,276	17,459	24,451	24,296	21,182									
Solyc11g065380	D111/G-patch domain protein (AHRD V3.3 *** A0A072VIM1_MEDTR)		F:GO:0003676	F:nucleic acid binding			IPR025239 (PFAM); IPR000467 (PFA	5,651	6,099	12,752	14,377	11,612									
Solyc11g065390	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT1G01570.2)		F:GO:0008375; C:GO	F:acetylglucosaminyltransferase activity; C:integral component			IPR006740 (PFAM); G3DSA:3.90.550	0,000	0,000	0,025	0,094	0,140									
Solyc11g065400	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT1G01570.2)		F:GO:0008375; C:GO	F:acetylglucosaminyltransferase activity; C:integral component			G3DSA:3.90.550.50 (GENE3D); IPR0	0,000	0,076	0,025	0,000	0,023									
Solyc11g065420	Transposon protein, putative, Mutator sub-class (AHRD V3.3 --* Q2R0S1_ORYSJ)		F:GO:0008270	F:zinc ion binding				11,397	8,903	7,798	7,549	7,911									
Solyc11g065425	Basic helix-loop-helix (bHLH) DNA-binding family protein (AHRD V3.3 --* AT4G17880.1)							1,458	1,088	0,663	1,000	0,945									
Solyc11g065490	Protein RETICULATA-RELATED 4, chloroplastic (AHRD V3.3 *** RER4_ARATH)		C:GO:0005739; C:GO	C:mitochondrion; C:chloroplast inner membrane			IPR021825 (PFAM); mobidb-lite (MOB	92,055	89,438	89,908	84,577	85,528									
Solyc11g065520	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G28960.2)						IPR036691 (G3DSA:3.60.10.GENE3D	15,135	19,083	6,966	11,162	8,908					0,680	0,003			up
Solyc11g065530	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G51440.1)		P:GO:0006629	P:lipid metabolic process			G3DSA:3.40.50.12520 (GENE3D); IPF	65,482	44,999	356,272	313,138	318,781									
Solyc11g065545	Vacuolar ATPase assembly integral membrane protein VMA21 homolog (AHRD V3.3 *** A0A0V0HJN7_SOLC		P:GO:0070072	P:vacuolar proton-transporting V-type ATPase complex assemb			IPR019013 (PFAM); mobidb-lite (MOB	179,483	134,022	111,792	86,540	84,377			-0,409	0,039				down	
Solyc11g065550	LOW QUALITY:Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT1G51890.4)							0,059	0,059	0,050	0,025	0,024									
Solyc11g065600	xyloglucan endotransglucosylase-hydrolase 4	xth4	F:GO:0004553; C:GO	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xylogluco	IPR000757 (PFAM); IPR010713 (PFA	0,021	0,062	0,000	0,025	0,023									
Solyc11g065610	LOW QUALITY:Vacuolar ATPase assembly integral membrane protein VMA21 homolog (AHRD V3.3 *-* A0A		C:GO:0005773; C:GO	C:vacuole; C:endoplasmic reticulum membrane; C:ER to Golgi transport vesicle membrane; C:integral c				0,407	0,393	0,198	0,436	0,404									
Solyc11g065620	Sulfite reductase (AHRD V3.3 *** H6WYS2_SOLLC)		F:GO:0020037; F:GO	F:heme binding; F:s	EC:1.8.7.1	Assimilatory sulfite re	IPR006066 (PRINTS); IPR006067 (PF	27,898	32,149	61,737	65,670	59,932									
Solyc11g065625	Phototropin 1 (AHRD V3.3 --* C1IDE6_9LAMI)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,102	0,105	0,212	0,166	0,211									
Solyc11g065630	Myosin-related family protein (AHRD V3.3 *** B9HNX7_POPTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,276	0,463	0,166	0,100	0,141									
Solyc11g065640	2Fe-2S ferredoxin (AHRD V3.3 *** A0A0B2PJW0_GLYSO)		F:GO:0009055; F:GO	F:electron transfer activity; F:2 iron, 2 sulfur cluster binding			IPR001055 (PRINTS); IPR001041 (PF	9,222	10,773	11,391	11,311	11,917									
Solyc11g065643	Luminal-binding protein (AHRD V3.3 --* BIP_SPIOL)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,101	0,025	0,000	0,000									
Solyc11g065660	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9RIC7_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			G3DSA:1.10.510.10 (GENE3D); IPR0	5,300	7,519	5,667	6,085	6,097									
Solyc11g065670	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR020783 (PFAM); IPR020784 (PFA	89,379	102,426	96,488	89,396	85,514									
Solyc11g065680	transmembrane protein (AHRD V3.3 *** AT2G01870.1)		C:GO:0009535; C:GO	C:chloroplast thylakoid membrane; C:integral component of men			PTHR37716 (PANTHER)	2,328	3,094	2,721	3,277	3,606									
Solyc11g065690	kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing protein (AHRD V3.3 --* AT1G16270.3)							24,977	24,727	35,777	38,332	35,251									
Solyc11g065700	Nuclear transcription factor Y subunit A-1-like protein (AHRD V3.3 *** A0A172ELD3_MORAL)		F:GO:0003700; P:GO	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRINT NF-YA	32,170	25,501	57,018	52,504	52,351									
Solyc11g065720	ABC transporter-like family-protein (AHRD V3.3 *** A0A072VNR4_MEDTR)	ABCC16	F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); G3DSA:3.40.50.3	0,019	0,000	0,000	0,000	0,000									
Solyc11g065730	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT3G20890.1)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	46,374	50,103	59,656	54,868	56,919									
Solyc11g065740	Chaperonin-like RbcX protein (AHRD V3.3 *** G7J266_MEDTR)		C:GO:0009570; F:GO	C:chloroplast stroma; F:protein folding chaperone; P:chaperone			IPR038052 (G3DSA:1.10.1200.GENE	5,080	7,853	10,768	10,704	10,683									
Solyc11g065750	Importin subunit alpha (AHRD V3.3 *-* A0A022RYG4_ERYGU)		F:GO:0005515	F:protein binding			IPR000225 (PFAM); IPR011989 (G3D	139,201	121,868	106,766	118,056	111,069									
Solyc11g065760	TK1-like deoxyribonucleoside kinase		F:GO:0004797; F:GO	F:thymidine kinase	EC:2.7.1.145; EC:2.7	Deoxynucleoside kin	G3DSA:3.40.50.300 (GENE3D); IPR0	5,940	4,669	0,902	0,412	0,397									
Solyc11g065770	Cytochrome P450, putative (AHRD V3.3 *** B9S4U7_RICCO)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc11g065820	Protein DETOXIFICATION (AHRD V3.3 *** K4D9J2_SOLLC)		P:GO:0006855; F:GO	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM); IPR002528 (F	11,802	7,481	7,674	6,402	8,219									
Solyc11g065830	2-oxoglutarate/malate translocator, chloroplastic (AHRD V3.3 *** A0A0B0P837_GOSAR)		F:GO:0005215; P:GO	F:transporter activity; P:sodium ion transport; C:membrane; P:tr			IPR001898 (PFAM); IPR001898 (TIGF	30,877	33,771	44,584	54,963	52,567									
Solyc11g065840	R2R3MYB transcription factor 46	R2R3MYB46	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,139	0,055	0,000	0,000	0,000									
Solyc11g065870	GTPase Der (AHRD V3.3 *** W9S707_9ROSA)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS); IPR006073 (PF	18,806	17,294	36,095	36,314	36,791									
Solyc11g065880	RNA-binding family protein (AHRD V3.3 *** A0A061FD24_THECC)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	23,936	23,353	34,448	30,933	31,840									
Solyc11g065890	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** E6Y2I1_HELAN)		F:GO:0016746	F:transferase activity, transferring acyl groups			IPR002123 (PFAM); IPR032098 (PFA	0,882	0,801	1,336	1,870	0,923									
Solyc11g065900	DNA replication complex GINS protein SLD5 (AHRD V3.3 *** K4D9J9_SOLLC)		P:GO:0006261	P:DNA-dependent DNA replication			G3DSA:1.20.58.1030 (GENE3D); IPR	21,190	21,355	17,906	18,391	18,340									
Solyc11g065910	Aspartic protease inhibitor 9 (AHRD V3.3 --* API9_SOLTU)						PR01217 (PRINTS); mobidb-lite (MOB	0,000	0,041	0,022	0,022	0,000									
Solyc11g065920	Xanthine dehydrogenase (AHRD V3.3 *** H6UJ41_CAMSI)		F:GO:0005506; F:GO	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR008274 (PFAM); IPR002888 (PFA	172,507	151,161	490,120	505,313	474,288									
Solyc11g065930	Xanthine dehydrogenase (AHRD V3.3 *** H6UJ41_CAMSI)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity; P:oxidation-reducti			G3DSA:3.30.365.10 (GENE3D); IPR0	33,995	31,472	36,517	34,923	37,490									
Solyc11g065940	ENTH/VHS family protein (AHRD V3.3 *** A0A061GXX0_THECC)						IPR013809 (PFAM); IPR008942 (G3D	28,696	23,957	24,591	21,131	24,371									
Solyc11g065950	Receptor protein kinase, putative (AHRD V3.3 *** B9T790_RICCO)		F:GO:0004672; F:GO	F:protein kinase activity; F:ubiquitin-protein transferase activity			G3DSA:3.30.200.20 (GENE3D); G3DS	38,616	28,348	50,223	47,645	44,329									
Solyc11g065960	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 --* M0ZPQ7_SOLTU)		F:GO:0004553; C:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; C:extra			mobidb-lite (MOBIDB_LITE)	1,940	1,319	1,552	1,732	1,488									
Solyc11g065970	Laccase (AHRD V3.3 *-* K4CA83_SOLLC)		F:GO:0005507; F:GO	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red			IPR008972 (G3DSA:2.60.40.GENE3D	0,078	0,039	0,075	0,145	0,023									
Solyc11g065980	U3 small nucleolar ribonucleoprotein protein imp4, putative (AHRD V3.3 *** B9RGD5_RICCO)		P:GO:0006364; F:GO	P:rRNA processing; F:snoRNA binding; C:small-subunit process			G3DSA:3.40.50.10480 (GENE3D); IPF	20,169	19,776	19,213	20,170	18,115									
Solyc11g065990	Actin (AHRD V3.3 *** ACT_GOSHI)		F:GO:0005524; C:GO	F:ATP binding; C:cytoplasm; C:cytoskeleton			IPR004000 (PRINTS); G3DSA:3.90.64	0,702	0,900	1,174	1,954	1,790									
Solyc11g066000	Cyclin-dependent protein kinase inhibitor SMR14 (AHRD V3.3 --* SMR14_ARATH)		P:GO:0032875	P:regulation of DNA endoreduplication			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,124	0,078	0,000	0,025	0,023									
Solyc11g066010	ATP synthase subunit epsilon (AHRD V3.3 *** W9SG58_9ROSA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,653	0,756	0,047	0,022	0,023									
Solyc11g066020	Ankyrin repeat family protein (AHRD V3.3 *** B9GJP4_POPTR)		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	142,163	108,427	28,181	21,096	32,595									
Solyc11g066040	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PZF9_ZOSMR)		F:GO:0004842; F:GO	F:ubiquitin-protein transferase activity; F:protein binding; P:cell			IPR013083 (G3DSA:3.30.40.GENE3D	22,964	18,873	21,551	19,204	23,621									
Solyc11g066050	LOW QUALITY:Dof zinc finger protein (AHRD V3.3 *** Q9M4G1_SOLTU)		F:GO:0003677; P:GO	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM Dof	1,738	1,310	0,875	0,778	0,723									
Solyc11g066065	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT5G63630.2)							0,040	0,019	0,068	0,000	0,024									
Solyc11g066070	Cysteine alpha-hairpin motif superfamily (AHRD V3.3 *** A0A103YFL5_CYNCS)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:mitochondrial translation			IPR031731 (PFAM); IPR017264 (PAN	12,811	12,716	19,094	17,927	16,687									
Solyc11g066080	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072VCD4_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR34054:SF2 (PANTHER); PTHR3	14,927	4,227	2,824	7,531	4,185	-1,788	0,000			1,404	0,000	down		up
Solyc11g066090	HSP20-like chaperones superfamily protein (AHRD V3.3 *** AT2G37570.1)						IPR008978 (G3DSA:2.60.40.GENE3D	6,002	5,255	4,471	4,309	5,805									
Solyc11g066100	heat shock protein 70 (AHRD V3.3 *** AT3G12580.1)		F:GO:0005524; C:GO	F:ATP binding; C:cy	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013126 (PRINTS); IPR013126 (PF	218,105	124,434	797,616	722,337	683,834	-0,783	0,015					down		
Solyc11g066110	Inner membrane protein (AHRD V3.3 *** S8C850_9LAMI)		C:GO:0016021; F:GO	C:integral component of membrane; F:membrane insertase acti			IPR001708 (PFAM); IPR028055 (TIGF	37,389	53,947	60,403	67,593	78,262	0,556	0,038	0,371	0,034			up	up	
Solyc11g066120	CLAVATA3/ESR (CLE)-related protein 46 (AHRD V3.3 --* CLE46_ARATH)						mobidb-lite (MOBIDB_LITE)	0,632	0,748	1,137	1,212	1,371									
Solyc11g066130	osmotin	TOMOLP	C:GO:0005576; C:GO	C:extracellular region; C:cell wall			IPR001938 (PRINTS); IPR037176 (G3	28,765	39,509	8,133	7,858	8,738									
Solyc11g066140	P-hydroxybenzoic acid efflux pump subunit aaeB (AHRD V3.3 *** A0A061GW63_THECC)		F:GO:0005515; C:GO	F:protein binding; C:plasma membrane; C:integral component of			PF13515 (PFAM); PTHR30509:SF22 (	0,279	0,140	0,068	0,170	0,071									
Solyc11g066150	UDP-glucuronate decarboxylase 1 (AHRD V3.3 *** Q6IVK5_TOBAC)		C:GO:0005737; P:GO	C:cytoplasm; P:D-x	EC:4.1.1.35	UDP-glucuronate dec	IPR016040 (PFAM); G3DSA:3.40.50.7	10,047	8,917	12,908	13,672	15,313									
Solyc11g066160	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677; F:GO	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS); IPR035425 (PF	8,156	8,109	2,632	1,928	2,096									
Solyc11g066170	Two-component response regulator (AHRD V3.3 *-* W9RGG7_9ROSA)		P:GO:0000160	P:phosphorelay signal transduction system			G3DSA:3.40.50.23 ARR-B	0,000	0,018	0,000	0,000	0,000									
Solyc11g066230	LOW QUALITY:Two-component response regulator (AHRD V3.3 *-* W9QMB4_9ROSA)		P:GO:0000160	P:phosphorelay signal transduction system			G3DSA:1.10.10.60 ARR-B	0,000	0,019	0,000	0,000	0,000									
Solyc11g066240	replication factor-A carboxy-terminal domain protein (AHRD V3.3 *** AT2G28105.2)						PTHR23273 (PANTHER); PTHR23273	0,929	0,805	1,073	1,116	1,155									
Solyc11g066250	Carboxypeptidase (AHRD V3.3 *** K4D9N3_SOLLC)		F:GO:0004185; P:GO	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	21,298	18,179	1,909	1,429	1,184									
Solyc11g066260	Vacuolar protein sorting-associated protein 24 like 1 (AHRD V3.3 *** A0A0B2QEZ9_GLYSO)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM); mobidb-lite (MOB	17,388	16,959	17,888	16,797	16,217									
Solyc11g066270	xyloglucan endotransglucosylase-hydrolase 6	xth6	F:GO:0004553; C:GO	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xylogluco	IPR016455 (PIRSF); IPR010713 (PFA	0,970	2,173	0,022	0,000	0,000	1,176	0,040					up		
Solyc11g066280	Ribosome production factor 1 (AHRD V3.3 *** A0A0B2P1B3_GLYSO)						G3DSA:3.40.50.10480 (GENE3D); IPF	53,469	52,237	13,354	9,814	14,087									
Solyc11g066290	Purple acid phosphatase 29 (AHRD V3.3 *** A0A193CCQ7_9ERIC)		F:GO:0016787	F:hydrolase activity			IPR011230 (PIRSF); IPR004843 (PFA	82,684	81,052	132,001	124,229	117,808									
Solyc11g066300	CRS2-associated factor 1 (AHRD V3.3 *** A0A072TTL7_MEDTR)		F:GO:0003723	F:RNA binding			IPR035920 (G3DSA:3.30.110.GENE3	6,785	6,814	7,752	7,595	8,404									
Solyc11g066310	transmembrane protein (AHRD V3.3 *** AT1G70505.4)		C:GO:0016021	C:integral component of membrane			PTHR12242:SF10 (PANTHER); PTHR	3,684	3,108	3,244	4,148	4,455									
Solyc11g066320	Exostosin family protein (AHRD V3.3 *** AT2G28110.1)		P:GO:0006486; F:GO	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM); PTHR11062:SF1	29,474	17,309	23,469	23,526	25,664	-0,740	0,005					down		
Solyc11g066330	Major facilitator superfamily protein (AHRD V3.3 *** AT2G28120.1)		C:GO:0016021	C:integral component of membrane			IPR010658 (PFAM); G3DSA:1.20.125	3,277	2,336	1,412	1,918	1,636									
Solyc11g066340	actin protein 2/3 complex subunit-like protein (AHRD V3.3 *** AT2G28130.1)		C:GO:0005634; P:GO	C:nucleus; P:DNA repair			PTHR37212 (PANTHER)	5,079	4,820	7,921	8,218	8,029									
Solyc11g066350	Shugoshin-1, putative (AHRD V3.3 *** B9SCJ5_RICCO)		C:GO:0000775; C:GO	C:chromosome, centromeric region; C:nucleus; P:meiotic chrom			IPR011515 (PFAM); mobidb-lite (MOB	0,260	0,232	0,000	0,095	0,048									
Solyc11g066360	DUF1635 family protein (AHRD V3.3 *** A0A072VBV9_MEDTR)						IPR012862 (PFAM); mobidb-lite (MOB	19,402	22,276	102,333	97,951	88,176									
Solyc11g066370	DNA ligase (AHRD V3.3 *** K4D9P5_SOLLC)		F:GO:0003677; F:GO	F:DNA binding; F:DI	EC:6.5.1.1	DNA ligase (ATP)	IPR012310 (PFAM); IPR000977 (TIGF	33,356	35,010	36,847	30,720	31,942									
Solyc11g066380	Domain of Uncharacterized protein function isoform 4 (AHRD V3.3 *** A0A061GYF6_THECC)						IPR010369 (PFAM); IPR021182 (PIRS	19,557	12,884	12,528	14,264	10,638									
Solyc11g066390	superoxide dismutase 3	sod3	P:GO:0006801; F:GO	P:superoxide metabolic process; F:metal ion binding			IPR001424 (PRINTS); IPR001424 (PF	37,624	49,701	24,287	19,234	23,224									
Solyc11g066400	Zinc finger family protein (AHRD V3.3 *** B9HQP7_POPTR)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM); C2H2	0,681	0,754	0,912	1,346	0,796									
Solyc11g066410	50S ribosomal protein L9 (AHRD V3.3 *** A0A0A9CWP8_ARUDO)		F:GO:0003735; C:GO	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036791 (G3DSA:3.10.430.GENE3	13,107	24,415	21,614	20,752	29,021	0,927	0,001	0,423	0,017			up	up	
Solyc11g066420	LOW QUALITY:Protein SENSITIVE TO PROTON RHIZOTOXICITY 1 (AHRD V3.3 *** A0A151SAJ5_CAJCA)		F:GO:0003676	F:nucleic acid binding			G3DSA:3.30.160.6 C2H2	0,061	0,372	0,022	0,048	0,095									
Solyc11g066440	lethal leaf spot 1	PAO	F:GO:0010277; F:GO	F:chlorophyllide a o	EC:1.13.12; EC:1.14	Acting on single donc	IPR017941 (PFAM); IPR036922 (G3D	82,956	114,337	284,514	337,341	327,518									
Solyc11g066450	transmembrane protein (AHRD V3.3 *** AT5G22875.3)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE); PTHR360	12,342	10,992	12,507	12,841	14,911									
Solyc11g066460	LOW QUALITY:DNA-binding storekeeper protein-related transcriptional regulator, putative (AHRD V3.3 *** A		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR007592 (PFAM); mobidb-lite (MOB	13,394	14,117	21,548	18,174	17,251									
Solyc11g066470	Pyridoxine/pyridoxamine 5'-phosphate oxidase (AHRD V3.3 --* A0A1D1ZJ14_9ARAE)							33,385	34,902	27,958	22,830	28,680									
Solyc11g066480	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain, putative (AHRD V3.3 *** A0A061		F:GO:0046872	F:metal ion binding			IPR032308 (PFAM); G3DSA:3.40.630	67,884	55,542	72,645	70,397	68,717									
Solyc11g066490	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0009506; C:GO	C:plasmodesma; C:integral component of membrane; C:anchore			IPR004864 (PFAM); PTHR31852:SF5	0,415	0,753	0,022	0,045	0,070									
Solyc11g066500	Ring/U-Box superfamily protein (AHRD V3.3 *-* AT2G27950.3)						PF13920 (PFAM); IPR013083 (G3DS/	33,288	40,771	63,158	64,260	64,926									
Solyc11g066510	RING/U-box superfamily protein (AHRD V3.3 *** AT2G27940.1)		F:GO:0008270; C:GO	F:zinc ion binding; C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	3,849	2,431	7,750	8,093	5,961									
Solyc11g066520	Carboxypeptidase (AHRD V3.3 *** K4D9Q9_SOLLC)		F:GO:0004185; P:GO	F:serine-type carbo	EC:3.4.21; EC:3.4.16	Acting on peptide bor	IPR001563 (PRINTS); IPR029058 (G3	0,556	0,874	0,072	0,072	0,072									
Solyc11g066530	pre-mRNA-splicing factor of RES complex protein (AHRD V3.3 --* AT1G31870.2)		C:GO:0005634; C:GO	C:nucleus; C:cytosol				0,021	0,000	0,000	0,000	0,000									
Solyc11g066540	HAD superfamily, subfamily IIIB acid phosphatase (AHRD V3.3 --* AT2G38600.2)							35,948	33,820	37,232	40,070	35,340									
Solyc11g066560	Vacuolar protein sorting-associated protein 41 homolog (AHRD V1 ***- B5X3G5_SALSA)		F:GO:0005515; P:GO	F:protein binding; P:intracellular protein transport; P:vesicle-me			IPR011990 (G3DSA:1.25.40.GENE3D	41,525	34,963	45,590	46,479	43,866									
Solyc11g066580	flavonoid 3`%2C5`-hydroxylase	F3'5'H	F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,979	1,526	0,047	0,050	0,000									
Solyc11g066590	Lysosomal Pro-X carboxypeptidase, putative (AHRD V3.3 *** B9SCN3_RICCO)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity			G3DSA:1.20.120.980 (GENE3D); IPR	1,258	2,531	0,506	0,590	0,612									
Solyc11g066600	Lysosomal Pro-X carboxypeptidase, putative (AHRD V3.3 *** B9SCN3_RICCO)		P:GO:0006508; F:GO	P:proteolysis; F:serine-type peptidase activity			IPR008758 (PFAM); G3DSA:1.20.120	0,094	0,385	0,000	0,050	0,071									
Solyc11g066610	AT1G08220-like protein (AHRD V3.3 *** A0A0G4ALR4_9ROSI)		C:GO:0005743; C:GO	C:mitochondrial inner membrane; C:integral component of mitoc			IPR007849 (PFAM); IPR007849 (PAN	7,254	7,158	11,959	11,472	11,844									
Solyc11g066620	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT5G22850.1)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR001461 (PRINTS); IPR032861 (PF	28,037	40,177	87,829	154,154	93,068					0,815	0,000			up
Solyc11g066630	AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT2G24681.1)							4,708	5,060	2,117	1,975	2,728									
Solyc11g066650	Kinase family protein (AHRD V3.3 *** B9MYL8_POPTR)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); IPR0	10,041	8,749	7,157	7,499	7,267									
Solyc11g066660	Magnesium transporter MRS2-like protein (AHRD V3.3 *** A0A072VBF4_MEDTR)		C:GO:0016020; P:GO	C:membrane; P:metal ion transport; F:metal ion transmembrane			G3DSA:1.20.58.340 (GENE3D); IPR0	28,104	25,393	9,370	10,400	16,286			0,790	0,008				up	
Solyc11g066665	Magnesium transporter MRS2-like protein (AHRD V3.3 *-* A0A072VBF4_MEDTR)		C:GO:0009941; P:GO	C:chloroplast envelope; P:thylakoid membrane organization; P:m			mobidb-lite (MOBIDB_LITE): mobidb-lit	28,129	26,226	9,196	11,055	16,677			0,852	0,006				up	
Solyc11g066670	Glycosyltransferase (AHRD V3.3 *** K4D9S4_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR	25,834	28,533	15,503	13,293	16,272									
Solyc11g066680	Glycosyltransferase (AHRD V3.3 *** K4D9S5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D); IPR	6,294	7,979	7,006	6,185	7,343									
Solyc11g066690	RecQ-mediated instability 2 (AHRD V3.3 *** A0A0B0NH03_GOSAR)		P:GO:0009555; P:GO	P:pollen development; P:regulation of sister chromatid segregat			G3DSA:2.40.50.140 (GENE3D); IPR0	0,879	1,508	0,308	0,125	0,210									
Solyc11g066700	GDSL esterase/lipase family protein		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	0,000	0,019	0,000	0,273	0,165									
Solyc11g066710	Phospholipid:diacylglycerol acyltransferase (AHRD V3.3 *** F8RNW6_RICCO)		P:GO:0006629; F:GO	P:lipid metabolic process; F:O-acyltransferase activity			IPR003386 (PFAM); IPR029058 (G3D	7,971	7,634	0,149	0,253	0,046									
Solyc11g066720	UDP-apiose/xylose synthase (AHRD V3.3 *** Q2I2N3_SOLTU)		F:GO:0003824; F:GO	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D); IPR0	132,647	142,019	20,228	14,727	19,790									
Solyc11g066730	phototropic-responsive NPH3 family protein		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D); IPR0	3,680	4,362	5,623	6,136	5,789									
Solyc11g066740	reticulata-like protein, putative (DUF3411) (AHRD V3.3 *** AT2G37860.4)		C:GO:0005739; C:GO	C:mitochondrion; C:chloroplast inner membrane; C:integral com			IPR021825 (PFAM); mobidb-lite (MOB	23,098	23,602	42,447	36,009	40,849									
Solyc11g066760	AP-2 complex subunit alpha-1 (AHRD V3.3 *** AP2A1_ARATH)		P:GO:0006886; P:GO	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR011989 (G3DSA:1.25.10.GENE3D	28,669	25,130	13,625	16,720	15,326									
Solyc11g066770	AP-2 complex subunit alpha (AHRD V3.3 *-* A0A151RV94_CAJCA)		P:GO:0006886; P:GO	P:intracellular protein transport; P:vesicle-mediated transport; C			IPR008152 (PFAM); IPR003164 (PFA	32,381	34,377	18,559	19,797	19,371									
Solyc11g066780	Nucleosome-remodeling factor subunit BPTF (AHRD V3.3 *** W9S0X5_9ROSA)		F:GO:0046872	F:metal ion binding			IPR028942 (PFAM); IPR019787 (PFA	27,445	26,509	29,325	32,002	30,279									
Solyc11g066790	Helicase protein with RING/U-box domain-containing protein (AHRD V3.3 *** AT5G43530.1)		F:GO:0003676; F:GO	F:nucleic acid binding; F:ATP binding; F:zinc ion binding; F:hydro			IPR000330 (PFAM); PF13923 (PFAM)	7,399	6,238	3,836	3,719	4,074									
Solyc11g066800	Amino acid transporter, putative (AHRD V3.3 *** B9SN74_RICCO)		P:GO:0003333; C:GO	P:amino acid transmembrane transport; C:plasma membrane; F			IPR013057 (PFAM); PTHR22950:SF3	0,059	0,182	0,050	0,025	0,070									
Solyc11g066810	Plasma-membrane choline transporter family protein (AHRD V3.3 --* AT3G04440.1)							0,203	0,159	0,096	0,125	0,119									
Solyc11g066820	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity, trans			IPR001173 (PFAM); IPR029044 (G3D	215,935	134,242	133,022	138,442	121,004	-0,657	0,049					down		
Solyc11g066830	Zinc finger transcription factor 68	C3H68	P:GO:0000398; F:GO	P:mRNA splicing, via spliceosome; F:RNA binding; F:metal ion b			IPR009145 (PRINTS); IPR012677 (G3	134,356	95,148	141,256	144,281	142,540									
Solyc11g066840	Histone deacetylase-like protein-like (AHRD V3.3 *** Q2XTD2_SOLTU)						G3DSA:2.60.120.340 (GENE3D); IPR	662,749	573,669	156,842	106,443	118,655					-0,556	0,040			down
Solyc11g066850	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S769_RICCO)		F:GO:0004519; F:GO	F:endonuclease activity; F:protein binding			IPR027434 (G3DSA:3.10.28.GENE3D	15,226	12,473	13,894	15,130	15,340									
Solyc11g066860	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,159	0,057	0,379	0,190	0,143									
Solyc11g066870	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein (AHRD V3.3 *** AT5G2264		F:GO:0008565; C:GO	F:protein transporter activity; C:chloroplast thylakoid membrane			IPR003409 (PFAM); G3DSA:2.20.110	47,911	59,471	51,999	46,112	56,728									
Solyc11g066880	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)		C:GO:0005576; F:GO	C:extracellular region; F:growth factor activity; P:cell population			IPR009438 (PFAM); PTHR33285:SF1	0,114	0,097	0,000	0,000	0,000									
Solyc11g066890	Arogenate dehydratase (AHRD V3.3 *** K4D9U6_SOLLC)		F:GO:0004664; P:GO	F:prephenate dehyc	EC:4.2.1.51	Prephenate dehydrat	G3DSA:3.40.190.10 (GENE3D); IPR0	14,922	36,135	295,962	251,032	268,112	1,300	0,000					up		
Solyc11g066900	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** A0A072VC14_MEDTR)		C:GO:0016020; F:GO	C:membrane; F:transmembrane transporter activity; P:transmem			IPR006043 (PFAM); mobidb-lite (MOB	17,129	15,590	9,860	14,080	11,710					0,519	0,020			up
Solyc11g066910	Syntaxin-like protein (AHRD V3.3 *** Q3HRZ4_SOLTU)		C:GO:0016020; P:GO	C:membrane; P:vesicle-mediated transport			G3DSA:1.20.5.110 (GENE3D); IPR00	14,023	12,655	12,586	11,958	12,155									
Solyc11g066920	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151R9G8_CAJCA)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,082	0,000	0,047	0,149	0,024									
Solyc11g066930	DUF868 family protein (DUF868) (AHRD V3.3 *** AT2G27770.1)		C:GO:0016020	C:membrane			IPR008586 (PFAM); PTHR31972:SF1	1,214	0,606	8,649	11,387	6,558									
Solyc11g066940	Wall-associated receptor kinase-like 20 (AHRD V3.3 --* A0A061E5G3_THECC)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane			PTHR33355 (PANTHER); PTHR33355	0,561	0,665	10,837	13,060	5,069			-1,095	0,000				down	
Solyc11g066950	Stress responsive A/B Barrel Domain-containing protein (AHRD V3.3 *** AT5G22580.1)		C:GO:0009507	C:chloroplast			G3DSA:3.30.70.100 (GENE3D); IPR0	1,260	1,553	0,046	0,000	0,023									
Solyc11g066960	TRNA ISOPENTENYLTRANSFERASE family protein (AHRD V3.3 *** B9HQU6_POPTR)		P:GO:0008033	P:tRNA processing			IPR018022 (PFAM); G3DSA:1.10.287	8,029	6,416	6,257	7,497	6,242									
Solyc11g066970	RAB6-interacting golgin (DUF662) (AHRD V3.3 *** AT2G27740.1)						IPR007033 (PFAM); mobidb-lite (MOB	0,434	0,503	0,000	0,045	0,000									

Solyc11g066990	Suppressor of gene silencing 3, putative (AHRD V3.3 *-* A0A061FQZ7_THECC)		P:GO:0031047	P:gene silencing by RNA			IPR005380 (PFAM): IPR038588 (G3D	49,155	52,245	69,693	68,656	66,561									
Solyc11g067000	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *** G7L5Z6_MED	ABCG51	F:GO:0005524: C:G(	F:ATP binding: C:m(	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR013581 (PFAM): IPR003439 (PFA	0,058	0,057	0,022	0,525	0,143									
Solyc11g067010	Protein BUD31 homolog 2 (AHRD V3.3 *** BD31B_ORYSJ)		C:GO:0005634	C:nucleus			IPR001748 (PRINTS): IPR001748 (PF	53,049	48,700	50,368	49,507	47,262									
Solyc11g067020	Histone deacetylase (AHRD V3.3 *** A0A0K9PTU8_ZOSMR)		F:GO:0004407: P:G(	F:histone deacetyla	EC:3.5.1.98	Histone deacetylase	IPR000286 (PRINTS): IPR003084 (PF	19,659	16,990	25,743	24,766	24,032									
Solyc11g067030	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G24560.1)		F:GO:0005524: C:G(	F:ATP binding: C:cytoplasm: P:tRNA processing: F:ligase activit			PTHR43033:SF4 (PANTHER): PTHR4:	0,518	0,454	0,439	0,504	0,472									
Solyc11g067040	Cytoplasmic tRNA 2-thiolation protein 1 (AHRD V3.3 --* A0A059BW08_EUCGR)		F:GO:0005524: C:G(	F:ATP binding: C:cytoplasm: P:tRNA processing: F:ligase activit			IPR014729 (G3DSA:3.40.50.GENE3D	0,485	0,685	0,385	0,510	0,332									
Solyc11g067050	MLFHVNVLIKSRNYYNSCKAEGIINFRYLLTMGASEAALQLLSGELSCQVRTSSILAKSN		F:GO:0033926	F:glycopeptide alph	EC:3.2.1.97	Endo-alpha-N-acetyl(	IPR024746 (PFAM): IPR012341 (G3D	39,940	38,356	36,915	35,578	36,340									
Solyc11g067060	low molecular weight protein-tyrosine phosphatase		F:GO:0004725: P:G(	F:protein tyrosine p	EC:3.1.3.16: EC:3.1.	Protein-serine/threor	IPR017867 (PRINTS): G3DSA:3.40.50	14,016	16,369	36,934	36,628	39,269									
Solyc11g067070	Protein kinase (AHRD V3.3 *** A7VL53_WHEAT)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (PFAM): mobidb-lite (MOB	11,541	8,500	35,465	30,463	29,363									
Solyc11g067075	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT4G29930.7)							0,516	0,209	0,868	0,803	0,848									
Solyc11g067080	Protein kinase like protein (AHRD V3.3 *** Q0WN21_ARATH)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	17,478	12,740	30,986	23,097	26,351					-0,421	0,049			down
Solyc11g067090	Peptidyl-prolyl cis-trans isomerase, putative (AHRD V3.3 *** A0A072VAB3_MEDTR)		P:GO:0000413: F:G(	P:protein peptidyl-pr	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR015943 (G3	14,912	12,922	15,347	14,561	14,721									
Solyc11g067100	60s acidic ribosomal family protein (AHRD V3.3 *** A9PCM7_POPTR)		F:GO:0003735: C:G(	F:structural constituent of ribosome: C:ribosome: P:translationa			IPR038716 (G3DSA:1.10.10.GENE3D	0,040	0,000	0,025	0,000	0,071									
Solyc11g067110	DNA polymerase epsilon catalytic subunit (AHRD V3.3 *-* AT1G08260.2)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.7	DNA-directed DNA po	IPR036397 (G3DSA:3.30.420.GENE3I	5,978	4,341	3,229	3,024	4,431									
Solyc11g067140	DNA polymerase epsilon catalytic subunit A (AHRD V3.3 *** W9R0V5_9ROSA)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.7	DNA-directed DNA po	IPR013697 (PFAM): IPR029703 (PAN	25,335	21,503	16,935	13,634	17,263									
Solyc11g067150	transmembrane protein (AHRD V3.3 *** AT4G04190.1)						PTHR36047 (PANTHER)	3,653	4,657	5,611	5,118	4,262									
Solyc11g067160	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** A0A072VAB6_MEDTR)						IPR023210 (PFAM): IPR036812 (G3D	54,199	61,756	232,727	261,970	259,658									
Solyc11g067180	Fatty acyl-CoA reductase (AHRD V3.3 *** K4D9X5_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			IPR013120 (PFAM): IPR033640 (PFA	0,040	0,039	1,183	0,847	0,680									
Solyc11g067190	Fatty acyl-CoA reductase (AHRD V3.3 *** K4D9X6_SOLLC)		F:GO:0080019	F:fatty-acyl-CoA reductase (alcohol-forming) activity			IPR033640 (PFAM): IPR013120 (PFA	0,021	0,039	0,000	0,000	0,023									
Solyc11g067200	Protein HIRA-like protein (AHRD V3.3 *** A0A0B0NK97_GOSAR)		F:GO:0005515: C:G(	F:protein binding: C:nucleus: P:chromatin organization: P:regula			IPR015943 (G3DSA:2.130.10.GENE3I	35,758	29,641	76,625	75,963	66,759									
Solyc11g067210	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XH63_CYNCS)		F:GO:0005515: F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,043	2,859	1,635	1,915	1,816									
Solyc11g067215	VEFS-Box of polycomb protein isoform 2 (AHRD V3.3 --* A0A061FZ24_THECC)							0,059	0,064	0,125	0,073	0,212									
Solyc11g067220	nudix hydrolase homolog 19 (AHRD V3.3 --* AT5G20070.1)							0,202	0,527	0,143	0,287	0,377									
Solyc11g067230	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** KTNA1_ARATH)		F:GO:0005524	F:ATP binding			G3DSA:1.20.58.280 (GENE3D): G3DS	51,476	49,662	50,214	50,261	50,422									
Solyc11g067240	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** KTNA1_ARATH)		F:GO:0005524	F:ATP binding			G3DSA:1.20.58.280 (GENE3D): G3DS	43,381	48,275	54,236	55,280	53,373									
Solyc11g067250	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4D9Y2_SOLLC)		F:GO:0003950: P:G(	F:NAD+ ADP-ribosy	EC:2.4.2.3	NAD(+) ADP-ribosylti	IPR012317 (PFAM): IPR036616 (G3D	5,989	9,453	2,419	4,401	0,509									
Solyc11g067255	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT5G42430.1)						mobidb-lite (MOBIDB_LITE)	1,356	1,271	2,549	2,725	2,260									
Solyc11g067260	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G22460.3)		C:GO:0005773: C:G(	C:vacuole: C:plant-type cell wall: C:plasmodesma: C:integral co			IPR000073 (PFAM): IPR029058 (G3D	47,026	47,583	81,339	85,882	80,217									
Solyc11g067270	Acylsugar acyltransferase 3 (AHRD V3.3 *** ASAT3_SOLLC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3I	0,952	2,507	0,025	0,025	0,000									
Solyc11g067280	MYB-CC type transfactor		F:GO:0003677	F:DNA binding			IPR001005 (PFAM G2-like	24,870	27,717	37,566	35,531	35,786									
Solyc11g067300	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	ABCB18	F:GO:0005524: C:G(	F:ATP binding: C:int	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): IPR003439 (PFA	3,546	3,965	2,773	3,023	2,492									
Solyc11g067320	Sulfotransferase (AHRD V3.3 *** K4D9Y9_SOLLC)		F:GO:0008146	F:sulfotransferase activity			IPR000863 (PFAM): G3DSA:3.40.50.3	0,078	0,036	0,167	0,176	0,234									
Solyc11g068360	LOW QUALITY:Disease resistance protein (AHRD V3.3 *** A0A068EUC5_SOLHA)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	6,550	4,976	2,003	1,814	2,119									
Solyc11g068370	bZIP transcription factor family protein (AHRD V3.3 *** AT1G08320.4)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR004827 (PFAM bZIP	0,390	0,628	0,050	0,097	0,213									
Solyc11g068390	LOW QUALITY:B-box type zinc finger protein with CCT domain-containing protein (AHRD V3.3 --* AT2G335(		P:GO:0009785	P:blue light signaling pathway			mobidb-lite (MOBIDB_LITE): IPR0403	0,000	0,019	0,000	0,050	0,000									
Solyc11g068400	Cytochrome b-c1 complex subunit 9 (AHRD V3.3 *** QCR9_SOLTU)		C:GO:0005750: P:G(	C:mitochondrial respiratory chain complex III: P:mitochondrial el			IPR036656 (G3DSA:1.20.5.GENE3D):	27,709	33,428	42,414	40,189	37,066									
Solyc11g068420	Ribosomal protein (AHRD V3.3 *** M1CHW0_SOLTU)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: P:translatio			IPR002143 (PIRSF): IPR028364 (PFA	210,257	194,745	138,749	119,369	130,190									
Solyc11g068430	Ferredoxin family protein (AHRD V3.3 *** B9HQ08_POPTR)		F:GO:0009055: P:G(	F:electron transfer activity: P:electron transport chain: F:2 iron.			IPR012675 (G3DSA:3.10.20.GENE3D	74,935	107,016	251,210	247,835	265,209									
Solyc11g068440	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SCU1_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00(	168,480	112,134	84,540	123,487	119,986									
Solyc11g068450	Biogenesis of lysosome-related organelles complex 1 subunit 1 (AHRD V3.3 *** A0A0B2PHL2_GLYSO)		C:GO:0031083	C:BLOC-1 complex			IPR009395 (PFAM): IPR009395 (PAN	7,068	6,547	6,269	5,902	6,252									
Solyc11g068460	Ef-hand calcium binding protein, putative (AHRD V3.3 *** B9SCV7_RICCO)		F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238.	11,816	8,969	16,662	16,683	13,857									
Solyc11g068465	asparagine synthetase 3 (AHRD V3.3 --* AT5G10240.2)							0,235	0,220	0,230	0,378	0,093									
Solyc11g068470	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XGK8_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	2,659	3,105	3,032	3,336	2,919									
Solyc11g068480	Nuclear factor Y (AHRD V3.3 *** A0A061GVH6_THECC)		F:GO:0046982	F:protein heterodimerization activity			IPR009072 (G3DS NF-YB	8,077	7,217	11,364	10,072	9,953									
Solyc11g068490	Ribosomal protein L31 (AHRD V3.3 *** AT5G55125.2)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			PTHR37264 (PANTHER)	32,488	34,688	46,016	48,524	40,734									
Solyc11g068500	Protein transport protein Sec24-like (AHRD V3.3 *** A0A0B2S359_GLYSO)		P:GO:0006886: P:G(	P:intracellular protein transport: P:endoplasmic reticulum to Gol(			IPR006900 (PFAM): G3DSA:2.30.30.3	45,661	42,995	39,735	46,982	45,104									
Solyc11g068510	copper ion binding protein (AHRD V3.3 *** AT2G27730.4)		F:GO:0005507: C:G(	F:copper ion binding: C:nucleolus: C:mitochondrial respiratory c			mobidb-lite (MOBIDB_LITE): mobidb-lit	69,493	71,780	104,477	100,391	108,013									
Solyc11g068515	Protein kinase superfamily protein (AHRD V3.3 --* AT1G54610.3)						mobidb-lite (MOBIDB_LITE)	4,722	8,992	3,147	2,772	4,364	0,954	0,018					up		
Solyc11g068520	Rho GTPase-activating protein (AHRD V3.3 *** A0A0K9PVR7_ZOSMR)		P:GO:0007165	P:signal transduction			IPR036936 (G3DSA:3.90.810.GENE3I	12,260	14,208	6,511	6,127	8,649									
Solyc11g068530	LOW QUALITY:FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT5G22390.1)						IPR021410 (PFAM): mobidb-lite (MOB	1,084	0,723	0,559	0,632	0,399									
Solyc11g068540	beta-alanine synthase		P:GO:0006596: F:G(	P:polyamine biosyn	EC:3.5.1.53	N-carbamoylputresci	IPR017755 (TIGRFAM): IPR036526 ((	118,201	105,081	120,276	103,144	114,106									
Solyc11g068550	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *** A0A072UVF!		P:GO:0009269: C:G(	P:response to desiccation; C:integral component of membrane			IPR004864 (PFAM): PTHR31852:SF7	29,639	24,943	19,098	15,034	18,074									
Solyc11g068560	Tropinone reductase (AHRD V3.3 --* TRN1_COCOF)		C:GO:0016020: C:G(	C:membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,075	0,192	0,100	0,000	0,000									
Solyc11g068580	Germin-like protein 1 (AHRD V3.3 *** B9MYQ6_POPTR)		F:GO:0030145: F:G(	F:manganese ion binding; F:nutrient reservoir activity			IPR001929 (PRINTS): IPR014710 (G3	0,000	0,021	0,025	0,000	0,000									
Solyc11g068610	Actin-related protein 2/3 complex subunit 2 (AHRD V3.3 *** N1R5B7_AEGTA)		C:GO:0005885: P:G(	C:Arp2/3 protein complex: P:Arp2/3 complex-mediated actin nuc			IPR034666 (G3DSA:3.30.1460.GENE:	12,305	13,246	15,046	14,230	13,519									
Solyc11g068620	NAC-domain protein	NAC096	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	0,324	1,076	0,166	0,218	0,803									
Solyc11g068630	Unknown protein (AHRD V3.3)							27,452	20,043	0,000	0,025	0,047									
Solyc11g068640	Protein TPLATE (AHRD V3.3 *** TPLAT_ARATH)		P:GO:0006897	P:endocytosis			mobidb-lite (MOBIDB_LITE): mobidb-lit	153,958	133,416	129,880	131,310	122,949									
Solyc11g068650	Mitochondrial fission protein ELM1 (AHRD V3.3 *** ELM1_ARATH)		P:GO:0000266: C:G(	P:mitochondrial fission; C:mitochondrial outer membrane			IPR009367 (PFAM): PTHR33986:SF8	33,974	39,408	63,154	61,892	59,884									
Solyc11g068660	OTU-like cysteine protease family protein (AHRD V3.3 *** B9HQ41_POPTR)		F:GO:0004843: F:G(	F:thiol-dependent ul	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.90.70.80 (GENE3D): IPR00:	45,030	47,099	60,694	64,310	60,261									
Solyc11g068670	Nicalin (AHRD V3.3 *** B9HQ38_POPTR)		P:GO:0009966: C:G(	P:regulation of signal transduction; C:membrane			G3DSA:3.40.630.10 (GENE3D): IPR0(	64,521	63,513	77,992	80,104	79,108									
Solyc11g068680	ATP synthase protein I (AHRD V3.3 *** A0A1D1ZEB6_9ARAE)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	8,148	10,216	13,215	11,918	14,563									
Solyc11g068690	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *-* AT5G22320.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	9,957	9,601	8,432	7,861	7,258									
Solyc11g068710	F-box family protein (AHRD V3.3 *** B9MYU0_POPTR)		C:GO:0016020	C:membrane			PTHR33736 (PANTHER): PTHR33736	96,509	67,214	22,100	27,835	28,089									
Solyc11g068720	Intracellular protein transporter USO1-like protein (AHRD V3.3 *** G7KAQ1_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,301	3,668	1,006	0,783	0,678									
Solyc11g068730	Nitrilase (AHRD V3.3 *** G4VV63_CAMSI)		P:GO:0006807	P:nitrogen compound metabolic process			IPR003010 (PFAM): IPR036526 (G3D	64,299	48,127	118,438	107,553	109,153									
Solyc11g068740	Methyl-CpG-binding domain-containing family protein (AHRD V3.3 *** A9PAN4_POPTR)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			G3DSA:3.30.890.10 (GENE3D): IPR0(	34,193	29,803	32,528	29,700	30,756									
Solyc11g068745	Diacylglycerol kinase (AHRD V3.3 --* B9RW81_RICCO)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,624	2,712	4,065	3,094	3,201									
Solyc11g068750	NAC domain protein, (AHRD V3.3 *** A0A061GVZ7_THECC)	NAC097	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	4,797	4,183	3,464	3,115	2,929									
Solyc11g068760	peptidyl-prolyl cis-trans isomerase G (AHRD V3.3 *** AT5G22280.1)		F:GO:0016853	F:isomerase activity			PTHR34564:SF3 (PANTHER): PTHR3	11,145	9,253	14,768	15,087	13,229									
Solyc11g068765	Gb:AAF02129.1, putative (AHRD V3.3 *** A0A061GVZ4_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,927	1,291	0,606	0,269	0,327									
Solyc11g068770	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 *** AT5G22250.1)		F:GO:0003676: F:G(	F:nucleic acid bindi	EC:3.1.13: EC:3.1.1!	Acting on ester bonds	IPR006941 (PFAM): IPR036397 (G3D	24,452	49,331	41,349	56,127	34,924	1,036	0,008			0,445	0,013	up		up
Solyc11g068780	LOW QUALITY:ovate family protein 30	OFP30	P:GO:0045892	P:negative regulation of transcription, DNA-templated			IPR006458 (TIGRFAM): IPR006458 (F	0,508	0,248	0,046	0,050	0,000									
Solyc11g068790	Protein FAM210B (AHRD V3.3 *** A0A0B2QJ22_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR009688 (PFAM): PTHR21377 (PAN	5,200	9,923	16,562	19,103	17,657	0,957	0,007					up		
Solyc11g068800	Transcription factor (E2F) (AHRD V3.3 *** Q9FNS0_OXYRB)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:transcription facto			IPR032198 (PFAM E2F/DP	7,670	7,956	8,575	7,336	7,916									
Solyc11g068810	Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B (AHRD V3.3 *** A0A0B0N9S9_GOSAR)							18,638	19,543	16,330	14,766	17,545									
Solyc11g068820	50S ribosomal protein L27		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001684 (PRINTS): IPR001684 (PF	67,201	123,102	87,018	92,475	137,633	0,901	0,001	0,659	0,000			up	up	
Solyc11g068830	bi-functional orotate phosphoribosyltransferase/orotidine-5'-phosphate decarboxylase-like protein		F:GO:0004588: F:G(	F:orotate phosphori	EC:4.1.1.23: EC:2.4.	Orotidine-5'-phospha	IPR000836 (PFAM): IPR001754 (PFA	179,393	167,066	153,983	135,122	145,679									
Solyc11g068870	Nuclear speckle splicing regulatory 1 (AHRD V3.3 *** A0A0B0NEG8_GOSAR)						IPR018612 (PFAM): mobidb-lite (MOB	46,615	34,153	69,836	63,066	61,669									
Solyc11g068880	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *-* A0A061GZN2_THECC)		F:GO:0004190: P:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR021109 (G3DSA:2.40.70.GENE3D	1,447	1,718	1,173	1,361	0,829									
Solyc11g068890	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G44220.1)		C:GO:0009506: C:G(	C:plasmodesma: C:integral component of membrane: C:anchore			IPR004864 (PFAM): PTHR31415:SF2	0,040	0,039	0,000	0,000	0,000									
Solyc11g068895	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G27260.1)		C:GO:0016021	C:integral component of membrane			PTHR31852 (PANTHER): PTHR31852	1,248	1,006	1,487	1,363	1,605									
Solyc11g068900	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G27260.1)		C:GO:0016021	C:integral component of membrane			IPR004864 (PFAM): mobidb-lite (MOB	41,359	42,526	50,546	44,581	46,370									
Solyc11g068910	Methyl-CpG binding domain containing protein, expressed (AHRD V3.3 *-* Q2QM23_ORYSJ)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			IPR001739 (PFAM): G3DSA:3.30.890.	8,578	5,647	4,342	3,851	4,755									
Solyc11g068920	U-box domain-containing family protein (AHRD V3.3 *** B9P691_POPTR)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR011989 (G3DSA:1.25.10.GENE3D	0,000	0,064	0,000	0,000	0,000									
Solyc11g068930	Ubiquitin-like modifier-activating enzyme atg7 (AHRD V3.3 *** A0A0B0P9S7_GOSAR)		C:GO:0005737: P:G(	C:cytoplasm: P:autophagy: F:ubiquitin-like modifier activating er			IPR032197 (PFAM): G3DSA:3.40.50.7	11,867	11,753	11,541	13,795	13,370									
Solyc11g068940	U-box domain-containing family protein (AHRD V3.3 *** B9IIL0_POPTR)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR011989 (G3DSA:1.25.10.GENE3D	0,000	0,436	0,274	0,414	0,585									
Solyc11g068950	BEL1-related homeotic protein 11 (AHRD V3.3 *** Q8LLE3_SOLTU)	BEL11	F:GO:0003677: P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR006563 (PFAM TALE	218,455	165,017	155,441	151,818	142,189									
Solyc11g068960	BHLH transcription factor-like protein (AHRD V3.3 *-* A0A072UK41_MEDTR)		F:GO:0003700: C:G(	F:DNA-binding transcription factor activity: C:nucleus: P:regulati			IPR025610 (PFAM): mobidb-lite (MOB	39,085	27,514	22,603	22,708	24,163									
Solyc11g068970	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G08440.1)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): PTHR31086:SF2:	0,804	0,690	0,131	0,050	0,046									
Solyc11g068980	Mitochondrial import inner membrane translocase subunit TIM22 (AHRD V3.3 *** A0A0B2PVQ5_GLYSO)		C:GO:0042721: P:G(	C:TIM22 mitochondrial import inner membrane insertion comple:			PF02466 (PFAM): mobidb-lite (MOBID	4,841	5,878	6,633	6,650	5,929									
Solyc11g068990	Unknown protein (AHRD V3.3)							16,006	15,302	14,982	16,798	14,909									
Solyc11g069000	T-complex protein 1 subunit beta (AHRD V3.3 *** TCPB_ARATH)		F:GO:0005524: P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR017998 (PRINTS): IPR027409 (G3	156,836	150,763	178,378	150,891	155,286									
Solyc11g069010	alpha-L-fucosidase 1 (AHRD V3.3 *** AT2G28100.1)		F:GO:0004560: P:G(	F:alpha-L-fucosidas	EC:3.2.1.51	Alpha-L-fucosidase	G3DSA:3.20.20.80 (GENE3D): IPR00(	17,468	20,033	12,439	12,430	15,290									
Solyc11g069020	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	0,450	1,407	0,241	0,216	0,424	1,648	0,024					up		
Solyc11g069040	glyoxalase 1		F:GO:0004462: F:G(	F:lactoylglutathione	EC:4.4.1.5	Lactoylglutathione ly:	IPR004361 (TIGRFAM): IPR029068 ((	51,707	48,179	31,185	28,367	33,545									
Solyc11g069050	4-coumarate:CoA ligase-like protein (AHRD V3.3 *** A0A089WWI7_BETPN)	4CL-like	F:GO:0003824	F:catalytic activity			IPR025110 (PFAM): IPR000873 (PFA	88,882	69,066	63,707	61,344	65,324									
Solyc11g069070	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT2G36950.1)		P:GO:0030001: F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	8,490	20,410	1,236	1,380	1,270	1,289	0,000					up		
Solyc11g069080	50S ribosomal L18 (AHRD V3.3 *** A0A0B0NQ41_GOSAR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR005484 (PFAM): G3DSA:3.30.420.	25,678	22,621	36,429	32,017	34,024									
Solyc11g069090	ABC transporter family protein (AHRD V3.3 *** AT5G60790.1)	ABCF6	F:GO:0005524: F:G(	F:ATP binding: F:AT	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0:	3274,014	2873,221	1688,262	1308,783	1428,071					-0,364	0,035			down
Solyc11g069110	vesicle-associated membrane protein 726 (AHRD V3.3 --* AT1G04760.2)							0,260	0,111	0,000	0,000	0,000									
Solyc11g069120	F-box family protein (AHRD V3.3 *** AT5G49610.1)		F:GO:0005515	F:protein binding			G3DSA:1.20.1280.50 (GENE3D): IPR(	2,894	3,042	2,911	3,416	2,802									
Solyc11g069125	beta glucosidase 7 (AHRD V3.3 --* AT3G62740.2)							2,613	1,927	3,092	2,687	2,376									
Solyc11g069130	BTB/POZ domain protein (AHRD V3.3 --* AT3G19920.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,512	1,755	4,128	4,572	4,492									
Solyc11g069140	RNA recognition motif (RRM)-containing protein (AHRD V3.3 --* AT4G12640.4)							2,414	2,123	4,388	5,743	4,777									
Solyc11g069150	Proteasome subunit beta type (AHRD V3.3 *** K4DA71_SOLLC)		F:GO:0004298: C:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR029055 (G3DSA:3.60.20.GENE3D	94,148	96,968	184,218	189,524	174,396									
Solyc11g069160	SUMO E3 ligase SIZ1 (AHRD V3.3 *** A0A0X9AQ43_SOLLC)		C:GO:0005634: F:G(	C:nucleus: F:zinc ion binding: P:cell growth: P:protein sumoylati(			IPR036361 (G3DSA:1.10.720.GENE3I	56,838	48,183	72,807	69,126	65,798									
Solyc11g069163	SUMO E3 ligase SIZ1 (AHRD V3.3 *** A0A0X9AQ43_SOLLC)		C:GO:0005634: F:G(	C:nucleus: F:zinc ion binding: P:cell growth: P:protein sumoylati(			IPR013083 (G3DSA:3.30.40.GENE3D	90,777	85,015	126,753	119,883	114,148									
Solyc11g069170	Transmembrane protein 209 (AHRD V3.3 *** A0A0B2QKQ1_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR019176 (PFAM): mobidb-lite (MOB	47,397	31,648	57,394	52,395	50,101	-0,555	0,038					down		
Solyc11g069180	Acyl-CoA dehydrogenase (AHRD V3.3 *** G7JQF7_MEDTR)		F:GO:0003995: F:G(	F:acyl-CoA dehydro	EC:1.3.99.3	Acting on the CH-CH	IPR013786 (PFAM): IPR009075 (PFA	19,235	17,746	5,441	5,394	8,138									
Solyc11g069190	auxin response factor 4	ARF4	F:GO:0003677: F:G(	F:DNA binding: F:protein binding: C:nucleus: P:regulation of tran			IPR010525 (PFAM ARF	539,872	437,402	59,906	47,771	57,962					-0,323	0,041			down
Solyc11g069210	Carbamoyl-phosphate synthase large chain (AHRD V3.3 *** A0A1D1YAI0_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,215	0,232	0,000	0,000	0,000									
Solyc11g069220	MLO-like protein (AHRD V3.3 *** K4DA78_SOLLC)		P:GO:0006952: C:G(	P:defense response; C:integral component of membrane			IPR004326 (PFAM): mobidb-lite (MOB	0,000	0,021	0,000	0,000	0,000									
Solyc11g069230	Syntaxin, putative (AHRD V3.3 *** B9S0N2_RICCO)		F:GO:0000149: F:G(	F:SNARE binding: F:SNAP receptor activity: P:intracellular prote			IPR000727 (PFAM): G3DSA:1.20.5.11	8,747	4,366	3,827	3,227	3,810	-0,971	0,003					down		
Solyc11g069240	Zinc finger family protein (AHRD V3.3 *** S8C619_9LAMI)		F:GO:0003676: F:G(	F:nucleic acid binding: F:DNA-binding transcription factor activit			G3DSA:3.30.160.6 C2H2	0,312	0,313	0,050	0,000	0,000									
Solyc11g069250	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7L2R9_MEDTR)		C:GO:0005886: P:G(	C:plasma membrane: P:plant-type secondary cell wall biogenesi			IPR000782 (PFAM): IPR036378 (G3D	0,336	0,450	0,000	0,000	0,024									
Solyc11g069260	ABC transporter family protein (AHRD V3.3 *** AT4G33460.1)	ABCI9	F:GO:0005524: F:G(	F:ATP binding: F:AT	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	6,670	8,955	7,981	7,580	8,635									
Solyc11g069270	Beta-galactosidase (AHRD V3.3 *** E3UVW7_SOLLC)	tbg5	F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			IPR001944 (PRINTS): IPR041392 (PF	107,301	104,583	159,032	153,144	168,851									
Solyc11g069280	Late embryogenesis abundant protein-related (AHRD V3.3 *** A0A061GV26_THECC)						IPR009646 (PFAM): PTHR31656:SF8	0,097	0,255	0,147	0,025	0,072									
Solyc11g069290	Pyridoxal biosynthesis protein PDX2 (AHRD V3.3 *** A0A151SGI6_CAJCA)		F:GO:0004359: P:G(	F:glutaminase activ	EC:3.5.1.2	Glutaminase	IPR002161 (TIGRFAM): IPR002161 (F	16,624	20,541	32,773	32,984	36,159									
Solyc11g069300	Kinase family protein (AHRD V3.3 *-* B9HQA2_POPTR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): mobic	50,058	54,888	86,265	87,789	80,879									
Solyc11g069320	F-box/kelch-repeat protein (AHRD V3.3 *** W9RH57_9ROSA)		F:GO:0005515	F:protein binding			IPR006652 (PFAM): IPR015915 (G3D	31,262	28,115	64,747	53,827	56,183									
Solyc11g069330	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *-*		F:GO:0008168	F:methyltransferase activity			IPR013216 (PFAM): PTHR33597 (PAN	144,770	147,144	120,321	149,174	88,786									
Solyc11g069340	Zinc finger transcription factor 69	C3H69	F:GO:0003676: P:G(	F:nucleic acid binding: P:RNA processing: F:RNA methyltransfer			IPR012677 (G3DS C3H	66,916	58,976	60,955	67,748	62,343									
Solyc11g069350	RING/U-box superfamily protein (AHRD V3.3 *** AT5G60580.3)		F:GO:0008270	F:zinc ion binding			IPR011016 (PFAM): IPR013083 (G3D	26,353	23,371	57,510	71,438	80,752			0,486	0,024				up	
Solyc11g069360	DHBP synthase RibB-like alpha/beta domain-containing protein (AHRD V3.3 *** AT5G60590.2)		F:GO:0003725	F:double-stranded RNA binding			IPR006070 (TIGRFAM): G3DSA:3.90.8	10,271	11,800	16,678	18,374	16,208									
Solyc11g069370	RuvB-like helicase (AHRD V3.3 *** K4DA93_SOLLC)		F:GO:0005524: C:G(	F:ATP binding: C:In	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR010339 (PFAM): G3DSA:1.10.8.60	31,357	29,369	47,024	45,689	43,822									
Solyc11g069380	Hydroxymethylbutenyl diphosphate (HMBPP) synthase	HDS	F:GO:0005506: P:G(	F:iron ion binding: F	EC:1.17.7.1: EC:1.1	(E)-4-hydroxy-3-meth	IPR004588 (TIGRFAM): IPR004588 (F	250,671	318,059	507,835	487,223	558,297									
Solyc11g069390	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT3G45230.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,943	0,841	1,320	1,007	0,888									
Solyc11g069400	Protein disulfide-isomerase (AHRD V3.3 *** K4DA96_SOLLC)		F:GO:0003756: P:G(	F:protein disulfide is	EC:5.3.4.1	Protein disulfide-ison	PR00421 (PRINTS): G3DSA:3.40.30.1	108,258	99,209	91,023	86,557	87,254									
Solyc11g069410	zinc finger, C3HC4 type family protein (AHRD V3.3 *** AT2G28430.1)		C:GO:0009536	C:plastid			PTHR37720 (PANTHER)	19,389	18,555	46,127	41,240	42,726									
Solyc11g069420	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7IRR9_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR35718 (PANTHER)	0,277	0,259	0,044	0,098	0,048									
Solyc11g069430	plasma membrane intrinsic protein 2.6	PIP2.6	F:GO:0015267: C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	444,515	274,205	309,012	325,549	334,435									
Solyc11g069440	60S ribosomal protein L12 (AHRD V3.3 *** Q6RJY1_CAPAN)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR020783 (PFAM): IPR020784 (PFA	111,255	102,238	111,563	99,744	100,003									
Solyc11g069450	LOW QUALITY:Senescence regulator (AHRD V3.3 *** A0A103XHC6_CYNCS)						IPR007608 (PFAM): mobidb-lite (MOB	40,645	36,764	22,742	28,457	24,521									
Solyc11g069460	Double-stranded RNA binding protein, putative (AHRD V3.3 *** B9SVC8_RICCO)		F:GO:0003725: C:G(	F:double-stranded RNA binding: C:cytoplasm: P:production of m			IPR014720 (PFAM): G3DSA:3.30.160.	12,044	15,524	2,479	2,792	3,098									
Solyc11g069470	Homeobox leucine-zipper protein (AHRD V3.3 *** Q8H962_ZINVI)		F:GO:0003677: F:G(	F:DNA binding; F:lipid binding			IPR001356 (PFAM HD-ZIP	48,259	44,347	20,191	19,366	18,986									
Solyc11g069480	CASP-like protein (AHRD V3.3 *** K4DAA4_SOLLC)		C:GO:0005886: C:G(	C:plasma membrane; C:integral component of membrane			IPR006702 (PFAM): PTHR32021 (PAN	27,474	21,837	26,959	25,251	23,327									
Solyc11g069490	SIT4 phosphatase-associated family protein (AHRD V3.3 *** B9HQ89_POPTR)						IPR007587 (PFAM): mobidb-lite (MOB	121,741	111,442	165,178	171,543	157,668									
Solyc11g069500	Auxin Response Factor 10A	ARF10	F:GO:0003677: F:G(	F:DNA binding: F:protein binding: C:nucleus: P:regulation of tran			G3DSA:3.10.20.9(ARF	56,685	41,479	75,743	61,656	75,136									
Solyc11g069510	GATA transcription factor (AHRD V3.3 *** V7C3K3_PHAVU)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans			IPR000679 (PFAM GATA	19,216	18,833	11,916	10,642	11,707									

Solyc11g069520	Sulfotransferase (AHRD V3.3 *** D7SKZ6_VITVI)		F:GO:0008146; C:G(	F:sulfotransferase activity; C:integral component of membrane			G3DSA:3.40.50.300 (GENE3D): mobic	25,176	19,953	25,953	26,079	24,601									
Solyc11g069530	Pleckstrin-like (PH) and lipid-binding START domain protein (AHRD V3.3 *** G7IRU5_MEDTR)		F:GO:0008289	F:lipid binding			IPR001849 (PFAM): IPR023393 (G3D	42,196	27,379	55,965	57,020	48,105	-0,597	0,021					down		
Solyc11g069540	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT2G28315.1)		C:GO:0016021	C:integral component of membrane			IPR004853 (PFAM): PTHR44159 (PAN	0,574	0,682	0,025	0,045	0,144									
Solyc11g069550	lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)		C:GO:0016021	C:integral component of membrane			IPR007877 (PFAM): IPR007877 (PAN	13,708	12,987	14,216	12,643	13,211									
Solyc11g069560	Glycosyl transferase, family 2 (AHRD V3.3 *** A0A124SHF0_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR029044 (G3DSA:3.90.550.GENE3I	3,233	1,360	0,049	0,000	0,024									
Solyc11g069570	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (AHRD V3.3 *** K4DAB3_SOLLC)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:cytokinin biosynthetic process; F:hydro			G3DSA:3.40.50.450 (GENE3D): IPR0:	9,947	8,282	1,292	1,243	1,834									
Solyc11g069580	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)		F:GO:0005216; P:G(	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR005821 (PFAM): IPR014710 (G3D	4,420	4,718	4,912	6,820	5,963									
Solyc11g069590	Kinase, putative (AHRD V3.3 *** B9SVB0_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	62,752	51,050	23,103	18,134	19,930									
Solyc11g069600	Zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 *** AT5G60710.1)		C:GO:0005886	C:plasma membrane			IPR036465 (G3DSA:3.40.50.GENE3D	15,668	11,293	7,446	6,862	7,071									
Solyc11g069610	Helicase protein MOM1 (AHRD V3.3 *-* W9SPW2_9ROSA)		P:GO:0006342	P:chromatin silencing			mobidb-lite (MOBIDB_LITE): mobidb-lit	28,088	22,336	20,281	22,487	22,284									
Solyc11g069620	Disease resistance protein (AHRD V3.3 *** A0A068EUA9_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR041118 (PFA	6,092	5,101	3,899	3,087	3,609									
Solyc11g069640	Carbonic anhydrase, putative (AHRD V3.3 *** B9STU9_RICCO)		F:GO:0004089; F:G(	F:carbonate dehydr	EC:4.2.1.1	Carbonic anhydrase	IPR001148 (PFAM): IPR036398 (G3D	0,042	0,064	0,000	0,000	0,000									
Solyc11g069650	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G71420.1)							0,381	0,191	0,000	0,000	0,024									
Solyc11g069660	Disease resistance protein (AHRD V3.3 *** A0A068EUB8_SOLHA)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	8,710	6,392	1,241	1,376	1,343									
Solyc11g069690	Protein disulfide-isomerase 5-1 (AHRD V3.3 *** PDI51_ARATH)		P:GO:0045454	P:cell redox homeostasis			IPR013766 (PFAM): G3DSA:3.40.30.1	8,077	9,085	12,323	10,818	10,262									
Solyc11g069700	Elongation factor 1-alpha (AHRD V3.3 *** EF1A_SOLLC)		F:GO:0003746; F:G(	F:translation elonga	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): IPR004161 (PF	119,702	162,751	85,458	68,421	76,755									
Solyc11g069710	ABC transporter family protein (AHRD V3.3 *** A0A097P9Q7_HEVBR)	ABCG28	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013525 (PFAM): G3DSA:3.40.50.3	21,705	15,977	8,835	5,953	9,151									
Solyc11g069720	Cell division cycle protein 48 homolog (AHRD V3.3 *** CDC48_CAPAN)		F:GO:0005524; F:G(	F:ATP binding; F:hydrolase activity			G3DSA:1.10.8.60 (GENE3D): IPR003:	181,078	171,057	243,191	212,193	222,961									
Solyc11g069730	LOW QUALITY:SH2 domain protein A (AHRD V3.3 --* AT1G17040.3)						PTHR36619 (PANTHER): PTHR36619	0,042	0,018	0,000	0,000	0,000									
Solyc11g069760	LOW QUALITY:High affinity nitrate transporter protein (AHRD V3.3 *-* Q84MZ8_TOBAC)		C:GO:0005886; C:G(	C:plasma membrane; C:plant-type vacuole membrane; F:nitrate			G3DSA:1.20.1250.20 (GENE3D): mob	0,000	0,021	0,000	0,000	0,000									
Solyc11g069770	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *** G7IU48_MEDTR)		F:GO:0003677; F:G(	F:DNA binding; F:protein dimerization activity			IPR002100 (PRIN M-type_MADS	1,049	0,594	0,263	0,200	0,377									
Solyc11g069780	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G60760.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	24,901	27,370	15,127	11,139	13,752									
Solyc11g069790	Chaperonin 60 alpha subunit (AHRD V3.3 *** Q9ZTV1_CANLI)		F:GO:0005524; C:G(	F:ATP binding; C:cytoplasm; P:protein refolding			IPR001844 (PRINTS): IPR002423 (PF	451,491	470,062	1288,614	1047,081	1240,797									
Solyc11g069800	Allene oxide synthase (AHRD V3.3 *** Q8RW06_SOLTU)		F:GO:0004497; F:G(	F:monooxygenase activity; F:iron ion binding; F:oxidoreductase			IPR002403 (PRINTS): IPR001128 (PF	19,204	28,131	9,459	11,669	12,957									
Solyc11g069810	OTU domain-containing (AHRD V3.3 *** A0A0B0PCH5_GOSAR)						G3DSA:3.90.70.80 (GENE3D): IPR00:	13,126	12,105	7,172	7,372	6,309									
Solyc11g069820	ABC transporter G family-like protein (AHRD V3.3 *** A0A072UJT7_MEDTR)	ABCG64	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	0,888	0,666	0,506	0,673	0,542									
Solyc11g069830	ATPase ASNA1 (AHRD V3.3 *** A0A1D1ZAT6_9ARAE)		F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0:	4,511	4,794	6,525	6,682	6,401									
Solyc11g069840	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G60720.1)		C:GO:0009507	C:chloroplast			IPR025757 (PFAM): IPR006869 (PFA	0,183	0,198	0,051	0,000	0,000									
Solyc11g069850	Telomere repeat-binding factor like-protein (AHRD V3.3 *-* A0A0K1SB99_REHGL)		F:GO:0003677	F:DNA binding			G3DSA:1.10.246.2 MYB_related	4,785	3,035	4,728	4,645	3,598									
Solyc11g069860	Glutaredoxin family protein (AHRD V3.3 *** AT5G20500.1)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR002109 (PFAM): G3DSA:3.40.30.1	29,424	28,850	59,127	50,051	48,778									
Solyc11g069890	BEL1-like homeodomain 8, putative (AHRD V3.3 *** A0A061GYR6_THECC)		F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			G3DSA:1.10.10.6(TALE	8,863	8,282	1,213	0,917	0,943									
Solyc11g069900	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT1G15490.2)						PTHR36040:SF2 (PANTHER): PTHR3(	1,422	1,406	0,025	0,022	0,000									
Solyc11g069910	DNA-directed RNA polymerase II subunit RPB11-like protein (AHRD V3.3 *** A0A0B0P734_GOSAR)		F:GO:0001055; C:G(	F:RNA polymerase	EC:2.7.7.6	DNA-directed RNA pc	IPR009025 (PFAM): IPR036603 (G3D	34,058	30,180	42,028	36,465	39,923									
Solyc11g069920	I2C6		F:GO:0043531	F:ADP binding			G3DSA:1.10.8.430 (GENE3D): IPR00:	0,642	0,693	0,025	0,047	0,095									
Solyc11g069925	Disease resistance protein (AHRD V3.3 *** A0A068EUA9_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	8,608	6,013	3,095	3,353	3,224									
Solyc11g069930	Disease resistance protein (AHRD V3.3 *-* B3IYJ6_CAPCH)		F:GO:0043531	F:ADP binding			IPR041118 (PFAM): PTHR23155:SF4	0,000	0,021	0,000	0,000	0,000									
Solyc11g069940	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)		F:GO:0009055; F:G(	F:electron transfer activity; F:protein disulfide oxidoreductase a			IPR011905 (TIGRFAM): G3DSA:3.40.:	108,368	47,921	12,767	6,984	9,624	-1,150	0,000			-0,868	0,014	down		down
Solyc11g069950	FtsH protease	ftsh	F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	PR00830 (PRINTS): IPR005936 (TIGF	61,807	56,834	98,595	96,542	94,395									
Solyc11g069960	RLK-1		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			G3DSA:1.10.510.10 (GENE3D): IPR0	0,275	1,388	0,025	0,072	0,832									
Solyc11g069970	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc11g069990	I2C5		F:GO:0005515; F:G(	F:protein binding; F:ADP binding			PR00364 (PRINTS): IPR001611 (PFA	14,649	11,742	5,734	5,065	6,532									
Solyc11g070010	Dynamin-related protein (AHRD V3.3 *** A0A1B0UTC3_TOBAC)		F:GO:0005525	F:GTP binding			IPR000375 (PFAM): PTHR11566:SF1:	0,099	0,197	0,000	0,000	0,048									
Solyc11g070020	Disease resistance protein (AHRD V3.3 *-* A0A068EUA5_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	6,366	6,914	10,088	9,748	9,952									
Solyc11g070030	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 *** NDHK_PHYPA)		F:GO:0008137; F:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR006138 (TIGRFAM): G3DSA:3.40.!	141,466	131,430	251,957	214,359	242,770									
Solyc11g070040	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S2U8_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	3,249	3,241	3,213	3,024	2,924									
Solyc11g070050	UPF0587 protein C1orf123-like protein (AHRD V3.3 *** A0A0B2Q6L6_GLYSO)						IPR008584 (PFAM): IPR008584 (PAN	14,517	14,922	17,380	16,018	17,183									
Solyc11g070055	Zinc finger CCCH domain-containing protein 39 (AHRD V3.3 *-* W9QMQ1_9ROSA)		F:GO:0046872	F:metal ion binding			PTHR12547:SF70 (PANTHER): PTHR	0,000	0,041	0,000	0,000	0,024									
Solyc11g070060	UPF0587 protein C1orf123-like protein (AHRD V3.3 *** A0A0B2Q6L6_GLYSO)						IPR008584 (PFAM): IPR008584 (PAN	9,866	12,329	13,374	10,252	17,108									
Solyc11g070070	Zinc finger transcription factor 70	C3H70	F:GO:0046872	F:metal ion binding			IPR000571 (PFAM C3H	1,867	2,323	2,375	2,326	2,328									
Solyc11g070100	Protein EARLY FLOWERING 3 (AHRD V3.3 *** A0A0B2RBI0_GLYSO)		P:GO:2000028	P:regulation of photoperiodism, flowering			mobidb-lite (MOBIDB_LITE): mobidb-lit	44,449	48,387	35,522	35,435	36,653									
Solyc11g070110	Clathrin interactor EPSIN 1 (AHRD V3.3 *** A0A0B2QBN6_GLYSO)		P:GO:0006623; F:G(	P:protein targeting to vacuole; F:clathrin binding			IPR008942 (G3DSA:1.25.40.GENE3D	11,923	11,188	23,312	26,304	21,177									
Solyc11g070120	Vacuolar protein sorting-associated protein 32 homolog 1 (AHRD V3.3 *** VP321_ARATH)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): G3DSA:1.10.287.	13,759	9,439	23,000	24,827	19,004									
Solyc11g070130	Profilin (AHRD V3.3 *** Q8VWR0_SOLLC)		F:GO:0003785; C:G(	F:actin monomer binding; C:cytoskeleton; C:cell cortex; P:seque			IPR005455 (PRINTS): IPR005455 (PF	435,641	388,690	382,892	305,878	334,178									
Solyc11g070140	Protein kinase (AHRD V3.3 *** A0A059LJU4_9CHLO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): IPR000719 (F	2,182	2,617	0,927	0,509	0,518									
Solyc11g070150	Histidine phosphotransfer protein (AHRD V3.3 *** I4IY29_POPCA)		P:GO:0000160	P:phosphorelay signal transduction system			IPR008207 (PFAM): IPR036641 (G3D	0,019	0,039	0,000	0,000	0,023									
Solyc11g070160	Sequence-specific DNA-binding transcription factor (AHRD V3.3 *** G7LDQ2_MEDTR)		F:GO:0003682	F:chromatin binding			G3DSA:2.30.30.140 (GENE3D): G3DS	7,492	7,237	8,543	8,521	8,259									
Solyc11g070170	Protein kinase family protein (AHRD V3.3 *** AT2G25760.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	17,534	25,371	10,600	9,765	11,341									
Solyc11g070180	LOW QUALITY:LOB domain-containing protein 27 (AHRD V3.3 --* AT3G47870.1)						mobidb-lite (MOBIDB_LITE)	0,699	0,558	5,337	5,413	4,135									
Solyc11g070190	spindle assembly checkpoint component (AHRD V3.3 --* AT3G28370.5)						PTHR36001 (PANTHER)	2,119	2,225	1,849	1,948	1,501									
Solyc11g071190	Mitogen-activated protein kinase kinase kinase 1 (AHRD V3.3 *** A0A151TDM7_CAJCA)		F:GO:0008270; F:G(	F:zinc ion binding; F:ubiquitin protein ligase activity			IPR007527 (PFAM): mobidb-lite (MOB	0,021	0,000	0,025	0,000	0,000									
Solyc11g071195	RING/U-box superfamily protein (AHRD V3.3 --* AT1G22500.1)		F:GO:0061630	F:ubiquitin protein ligase activity			IPR013083 (G3DSA:3.30.40.GENE3D	0,042	0,018	0,000	0,000	0,000									
Solyc11g071200	GRAS family transcription factor (AHRD V3.3 --* AT2G37650.2)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,846	1,244	0,411	0,172	0,212									
Solyc11g071205	Profilin (AHRD V3.3 *** Q8VWR0_SOLLC)		F:GO:0003785; C:G(	F:actin monomer binding; C:cell cortex; P:sequestering of actin			IPR005455 (PRINTS): IPR005455 (PF	28,513	23,769	22,905	18,038	19,575									
Solyc11g071210	Profilin (AHRD V3.3 --* A0A0D3EBU1_BRAOL)		F:GO:0003779; C:G(	F:actin binding; C:cytoskeleton				1,362	1,615	2,000	1,474	1,320									
Solyc11g071220	Transcription factor CPC (AHRD V3.3 *** A0A1D1ZLD7_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	15,659	15,236	24,093	25,635	22,015									
Solyc11g071230	Beta-1,3-glucuronyltransferase, putative (AHRD V3.3 *** B9RS38_RICCO)		F:GO:0015018; C:G(	F:galactosylgalacto	EC:2.4.1.17; EC:2.4.	Glucuronosyltransfer	IPR029044 (G3DSA:3.90.550.GENE3I	3,248	3,151	1,136	1,245	0,844									
Solyc11g071240	U-box domain-containing protein 26 (AHRD V3.3 *** A0A151TDP3_CAJCA)						IPR011989 (G3DSA:1.25.10.GENE3D	2,452	1,922	0,100	0,215	0,023									
Solyc11g071250	Protein EMBRYONIC FLOWER 1-like protein (AHRD V3.3 *** A0A0B0NHJ8_GOSAR)		P:GO:0009910; P:G(	P:negative regulation of flower development; P:negative regulat			mobidb-lite (MOBIDB_LITE): mobidb-lit	22,114	21,389	24,117	23,783	24,223									
Solyc11g071260	DnaJ / Sec63 Brl domains-containing protein (AHRD V3.3 --* AT1G79940.4)							18,298	18,165	32,408	33,195	30,290									
Solyc11g071270	ENTH/VHS/GAT family protein (AHRD V3.3 *** A0A061GKP2_THECC)		C:GO:0005622; P:G(	C:intracellular; P:intracellular protein transport			IPR038425 (G3DSA:1.20.58.GENE3D	33,461	23,493	40,774	43,317	38,636									
Solyc11g071280	4-amino-4-deoxychorismate lyase		F:GO:0003824	F:catalytic activity			IPR001544 (PFAM): G3DSA:3.20.10.1	23,353	29,061	10,669	9,119	10,408									
Solyc11g071290	Alcohol dehydrogenase (AHRD V3.3 *** I6N8Z5_OLEEU)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): G3DSA:3.40.50.7	0,115	0,095	0,000	0,000	0,000									
Solyc11g071300	Myb (AHRD V3.3 *** Q948S6_TOBAC)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	2,006	1,330	0,331	0,633	0,330									
Solyc11g071310	LOW QUALITY:Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM): PTHR14255 (PAN	0,169	0,000	0,000	0,000	0,000									
Solyc11g071320	50S ribosomal protein L27 (AHRD V3.3 *** W9QGR1_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001684 (PRINTS): IPR001684 (PF	44,658	39,454	53,981	46,660	48,085									
Solyc11g071330	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT3G24570.1)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM): IPR007248 (PAN	1,252	1,674	3,821	3,424	3,579									
Solyc11g071340	FRIGIDA-like protein (AHRD V3.3 *** A0A061GN61_THECC)		P:GO:0009908; P:G(	P:flower development; P:cell differentiation			IPR012474 (PFAM): mobidb-lite (MOB	4,275	4,008	5,348	5,722	5,314									
Solyc11g071350	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G08440.1)		P:GO:0015743	P:malate transport			IPR020966 (PFAM): PTHR31086 (PAN	0,061	0,039	0,000	0,000	0,000									
Solyc11g071360	LOW QUALITY:Cytochrome b561 and DOMON domain-containing protein At5g47530 (AHRD V3.3 --* B561J_ARATH)							0,115	0,161	0,000	0,000	0,000									
Solyc11g071370	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9GHN6_POPTR)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	2,931	3,575	6,746	5,579	6,269									
Solyc11g071380	LOW QUALITY:Clavata3/ESR (CLE) gene family member (AHRD V3.3 --* A0A072UKM6_MEDTR)						mobidb-lite (MOBIDB_LITE): PTHR363	0,021	0,055	0,000	0,048	0,000									
Solyc11g071390	LOW QUALITY:I2C7		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,634	1,048	0,000	0,000	0,000									
Solyc11g071400	I2C3		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,991	0,980	0,516	0,310	0,236									
Solyc11g071410	Disease resistance protein (AHRD V3.3 *-* B3IYJ6_CAPCH)		F:GO:0043531	F:ADP binding			IPR041118 (PFAM): PTHR23155 (PAN	3,614	2,841	1,570	1,102	1,530									
Solyc11g071420	I2C2		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	4,921	3,407	0,980	1,061	0,938									
Solyc11g071423	Disease resistance protein (AHRD V3.3 *** A0A068EW38_SOLLC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	7,265	4,940	3,866	2,964	3,600									
Solyc11g071427	multidrug resistance-associated protein 6 (AHRD V3.3 --* AT3G21250.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,649	1,888	1,657	1,622	1,556									
Solyc11g071440	Pyridine nucleotide-disulfide oxidoreductase family protein (AHRD V3.3 *** B9GHZ7_POPTR)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00368 (PRINTS): IPR023753 (PFA	0,275	0,702	0,050	0,025	0,306									
Solyc11g071450	Actin (AHRD V3.3 --* A0A059LSL6_9CHLO)							1,133	0,803	0,677	0,486	0,797									
Solyc11g071460	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G24190.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	8,281	13,851	2,405	1,963	2,668	0,772	0,036					up		
Solyc11g071470	Agmatine coumaroyltransferase-2 (AHRD V3.3 *** A0A199W5X9_ANACO)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,355	0,925	0,121	0,354	0,396									
Solyc11g071480	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (AHRD V3. HCT		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,021	0,094	0,000	0,000	0,000									
Solyc11g071490	60S ribosomal protein L30 (AHRD V3.3 *** RL30_LUPLU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome			IPR004038 (PFAM): IPR029064 (G3D	29,036	33,987	28,614	25,678	24,318									
Solyc11g071500	Myb family transcription factor family protein (AHRD V3.3 *-* B9H5N1_POPTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	16,410	10,338	13,532	11,897	11,297									
Solyc11g071510	Glycosyl hydrolase (AHRD V3.3 *-* N0DW43_9CARY)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			PTHR36394 (PANTHER)	33,082	28,204	35,728	35,684	32,010									
Solyc11g071520	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A072VNE5_MEDTR)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM): G3DSA:3.20.20.8	1,292	1,404	0,779	1,081	0,732									
Solyc11g071535	Unknown protein (AHRD V3.3)							0,078	0,000	0,051	0,125	0,071									
Solyc11g071540	TATA box-binding protein associated factor RNA polymerase I subunit B-like protein (AHRD V3.3 *** A0A072		F:GO:0001164; P:G(	F:RNA polymerase I CORE element sequence-specific DNA bin			IPR021752 (PFAM): mobidb-lite (MOB	21,583	21,800	39,049	43,415	37,335									
Solyc11g071550	Amidase family protein (AHRD V3.3 *** Q94GC8_SOLDE)		F:GO:0016740	F:transferase activity			IPR036928 (G3DSA:3.90.1300.GENE	3,129	7,095	1,124	2,389	4,138	1,200	0,022	1,883	0,000			up	up	
Solyc11g071560	Hsp20/alpha crystallin family protein (AHRD V3.3 *** Q94GC7_SOLDE)	Hsp27.5	C:GO:0016021	C:integral component of membrane			IPR008978 (G3DSA:2.60.40.GENE3D	0,122	0,154	0,051	0,022	0,070									
Solyc11g071570	Gamma-tubulin complex component (AHRD V3.3 *** A0A0V0IYY8_SOLCH)		C:GO:0000922; C:G(	C:spindle pole; C:microtubule organizing center; P:microtubule n			IPR041470 (PFAM): PTHR19302:SF3	7,225	6,963	2,467	3,603	3,293									
Solyc11g071575	Gamma-tubulin complex component (AHRD V3.3 *-* A0A0V0IYY8_SOLCH)		C:GO:0000922; C:G(	C:spindle pole; C:microtubule organizing center; P:microtubule n			IPR040457 (PFAM): G3DSA:1.20.120.	4,449	4,282	2,737	2,043	2,123									
Solyc11g071600	aldehyde oxidase	ao3	F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR000674 (PFAM): IPR002346 (PFA	0,438	2,113	0,296	0,641	0,923	2,266	0,000					up		
Solyc11g071610	aldehyde oxidase		F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR002346 (PFAM): IPR016208 (PIRS	3,146	6,944	1,660	1,873	2,046	1,168	0,006					up		
Solyc11g071620	aldehyde oxidase	ao1	F:GO:0005506; F:G(	F:iron ion binding; F:electron transfer activity; F:iron-sulfur clust			IPR001041 (PFAM): IPR002346 (PFA	30,898	78,704	7,571	9,582	10,909	1,376	0,000					up		
Solyc11g071640	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR001764 (PF	18,085	17,836	28,638	39,496	32,865					0,466	0,017			up
Solyc11g071650	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001764 (PRINTS): IPR036962 (G3	0,112	0,072	0,050	0,022	0,000									
Solyc11g071660	Ras-induced vulval development antagonist protein (AHRD V3.3 *** A0A072TNN4_MEDTR)		F:GO:0003682; P:G(	F:chromatin binding; P:Notch signaling pathway; P:negative reg			IPR009269 (PFAM): mobidb-lite (MOB	95,572	93,898	91,000	79,465	81,917									
Solyc11g071670	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RN92_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,110	2,026	1,868	1,324	1,555									
Solyc11g071680	Tousled-like protein (AHRD V3.3 *** B2YHW0_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	27,647	21,336	40,505	40,354	38,648									
Solyc11g071690	Zinc knuckle family protein, putative (AHRD V3.3 *** A0A061F6F6_THECC)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding			G3DSA:4.10.60.10 (GENE3D): IPR00	37,649	28,517	23,298	20,246	20,694									
Solyc11g071700	Ubiquitin carboxyl-terminal hydrolase 12-like protein (AHRD V3.3 *** A0A0B0PTR8_GOSAR)		F:GO:0005515; P:G(	F:protein binding; P	EC:3.4.19.12	Ubiquitinyl hydrolase	G3DSA:3.10.20.90 (GENE3D): G3DS/	111,195	99,708	124,815	135,966	127,300									
Solyc11g071710	Chaperone DnaJ (AHRD V3.3 *** A0A0B0PGQ8_GOSAR)		C:GO:0016021; F:G(	C:integral component of membrane; F:isomerase activity			PTHR15852:SF25 (PANTHER): PTHR	5,769	5,744	6,946	8,658	8,131									
Solyc11g071720	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GZL6_THECC)		F:GO:0016787	F:hydrolase activity			IPR013094 (PFAM): IPR029058 (G3D	0,649	0,823	0,899	0,979	1,131									
Solyc11g071730	Kinesin, putative (AHRD V3.3 *** B9SS38_RICCO)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	0,834	1,384	0,071	0,245	0,163									
Solyc11g071740	Calmodulin-like protein (AHRD V1 ***- Q0VJ70_DATME)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	6,448	7,048	5,628	10,103	9,139									
Solyc11g071750	Calmodulin-like protein (AHRD V1 ***- Q0VJ70_DATME)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	0,021	0,061	0,075	0,216	0,116									
Solyc11g071760	regulator of gene silencing AY642285		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): IPR0(	0,213	0,311	0,945	1,916	0,866									
Solyc11g071770	Translation elongation factor, putative (AHRD V3.3 *** B9RPP6_RICCO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS): G3DSA:3.40.5(	26,251	30,321	29,152	24,600	27,326									
Solyc11g071780	LOW QUALITY:B-class MADS-box protein AP3-2 (AHRD V3.3 --* G2XKB5_PHATN)						mobidb-lite (MOBIDB_LITE): PTHR332	0,396	0,476	0,344	0,171	0,259									
Solyc11g071790	Succinate dehydrogenase subunit 6, mitochondrial (AHRD V3.3 *** SDH6_ARATH)		C:GO:0005749	C:mitochondrial respiratory chain complex II, succinate dehydro			IPR034574 (PANTHER)	51,088	50,572	100,360	82,750	90,785									
Solyc11g071800	Strictosidine synthase, putative (AHRD V3.3 *** B9RJ21_RICCO)		P:GO:0009058; F:G(	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR011042 (G3DSA:2.120.10.GENE3I	40,783	31,337	24,121	20,103	24,299									
Solyc11g071810	fasciated	FASCIATED	P:GO:0007275	P:multicellular organism development			IPR036910 (G3DS YABBY	9,371	8,635	28,992	42,671	34,672					0,562	0,035			up
Solyc11g071820	Kinase family protein (AHRD V3.3 *** D7M0T2_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	17,446	13,733	8,162	12,238	11,325									
Solyc11g071830	DnaJ protein homolog (AHRD V3.3 *** DNJH_CUCSA)		F:GO:0005524; P:G(	F:ATP binding; P:protein folding; P:response to heat; F:heat shc			IPR001623 (PRINTS): IPR001623 (PF	5,882	4,559	7,223	8,449	8,197									
Solyc11g071840	SUN-like protein 31	SUN31	F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 (GENE3D): IPR00(	32,738	28,745	22,046	22,567	24,413									
Solyc11g071850	core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** AT3G52060		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR31042:SF4	13,298	10,964	8,482	7,104	8,562									
Solyc11g071860	hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein (AHRD V3.3 --* AT3(		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE)	4,850	3,648	8,888	9,626	7,770									
Solyc11g071865	RING-H2 finger protein ATL48 (AHRD V3.3 *-* ATL48_ARATH)		C:GO:0016021	C:integral component of membrane			IPR007667 (PFAM): PTHR12297 (PAN	0,000	0,018	0,000	0,049	0,071									
Solyc11g071870	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A1D1ZAB9_9ARAE)		F:GO:0005524; P:G(	F:ATP binding; P:ubiquitin-dependent protein catabolic process;			IPR000608 (PFAM): IPR016135 (G3D	7,693	8,133	9,914	9,361	7,037									
Solyc11g071880	receptor-like kinase2		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM): IPR000719 (PFA	0,021	0,055	0,000	0,000	0,000									
Solyc11g071890	Outer envelope protein 80 (AHRD V3.3 *** W9RH86_9ROSA)		C:GO:0019867	C:outer membrane			G3DSA:2.40.160.50 (GENE3D): IPR0(	4,006	3,574	3,479	4,137	3,907									
Solyc11g071910	GTP-binding family protein (AHRD V3.3 *** D7KI21_ARALL)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): G3DSA:3.40.5(	59,717	66,072	79,816	78,091	80,606									
Solyc11g071920	Serine/threonine-protein phosphatase (AHRD V3.3 *** K4DAP9_SOLLC)		F:GO:0004721; F:G(	F:phosphoprotein pl	EC:3.1.3.16	Protein-serine/threor	IPR006186 (PRINTS): IPR029052 (G3	75,306	65,271	86,648	90,213	84,024									
Solyc11g071930	DnaJ domain containing protein, expressed (AHRD V3.3 *** Q10NS2_ORYSJ)						IPR001623 (PRINTS): IPR001623 (PF	19,745	18,656	33,035	28,617	26,828									
Solyc11g071940	FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT5G19260.1)						IPR021410 (PFAM): mobidb-lite (MOB	0,117	0,137	0,000	0,000	0,000									
Solyc11g071950	ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** AT5G22040.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,557	7,421	10,124	9,490	8,313									
Solyc11g071960	Sulfhydryl oxidase (AHRD V3.3 *** K4DAQ3_SOLLC)		F:GO:0016971; P:G(	F:flavin-linked sulfh	EC:1.8.3.2	Thiol oxidase	IPR036774 (G3DSA:1.20.120.GENE3I	1,363	1,651	1,977	1,723	1,859									
Solyc11g071970	Protein kinase (AHRD V3.3 *** Q2HSJ8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:3.30.200.	13,445	10,800	4,715	5,085	4,980									
Solyc11g071990	Apoptosis-inducing factor, putative (AHRD V3.3 *** B9SD10_RICCO)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			PR00368 (PRINTS): IPR023753 (PFA	0,526	1,337	0,219	0,416	0,545									
Solyc11g071995	Disease resistance protein (AHRD V3.3 *** A0A068EUT9_SOLHA)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	12,633	10,275	6,416	5,813	8,087									

Solyc11g072000	Disease resistance protein (AHRD V3.3 *-* B3IYJ6_CAPCH)		F:GO:0043531	F:ADP binding			IPR041118 (PFAM): PTHR23155:SF4	0,000	0,019	0,000	0,000	0,000									
Solyc11g072010	Homoserine dehydrogenase (AHRD V3.3 *** K4DAQ8_SOLLC)		P:GO:0006520: P:G	P:cellular amino acid metabolic process; P:oxidation-reduction			G3DSA:3.30.360.10 (GENE3D): IPR0	30,246	30,175	58,106	52,710	56,283									
Solyc11g072030	Lipid transfer protein (AHRD V3.3 *** B7FFE5_MEDTR)		C:GO:0016020	C:membrane			G3DSA:1.10.110.10 (GENE3D): IPR0	6,966	7,339	1,963	1,126	1,449									
Solyc11g072040	GDSL esterase/lipase (AHRD V3.3 *** W9RH15_9ROSA)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM): IPR036514 (G3D	13,219	6,815	2,939	3,073	3,532	-0,927	0,003					down		
Solyc11g072050	F-box/WD-40 repeat-containing protein (AHRD V3.3 *** W9R2N4_9ROSA)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	22,472	27,617	24,588	20,257	23,020									
Solyc11g072055	CHY-type/CTCHY-type/RING-type Zinc finger protein (AHRD V3.3 --* AT5G25560.6)							0,019	0,039	0,000	0,000	0,000									
Solyc11g072060	MYB-related transcription factor (AHRD V3.3 *** A0A059PSR6_SALMI)	R2R3MYB97	F:GO:0003677	F:DNA binding			IPR001005 (PFAM: MYB	1,707	0,770	0,075	0,075	0,000									
Solyc11g072070	BTB-POZ and MATH domain protein (AHRD V3.3 *** B9VXZ7_CAPAN)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): IPR0	27,955	23,369	41,630	38,686	38,208									
Solyc11g072080	Kelch repeat-containing F-box family protein (AHRD V3.3 *** D7M5E9_ARALL)		F:GO:0005515	F:protein binding			IPR015915 (G3DSA:2.120.10.GENE3	5,079	3,527	4,122	3,538	3,946									
Solyc11g072090	Translation initiation factor eIF-2B subunit gamma (AHRD V3.3 *** A0A0B2SSR8_GLYSO)		P:GO:0009058: F:G	P:biosynthetic process; F:nucleotidyltransferase activity			G3DSA:2.160.10.10 (GENE3D): IPR0	20,638	19,568	21,355	18,640	19,554									
Solyc11g072100	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	3,488	3,930	4,075	5,571	4,471									
Solyc11g072110	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR005123 (PFA	35,977	38,048	14,972	14,911	22,106			0,558	0,004				up	
Solyc11g072120	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			IPR005123 (PFAM): IPR027443 (G3D	43,372	37,123	31,184	27,001	34,986									
Solyc11g072130	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR005123 (PFA	0,927	0,978	0,777	0,341	0,680									
Solyc11g072140	Protein kinase family protein (AHRD V3.3 *** B5RHV5_MUSBA)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR009072 (G3DSA:1.10.20.GENE3D	0,037	0,019	0,047	0,000	0,000									
Solyc11g072150	Nuclear transcription factor Y subunit C8 (AHRD V3.3 *** I3TAY5_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			IPR003958 (PFAM: NF-YC	0,283	0,253	0,646	0,512	0,519									
Solyc11g072160	Ubiquitin-associated domain-containing family protein (AHRD V3.3 *** B9HPT6_POPTR)		F:GO:0005515	F:protein binding			G3DSA:1.10.8.10 (GENE3D): mobidb-	16,774	16,955	36,837	35,628	35,630									
Solyc11g072170	Tryptophan/tyrosine permease (AHRD V3.3 *** AT5G19500.1)		P:GO:0003333: C:G	P:amino acid transmembrane transport; C:integral component o			IPR018227 (PFAM): IPR013059 (PAN	6,691	5,766	9,451	10,026	11,142									
Solyc11g072180	THO complex subunit 7 (AHRD V3.3 *** A0A0B0PUA3_GOSAR)		C:GO:0000445: P:G	C:THO complex part of transcription export complex; P:mRNA p			IPR008501 (PFAM): mobidb-lite (MOB	17,702	16,005	9,414	8,378	9,778									
Solyc11g072190	Elongation factor 1-beta', putative (AHRD V3.3 *** Q6L4C2_SOLDE)		F:GO:0003746: P:G	F:translation elongation factor activity; P:translational elongatio			IPR014717 (G3DSA:3.30.70.GENE3D	528,342	512,770	268,958	233,756	252,042									
Solyc11g072220	Ulp1 protease family protein, putative (AHRD V3.3 *** Q6L4B6_SOLDE)		P:GO:0006508: F:G	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:3.30.310.130 (GENE3D): G3D	4,917	6,249	8,117	8,539	8,209									
Solyc11g072230	LOW QUALITY:Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SWP3_RICCO)		F:GO:0004553: P:G	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	0,616	0,240	1,073	1,312	1,289									
Solyc11g072240	Calmodulin 4	CaM4	F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM): G3DSA:1.10.238	115,712	129,592	172,594	182,487	159,207									
Solyc11g072250	LOW QUALITY:Polyprotein, putative (AHRD V3.3 *-* Q6L4B3_SOLDE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,119	0,121	0,118	0,197	0,094									
Solyc11g072260	40S ribosomal protein S13 (AHRD V3.3 *** RS13_SOYBN)		F:GO:0003735: C:G	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:1.10.287.10 (GENE3D): IPR0	29,400	34,657	43,807	41,482	39,144									
Solyc11g072270	Calmodulin, putative (AHRD V3.3 *** B9RBR8_RICCO)		F:GO:0005509	F:calcium ion binding			G3DSA:1.10.238.10 (GENE3D): G3DS	37,561	36,386	33,877	34,557	33,314									
Solyc11g072280	65-kDa microtubule-associated-like protein (AHRD V3.3 *** G7KNR9_MEDTR)		P:GO:0000226: F:G	P:microtubule cytoskeleton organization; F:microtubule binding			G3DSA:1.20.58.1520 (GENE3D): PF0	4,405	3,640	1,802	2,161	2,119									
Solyc11g072290	cysteine and histidine-rich domain-containing protein RAR1 (AHRD V3.3 *** AT5G51700.1)						IPR007051 (PFAM): PTHR12621:SF9	18,434	20,561	23,289	22,920	22,684									
Solyc11g072300	ACI13	aci13					mobidb-lite (MOBIDB_LITE): mobidb-lit	12,723	10,241	15,179	13,473	14,025									
Solyc11g072310	gibberellin 20-oxidase-3		F:GO:0016491: P:G	F:oxidoreductase activity; P:oxidation-reduction process			PR00682 (PRINTS): IPR027443 (G3D	2,542	5,849	27,153	45,144	39,363	1,223	0,010			0,740	0,013	up		up
Solyc11g072320	Arginine/serine-rich splicing factor RSP41, putative (AHRD V3.3 *-* Q0KIM7_SOLDE)		P:GO:0000160: F:G	P:phosphorelay signal transduction system; F:DNA binding			IPR018972 (PFAM): G3DSA:3.40.50.2	33,724	29,934	92,333	94,607	101,268									
Solyc11g072330	Two-component response regulator (AHRD V3.3 *-* W9QMB4_9ROSA)		P:GO:0000160: F:G	P:phosphorelay signal transduction system; F:DNA binding			IPR001005 (PFAM: ARR-B	0,141	0,140	0,276	0,172	0,141									
Solyc11g072340	Arginine/serine-rich splicing factor RSP41, putative (AHRD V3.3 *** Q0KIM7_SOLDE)		P:GO:0000398: F:G	P:mRNA splicing, via spliceosome; F:nucleic acid binding; C:spli			IPR000504 (PFAM): IPR012677 (G3D	11,714	12,428	12,842	10,684	11,530									
Solyc11g072380	Vicilin-like antimicrobial peptides 2-2 (AHRD V3.3 *** W9SCA8_9ROSA)		F:GO:0045735	F:nutrient reservoir activity			IPR014710 (G3DSA:2.60.120.GENE3	48,381	52,771	5,337	13,692	2,026									
Solyc11g072390	Something about silencing protein sas10, putative (AHRD V3.3 *** B9SX55_RICCO)		P:GO:0000462: C:G	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSI			IPR007146 (PFAM): IPR018972 (PFA	16,224	16,422	15,920	16,732	15,769									
Solyc11g072400	Defects in morphology protein 1 (AHRD V3.3 *** G7JQI6_MEDTR)		F:GO:0045145	F:single-stranded D	EC:3.1.11; EC:3.1.1	Acting on ester bonds	IPR019190 (PFAM): mobidb-lite (MOB	1,898	1,370	3,120	2,692	2,401									
Solyc11g072410	Adenylate kinase isoenzyme 6 homolog (AHRD V3.3 *** G8Z291_SOLLC)		F:GO:0004017: F:G	F:adenylate kinase	EC:2.7.4.4; EC:2.7.4	Nucleoside-phosphat	G3DSA:3.40.50.300 (GENE3D): PF13	14,820	15,776	28,823	28,927	23,649									
Solyc11g072430	RNA ligase isoform 1 (AHRD V3.3 *-* Q0WZC2_WHEAT)		F:GO:0003972: P:G	F:RNA ligase (ATP)	EC:6.5.1.3	RNA ligase (ATP)	mobidb-lite (MOBIDB_LITE): mobidb-lit	62,045	52,246	89,274	90,160	90,319									
Solyc11g072440	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G02970.1)		C:GO:0016021	C:integral component of membrane			IPR000073 (PFAM): mobidb-lite (MOB	31,498	22,582	64,204	53,386	56,962									
Solyc11g072450	ATP synthase subunit d, mitochondrial (AHRD V3.3 *** A0A0B2NZE9_GLYSO)		C:GO:0000276: F:G	C:mitochondrial proton-transporting ATP synthase complex, cou			IPR036228 (G3DSA:1.20.58.GENE3D	135,697	142,690	293,587	272,013	261,466									
Solyc11g072460	NEDD8-activating enzyme E1 regulatory subunit (AHRD V3.3 *** K4DAV3_SOLLC)		F:GO:0019781: P:G	F:NEDD8 activating enzyme activity; P:protein neddylation			G3DSA:3.40.50.720 (GENE3D): IPR0	16,122	13,148	18,866	18,003	16,580									
Solyc11g072470	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)						IPR004883 (PFAM: LBD	5,571	11,962	75,126	96,027	68,038	1,126	0,011			0,357	0,034	up		up
Solyc11g072480	Tetraspanin (AHRD V3.3 *** A0A103XGG0_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	6,187	17,552	2,618	3,514	3,610	1,527	0,000					up		
Solyc11g072490	Interactor of constitutive active ROPs-like protein (AHRD V3.3 *** A0A072ULW0_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	74,734	74,110	3,447	12,178	8,083			1,224	0,000	1,821	0,000		up	up
Solyc11g072500	Dof domain, zinc finger family protein (AHRD V3.3 *** Q6L3K2_SOLDE)		F:GO:0003677: P:G	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003851 (PFAM: Dof	2,801	6,514	1,014	0,742	1,204	1,239	0,003					up		
Solyc11g072510	Cinnamoyl-CoA reductase (AHRD V3.3 *** C3VPA5_9ERIC)	CCR	F:GO:0003824: F:G	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0	15,573	16,537	5,498	4,011	7,563									
Solyc11g072520	Arogenate dehydratase (AHRD V3.3 *** M1CDP7_SOLTU)		F:GO:0004664: P:G	F:prephenate dehyc	EC:4.2.1.51	Prephenate dehydrat	G3DSA:3.30.70.260 (GENE3D): G3DS	30,837	30,027	42,800	37,055	38,945									
Solyc11g072530	V-type proton ATPase subunit a (AHRD V3.3 *** K4DAW0_SOLLC)		C:GO:0000220: F:G	C:vacuolar proton-transporting V-type ATPase, V0 domain; F:pr			IPR026028 (PIRSF): IPR002490 (PFA	28,178	30,190	16,910	18,941	19,264									
Solyc11g072540	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G45620.1)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	70,482	60,570	110,550	91,648	100,565									
Solyc11g072550	4,5-dioxygenase-like protein (AHRD V3.3 *** A0A0G2UQT9_9CARY)		P:GO:0006725: F:G	P:cellular aromatic compound metabolic process; F:ferrous iron			G3DSA:3.40.830.10 (GENE3D): IPR0	38,174	60,822	60,050	57,216	58,310									
Solyc11g072560	Major Facilitator Superfamily protein (AHRD V3.3 *** Q6L3J2_SOLDE)		C:GO:0016020: F:G	C:membrane; F:transmembrane transporter activity; P:transmem			G3DSA:1.20.1250.20 (GENE3D): IPR	0,000	0,078	0,000	0,050	0,023									
Solyc11g072580	Major facilitator superfamily protein (AHRD V3.3 *** AT3G45660.3)		C:GO:0016020: F:G	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125	3,094	1,258	0,780	0,357	0,499	-1,270	0,029					down		
Solyc11g072590	CCR4-NOT transcription complex subunit 4 (AHRD V3.3 *** W9SKU7_9ROSA)		F:GO:0003676: F:G	F:nucleic acid binding; F:ubiquitin-protein transferase activity; C			IPR013083 (G3DSA:3.30.40.GENE3D	149,084	139,131	152,792	151,673	155,353									
Solyc11g072600	APETALA2d	AP2d	F:GO:0003677: F:G	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PFAM: AP2	4,697	14,747	1,462	0,610	1,225	1,672	0,000					up		
Solyc11g072610	DNA repair (Rad51) family protein (AHRD V3.3 *-* AT2G28560.6)		F:GO:0000400: P:G	F:four-way junction	EC:3.6.1.3; EC:3.6.1	Adenosinetriphosphatase; Nucleoside-triphosphate phosphat		0,689	0,729	0,790	1,004	0,707									
Solyc11g072615	DNA repair (Rad51) family protein (AHRD V3.3 *** AT2G28560.1)		P:GO:0000724: F:G	P:double-strand bre	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	3,173	2,692	2,311	2,740	2,429									
Solyc11g072620	LOW QUALITY:G patch domain-containing protein 1 (AHRD V3.3 --* A0A1D1XCL3_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,063	0,601	0,150	0,447	0,116									
Solyc11g072630	mitogen-activated protein kinase 4	mapk4	F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): PIRS	8,670	10,375	9,268	15,032	15,115			0,699	0,033	0,696	0,042		up	up
Solyc11g072645	Zinc binding dehydrogenase, putative (AHRD V3.3 *** B9SW66_RICCO)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): IPR0	17,154	19,644	37,922	31,310	38,586									
Solyc11g072650	Zinc binding dehydrogenase, putative (AHRD V3.3 *** B9SW66_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013154 (PFAM): IPR013149 (PFA	0,598	0,613	0,072	0,000	0,000									
Solyc11g072660	Protein kinase-like protein (AHRD V3.3 *** Q6TKQ5_VITAE)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRS	56,389	49,729	45,540	58,444	56,836									
Solyc11g072670	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT4G00830.6)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,656	2,435	1,864	1,225	1,456									
Solyc11g072680	LOW QUALITY:Fasciclin-like arabinogalactan family protein, putative (AHRD V3.3 *-* A0A061G6S2_THECC		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,158	0,290	0,122	0,144	0,119									
Solyc11g072690	LES294902 3-desoxy-D-manno octulosonic acid-8-phosphate synthase	kdsa	C:GO:0005737: F:G	C:cytoplasm; F:3-de	EC:2.5.1.55	3-deoxy-8-phosphoo	IPR006218 (PFAM): IPR013785 (G3D	24,486	26,672	17,304	14,498	15,816									
Solyc11g072700	LOW QUALITY:transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT1G07850.1)		F:GO:0008375: C:G	F:acetylglucosaminyltransferase activity; C:integral component			IPR006740 (PFAM): G3DSA:3.90.550	0,280	0,178	0,097	0,122	0,023									
Solyc11g072710	phototropin 1	phot1	F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000014 (TIGRFAM): G3DSA:3.30.	479,485	394,020	174,502	155,278	192,159									
Solyc11g072720	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A061GXV0_THECC)		F:GO:0005515	F:protein binding			G3DSA:3.30.710.10 (GENE3D): mobi	8,657	7,441	10,346	7,385	8,401									
Solyc11g072730	DNA-directed RNA polymerase subunit (AHRD V3.3 *** K4DAY0_SOLLC)		F:GO:0003677: F:G	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA p	G3DSA:1.20.120.1280 (GENE3D): IPF	18,451	17,166	26,002	25,717	22,137									
Solyc11g072740	Protein BPS1, chloroplastic (AHRD V3.3 --* A0A0B2Q6K6_GLYSO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	10,646	13,929	12,950	12,675	10,473									
Solyc11g072750	Chitinase (AHRD V3.3 *** G7KL79_MEDTR)		P:GO:0005975	P:carbohydrate metabolic process			IPR000677 (PRINTS): G3DSA:3.20.2	0,481	0,620	0,709	0,653	0,778									
Solyc11g072760	Chitinase (AHRD V3.3 *** G7KL79_MEDTR)		P:GO:0005975	P:carbohydrate metabolic process			IPR000677 (PRINTS): G3DSA:3.20.2	0,357	0,693	0,817	0,610	0,729									
Solyc11g072770	WUSCHEL-related homeobox protein (AHRD V3.3 *-* A0A097I3L1_ROSCN)		F:GO:0003677	F:DNA binding			IPR001356 (PFAM: WOX	0,000	0,043	0,025	0,000	0,000									
Solyc11g072790	WUSCHEL-like homeobox protein (AHRD V3.3 *-* F6MIV6_ORYSJ)		F:GO:0003677	F:DNA binding			IPR001356 (PFAM: WOX	0,019	0,000	0,000	0,000	0,000									
Solyc11g072800	Respiratory burst oxidase-like protein (AHRD V3.3 *** G7L3G1_MEDTR)		F:GO:0004601: F:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR000778 (PRINTS): IPR013130 (PF	0,837	1,111	0,187	0,191	0,164									
Solyc11g072810	Nuclear factor related to kappa-B-binding protein (AHRD V3.3 *** W9QSQ0_9ROSA)		C:GO:0031011	C:Ino80 complex			mobidb-lite (MOBIDB_LITE): mobidb-lit	75,201	67,631	82,374	78,234	81,073									
Solyc11g072820	Kinesin-related protein (AHRD V3.3 *** A0A0B0ND48_GOSAR)		F:GO:0003777: F:G	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	4,827	3,966	0,898	0,586	0,846									
Solyc11g072830	Chitinase (AHRD V3.3 *** G7KL79_MEDTR)		P:GO:0005975	P:carbohydrate metabolic process			IPR000677 (PRINTS): G3DSA:3.20.2	0,538	0,716	0,143	0,120	0,140									
Solyc11g072840	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR009072 (G3	5,146	5,552	1,062	0,472	0,541									
Solyc11g072850	CCT motif family protein (AHRD V3.3 *** A0A061GWL0_THECC)		F:GO:0005515	F:protein binding			IPR010402 (PFAM): PTHR31319:SF2	1,142	0,845	0,187	0,142	0,164									
Solyc11g072860	histone H4 (AHRD V3.3 *** AT2G28740.1)		F:GO:0003677: F:G	F:DNA binding; F:protein heterodimerization activity			IPR001951 (PRINTS): IPR009072 (G3	21,576	22,423	3,722	2,261	2,727									
Solyc11g072880	Calcium-transporting ATPase (AHRD V3.3 *** A0A103XD00_CYNCS)		F:GO:0000166: C:G	F:nucleotide binding; C:integral component of membrane			PR00119 (PRINTS): G3DSA:1.20.111	349,220	321,726	297,047	370,628	344,804									
Solyc11g072890	LOW QUALITY:Sulfate transporter 1.2 (AHRD V3.3 *** A0A1D1YKN7_9ARAE)						PTHR35304 (PANTHER)	13,440	11,985	65,859	58,118	54,385									
Solyc11g072900	BTB/POZ domain-containing protein (AHRD V3.3 *** AT5G60050.1)						IPR038920 (PANTHER): PTHR31060:	0,215	0,158	0,264	0,169	0,120									
Solyc11g072910	Kinase (AHRD V3.3 *** A0A061GXM4_THECC)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	18,345	18,425	16,448	17,155	16,411									
Solyc11g072920	Peroxidase (AHRD V3.3 *** K4DAZ8_SOLLC)		F:GO:0004601: P:G	F:peroxidase activit	EC:1.11.1.7	Peroxidase	IPR002016 (PRINTS): IPR000823 (PF	0,040	0,039	0,140	0,051	0,140									
Solyc11g072930	Leucine-rich repeat transmembrane protein kinase protein, putative (AHRD V3.3 *** A0A061GWK2_THECC)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	1,104	1,679	0,470	0,736	1,078									
Solyc11g072940	CCR4-NOT transcription complex subunit 2 (AHRD V3.3 *** G7IUA4_MEDTR)		C:GO:0005634: P:G	C:nucleus; P:regulation of transcription, DNA-templated; C:CCR			IPR007282 (PFAM): IPR038635 (G3D	55,813	44,352	75,491	79,329	74,872									
Solyc11g072950	E3 UFM1-protein ligase 1 (AHRD V3.3 *** A0A103XPK8_CYNCS)		F:GO:0016874	F:ligase activity			IPR018611 (PFAM): mobidb-lite (MOB	45,109	42,989	66,558	65,077	65,318									
Solyc11g072960	Ankyrin repeat family protein (AHRD V3.3 *** AT1G07710.2)		F:GO:0005515	F:protein binding			IPR036770 (G3DSA:1.25.40.GENE3D	0,000	0,039	0,000	0,000	0,046									
Solyc11g072970	Nudix hydrolase 9 (AHRD V3.3 *** A0A151TN32_CAJCA)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D): IPR00	20,232	15,236	17,659	17,113	16,318									
Solyc11g072990	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4DB05_SOLLC)		P:GO:0006633: C:G	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR012392 (PIRSF): IPR013601 (PFA	6,977	12,373	0,261	0,375	0,212									
Solyc11g073010	LOW QUALITY:Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9HCA8_POPTR)		C:GO:0000145: P:G	C:exocyst; P:exocytosis			IPR004140 (PFAM): mobidb-lite (MOB	4,236	1,434	1,412	5,925	2,144	-1,526	0,010			2,054	0,000	down		up
Solyc11g073020	Chloroplast-targeted copper chaperone protein, putative (AHRD V3.3 *** A0A061GXQ1_THECC)		P:GO:0030001: F:G	P:metal ion transport; F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,357	0,331	0,025	0,025	0,000									
Solyc11g073050	ethylene-responsive small GTP-binding protein	er43	F:GO:0003924: F:G	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR005225 (TIGF	38,658	48,103	17,155	15,438	18,579									
Solyc11g073060	Zinc finger family protein (AHRD V3.3 *** B9HM54_POPTR)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM): C2H2	2,614	0,368	0,250	0,789	0,188	-2,800	0,000					down		
Solyc11g073080	Methyl-CpG-binding domain-containing family protein (AHRD V3.3 *** B9HPK6_POPTR)		F:GO:0003677: C:G	F:DNA binding; C:nucleus			IPR001739 (PFAM): G3DSA:3.30.890	9,661	16,514	2,545	2,880	2,800									
Solyc11g073090	nuclease (AHRD V3.3 *** AT3G63270.1)						IPR027806 (PFAM): PTHR22930 (PAN	0,962	1,092	1,441	1,307	1,739									
Solyc11g073100	RNA binding protein, putative isoform 1 (AHRD V3.3 *-* A0A061H044_THECC)						mobidb-lite (MOBIDB_LITE)	0,455	0,298	0,386	0,382	0,494									
Solyc11g073110	UPSTREAM OF FLC protein (DUF966) (AHRD V3.3 *** AT5G59790.1)						IPR010369 (PFAM): IPR021182 (PIRS	8,617	5,650	0,653	0,615	1,499									
Solyc11g073120	R2R3MYB transcription factor 58	R2R3MYB58	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6 MYB	8,737	5,615	5,690	7,057	7,554									
Solyc11g073130	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase (AHRD V3.3 *** K4DB19_SOLLC)		C:GO:0005789: P:G	C:endoplasmic retic	EC:4.2.1.134	Very-long-chain (3R)-	IPR007482 (PFAM): PTHR11035:SF2	1,264	2,954	0,219	0,312	0,656	1,244	0,017					up		
Solyc11g073140	LOW QUALITY:late embryogenesis abundant protein-related / LEA protein-like protein (AHRD V3.3 *-* AT3G19430.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,000	0,075	0,175	0,165									
Solyc11g073150	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)						IPR009646 (PFAM): mobidb-lite (MOB	0,000	0,039	0,483	0,712	0,704									
Solyc11g073160	3,4-dihydroxy-2-butanone-4-phosphate synthase, GTP cyclohydrolase II (AHRD V3.3 *** A0A0K9PRA8_ZOS		F:GO:0003935: F:G	F:GTP cyclohydrola	EC:3.5.4.25; EC:4.1.	GTP cyclohydrolase	IPR000422 (PFAM): G3DSA:3.90.870	8,365	13,141	16,018	22,102	30,269			0,918	0,000	0,471	0,043		up	up
Solyc11g073170	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GXP2_THECC)		C:GO:0016021	C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,061	0,266	0,264	0,423									
Solyc11g073180	TOX high mobility group box protein, putative (DUF1635) (AHRD V3.3 *** AT2G28690.1)						IPR012862 (PFAM): IPR012862 (PAN	0,061	0,043	0,223	0,167	0,449									
Solyc11g073190	UDP-galactose transporter 5 (AHRD V3.3 *** AT3G46180.1)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM): PTHR10778 (PAN	12,247	9,299	10,873	10,214	11,021									
Solyc11g073200	Glutelin type-A 2 (AHRD V3.3 *** A0A199V5M8_ANACO)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS): IPR006045 (PF	32,042	26,489	31,101	32,345	31,653									
Solyc11g073210	11S seed storage protein (AHRD V3.3 *** A0A0A0VHH8_ORYRU)		F:GO:0045735	F:nutrient reservoir activity			IPR006044 (PRINTS): IPR006045 (PF	0,117	0,094	0,238	0,500	0,445									
Solyc11g073220	DNA repair protein RAD51 (AHRD V3.3 *** A0A072UK69_MEDTR)		F:GO:0003677: F:G	F:DNA binding; F:A	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	0,801	0,731	0,548	0,718	0,399									
Solyc11g073230	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K7B7_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR011990 (G3D	2,812	2,994	2,664	2,850	3,036									
Solyc11g073240	Transmembrane proteins 14C (AHRD V3.3 *-* AT3G43520.1)		C:GO:0016020	C:membrane			IPR005349 (PFAM): G3DSA:1.20.58.1	33,113	40,086	63,931	68,814	64,722									
Solyc11g073250	Histone H2A (AHRD V3.3 *** K4DB31_SOLLC)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR007125 (PF	36,436	38,127	43,524	40,005	39,268									
Solyc11g073255	ARM repeat superfamily protein (AHRD V3.3 --* AT1G77600.3)							1,442	1,403	1,048	1,119	1,530									
Solyc11g073260	Histone H2A (AHRD V3.3 *** K4DB32_SOLLC)		C:GO:0000786: F:G	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodime			IPR002119 (PRINTS): IPR009072 (G3	0,019	0,000	0,000	0,000	0,000									
Solyc11g073270	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XPT2_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	9,283	6,241	5,413	6,148	6,729									
Solyc11g073280	RNA-binding (RRM/RBD/RNP motifs) family protein		F:GO:0003676	F:nucleic acid binding			IPR000504 (PFAM): IPR012677 (G3D	68,756	69,828	73,635	64,365	67,652									
Solyc11g073300	K-stimulated pyrophosphate-energized sodium pump protein (AHRD V3.3 *** AT5G59960.1)		C:GO:0005634: C:G	C:nucleus; C:endoplasmic reticulum; C:integral component of m			PTHR45099 (PANTHER)	32,077	30,219	35,953	38,745	33,104									
Solyc12g005000	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IXN1_MEDTR)						PTHR33647 (PANTHER): PTHR33647	0,185	0,476	0,125	0,072	0,095									
Solyc12g005010	actin cytoskeleton-regulatory complex pan-like protein (AHRD V3.3 *** AT1G50660.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	66,637	48,503	29,881	23,755	26,872									
Solyc12g005020	RING/U-box superfamily protein (AHRD V3.3 *** AT3G20395.1)		C:GO:0016021	C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	21,867	14,518	0,925	0,261	1,270									
Solyc12g005030	Protein kinase (AHRD V3.3 *** Q9AR92_MEDSA)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	37,499	26,856	16,612	11,312	16,938					-0,552	0,024			down
Solyc12g005050	HAUS augmin-like complex subunit 4 (AHRD V3.3 *** A0A0B2P0N3_GLYSO)		P:GO:0051225: C:G	P:spindle assembly; C:HAUS complex			IPR029327 (PFAM): IPR029327 (PAN	8,219	7,068	5,927	5,694	5,940									
Solyc12g005070	CASP-like protein (AHRD V3.3 *** K4DB45_SOLLC)		C:GO:0005886: C:G	C:plasma membrane; C:integral component of membrane; F:4 ir			IPR006459 (TIGRFAM): IPR006702 (F	0,598	0,718	0,487	0,323	0,566									
Solyc12g005080	alpha - ketoglutarate dehydrogenase subunit E2		F:GO:0004149: P:G	F:dihydrolipoyllysine	EC:2.3.1.61	Dihydrolipoyllysine-re	G3DSA:2.40.50.100 (GENE3D): IPR0	53,888	52,732	80,766	80,663	77,928									
Solyc12g005090	Vacuolar protein sorting-associated protein 35 (AHRD V3.3 *** V4V8H5_9ROSI)		P:GO:0015031: C:G	P:protein transport; C:retromer, cargo-selective complex; P:retr			IPR005378 (PFAM): IPR029705 (PAN	9,433	8,494	14,109	14,920	12,704									
Solyc12g005093	Esophageal cancer associated protein, putative (AHRD V3.3 *-* B9STX6_RICCO)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): IPR0297	4,753	3,484	5,781	5,594	6,383									
Solyc12g005095	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.5)							0,000	0,000	0,022	0,000	0,000									
Solyc12g005097	histone-lysine N-methyltransferase SUVR5 (AHRD V3.3 --* AT2G23740.6)							0,000	0,000	0,000	0,025	0,000									
Solyc12g005110	AT hook motif-containing protein, putative (AHRD V3.3 *** A0A061F4V0_THECC)		F:GO:0043565	F:sequence-specific DNA binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,863	4,169	3,391	3,719	3,666									
Solyc12g005120	inositol-1%2C4%2C5-trisphosphate 5-phosphatase (AHRD V3.3 *-* AT5G54870.2)						PTHR31354 (PANTHER): PTHR31354	1,510	1,719	2,302	2,926	2,260									
Solyc12g005130	inositol-1%2C4%2C5-trisphosphate 5-phosphatase (AHRD V3.3 *** AT4G27020.1)						PTHR31354 (PANTHER): PTHR31354	3,842	3,626	5,465	7,085	4,880									
Solyc12g005140	Major facilitator superfamily protein (AHRD V3.3 *** AT5G54860.1)		C:GO:0016021	C:integral component of membrane			IPR004324 (TIGRFAM): IPR039309 (F	4,062	4,018	7,458	7,447	6,930									
Solyc12g005150	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** A0A097PK87_SOLLC),Pfam:PF01190						PF01190 (PFAM): PTHR38400 (PANT	186,313	112,966	60,427	43,392	49,732	-0,694	0,016			-0,474	0,001	down		down
Solyc12g005160	Kinase family protein (AHRD V3.3 *** U5GUL9_POPTR)		F:GO:0004672: F:G	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	0,000	0,043	0,000	0,000	0,000									
Solyc12g005170	Cytochrome P450 family protein (AHRD V3.3 *** A0A072UZE3_MEDTR)		F:GO:0005506: F:G	F:iron ion binding; F:oxidoreductase activity, acting on paired d			IPR002401 (PRINTS): IPR036396 (G3	0,075	0,167	0,025	0,050	0,000									
Solyc12g005180	Chloroplast lipocalin (AHRD V3.3 *** Q38JB4_SOLTU)		F:GO:0036094	F:small molecule binding			IPR012674 (G3DSA:2.40.128.GENE3	44,663	64,339	56,836	48,554	70,282	0,553	0,022					up		
Solyc12g005200	Electron transfer flavoprotein alpha subunit (AHRD V3.3 *** B9I0B5_POPTR)		F:GO:0009055: F:G	F:electron transfer activity; F:flavin adenine dinucleotide binding			IPR014731 (PFAM): G3DSA:3.40.50.1	9,305	9,548	20,624	19,397	20,025									
Solyc12g005210	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 --* AT3G05860.3)		F:GO:0003677: F:G	F:DNA binding; F:protein dimerization activity			IPR036879 (G3DS M-type_MADS	0,021	0,000	0,025	0,000	0,000									
Solyc12g005220	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT5G54780.1)		F:GO:0005096: C:G	F:GTPase activator activity; C:cell; P:intracellular protein transp			IPR000195 (PFAM): G3DSA:1.10.8.27	2,630	2,169	4,402	3,900	4,041									
Solyc12g005230	Breast carcinoma-amplified sequence 3 (AHRD V3.3 *** A0A0B0NHS9_GOSAR)		F:GO:0005515	F:protein binding			IPR000195 (PFAM): IPR015943 (G3D	7,697	7,489	4,874	4,406	5,316									

Solyc12g005240	Plant/F3H11-7 protein (AHRD V3.3 *** G7IHE1_MEDTR)		C:GO:0009507	C:chloroplast			IPR018962 (PFAM): PTHR36365 (PAN	0,361	1,819	0,137	0,225	0,546	2,343	0,000					up		
Solyc12g005250	Kinesin-like protein (AHRD V3.3 *** K4DB63_SOLLC)		F:GO:0003777; F:GC	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR036961 (G3	10,001	8,731	1,139	1,233	1,805									
Solyc12g005260	Kinesin-like protein (AHRD V3.3 *-* M1BZ06_SOLTU)		F:GO:0003777; F:GC	F:microtubule motor	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE)	1,728	1,106	0,121	0,142	0,094									
Solyc12g005270	Histone H2A (AHRD V3.3 *** K4DB65_SOLLC)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimer			IPR002119 (PRINTS): IPR009072 (G3	55,159	51,137	85,765	75,500	75,442									
Solyc12g005280	tRNA (guanine(37)-N1)-methyltransferase (AHRD V3.3 *** K4DB66_SOLLC)		F:GO:0009019; P:GC	F:tRNA (guanine-N1-)-methyltransferase activity; P:tRNA methy			G3DSA:3.40.50.150 (GENE3D): G3DS	3,658	3,883	5,638	5,954	7,227									
Solyc12g005290	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IT75_SOLCH)		F:GO:0004674; F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001245 (PFAM): G3DSA:3.30.200	30,154	22,246	16,592	26,841	21,815					0,696	0,000			up
Solyc12g005300	Chlorophyllase (AHRD V3.3 *** A0A165YG74_POAPR)	CLH4	P:GO:0015996; F:GC	P:chlorophyll catabo	EC:3.1.1.14; EC:3.1.	Chlorophyllase; Carb	IPR041127 (PFAM): IPR029058 (G3D	0,213	0,465	1,600	1,681	1,330									
Solyc12g005310	Auxin-responsive GH3 family protein (AHRD V3.3 *** AT5G54510.1)						IPR004993 (PFAM): PTHR31901:SF2	0,156	0,124	0,146	0,246	0,537									
Solyc12g005330	Ribosomal protein L2 family (AHRD V3.3 *** AT4G36130.1)		F:GO:0003735; C:GC	F:structural constituent of ribosome; C:ribosome; P:translation			IPR022666 (PFAM): IPR022669 (PFA	254,337	255,874	151,909	146,049	147,936									
Solyc12g005340	GRAS family transcription factor (AHRD V3.3 *** D4QD66_DIACA)	GRAS	F:GO:0003700; C:GC	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR005202 (PFAM GRAS	254,559	171,270	65,923	187,463	108,909			0,721	0,012	1,509	0,000		up	up
Solyc12g005350	Dihydroflavonol 4-reductase-like protein (AHRD V3.3 *** A0A072UNZ6_MEDTR)	DFR	F:GO:0003824; F:GC	F:catalytic activity; F:coenzyme binding			G3DSA:3.40.50.720 (GENE3D): IPR0(	23,596	20,594	12,108	12,135	14,838									
Solyc12g005360	MAP kinase kinase kinase 83	MAPKKK83	F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	0,042	0,018	0,000	0,000	0,000									
Solyc12g005390	Vesicle-associated protein 4-2 (AHRD V3.3 *** VAP42_ARATH)		C:GO:0005789	C:endoplasmic reticulum membrane			IPR000535 (PFAM): IPR013783 (G3D	16,773	18,993	23,541	28,905	26,568									
Solyc12g005400	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9SIE1_RICCO)		F:GO:0005216; P:GC	F:ion channel activity; P:ion transport; C:membrane; P:transmer			IPR014710 (G3DSA:2.60.120.GENE3	0,809	2,252	1,302	2,378	1,695	1,491	0,004					up		
Solyc12g005410	Sodium Bile acid symporter family (AHRD V3.3 *** AT1G78560.1)		C:GO:0016020	C:membrane			IPR038770 (G3DSA:1.20.1530.GENE	14,004	16,604	12,002	13,556	14,500									
Solyc12g005420	Zinc finger, B-box (AHRD V3.3 *** A0A103Y421_CYNCS)	BBX23	F:GO:0008270	F:zinc ion binding			IPR000315 (PFAM DBB	0,565	1,199	0,272	0,858	0,069									
Solyc12g005430	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR023213 (G3DSA:3.30.559.GENE3	11,463	9,560	0,442	0,117	0,329									
Solyc12g005440	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than amino			IPR003480 (PFAM): IPR023213 (G3D	0,021	0,000	0,000	0,022	0,023									
Solyc12g005450	Kinase family protein (AHRD V3.3 *** D7LY50_ARALL)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF): G3DSA:1.10.5	1,852	1,850	0,267	0,270	0,186									
Solyc12g005465	Early nodulin-like protein (AHRD V3.3 *** A0A072VAV5_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,019	0,058	0,000	0,000	0,000									
Solyc12g005470	RING/U-box superfamily protein (AHRD V3.3 *** AT2G20650.2)		F:GO:0008270; C:GC	F:zinc ion binding; C:integral component of membrane; F:ligase			IPR013083 (G3DSA:3.30.40.GENE3D	15,401	12,198	23,592	28,665	27,485									
Solyc12g005480	targeting protein for XKLP2 (AHRD V3.3 *** AT1G03780.2)		C:GO:0005819; C:GC	C:spindle; C:microtubule; P:activation of protein kinase activity;			IPR027329 (PFAM): IPR027330 (PFA	0,330	0,912	0,025	0,047	0,023									
Solyc12g005490	LOW QUALITY:transmembrane protein, putative (DUF679 domain membrane protein 7) (AHRD V3.3 *** AT4		C:GO:0005783; P:GC	C:endoplasmic reticulum; P:abscission; P:dehiscence; C:integra			IPR007770 (PFAM): IPR007770 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc12g005500	Prohibitin, putative (AHRD V3.3 *** B9RVS2_RICCO)		C:GO:0016020	C:membrane			IPR000163 (PRINTS): IPR001107 (PF	0,000	0,277	0,000	0,022	0,071									
Solyc12g005520	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *-* AT1G12220.3)		F:GO:0043531	F:ADP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	0,019	0,057	0,000	0,000	0,000									
Solyc12g005530	Nucleotide-binding site leucine-rich repeat protein (AHRD V3.3 *-* H9B299_9ERIC)		F:GO:0043531	F:ADP binding			IPR002182 (PFAM): PTHR43909 (PAN	0,019	0,096	0,000	0,072	0,000									
Solyc12g005540	Disease resistance protein (AHRD V3.3 *-* W9R405_9ROSA)		F:GO:0043531	F:ADP binding			PTHR43906 (PANTHER): PTHR43906	0,000	0,041	0,000	0,000	0,000									
Solyc12g005550	Gamma-tubulin complex component (AHRD V3.3 --* A0A0K9RPK1_SPIOL)							0,037	0,140	0,000	0,049	0,000									
Solyc12g005560	LOW QUALITY:Micronuclear linker histone polyprotein-like protein (AHRD V3.3 *** A0A061E2Z9_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,458	2,922	0,000	0,025	0,047									
Solyc12g005570	1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase (AHRD V3.3 *** A0A0B0PDZ2_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR352	41,534	49,108	58,736	53,513	58,358									
Solyc12g005590	Organic solute transporter ostalpha protein (AHRD V3.3 *** G7J9A4_MEDTR)		P:GO:0009626	P:plant-type hypersensitive response			IPR005178 (PFAM): mobidb-lite (MOB	16,258	16,651	24,132	22,630	23,344									
Solyc12g005600	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G28240.1)						IPR022251 (PFAM): PTHR33090:SF1	0,000	0,021	0,000	0,050	0,000									
Solyc12g005610	Leucine-rich receptor-like kinase family protein (AHRD V3.3 *-* G7L9I8_MEDTR)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR013210 (PFA	0,101	0,037	0,000	0,025	0,000									
Solyc12g005620	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT2G33170.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	0,202	0,204	0,000	0,000	0,046									
Solyc12g005630	Cytochrome b6-f complex iron-sulfur subunit (AHRD V3.3 *** K4DBA1_SOLLC)		F:GO:0009496; P:GC	F:plastoquinol--plas	EC:1.1.9; EC:1.1.9.1	Acting on diphenols a	IPR005805 (PRINTS): G3DSA:1.20.5.	98,118	201,105	66,550	83,241	172,402	1,062	0,000	1,370	0,000			up	up	
Solyc12g005640	R2R3MYB transcription factor 68	R2R3MYB68	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6C MYB	0,097	0,344	0,000	0,000	0,024									
Solyc12g005660	Zinc finger, B-box (AHRD V3.3 *-* A0A103Y7X2_CYNCS)	BBX28	F:GO:0008270	F:zinc ion binding			IPR000315 (PFAM): mobidb-lite (MOB	6,945	8,453	2,573	1,937	2,987									
Solyc12g005670	HAK5	HAK5	F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (TIGRFAM): IPR003855 (F	0,000	0,019	0,000	0,047	0,047									
Solyc12g005680	Potassium transporter (AHRD V3.3 *** M1B2Q5_SOLTU)		F:GO:0015079; C:GC	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): IPR003855 (TIGF	0,140	0,196	0,096	0,022	0,093									
Solyc12g005700	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769 (PAN	0,197	0,214	0,069	0,000	0,000									
Solyc12g005710	Blue copper protein (AHRD V3.3 *** W9S2S3_9ROSA)		F:GO:0009055	F:electron transfer activity			IPR008972 (G3DSA:2.60.40.GENE3D	0,000	0,000	0,000	0,049	0,000									
Solyc12g005720	Cysteine-rich RLK (Receptor-like kinase) protein (AHRD V3.3 *** G7IKM1_MEDTR)						IPR038408 (G3DSA:3.30.430.GENE3	0,000	0,082	0,022	0,000	0,000									
Solyc12g005730	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:integral component			G3DSA:3.90.550.50 (GENE3D): IPR0(	4,409	3,742	27,370	29,362	22,588									
Solyc12g005740	LOW QUALITY:C2H2-like zinc finger protein (AHRD V3.3 --* AT2G18490.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	2,397	6,359	0,134	0,047	0,256	1,432	0,001					up		
Solyc12g005750	LOW QUALITY:Zinc finger protein CONSTANS-LIKE 14 (AHRD V3.3 *** W9SAN7_!	BBX16	F:GO:0008270	F:zinc ion binding			PTHR31717:SF26 (PANTHER): PTHR:	0,542	1,244	0,000	0,000	0,070									
Solyc12g005760	Peroxisome biogenesis protein 22 (AHRD V3.3 *** A0A0B2RXJ0_GLYSO)		P:GO:0007031	P:peroxisome organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	32,205	29,604	21,838	22,578	24,400									
Solyc12g005770	Zinc finger transcription factor 71	C3H71	F:GO:0046872	F:metal ion binding			mobidb-lite (MOBII C3H	38,045	41,259	49,925	52,282	50,246									
Solyc12g005780	TraB family protein (AHRD V3.3 *** A0A072UIY1_MEDTR)		C:GO:0031307	C:integral component of mitochondrial outer membrane			IPR002816 (PFAM): PTHR21530 (PAN	64,596	51,919	81,167	71,134	74,050									
Solyc12g005800	Myb transcription factor (AHRD V3.3 *** A0A072UKM9_MEDTR)		C:GO:0005634; P:GC	C:nucleus; P:cell differentiation; F:sequence-specific DNA bindi			IPR015495 (PANTHER): PTHR10641:	0,000	0,103	0,025	0,047	0,024									
Solyc12g005820	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G27660.1)		P:GO:0010089	P:xylem development			mobidb-lite (MOBIDB_LITE): mobidb-lit	11,956	10,058	2,088	1,023	1,505					-1,023	0,036			down
Solyc12g005830	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GU68_POPTR)		F:GO:0003677; F:GC	F:DNA binding; F:lipid binding			IPR001356 (PFAM HD-ZIP	1,893	2,885	0,000	0,000	0,000									
Solyc12g005840	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT3G21700.3)		F:GO:0003924; F:GC	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): G3DSA:3.40.50.3	13,662	17,929	1,794	1,328	2,692									
Solyc12g005850	Protein DETOXIFICATION (AHRD V3.3 *** K4DBC3_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (TIGRFAM): IPR002528 (F	11,459	17,777	27,725	36,324	33,725	0,661	0,036					up		
Solyc12g005860	Aconitate hydratase (AHRD V3.3 *** K4DBC4_SOLLC)		F:GO:0003994; F:GC	F:aconitate hydrata	EC:4.2.1.3	Aconitate hydratase	IPR001030 (PRINTS): IPR015928 (G3	197,408	211,494	260,629	305,871	327,766									
Solyc12g005870	NEDD8-activating enzyme E1 regulatory subunit (AHRD V3.3 *** K4DBC5_SOLLC)		F:GO:0019781; P:GC	F:NEDD8 activating enzyme activity; P:protein neddylation			IPR000594 (PFAM): G3DSA:3.40.50.7	20,268	17,193	34,462	41,036	37,310									
Solyc12g005875	NEDD8-activating enzyme E1 regulatory subunit (AHRD V3.3 *-* K4DBC5_SOLLC)		F:GO:0019781; P:GC	F:NEDD8 activating enzyme activity; P:protein neddylation			G3DSA:3.40.50.720 (GENE3D): PTHF	6,071	5,180	11,499	12,596	11,280									
Solyc12g005880	Hexosyltransferase (AHRD V3.3 *** K4DBC6_SOLLC)		P:GO:0006486; F:GC	P:protein glycosylation; F:galactosyltransferase activity; C:mem			G3DSA:3.90.550.50 (GENE3D): IPR0(	18,994	14,294	10,830	8,309	10,220									
Solyc12g005890	MYB-related transcription factor (AHRD V3.3 *** A0A075BMI0_SALMI)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB_related	0,038	0,145	0,000	0,075	0,000									
Solyc12g005900	RecQ-mediated genome instability protein 1 (AHRD V3.3 *** A0A151RRF7_CAJCA)		F:GO:0000166; C:GC	F:nucleotide binding; C:RecQ helicase-Topo III complex			IPR013894 (PFAM): G3DSA:2.40.50.7	11,877	9,145	11,145	10,263	10,473									
Solyc12g005910	B-cell receptor-associated 31-like protein (AHRD V3.3 *** A0A103XE39_CYNCS)		C:GO:0005783; P:GC	C:endoplasmic reticulum; P:intracellular protein transport; C:inte			mobidb-lite (MOBIDB_LITE): mobidb-lit	23,234	36,961	15,726	18,224	18,069	0,695	0,030					up		
Solyc12g005920	Fimbrin-like family protein (AHRD V3.3 *** B9I148_POPTR)		F:GO:0051015; P:GC	F:actin filament binding; P:actin filament bundle assembly			IPR001715 (PFAM): IPR036872 (G3D	0,084	0,341	0,051	0,125	0,071									
Solyc12g005930	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT3G07890.5)		F:GO:0005096; C:GC	F:GTPase activator activity; C:cell; P:intracellular protein transp			G3DSA:1.10.472.80 (GENE3D): G3DS	30,414	23,070	145,247	131,422	122,719									
Solyc12g005940	1-aminocyclopropane-1-carboxylate oxidase 1 (AHRD V3.3 *** ACCO1_SOLLC)	ACO2	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3	0,306	1,271	0,544	0,896	0,492									
Solyc12g005950	COP1 homolog	COP1	F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR013083 (G3	69,575	52,562	78,884	70,610	69,965									
Solyc12g005960	Ethylene-responsive transcription factor, putative (AHRD V3.3 *-* B9SYX3_RICCO	ERF.F6	F:GO:0003677; F:GC	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRINT ERF	12,174	11,639	13,826	15,139	11,663									
Solyc12g005970	LOW QUALITY:Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *-* AT5G35450.2)		F:GO:0043531	F:ADP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	8,111	8,046	5,562	5,928	5,453									
Solyc12g005980	Ubiquitin and WLM domain-containing protein (AHRD V3.3 *** A0A0B0N1Y2_GOSAR)						IPR013536 (PFAM): G3DSA:3.10.20.9	56,272	43,446	92,145	111,782	97,224									
Solyc12g005990	Dual specificity protein phosphatase, putative (AHRD V3.3 *** B9SSI3_RICCO)		P:GO:0006470; F:GC	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR000340 (PFAM): IPR029021 (G3D	17,451	16,540	17,149	17,540	16,914									
Solyc12g006000	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT1G05020.1)		F:GO:0005545; C:GC	F:1-phosphatidylinositol binding; C:clathrin-coated vesicle; F:cla			IPR008942 (G3DSA:1.25.40.GENE3D	3,392	2,510	0,779	1,088	1,696									
Solyc12g006010	Small ubiquitin-related modifier (AHRD V3.3 *** K4DBD9_SOLLC)		F:GO:0005515; P:GC	F:protein binding; P:protein sumoylation			G3DSA:3.10.20.90 (GENE3D): IPR02:	63,781	60,615	84,057	77,125	74,891									
Solyc12g006030	Methyltransferase-like protein 5 (AHRD V3.3 *** A0A151TIR0_CAJCA)		F:GO:0008168	F:methyltransferase activity			IPR007848 (PFAM): G3DSA:3.40.50.1	0,818	0,993	1,066	0,840	0,632									
Solyc12g006040	NBS-LRR protein (AHRD V3.3 *** Q9SM52_SOLAC)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	8,259	9,109	23,977	23,530	22,067									
Solyc12g006050	Major facilitator superfamily protein (AHRD V3.3 *** AT3G21670.1)		C:GO:0016020; F:GC	C:membrane; F:transmembrane transporter activity; P:transmer			IPR000109 (PFAM): G3DSA:1.20.125	0,433	0,716	1,623	1,280	2,540									
Solyc12g006060	DNA-BINDING TRANSCRIPTION FACTOR 2 (AHRD V3.3 --* AT3G18380.3)		F:GO:0003682	F:chromatin binding			G3DSA:2.30.30.140 (GENE3D): IPR0:	8,561	6,805	13,664	13,952	14,882									
Solyc12g006110	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)		C:GO:0016021; C:GC	C:integral component of membrane; C:anchored component of r			IPR000782 (PFAM): IPR036378 (G3D	0,967	0,482	0,000	0,000	0,072									
Solyc12g006120	Nuclear transcription factor Y protein (AHRD V3.3 *** G7K4Q5_MEDTR)		F:GO:0046982	F:protein heterodimerization activity			PR00615 (PRINTS NF-YB	4,464	5,164	7,994	6,827	8,026									
Solyc12g006140	Cab-5 gene encoding chlorophyll a/b-binding protein	cab5a	P:GO:0009765; C:GC	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	25,082	143,633	9,325	19,471	37,835	2,545	0,000	2,010	0,000	1,062	0,001	up	up	up
Solyc12g006160	Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT3G07760.5)		F:GO:0005515	F:protein binding			G3DSA:1.10.150.50 (GENE3D): IPR0(	33,769	27,188	53,491	52,659	43,348									
Solyc12g006170	WRKY transcription factor 14	WRKY14	F:GO:0003700; P:GC	F:DNA-binding transcription factor activity; P:regulation of transc			IPR036576 (G3DS WRKY	26,998	25,235	39,526	42,474	37,028									
Solyc12g006175	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT5G67385.5)							0,080	0,043	0,121	0,097	0,095									
Solyc12g006180	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	73,488	62,891	70,391	63,990	62,891									
Solyc12g006220	calcium ion-binding protein (AHRD V3.3 *** AT4G12700.1)		C:GO:0005794; C:GC	C:Golgi apparatus; C:integral component of membrane			PTHR31469:SF2 (PANTHER): PTHR3	3,193	2,952	0,353	0,196	0,564									
Solyc12g006225	serine-rich protein-like protein (AHRD V3.3 *-* AT5G55980.1)						PTHR33132 (PANTHER): PTHR33132	0,270	0,259	3,317	2,266	1,866									
Solyc12g006230	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DMB3_THECC)		C:GO:0016021; F:GC	C:integral component of membrane; F:ligase activity			IPR001841 (PFAM): IPR013083 (G3D	5,764	9,422	37,530	24,277	23,291			-0,691	0,000	-0,622	0,003		down	down
Solyc12g006240	CONSTANS-like zinc finger protein (AHRD V3.3 *** A0A023GS52_SOYBN)	BBX7	F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR010402 (PFAM DBB	1,270	1,285	6,708	8,352	5,611									
Solyc12g006250	Protein transport protein SFT2, putative (AHRD V3.3 *** B9SF26_RICCO)		C:GO:0016021; P:GC	C:integral component of membrane; P:vesicle-mediated transpo			IPR007305 (PFAM): PTHR23137:SF1	5,188	3,846	4,098	5,091	4,529									
Solyc12g006260	L-fucokinase/GDP-L-fucose pyrophosphorylase (AHRD V3.3 --* AT1G01220.7)							6,636	2,785	5,009	7,812	8,855	-1,220	0,038					down		
Solyc12g006270	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, putative isoform 1 (AHRD V3.3 *** A0A061DKZ		P:GO:0007142	P:male meiosis II			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,881	1,797	0,277	0,217	0,188									
Solyc12g006290	Reticulon-like protein (AHRD V3.3 *** M1CT78_SOLTU)		C:GO:0005789; C:GC	C:endoplasmic reticulum membrane; C:integral component of me			IPR003388 (PFAM): PTHR10994 (PAN	36,529	37,697	50,172	45,829	46,487									
Solyc12g006300	WD-repeat protein, putative (AHRD V3.3 *** B9RGK0_RICCO)		F:GO:0005515	F:protein binding			PTHR22838:SF6 (PANTHER): PTHR2:	3,255	2,878	3,610	3,823	2,945									
Solyc12g006310	Endoplasmic reticulum vesicle transporter protein (AHRD V3.3 *** AT3G22290.2)		C:GO:0016021; F:GC	C:integral component of membrane; F:isomerase activity			IPR012936 (PFAM): IPR039542 (PFA	9,958	8,632	11,333	13,107	10,889									
Solyc12g006320	RNA helicase DEAD35	DEAD35	F:GO:0003676; F:GC	F:nucleic acid binding; F:ATP binding			IPR011545 (PFAM): G3DSA:3.40.50.3	245,753	203,556	277,579	281,857	296,744									
Solyc12g006340	Auxin Response Factor 6	ARF6A	F:GO:0003677	F:DNA binding			IPR015300 (G3DSA:2.40.330.GENE3	15,936	14,354	12,332	13,480	12,957									
Solyc12g006350	Auxin response factor (AHRD V3.3 *-* M1CTA3_SOLTU)		F:GO:0003677	F:DNA binding			IPR015300 (G3DSA:2.40.330.GENE3	12,717	12,049	12,062	12,025	13,192									
Solyc12g006360	Protein DETOXIFICATION (AHRD V3.3 *** K4DBH3_SOLLC)		P:GO:0006855; F:GC	P:drug transmembrane transport; F:drug transmembrane transpo			IPR002528 (PFAM): IPR002528 (TIGF	6,269	2,812	1,323	7,080	3,281	-1,125	0,023	1,289	0,010	2,394	0,000	down	up	up
Solyc12g006370	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06620.1)		F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR001613 (PRINTS): G3DSA:3.90.66	4,091	3,219	2,891	4,582	3,347									
Solyc12g006380	2-oxoglutarate-dependent dioxygenase	odd	F:GO:0016491; P:GC	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	1,387	5,450	0,099	0,047	0,330	1,992	0,001					up		
Solyc12g006410	UDP-glucose 4-epimerase, putative (AHRD V3.3 *** B9SV82_RICCO)		F:GO:0003978; P:GC	F:UDP-glucose 4-e	EC:5.1.3.2	UDP-glucose 4-epim	IPR016040 (PFAM): G3DSA:3.90.25.1	0,019	0,080	0,025	0,025	0,071									
Solyc12g006420	Topoisomerase II-associated protein PAT1 (AHRD V3.3 *** AT4G14990.1)		P:GO:0000290	P:deadenylation-dependent decapping of nuclear-transcribed ml			mobidb-lite (MOBIDB_LITE): mobidb-lit	229,532	127,098	96,654	215,849	176,799	-0,829	0,021	0,868	0,000	1,160	0,000	down	up	up
Solyc12g006440	LOW QUALITY:3-isopropylmalate dehydratase large subunit (AHRD V3.3 *** A0A0B0MEL1_GOSAR)		C:GO:0016021	C:integral component of membrane			PTHR37225 (PANTHER)	0,201	0,778	0,137	0,170	0,142									
Solyc12g006450	gamma-aminobutyrate transaminase subunit precursor isozyme 3		F:GO:0008483; F:GC	F:transaminase activity; F:pyridoxal phosphate binding			IPR015421 (G3DSA:3.40.640.GENE3	15,672	14,423	24,474	38,997	26,794					0,678	0,000			up
Solyc12g006460	Cytochrome P450 (AHRD V3.3 *** A0A124SDJ5_CYNCS)		F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS): IPR001128 (PF	22,481	21,674	6,168	4,527	8,575									
Solyc12g006470	viroid RNA-binding protein	GABA-TP2	F:GO:0008483; F:GC	F:transaminase activity; F:pyridoxal phosphate binding			IPR005814 (PFAM): IPR015421 (G3D	98,524	99,014	8,724	7,200	17,546			1,000	0,007				up	
Solyc12g006480	Nuclear pore complex Nup205-like protein (AHRD V3.3 *** G7L0K5_MEDTR)		C:GO:0005643	C:nuclear pore			IPR021827 (PFAM): PTHR31344 (PAN	74,935	59,566	62,352	63,045	61,567									
Solyc12g006490	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061GNR0_T		F:GO:0008375; C:GC	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297:SF9	14,705	13,226	21,956	20,829	19,602									
Solyc12g006500	Nucleotide-sugar transporter family protein (AHRD V3.3 *** AT5G25400.1)		C:GO:0005768; C:GC	C:endosome; C:trans-Golgi network; F:antiporter activity; C:inte			IPR004853 (PFAM): mobidb-lite (MOB	13,135	11,994	10,037	7,076	7,622									
Solyc12g006510	Terpene cyclase/mutase family member (AHRD V3.3 *** M1BRW8_SOLTU)		F:GO:0016866	F:intramolecular transferase activity			IPR032697 (PFAM): IPR018333 (TIGF	0,157	0,158	0,000	0,151	0,023									
Solyc12g006520	Terpene cyclase/mutase family member (AHRD V3.3 *** M1BMW2_SOLTU)		F:GO:0016866	F:intramolecular transferase activity			IPR032696 (PFAM): IPR032697 (PFA	55,313	35,742	0,711	0,437	0,633									
Solyc12g006530	Terpene cyclase/mutase family member (AHRD V3.3 *** M1BMW3_SOLTU)		F:GO:0016866	F:intramolecular transferase activity			IPR032697 (PFAM): G3DSA:1.50.10.2	32,642	20,611	5,909	4,007	5,381									
Solyc12g006540	Signal peptidase I (AHRD V3.3 *** K4DBJ1_SOLLC)		P:GO:0006465; F:GC	P:signal peptide processing; F:peptidase activity; C:membrane			IPR001733 (PRINTS): IPR001733 (TIG	78,807	76,173	124,886	123,181	111,468									
Solyc12g006550	Ribosome biogenesis regulatory protein homolog (AHRD V3.3 *** RRS1_ARATH)		C:GO:0005634; P:GC	C:nucleus; P:ribosome biogenesis			IPR007023 (PFAM): mobidb-lite (MOB	149,375	129,251	92,682	98,799	90,363									
Solyc12g006560	Early nodulin-93 (AHRD V3.3 *** A0A061GV12_THECC)		C:GO:0016021	C:integral component of membrane			IPR005050 (PFAM): IPR005050 (PAN	2,157	1,122	0,144	0,244	0,538									
Solyc12g006570	Sesquiterpene synthase (AHRD V3.3 *** G5CV52_SOLLC)		F:GO:0000287; F:GC	F:magnesium ion binding; F:terpene synthase activity			IPR001906 (PFAM): IPR008949 (G3D	1,191	2,468	0,393	0,486	0,724									
Solyc12g006575	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9IKK7_POPTR)		F:GO:0005515; F:GC	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR011990 (G3D	6,544	6,037	5,108	4,885	6,830									
Solyc12g006580	cytochrome P450, family 705, subfamily A, polypeptide 30 (AHRD V3.3 --* AT3G20940.1)							0,000	0,018	0,000	0,000	0,023									
Solyc12g006590	Zinc finger protein-like protein (AHRD V3.3 *** Q3S345_GOSHI)		F:GO:0046872	F:metal ion binding			G3DSA:4.10.1060.10 (GENE3D): IPR(	6,424	7,143	3,169	2,300	3,331									
Solyc12g006600	Zinc finger protein-like protein (AHRD V3.3 *** Q3S345_GOSHI)		F:GO:0046872	F:metal ion binding			G3DSA:4.10.1060.10 (GENE3D): IPR(	0,042	0,061	0,686	0,678	0,826									
Solyc12g006610	zinc finger (Ran-binding) family protein (AHRD V3.3 --* AT2G17975.2)						PTHR23111 (PANTHER): PTHR23111	0,000	0,000	0,065	0,048	0,000									
Solyc12g006620	Zinc finger transcription factor 72	C3H72	F:GO:0046872	F:metal ion binding			IPR041686 (PFAM): G3DSA:4.10.100	2,465	2,344	0,830	1,189	0,683									
Solyc12g006630	Dynein light chain-like protein (AHRD V3.3 *-* Q8RV44_ORYSJ)		P:GO:0007017; C:GC	P:microtubule-based process; C:dynein complex			IPR037177 (G3DSA:3.30.740.GENE3	2,099	1,340	0,047	0,000	0,093									
Solyc12g006640	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)		F:GO:0016829	F:lyase activity			IPR004360 (PFAM): IPR029068 (G3D	0,310	0,159	0,000	0,000	0,000									
Solyc12g006650	RNA polymerase II transcription mediator (AHRD V3.3 *** A0A097PP20_SOLLC)		F:GO:0003712; P:GC	F:transcription coregulator activity; P:regulation of transcription			IPR019313 (PFAM): IPR019313 (PAN	17,444	14,658	19,414	19,796	19,449									
Solyc12g006660	testis- and ovary-specific PAZ domain protein (AHRD V3.3 *** AT5G20120.2)		C:GO:0016021	C:integral component of membrane			PTHR31134:SF1 (PANTHER): IPR033	2,426	1,474	0,790	0,876	1,055									
Solyc12g006670	Sel1-like repeats-containing protein		F:GO:0005515	F:protein binding			IPR006597 (PFAM): IPR011990 (G3D	13,496	11,286	23,436	23,105	21,719									
Solyc12g006680	Early nodulin 93 protein (AHRD V3.3 *** A3FGC9_9ROSI)		C:GO:0016021	C:integral component of membrane			IPR005050 (PFAM): PTHR33605:SF2	4,112	1,490	0,124	0,273	0,047									
Solyc12g006690	Protein kinase G11A (AHRD V3.3 *** A0A151S8P4_CAJCA)		F:GO:0004672; F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): mobidb-lite (MOB	1,528	1,641	0,588	0,376	0,681									
Solyc12g006700	Mitogen-activated protein kinase kinase kinase 1 isoform 1 (AHRD V3.3 *** A0A061GM60_THECC)						IPR012866 (PFAM): mobidb-lite (MOB	80,856	98,817	79,096	73,532	73,607									
Solyc12g006710	Tudor domain protein (AHRD V3.3 *** A0A072V9B3_MEDTR)		C:GO:0005739	C:mitochondrion			G3DSA:2.40.50.770 (GENE3D): IPR0	12,095	12,718	11,527	12,144	12,415									
Solyc12g006720	LOW QUALITY:calcium-dependent lipid-binding family protein (AHRD V3.3 --* AT1G48090.6)						mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,050	0,000	0,000									
Solyc12g006730	LOW QUALITY:glutathione S-transferase zeta 1 (AHRD V3.3 --* AT2G02390.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,064	0,000	0,000	0,000									
Solyc12g006740	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT2G40640.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,040	0,000	0,025	0,000	0,046									
Solyc12g006760	glutathione S-transferase zeta 1 (AHRD V3.3 --* AT2G02390.2)						mobidb-lite (MOBIDB_LITE): PTHR370	0,099	0,586	0,025	0,097	0,046									
Solyc12g006770	glutathione S-transferase zeta 1 (AHRD V3.3 --* AT2G02390.2)						mobidb-lite (MOBIDB_LITE): PTHR370	0,334	0,373	0,412	0,368	0,355									
Solyc12g006790	Argonaute10b	AGO10b	F:GO:0003676; F:GC	F:nucleic acid binding; F:protein binding			G3DSA:3.40.50.2300 (GENE3D): IPR(	0,521	0,669	0,071	0,050	0,046									
Solyc12g006800	Two-component response regulator (AHRD V3.3 *** W9R8R3_9ROSA)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	2,589	2,816	2,191	2,388	2,620									
Solyc12g006810	SOUL heme-binding family protein (AHRD V3.3 *** AT5G20140.1)						IPR006917 (PFAM): IPR018790 (PFA	5,823	12,580	5,644	6,753	14,357	1,138	0,000	1,345	0,000			up	up	
Solyc12g006820	3-ketoacyl-CoA synthase (AHRD V3.3 *** M0ZKJ4_SOLTU)		P:GO:0006633; C:GC	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR012392 (PIRSF): IPR013747 (PFA	0,038	0,000	0,000	0,000	0,000									
Solyc12g006830	Histone H2A (AHRD V3.3 *** M0ZKK1_SOLTU)		C:GO:0000786; F:GC	C:nucleosome; F:DNA binding; C:nucleus; F:protein heterodimer			IPR002119 (PRINTS): IPR007125 (PF	18,680	22,033	25,118	24,016	25,630									
Solyc12g006840	Serine/threonine-protein kinase (AHRD V3.3 *** K9LQT0_ARATH)		F:GO:0004674; F:GC	F:protein serine/thre	EC:2.7.11	Transferring phospho	IPR001480 (PFAM): IPR001245 (PFA	0,379	1,580	0,294	0,454	0,826									
Solyc12g006850	LELKT1GEN L.esculentum potassium channel	lkt1	F:GO:0005249; F:GC	F:voltage-gated potassium channel activity; F:protein binding; P			IPR003938 (PRINTS): IPR036770 (G3	1,246	7,505	0,738	0,620	0,679	2,607	0,000					up		
Solyc12g006860	brassinosteroid hydroxylase	CYP734A8	F:GO:0005506; F:GC	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	0,549	0,938	0,632	1,024	0,492									

Solyc12g006870	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A0B2RN42_GLYSO)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	46,448	47,849	63,622	62,476	64,828									
Solyc12g006880	PPPDE thiol peptidase family protein, putative (AHRD V3.3 *** I3T9Q3_MEDTR)						IPR008580 (PFAM): G3DSA:3.90.172(	6,162	6,410	19,813	21,937	16,323									
Solyc12g006890	Lipase class 3 family protein (AHRD V3.3 --* A0A061RUU6_9CHLO)							10,689	10,222	13,520	13,205	13,359									
Solyc12g006910	Cadmium tolerant 1 (AHRD V3.3 *** B5BSU1_9POAL)						IPR028144 (PFAM): PTHR35470 (PAN	0,137	0,062	0,332	0,412	0,164									
Solyc12g006920	Serine/threonine protein phosphatase 2A regulatory subunit B (AHRD V3.3 *** B9HTC9_POPTR)		C:GO:0000159; P:G(	C:protein phosphatase type 2A complex; P:signal transduction;			IPR011989 (G3DSA:1.25.10.GENE3D	28,766	34,222	27,208	30,187	27,479									
Solyc12g006930	Acyl-[acyl-carrier-protein] hydrolase (AHRD V3.3 *** K4DBN0_SOLLC)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:thiolester hydrolase activity			IPR002864 (PFAM): G3DSA:3.10.129	268,194	177,224	81,978	87,280	88,996									
Solyc12g006940	RING/U-box superfamily protein (AHRD V3.3 *** A0A061G9Z9_THECC)		F:GO:0008270; C:G(	F:zinc ion binding; C:integral component of membrane; F:ligase			IPR013083 (G3DSA:3.30.40.GENE3D	37,324	35,213	32,980	31,291	33,246									
Solyc12g006960	Sulfate transporter, putative (AHRD V3.3 *** B9RPC1_RICCO)		F:GO:0008271; C:G(	F:secondary active sulfate transmembrane transporter activity;			IPR036513 (G3DSA:3.30.750.GENE3	0,000	0,039	0,000	0,000	0,000									
Solyc12g006970	50S ribosomal protein L22, chloroplastic (AHRD V3.3 --* RK22_OENPA)							25,969	17,863	34,540	45,726	37,047									
Solyc12g006980	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *-* A0A0K9PTR8_ZOSMR)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): IPR032675 (G3D	129,663	88,131	129,645	184,789	175,880					0,515	0,031			up
Solyc12g006990	Arf GTPase activating protein (AHRD V3.3 *** A0A103Y2E2_CYNCS)		F:GO:0005096	F:GTPase activator activity			IPR001164 (PRINTS): IPR001164 (PF	67,868	74,451	60,748	64,035	64,293									
Solyc12g006993	delay of germination 1 (AHRD V3.3 --* AT5G45830.6)							0,121	0,202	0,168	0,149	0,094									
Solyc12g006997	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061GN86_THECC)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			IPR006121 (PFAM): G3DSA:3.30.70.1	0,294	0,057	0,050	0,347	0,399									
Solyc12g007000	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *-* AT5G19590.2)						IPR007493 (PFAM): IPR036758 (G3D	53,882	38,343	66,619	66,213	61,100									
Solyc12g007010	fe-S cluster assembly factor HCF101		F:GO:0005524	F:ATP binding			IPR002744 (PFAM): G3DSA:3.40.50.3	46,547	78,011	40,276	47,105	84,250	0,772	0,001	1,061	0,000			up	up	
Solyc12g007020	DUF936 family protein (AHRD V3.3 *** A0A072UQI4_MEDTR)		C:GO:0005829; F:G(	C:cytosol; F:microtubule binding			IPR010341 (PFAM): mobidb-lite (MOB	0,779	0,610	0,097	0,100	0,047									
Solyc12g007030	Aldehyde dehydrogenase, putative (AHRD V3.3 *** B9RKT6_RICCO)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR015590 (PFAM): IPR016162 (G3D	5,995	9,434	3,975	5,741	7,385			0,886	0,002				up	
Solyc12g007040	LOW QUALITY:FKBP-like peptidyl-prolyl cis-trans isomerase family protein (AHRD V3.3 --* AT4G26555.2)						PTHR33168:SF12 (PANTHER): PTHR:	0,021	0,000	0,141	0,171	0,024									
Solyc12g007050	LOW QUALITY:Arabinogalactan peptide-like protein (AHRD V3.3 *** G7J699_MEDTR)		C:GO:0005886; C:G(	C:plasma membrane; C:integral component of membrane; C:anc			IPR009424 (PFAM): IPR009424 (PAN	2,220	1,827	0,841	2,282	1,571					1,425	0,008			up
Solyc12g007060	LOW QUALITY:serine-rich protein-like protein (AHRD V3.3 --* AT5G55980.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,051	3,081	4,131	2,338	2,565									
Solyc12g007070	SolycHsfC1	HSF-12	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	8,283	11,679	88,070	105,939	68,004									
Solyc12g007080	Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G17150.6)							0,019	0,081	0,838	1,046	0,403									
Solyc12g007090	Tyrosine-protein phosphatase non-receptor type 6 (AHRD V3.3 *** A0A1D1XLX7_9ARAE)						PTHR35757 (PANTHER)	24,305	18,931	133,762	127,106	120,353									
Solyc12g007100	AAA-type ATPase family protein / ankyrin repeat family protein (AHRD V3.3 *** AT3G24530.1)		F:GO:0005515; F:G(	F:protein binding; F:ATP binding			IPR000641 (PRINTS): IPR002110 (PF	43,758	37,149	27,989	33,937	35,949									
Solyc12g007110	Receptor-like kinase (AHRD V3.3 *** G7KPX0_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	74,891	87,714	81,301	83,995	92,259									
Solyc12g007120	Chloroplast processing peptidase-like protein (AHRD V3.3 *** A0A0B0P629_GOSAR)		P:GO:0006508; F:G(	P:proteolysis; F:serine-type peptidase activity; C:membrane			IPR000223 (PRINTS): G3DSA:2.10.1(	4,089	4,934	10,247	10,112	12,243									
Solyc12g007130	Like-COV protein (AHRD V3.3 *** G7L895_MEDTR)		C:GO:0005794; P:G(	C:Golgi apparatus; P:stem vascular tissue pattern formation; C:			IPR007462 (PFAM): mobidb-lite (MOB	10,417	8,306	16,160	16,376	15,090									
Solyc12g007140	Actin-binding LIM 3 (AHRD V3.3 *** A0A0B0MT11_GOSAR)						IPR025486 (PFAM): IPR032795 (PFA	8,701	10,242	6,986	6,138	5,782									
Solyc12g007150	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 *** AT1G52240.1)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			G3DSA:1.20.58.2010 (GENE3D): G3D	0,157	0,265	0,075	0,000	0,024									
Solyc12g007160	ABIL1-like protein (AHRD V3.3 *** B7FL53_MEDTR)						IPR028457 (PANTHER): PTHR10460:	0,394	1,185	0,075	0,025	0,023									
Solyc12g007170	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857; F:G(	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	IPR001753 (PFAM): G3DSA:3.90.226	96,915	94,774	162,169	158,572	163,069									
Solyc12g007180	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 *** A0A061GMK6_THECC)						IPR005172 (PFAM CPP	5,535	4,555	23,976	27,484	22,494									
Solyc12g007190	Tesmin/TSO1-like CXC domain-containing protein (AHRD V3.3 --* A0A061GMK6_THECC)						mobidb-lite (MOBIDB_LITE)	1,141	0,818	2,694	3,480	2,425									
Solyc12g007200	Protein kinase (AHRD V3.3 *** A0A0K9PBK2_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	59,907	40,736	34,005	33,686	33,964									
Solyc12g007210	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	0,040	0,140	0,000	0,050	0,000									
Solyc12g007220	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmem			IPR000109 (PFAM): G3DSA:1.20.125	0,019	0,000	0,000	0,000	0,000									
Solyc12g007230	auxin-regulated IAA8	IAA8	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-(			G3DSA:3.10.20.90 (GENE3D): IPR03:	22,459	23,115	8,830	9,403	12,426									
Solyc12g007240	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT4G28840.1)		F:GO:0003700	F:DNA-binding transcription factor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,399	0,346	0,355	0,274	0,116									
Solyc12g007280	Casein kinase family protein (AHRD V3.3 *** B9ILR0_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	60,631	60,303	62,621	62,177	61,153									
Solyc12g007290	LOW QUALITY:Unknown protein (AHRD V3.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,683	0,785	0,615	0,231	0,448									
Solyc12g007300	LOW QUALITY:B3 domain-containing protein, putative (AHRD V3.3 *** A0A061GNJ5_THECC)		F:GO:0003677	F:DNA binding			IPR003340 (PFAM B3	1,178	1,753	8,799	10,327	7,059									
Solyc12g007310	Lactoylglutathione lyase (AHRD V3.3 *** A0A059CVI9_EUCGR)		F:GO:0004462; F:G(	F:lactoylglutathione	EC:4.4.1.5	Lactoylglutathione ly:	IPR029068 (G3DSA:3.10.180.GENE3	40,153	55,565	105,616	113,852	124,222									
Solyc12g007320	RING/U-box superfamily protein (AHRD V3.3 *** AT4G28890.1)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (PFAM): IPR013083 (G3D	0,038	0,021	0,051	0,092	0,070									
Solyc12g008320	Sugar transporter protein 18	STP18	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS): G3DSA:1.20.12	0,075	0,036	0,322	0,739	0,236									
Solyc12g008330	F-box protein, putative (AHRD V3.3 *-* A2Q1T0_MEDTR)						IPR032675 (G3DSA:3.80.10.GENE3D	17,272	14,892	9,120	11,016	9,593									
Solyc12g008340	Exostosin family protein (AHRD V3.3 *** AT5G19670.2)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glyco			IPR040911 (PFAM): PTHR11062:SF8	16,037	14,737	6,769	5,422	6,549									
Solyc12g008350	dehydration responsive element binding protein 2	dreb2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN ERF	25,145	23,127	3,436	2,144	3,278									
Solyc12g008360	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 (AHRD V3.3 *** W9RM44_9R(		F:GO:0004576; P:G(	F:oligosaccharyl transferase activity; P:protein glycosylation; C			IPR003674 (PFAM): G3DSA:3.40.50.1	126,826	121,398	132,888	133,682	130,653									
Solyc12g008370	SNW domain-containing 1 (AHRD V3.3 *** A0A0B0PGB0_GOSAR)		P:GO:0000398; C:G(	P:mRNA splicing, via spliceosome; C:spliceosomal complex			IPR004015 (PFAM): mobidb-lite (MOB	185,158	126,760	154,824	119,324	129,729					-0,372	0,025			down
Solyc12g008380	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** I3SWH2_MEDTR)		C:GO:0005773; P:G(	C:vacuole; P:response to chitin			IPR008480 (PFAM): PTHR33265:SF8	0,354	0,421	0,047	0,050	0,046									
Solyc12g008390	golgin Putative 1 (AHRD V3.3 *** AT2G19950.2)		P:GO:0007030	P:Golgi organization			mobidb-lite (MOBIDB_LITE): mobidb-lit	39,924	32,110	39,408	39,386	38,568									
Solyc12g008395	Golgin candidate 1 (AHRD V3.3 *-* GOGC1_ARATH)		P:GO:0007030	P:Golgi organization			IPR019177 (PFAM): PTHR13815:SF5	19,447	17,937	21,244	19,859	18,574									
Solyc12g008400	Receptor-kinase, putative (AHRD V3.3 *-* B9RVA8_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PR00019 (PRINTS): IPR001611 (PFA	2,520	2,885	0,091	0,217	0,329									
Solyc12g008420	RNA-dependent RNA polymerase (AHRD V3.3 *** K4DBS9_SOLLC)		F:GO:0003968	F:RNA-directed 5'-3	EC:2.7.7.48	RNA-directed RNA p(	IPR007855 (PFAM): mobidb-lite (MOB	50,308	39,771	15,996	14,015	19,549									
Solyc12g008430	Malic enzyme (AHRD V3.3 *** M0ZHN3_SOLTU)		F:GO:0004471; F:G(	F:malate dehydrog(	EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS): IPR012301 (PF	0,758	0,741	64,903	97,242	116,253			0,838	0,018				up	
Solyc12g008450	initiator tRNA phosphoribosyl transferase family protein (AHRD V3.3 *** AT2G40570.1)		P:GO:0019988; F:G(	P:charged-tRNA amino acid modification; F:tRNA A64-2'-O-ribos			IPR029021 (G3DSA:3.90.190.GENE3	8,034	7,639	10,203	10,644	9,247									
Solyc12g008460	Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT4G15450.1)		C:GO:0005886	C:plasma membrane			IPR009686 (PFAM): PTHR21068 (PAN	2,830	1,944	1,274	1,700	1,508									
Solyc12g008470	Cytochrome b5 (AHRD V3.3 *** A0A0B0P428_GOSAR)		C:GO:0016021; F:G(	C:integral component of membrane; F:heme binding; F:metal ior			IPR001199 (PFAM): IPR036400 (G3D	19,292	15,588	12,467	10,924	12,043									
Solyc12g008473	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G55530.3)		F:GO:0008270; P:G(	F:zinc ion binding; P:protein ubiquitination; F:ligase activity; F:ul			IPR001841 (PFAM): IPR013083 (G3D	0,077	0,041	0,025	0,025	0,046									
Solyc12g008477	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G19950.3)		C:GO:0005737; F:G(	C:cytoplasm; F:zinc ion binding; P:protein ubiquitination; F:ligas(			IPR001841 (PFAM): IPR013083 (G3D	0,037	0,043	0,025	0,000	0,000									
Solyc12g008480	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G60360.1)		F:GO:0008270; F:G(	F:zinc ion binding; F:ligase activity; F:metal ion binding			IPR001841 (PFAM): IPR013083 (G3D	0,038	0,000	0,000	0,000	0,000									
Solyc12g008490	Nucleotide-diphospho-sugar transferase domain protein (AHRD V3.3 *** G7L7F4_MEDTR)		F:GO:0016757	F:transferase activity, transferring glycosyl groups			IPR025993 (PFAM): IPR029044 (G3D	25,697	21,402	19,145	20,902	20,084									
Solyc12g008500	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9PZN1_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR032675 (G3DSA:3.80.10.GENE3D	3,032	10,992	5,240	7,101	8,725	1,881	0,000	0,736	0,006			up	up	
Solyc12g008510	Phosphotransferase (AHRD V3.3 *** K4DBT9_SOLLC)	hxk3	P:GO:0001678; F:G(	P:cellular glucose h	EC:2.7.1.1	Hexokinase	PR00475 (PRINTS): G3DSA:3.30.420	0,903	0,978	0,286	0,856	0,873									
Solyc12g008520	SUN-like protein 32	SUN32	F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 (GENE3D): IPR00(	0,355	0,393	0,146	0,139	0,000									
Solyc12g008530	Pectinesterase (AHRD V3.3 *** K4DBU1_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase a(	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR012334 (G3DSA:2.160.20.GENE3	3,098	3,350	0,642	0,931	1,201									
Solyc12g008540	Peptidase M28 family protein (AHRD V3.3 *-* AT5G19740.1)		F:GO:0004180; P:G(	F:carboxypeptidase activity; P:proteolysis			G3DSA:3.40.630.10 (GENE3D): IPR0(	1,506	1,168	0,801	0,730	1,012									
Solyc12g008550	Peptidase M28 family protein (AHRD V3.3 *-* AT5G19740.1)		F:GO:0004180; P:G(	F:carboxypeptidase activity; P:proteolysis			IPR007365 (PFAM): IPR036757 (G3D	35,844	25,315	18,575	15,025	16,026									
Solyc12g008570	Arginyl-tRNA synthetase-like protein (AHRD V3.3 *** V5RAL0_CAMSI)		F:GO:0004814; F:G(	F:arginine-tRNA lig	EC:6.1.1.19	Arginine--tRNA ligase	IPR001278 (PRINTS): G3DSA:1.10.73	63,065	65,913	77,917	76,059	78,157									
Solyc12g008580	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RKF7_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR012946 (PFAM): G3DSA:3.20.20.8	16,435	10,626	4,916	3,370	5,334									
Solyc12g008590	Profilin (AHRD V3.3 *** A0A0V0HAW8_SOLCH)		F:GO:0003779; C:G(	F:actin binding; C:cell wall; C:nucleolus; C:spindle; C:cytosol; C:			IPR005455 (PRINTS): IPR005455 (PF	145,200	145,370	158,113	141,653	146,985									
Solyc12g008600	DUF1005 family protein (DUF1005) (AHRD V3.3 *** AT4G29310.1)		C:GO:0009505	C:plant-type cell wall			IPR010410 (PFAM): PTHR31317:SF2	3,525	1,645	3,393	5,222	5,933			0,810	0,028				up	
Solyc12g008605	CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)							0,059	0,041	0,200	0,072	0,095									
Solyc12g008610	transmembrane protein (AHRD V3.3 --* AT5G27440.1)		C:GO:0016021	C:integral component of membrane				0,240	0,459	0,169	0,373	0,261									
Solyc12g008620	Protein-tyrosine phosphatase mitochondrial 1, mitochondrial, putative (AHRD V3.3 *** B9RKE9_RICCO)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR029021 (G3DSA:3.90.190.GENE3	27,632	21,621	42,565	37,588	36,638									
Solyc12g008630	Mitochondrial-processing peptidase subunit alpha (AHRD V3.3 *** MPPA_SOLTU)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			G3DSA:3.30.830.10 (GENE3D): IPR0(	224,580	227,126	381,345	346,248	347,452									
Solyc12g008640	Gamma-glutamyltranspeptidase 1 (AHRD V3.3 *** A0A0B0NB37_GOSAR)		F:GO:0005506; C:G(	F:iron ion binding; (	EC:3.4.19; EC:1.13.9	Acting on peptide bor	PR01210 (PRINTS): IPR000101 (TIGF	141,708	70,412	248,209	204,008	190,521	-0,980	0,000					down		
Solyc12g008650	Myo-inositol oxygenase (AHRD V3.3 *** C6K2L2_SOLLC)	MIOX	F:GO:0005506; C:G(	F:iron ion binding; (	EC:1.13.99.1	Inositol oxygenase	IPR007828 (PFAM): PTHR12588:SF1	0,301	0,486	0,000	0,000	0,000									
Solyc12g008660	Zinc finger transcription factor 73	C3H73	F:GO:0046872	F:metal ion binding			G3DSA:4.10.1000_C3H	8,938	14,626	3,896	3,793	4,920									
Solyc12g008665	Meiotic nuclear division protein 1 homolog (AHRD V3.3 *** M0ZHL5_SOLTU)		C:GO:0005634; P:G(	C:nucleus; P:double-strand break repair; P:embryo sac develop			IPR005647 (PIRSF): IPR040453 (PFA	0,000	0,021	0,000	0,000	0,000									
Solyc12g008670	blind-like4	R2R3MYB90	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,000	0,043	0,000	0,000	0,000									
Solyc12g008680	RNA-binding CRS1 / YhbY (CRM) domain protein (AHRD V3.3 --* AT3G27550.3)							0,059	0,000	0,000	0,000	0,000									
Solyc12g008690	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9RQ74_RICCO)		F:GO:0016787	F:hydrolase activity			G3DSA:3.30.70.360 (GENE3D): IPR0(	27,497	22,632	43,834	35,736	41,562									
Solyc12g008700	peroxisomal ABC transporter 1 (AHRD V3.3 --* AT4G39850.4)						mobidb-lite (MOBIDB_LITE)	71,569	90,373	80,234	71,827	71,885									
Solyc12g008710	Peptidase M16 family protein (AHRD V3.3 *** D7MM64_ARALL)		F:GO:0003824; F:G(	F:catalytic activity; F:metal ion binding			IPR011765 (PFAM): G3DSA:3.30.830	51,947	41,164	77,693	79,730	78,158									
Solyc12g008720	60S ribosomal protein L31 (AHRD V3.3 *** W9QLF2_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000054 (PFAM): IPR023621 (G3D	174,010	198,290	140,088	122,821	129,428									
Solyc12g008730	Mitochondrial ATP synthase subunit G protein (AHRD V3.3 *** AT4G26210.2)		C:GO:0000276; F:G(	C:mitochondrial proton-transporting ATP synthase complex, cou			IPR006808 (PFAM): IPR006808 (PAN	52,963	58,600	78,273	78,394	71,094									
Solyc12g008750	Splicing factor U2af large subunit B (AHRD V3.3 *** A0A0M9UMX0_NICAT)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:mRNA processing			IPR012677 (G3DSA:3.30.70.GENE3D	115,636	114,501	135,759	119,567	127,477									
Solyc12g008760	arginine methyltransferase 11 (AHRD V3.3 *** AT4G29510.1)		P:GO:0006479; F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D): G3DS	27,722	30,839	31,926	31,246	27,172									
Solyc12g008770	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT4G26180.1)		C:GO:0005743; F:G(	C:mitochondrial inner membrane; F:transmembrane transporter			IPR002067 (PRINTS): IPR002167 (PF	16,880	14,209	12,781	11,584	12,536									
Solyc12g008780	Serine acetyltransferase family protein (AHRD V3.3 *** U5FSS1_POPTR)		C:GO:0005737; P:G(	C:cytoplasm; P:cys	EC:2.3.1.3	Serine O-acetyltrans	IPR005881 (TIGRFAM): G3DSA:1.10.:	7,189	5,650	15,436	12,585	13,532									
Solyc12g008790	Acyl--UDP-N-acetylglucosamine O-acyltransferase (AHRD V3.3 *** D7MCK7_ARALL)		P:GO:0008610; F:G(	P:lipid biosynthetic	EC:2.3.1.129	Acyl-[acyl-carrier-pro	IPR029098 (PFAM): G3DSA:2.160.10	11,434	8,745	11,005	10,247	10,669									
Solyc12g008800	Myb-like transcription factor family protein, putative (AHRD V3.3 *** A0A061GMU9_THECC)		F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB_related	0,608	1,235	0,615	1,303	1,200									
Solyc12g008810	Embryo defective 2752 (AHRD V3.3 *** A0A061GTL0_THECC)		C:GO:0016021	C:integral component of membrane			IPR037759 (PANTHER)	22,209	21,845	36,725	36,025	32,042									
Solyc12g008830	GATA-like transcription factor (AHRD V3.3 *** I3VFF1_TOBAC)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR000679 (PFAM GATA	0,038	0,135	0,000	0,025	0,070									
Solyc12g008840	beta-galactosidase 4	TBG4	F:GO:0004553; F:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): G3DSA:3.20.2(	18,309	17,030	479,930	790,108	533,878					0,721	0,001			up
Solyc12g008850	Lysine-specific histone demethylase 1 homolog 1 (AHRD V3.3 *** LDL1_ARATH)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR036188 (G3DSA:3.50.50.GENE3D	0,077	0,058	0,094	0,147	0,070									
Solyc12g008860	transmembrane protein (AHRD V3.3 *-* AT4G29735.1)		P:GO:0006487; C:G(	P:protein N-linked glycosylation; C:oligosaccharyltransferase I (			IPR007915 (PFAM): IPR007915 (PAN	0,042	0,000	0,047	0,000	0,000									
Solyc12g008890	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *-* I0IUQ9_SOLLC)		P:GO:0006487; P:G(	P:protein N-linked g	EC:1.5.99.12	Cytokinin dehydroge	IPR016170 (G3DSA:3.40.462.GENE3	27,103	23,221	36,597	30,084	32,188									
Solyc12g008900	cytokinin oxidase6	CKX6	P:GO:0009690; F:G(	P:cytokinin metabol	EC:1.5.99.12	Cytokinin dehydroge	IPR016170 (G3DSA:3.40.462.GENE3	8,806	8,369	0,342	0,175	0,232									
Solyc12g008910	translation initiation factor SUI1 family protein		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			G3DSA:3.30.780.10 (GENE3D): IPR0(	20,109	19,877	22,256	22,743	20,803									
Solyc12g008920	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ9_SOLLC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process; F:FAI			IPR006094 (PFAM): IPR016167 (G3D	0,042	0,000	0,000	0,000	0,000									
Solyc12g008930	Basic helix loop helix (BHLH) DNA-binding family protein (AHRD V3.3 *** G7IIK9_MEDTR)		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (PFAM): IPR036638 (G3D	0,000	0,696	0,000	0,000	0,168									
Solyc12g008940	Nucleosome assembly protein 1-1 (AHRD V3.3 *** NAP1A_TOBAC)		C:GO:0005634; P:G(	C:nucleus; P:nucleosome assembly			G3DSA:3.30.1120.90 (GENE3D): IPR(	118,128	139,820	83,510	80,076	93,222									
Solyc12g008950	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT2G47240.4)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,384	5,666	1,450	1,400	1,666									
Solyc12g008960	Calmodulin-binding family protein (AHRD V3.3 *** A0A061GKK0_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	5,364	4,809	1,270	2,810	1,951					1,134	0,011			up
Solyc12g008970	O-acyltransferase (AHRD V3.3 *** K4DBY5_SOLLC)		F:GO:0004144; P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR014371 (PIRSF): IPR027251 (PTH	23,422	42,575	26,174	29,968	30,443									
Solyc12g008980	Delta	E-LCY	P:GO:0016117; F:G(	P:carotenoid biosynthetic process; F:oxidoreductase activity, a			PR00411 (PRINTS): IPR010108 (TIGF	5,330	13,373	1,765	2,195	4,432	1,357	0,008	1,315	0,000			up	up	
Solyc12g008990	Kinase family protein (AHRD V3.3 *** D7MM98_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ubiquitin-protein transferase activity			IPR006016 (PFAM): IPR014729 (G3D	1,343	1,655	0,670	0,586	0,773									
Solyc12g009000	LOW QUALITY:Harbinger transposase-derived nuclease (AHRD V3.3 *** A0A103Y2W0_CYNCS)						IPR027806 (PFAM): PTHR22930:SF1	317,163	249,561	89,459	286,183	134,164					1,678	0,000			up
Solyc12g009010	Kinase family protein (AHRD V3.3 *** B9HDX0_POPTR)		F:GO:0004674; F:G(	F:protein serine/thr	EC:2.7.11	Transferring phospho	IPR000719 (PFAM): PTHR24356:SF2	1,503	2,522	2,455	1,888	1,920									
Solyc12g009015	Chalcone--flavonone isomerase 3 (AHRD V3.3 --* CFI3_SOYBN)	CHI						0,040	0,000	0,000	0,000	0,000									
Solyc12g009020	MAP kinase kinase 1	MAPKK1	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): PIRSF000654 (	31,265	54,677	32,615	40,319	37,836	0,831	0,037					up		
Solyc12g009030	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT4G29830.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	18,520	16,320	22,313	18,620	21,752									
Solyc12g009040	Long chain acyl-CoA synthetase (AHRD V3.3 *** Q5W6W7_ORYSJ)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): PTHR43272 (PAN	1,602	0,845	2,120	1,095	2,325									
Solyc12g009050	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR001289 (PRIN NF-YA	1,314	1,114	2,283	1,454	2,546									
Solyc12g009060	SNF7 family protein		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): mobidb-lite (MOB	109,124	141,342	140,559	154,144	142,645									
Solyc12g009065	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GT61_THECC)		C:GO:0016021	C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,000	0,044	0,000	0,000									
Solyc12g009070	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A151SSR0_CAJCA)							3,907	8,234	0,929	1,777	2,750			1,541	0,000				up	
Solyc12g009075	centromere protein O (AHRD V3.3 --* AT5G10710.3)							0,000	0,000	0,025	0,025	0,046									
Solyc12g009080	OBP3-RESPONSIVE GENE 4 family protein (AHRD V3.3 *** U5FFX8_POPTR)		C:GO:0009536; P:G(	C:plastid; P:response to salicylic acid			PTHR35710 (PANTHER)	23,092	17,765	27,587	27,261	25,516									
Solyc12g009090	Succinate dehydrogenase subunit 4, mitochondrial (AHRD V3.3 --* SDH4_ARATH)							21,701	20,165	26,301	22,982	23,368									
Solyc12g009100	FRIGIDA interacting protein 1 (AHRD V3.3 *** AT2G06005.1)		C:GO:0005765; C:G(	C:lysosomal membrane; C:late endosome; C:integral componen			IPR029399 (PFAM): IPR029399 (PAN	10,787	8,547	16,860	17,695	13,975									
Solyc12g009110	O-methyltransferase, putative (AHRD V3.3 *** B9SUX6_RICCO)		F:GO:0008171; F:G(	F:O-methyltransferase activity; F:protein dimerization activity			IPR016461 (PIRSF): IPR001077 (PFA	0,021	0,000	1,588	1,460	0,517									
Solyc12g009120	RING-box protein (AHRD V3.3 *** Q2PYP4_ARAHY)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	31,099	27,909	52,458	42,648	40,458									
Solyc12g009130	LURP-one-like protein (AHRD V3.3 *** G7IGE6_MEDTR)						IPR038595 (G3DSA:3.20.90.GENE3D	0,000	0,000	0,068	0,147	0,071									
Solyc12g009140	Proteasome subunit alpha type (AHRD V3.3 *** A0A0V0HRW3_SOLCH)		F:GO:0004298; P:G(	F:threonine-type en	EC:3.4.25	Acting on peptide bor	IPR001353 (PFAM): IPR000426 (PFA	95,621	98,756	179,829	176,995	164,899									
Solyc12g009150	TRICHOME BIREFRINGENCE-LIKE 16 (AHRD V3.3 *** AT5G20680.5)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:acetyl			IPR026057 (PFAM): IPR025846 (PFA	39,701	39,492	67,829	73,316	62,390									
Solyc12g009160	inter-alpha-trypsin inhibitor heavy chain-like protein (AHRD V3.3 *** AT1G19110.1)						IPR002035 (PFAM): IPR036465 (G3D	18,804	25,403	20,935	21,958	22,956									
Solyc12g009170	Small nuclear ribonucleoprotein LSM1 (AHRD V3.3 *** B6SKB6_MAIZE)		P:GO:0016071; C:G(	P:mRNA metabolic process; C:protein-containing complex; C:int			IPR001163 (PFAM): G3DSA:2.30.30.1	0,444	0,564	0,075	0,051	0,024									
Solyc12g009180	RmlC-like jelly roll fold protein (AHRD V3.3 *** AT1G19130.1)						IPR014710 (G3DSA:2.60.120.GENE3	45,132	49,951	23,798	18,598	22,784									
Solyc12g009190	Receptor-like kinase, putative (AHRD V3.3 *** A0A072TMR8_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR001611 (PFAM): IPR013210 (PFA	0,019	0,670	0,000	0,025	0,213									
Solyc12g009200	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4DC08_SOLLC)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR022796 (PFAM): IPR023329 (G3D	0,410	2,575	0,430	1,244	2,853	2,642	0,000	2,685	0,000			up	up	
Solyc12g009210	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G42950.1)	PG58-1	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	28,177	27,270	49,211	42,271	40,386									
Solyc12g009220	jasmonate ZIM-domain protein 1		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:response to wounding; P:regulat			IPR010399 (PFAM): IPR018467 (PFA	3,072	17,675	4,219	2,993	3,629	2,550	0,000					up		
Solyc12g009230	RNA-binding protein (AHRD V3.3 *** A0A0K9PBY9_ZOSMR)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	9,960	11,594	12,602	12,510	13,146									
Solyc12g009240	Ethylene-responsive transcription factor ERF017 (AHRD V3.3 *** ERF17_ARATH)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:reg			IPR001471 (PRIN ERF	89,031	4,358	21,030	73,738	13,407	-4,325	0,000			1,814	0,000	down		up
Solyc12g009245	20 kDa chaperonin family protein (AHRD V3.3 *-* B9INC6_POPTR)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding			IPR037124 (G3DSA:2.30.33.GENE3D	0,021	0,021	0,000	0,000	0,024									
Solyc12g009250	Chaperonin (AHRD V3.3 *** Q69QD5_ORYSJ)		C:GO:0005737; P:G(	C:cytoplasm; P:protein folding; F:transition metal ion binding; P:(			IPR020818 (PRINTS): IPR037124 (G3	151,488	218,203	157,563	138,319	211,209	0,552	0,047	0,420	0,013			up	up	
Solyc12g009260	3-oxoacyl-[acyl-carrier-protein] synthase (AHRD V3.3 *** K4DC14_SOLLC)		P:GO:0006633; F:G(	P:fatty acid biosynthetic process; F:transferase activity, transfe			IPR014030 (PFAM): IPR017568 (TIGF	3,593	4,167	3,218	2,868	3,871									
Solyc12g009270	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061GSW0_THECC)		F:GO:0004857	F:enzyme inhibitor activity			IPR006501 (TIGRFAM): IPR006501 (I	19,584	12,608	4,557	5,004	3,083									

Solyc12g009300	sucrose synthase (SuSy)	SUS1	P:GO:0005985: F:G(	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	IPR012820 (TIGRFAM): G3DSA:3.10.	999,255	914,158	41,725	30,724	41,335									
Solyc12g009310	Protein kinase superfamily protein (AHRD V3.3 *** AT2G07180.2)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	1,851	2,174	1,009	0,687	0,920									
Solyc12g009340	MAP kinase kinase kinase 84	MAPKKK84	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PRINTS): PIRSF000654 (	28,867	33,865	39,046	40,207	39,242									
Solyc12g009350	Protein kinase (AHRD V3.3 *** A0A0K9NJ18_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): PIRS	0,038	0,000	0,000	0,000	0,000									
Solyc12g009370	Protein kinase (AHRD V3.3 *-* A0A0K9NJ18_ZOSMR)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510.	0,000	0,019	0,000	0,000	0,000									
Solyc12g009380	Ribosomal protein S17 (AHRD V3.3 *** U5FIK1_POPTR)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000266 (PRINTS): G3DSA:2.40.5(	6,362	6,818	7,507	6,494	6,376									
Solyc12g009390	Zinc finger transcription factor 75	C3H75	F:GO:0046872	F:metal ion binding			IPR000571 (PFAM C3H	6,753	8,867	13,356	14,244	12,062									
Solyc12g009400	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** K4DC28_SOLLC)		F:GO:0004739: P:G(	F:pyruvate dehydro	EC:1.2.4.1	Pyruvate dehydroger	IPR001017 (PFAM): IPR017597 (TIGF	48,020	56,151	97,309	100,824	102,841									
Solyc12g009410	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** K4DC29_SOLLC)		F:GO:0004739: P:G(	F:pyruvate dehydro	EC:1.2.4.1	Pyruvate dehydroger	IPR001017 (PFAM): G3DSA:3.40.50.9	76,761	77,859	133,545	153,071	145,222									
Solyc12g009415	NBS-LRR protein (AHRD V3.3 *-* Q9SM52_SOLAC)		F:GO:0043531	F:ADP binding			IPR002182 (PFAM): G3DSA:3.40.50.3	0,000	0,018	0,000	0,000	0,023									
Solyc12g009420	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G57510.1)	PG70	F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	2,805	2,275	1,168	0,804	1,299									
Solyc12g009425	Pectin lyase-like superfamily protein (AHRD V3.3 *-* AT1G80170.2)		F:GO:0004650: P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	1,446	1,299	0,574	0,525	0,564									
Solyc12g009430	FkbM family methyltransferase (AHRD V3.3 *** AT2G26680.1)		C:GO:0005794: C:G(	C:Golgi apparatus; C:plasma membrane; C:integral component (			G3DSA:3.40.50.150 (GENE3D): IPR0(	8,107	4,878	7,001	6,369	6,711									
Solyc12g009440	Chaperone DnaJ (AHRD V3.3 *** A0A0B0P8V3_GOSAR)		C:GO:0009507	C:chloroplast			PTHR15852:SF26 (PANTHER): PTHR	27,496	41,801	34,683	29,883	37,279	0,631	0,009					up		
Solyc12g009450	Disease resistance protein (CC-NBS-LRR class) family (AHRD V3.3 *** AT5G35450.2)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	0,379	0,473	0,538	0,568	0,446									
Solyc12g009470	yellow-green-2	yg2/GUN2	F:GO:0004392: P:G(	F:heme oxygenase	EC:1.14.99.3	Acting on paired don(	IPR016053 (PFAM): IPR016951 (PIRS	28,801	36,172	58,547	51,443	58,047									
Solyc12g009480	SPX domain-containing family protein (AHRD V3.3 *** B9IMZ5_POPTR)		P:GO:0016036	P:cellular response to phosphate starvation			IPR004331 (PFAM): mobidb-lite (MOB	9,413	8,092	4,510	3,158	4,695									
Solyc12g009490	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9QRX0_9ROSA)		F:GO:0003677: F:G(	F:DNA binding: F:DNA-binding transcription factor activity: P:rec			IPR001471 (PRIN ERF	9,025	6,333	0,000	0,000	0,000									
Solyc12g009500	Elongator complex protein 6 (AHRD V3.3 *** ELP6_ARATH)		P:GO:0002098: C:G(	P:tRNA wobble uridine modification: C:Elongator holoenzyme co			G3DSA:3.40.50.300 (GENE3D): IPR0	20,566	23,473	13,206	11,103	12,959									
Solyc12g009510	Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	0,042	0,233	0,000	0,025	0,094									
Solyc12g009520	Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR013210 (PFA	8,627	37,659	2,343	2,724	4,498	2,144	0,004	0,937	0,004			up	up	
Solyc12g009550	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT3G24240.1		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR032675 (G3D	0,000	0,039	0,000	0,025	0,000									
Solyc12g009560	EIN3-binding F-box protein 1	EBF2	F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	62,726	96,119	237,558	307,513	163,441			-0,543	0,018				down	
Solyc12g009570	calcineurin B-like interacting protein kinase	cipk	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.310.80 (GENE3D): G3DS	13,679	10,264	7,717	6,908	7,191									
Solyc12g009580	CRABS CLAW 5b	YABBY5b	P:GO:0007275	P:multicellular organism development			IPR036910 (G3DS YABBY	0,131	0,078	0,000	0,000	0,000									
Solyc12g009590	Methyl-CpG-binding domain protein (AHRD V3.3 *-* G7JE44_MEDTR)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus			G3DSA:3.30.890.10 (GENE3D): IPR0(	16,908	14,369	34,138	32,300	29,769									
Solyc12g009600	Thylakoid lumenal 16.5 kDa protein (AHRD V3.3 *** A0A061GNW6_THECC)		P:GO:0010206	P:photosystem II repair			IPR038862 (PANTHER)	5,542	13,220	3,682	4,928	9,743	1,282	0,005	1,389	0,000			up	up	
Solyc12g009610	RabGAP/TBC domain-containing protein (AHRD V3.3 *** AT5G52580.1)		F:GO:0005096: C:G(	F:GTPase activator activity: C:cell: P:intracellular protein transp			G3DSA:1.10.472.80 (GENE3D): IPR0	212,747	216,834	131,790	148,210	132,998									
Solyc12g009620	Ubiquitin system component Cue protein (AHRD V3.3 *** AT5G32440.3)		F:GO:0005515	F:protein binding			PTHR31245:SF1 (PANTHER): PTHR3	30,857	26,443	43,809	39,807	36,744									
Solyc12g009630	Calcium-binding family protein (AHRD V3.3 *** B9HA89_POPTR)		F:GO:0005509	F:calcium ion binding			PR01697 (PRINTS): IPR002048 (PFA	1,136	0,944	0,840	0,784	0,611									
Solyc12g009640	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061G8Z6_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity			IPR008906 (PFAM): IPR003656 (PFA	70,256	71,153	73,978	61,750	68,342									
Solyc12g009650	Sl proline-rich protein						IPR027923 (PFAM): G3DSA:1.10.110	2,280	7,076	0,786	0,597	0,828	1,660	0,012					up		
Solyc12g009660	Exostosin family protein (AHRD V3.3 *** AT5G20260.2)		P:GO:0006486: F:G(	P:protein glycosylation: F:transferase activity, transferring glycc			IPR040911 (PFAM): IPR004263 (PAN	0,159	0,292	0,000	0,000	0,000									
Solyc12g009680	ADIPOR-like receptor (AHRD V3.3 *** W9SGZ8_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR004254 (PFAM): PTHR20855:SF3	3,231	2,621	4,233	4,190	3,709									
Solyc12g009700	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *-* AT1G05500.1)		F:GO:0008289	F:lipid binding			IPR039010 (PFAM): PTHR10774 (PAN	0,019	0,041	0,000	0,000	0,000									
Solyc12g009770	LOW QUALITY:Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A097BR55_GOSBA)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,832	1,287	0,212	0,700	2,360			3,377	0,000				up	
Solyc12g009780	LOW QUALITY:Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	0,084	0,204	0,025	0,025	0,242									
Solyc12g009790	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G05500.1)		F:GO:0008289	F:lipid binding			IPR000008 (PRINTS): IPR000008 (PF	19,478	20,017	7,458	7,732	8,666									
Solyc12g009800	Purple acid phosphatase (AHRD V3.3 *** K4DC68_SOLLC)		F:GO:0003993: F:G(	F:acid phosphatase	EC:3.1.3.2	Acid phosphatase	IPR004843 (PFAM): IPR015914 (PFA	34,721	36,359	0,909	0,645	1,074									
Solyc12g009810	UDP-N-acetylglucosamine transferase subunit ALG13-like protein (AHRD V3.3 *** W9QX49_9ROSA)		P:GO:0006488: F:G(	P:dolichol-linked oligosaccharide biosynthetic process: F:transf(			G3DSA:3.40.50.2000 (GENE3D): IPR(	42,875	37,402	38,292	38,590	36,167									
Solyc12g009820	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** G7JGJ5_MEDTR)		P:GO:0009247: F:G(	P:glycolipid biosynthetic process: F:transferase activity, transfe			IPR009695 (PFAM): IPR007235 (PFA	17,379	11,019	4,246	3,869	3,205									
Solyc12g009830	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GPA7_THECC)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	16,199	12,900	26,215	25,234	21,769									
Solyc12g009840	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)		F:GO:0004427: F:G(	F:inorganic diphosp	EC:3.6.1.1	Inorganic diphosphat	IPR004131 (PIRSF): IPR004131 (PFA	27,055	31,047	7,347	4,874	6,337									
Solyc12g009860	Arginine decarboxylase (AHRD V3.3 --* G4V2J2_MATIN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	17,967	20,496	15,331	15,529	14,475									
Solyc12g009870	LOW QUALITY:Leucine-rich repeat family protein (AHRD V3.3 *** AT1G15740.1)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	0,000	0,000	0,000	0,225	0,023									
Solyc12g009880	LOW QUALITY:Serine-rich protein-related (AHRD V3.3 *** A0A061GN42_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	9,725	6,794	3,286	3,751	4,770									
Solyc12g009890	Vacuolar ATPase subunit H protein (AHRD V3.3 *** B6SIW6_MAIZE)		C:GO:0000221: P:G(	C:vacuolar proton-t	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR004908 (PFAM): IPR038497 (G3D	25,912	27,068	23,633	26,517	27,719									
Solyc12g009920	Glycosyltransferase (AHRD V3.3 *** A0A0V0I412_SOLCH)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	3,030	4,411	0,425	0,795	1,405									
Solyc12g009925	Glutamyl-tRNA reductase 2, chloroplastic (AHRD V3.3 --* HEM12_ARATH)	HEMA/GluTR						0,042	0,043	0,025	0,000	0,000									
Solyc12g009930	Glycosyltransferase (AHRD V3.3 *** K4DC81_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	20,592	29,236	0,258	0,401	0,493									
Solyc12g009940	Glycosyltransferase (AHRD V3.3 *** K4DC82_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	6,363	6,713	4,750	3,991	4,183									
Solyc12g009960	Eukaryotic translation initiation factor iso4G (AHRD V3.3 *** K7T8S0_SOLLC)		F:GO:0003723: F:G(	F:RNA binding; F:protein binding			IPR003890 (PFAM): IPR003891 (PFA	359,869	313,489	330,840	287,293	299,852									
Solyc12g009970	Ribosomal RNA small subunit methyltransferase G (AHRD V3.3 *** A0A0B0NU00_GOSAR)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	21,224	31,069	10,461	9,443	10,707									
Solyc12g009980	UPF0133 protein (AHRD V3.3 *** A0A0B2RBJ9_GLYSO)		F:GO:0003677	F:DNA binding			IPR036894 (G3DSA:3.30.1310.GENE	23,168	30,797	30,166	27,122	32,166									
Solyc12g009990	signal recognition particle receptor alpha subunit family protein (AHRD V3.3 *** AT4G30600.2)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.120.140 (GENE3D): IPR(	131,047	139,302	199,097	194,765	189,938									
Solyc12g010000	Early nodulin-like protein (AHRD V3.3 *** G7J9U0_MEDTR)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,000	0,000	0,025	0,000	0,000									
Solyc12g010010	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9STR6_RICCO)		F:GO:0005249: F:G(	F:voltage-gated potassium channel activity: F:protein binding: P			IPR003938 (PRINTS): IPR005821 (PF	69,596	74,104	87,477	89,681	87,339									
Solyc12g010015	Small nuclear ribonucleoprotein family protein (AHRD V3.3 -** AT3G62840.1)		F:GO:0005249: C:G(	F:voltage-gated potassium channel activity: C:integral component of membrane: P:potassium ion transn				0,161	0,370	0,194	0,219	0,140									
Solyc12g010020	Leucine aminopeptidase A1	LapA1	F:GO:0004177: C:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	G3DSA:3.40.630.10 (GENE3D): IPR0(	0,224	1,178	0,340	0,241	0,375									
Solyc12g010025	Leucine aminopeptidase (AHRD V3.3 *** U3PLK3_TOBAC)		F:GO:0004177: C:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR011356 (PRINTS): IPR000819 (PF	0,021	0,082	0,047	0,025	0,094									
Solyc12g010030	Leucine aminopeptidase (AHRD V3.3 *-* U3PLK3_TOBAC)		F:GO:0004177: C:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR000819 (PFAM): G3DSA:3.40.630	0,080	0,277	0,047	0,048	0,232									
Solyc12g010040	leucine aminopeptidase A	aci29	F:GO:0004177: C:G(	F:aminopeptidase a	EC:3.4.11	Acting on peptide bor	IPR011356 (PRINTS): G3DSA:3.40.63	335,549	299,559	535,038	460,330	479,365									
Solyc12g010050	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9STQ9_RICCO)		P:GO:0006284: F:G(	P:base-excision rep	EC:3.2.2.21: EC:3.2.	DNA-3-methyladenine	IPR005019 (PFAM): G3DSA:1.10.340	8,452	5,718	0,508	0,201	0,401									
Solyc12g010060	Eukaryotic translation initiation factor 5A (AHRD V3.3 *** Q6S021_CAPAN)		F:GO:0003746: P:G(	F:translation elongation factor activity: P:translational frameshif			IPR001884 (TIGRFAM): G3DSA:2.40.	34,610	34,311	23,524	27,418	26,139									
Solyc12g010070	LOW QUALITY:MUTL protein homolog 3 (AHRD V3.3 --* AT4G35520.8)							0,157	0,083	0,025	0,075	0,072									
Solyc12g010080	BTB/POZ domain-containing protein (AHRD V3.3 *** W9QLB4_9ROSA)		F:GO:0003824: F:G(	F:catalytic activity: F:protein binding: P:protein homooligomeriza			G3DSA:3.30.710.10 (GENE3D): IPR0(	0,019	0,000	0,000	0,000	0,000									
Solyc12g010100	BTB/POZ domain-containing protein (AHRD V3.3 *** W9QLB4_9ROSA)		F:GO:0005515: P:G(	F:protein binding; P:protein homooligomerization			G3DSA:3.30.710.10 (GENE3D): IPR0(	0,205	0,079	0,022	0,000	0,000									
Solyc12g010110	Formin-like protein (AHRD V3.3 *** K4DC98_SOLLC)						IPR014020 (PFAM): G3DSA:1.20.58.2	24,211	23,721	39,818	51,362	40,938									
Solyc12g010115	Cathechol O-methyltransferase (AHRD V3.3 -** B0ZR84_PINSY)							2,423	2,766	4,786	6,065	4,758									
Solyc12g010120	Reticulon-like protein (AHRD V3.3 *** K4DC99_SOLLC)		C:GO:0005789: C:G(	C:endoplasmic reticulum membrane: C:integral component of me			IPR003388 (PFAM): mobidb-lite (MOB	8,404	6,704	10,046	12,763	8,538									
Solyc12g010140	Aldolase-type TIM barrel family protein (AHRD V3.3 --* AT3G14150.7)							8,781	16,071	23,252	29,498	17,283	0,898	0,004	-0,431	0,037			up	down	
Solyc12g010150	Cytochrome C oxidase, subunit VIb family protein (AHRD V3.3 *** G7JGS6_MEDTR)		C:GO:0005739	C:mitochondrion			IPR003213 (PFAM): PTHR11387:SF2(	5,009	4,478	9,345	8,916	8,135									
Solyc12g010160	LOW QUALITY:syntaxin of plants 41 (AHRD V3.3 --* AT5G26980.3)							0,155	0,075	0,118	0,100	0,070									
Solyc12g010170	bHLH transcription factor 070		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	0,197	0,221	0,097	0,166	0,282									
Solyc12g010180	Anthranilate synthase (AHRD V3.3 *** A0A0K9PKR0_ZOSMR)		P:GO:0000162: F:G(	P:tryptophan biosyr	EC:4.1.3.27	Anthranilate synthase	PR00096 (PRINTS): PR00099 (PRINT	23,604	27,244	45,937	42,719	43,161									
Solyc12g010190	LOW QUALITY:Sucrose-phosphate synthase 2 (AHRD V3.3 --* A0A151U227_CAJCA)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,037	0,000	0,025	0,000									
Solyc12g010200	Hexosyltransferase (AHRD V3.3 *** K4DCA7_SOLLC)		F:GO:0047262	F:polygalacturonate	EC:2.4.1.43	Polygalacturonate 4-	IPR002495 (PFAM): IPR029044 (G3D	4,932	3,391	30,173	36,699	26,322									
Solyc12g010220	ABC transporter family protein (AHRD V3.3 *** A0A097P9R6_HEVBR)	ABCI10	F:GO:0005215: F:G(	F:transporter activit	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	4,182	4,713	5,880	5,712	5,540									
Solyc12g010230	Calcineurin-like metallo-phosphoesterase superfamily protein, putative (AHRD V3.3 *** A0A061GI89_THECC)						IPR029052 (G3DSA:3.60.21.GENE3D	3,841	3,962	1,468	1,312	2,210									
Solyc12g010233	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061FVD3_THECC)		F:GO:0003677: F:G(	F:DNA binding; F:protein dimerization activity			IPR025525 (PFAM): IPR008906 (PFA	0,811	0,306	0,459	0,490	0,564									
Solyc12g010237	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD V3.3 --* AT1G11100.5)							2,295	1,134	1,848	2,317	2,051									
Solyc12g010300	LOW QUALITY:growth-regulating factor 9 (AHRD V3.3 --* AT2G45480.3)							2,137	1,266	2,150	1,817	1,365									
Solyc12g010310	Zinc finger CCCH domain-containing protein 32 (AHRD V3.3 --* C3H32_ORYSJ)							11,586	7,380	10,476	10,491	10,600									
Solyc12g010320	temperature-induced lipocalin	til	F:GO:0005215	F:transporter activity			IPR002446 (PRINTS): IPR022271 (PII	157,095	167,361	1638,610	1253,574	1212,309			-0,438	0,031				down	
Solyc12g010330	Two-component response regulator (AHRD V3.3 *** W9RL08_9ROSA)		P:GO:0000160: F:G(	P:phosphorelay signal transduction system: F:DNA binding: F:D			IPR001005 (PFAM ARR-B	20,670	18,496	32,659	37,222	34,263									
Solyc12g010340	PHD finger-like domain-containing protein 5A (AHRD V3.3 *** PHF5A_ARATH)		P:GO:0000398: C:G(	P:mRNA splicing, via spliceosome: C:U2 snRNP: C:U12-type sp			IPR005345 (PFAM): IPR005345 (PAN	16,278	14,622	25,245	21,387	22,675									
Solyc12g010350	60S ribosomal protein L39 (AHRD V3.3 *** RL39_MAIZE)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR023626 (G3DSA:1.10.1620.GENE	70,972	83,209	52,556	43,620	45,440									
Solyc12g010360	Plasma membrane ATPase (AHRD V3.3 *** M1ADF7_SOLTU)		F:GO:0000166: F:G(	F:nucleotide binding	EC:3.6.1.3: EC:3.6.3	Adenosinetriphospha	IPR001757 (PRINTS): PR00119 (PRIN	0,040	0,000	0,025	0,025	0,000									
Solyc12g010370	Ultrapetala (AHRD V3.3 *** A0A0D4D604_CROSA)		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; C:cytosol			IPR020533 (PANTHER): IPR020533 (I	0,000	0,000	0,000	0,000	0,024									
Solyc12g010380	adenylate kinase family protein (AHRD V3.3 *** AT5G35170.1)		F:GO:0004017: F:G(	F:adenylate kinase	EC:2.7.4.4: EC:2.7.4	Nucleoside-phosphat	IPR018962 (PFAM): PF00406 (PFAM)	37,833	58,869	32,060	35,968	46,336	0,663	0,019	0,529	0,001			up	up	
Solyc12g010390	Transmembrane 9 superfamily member (AHRD V3.3 *** M1AD53_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): IPR004240 (PAN	234,622	353,220	160,299	157,456	150,041	0,617	0,047					up		
Solyc12g010400	Zinc finger, SWIM-type (AHRD V3.3 *** A0A118JSI3_CYNCS)						PTHR35121:SF2 (PANTHER): PTHR3	151,693	156,379	133,432	117,948	135,660									
Solyc12g010410	Homeobox protein knotted-1, putative (AHRD V3.3 *** B9RNZ6_RICCO)		F:GO:0003677: C:G(	F:DNA binding: C:nucleus: P:regulation of transcription, DNA-ter			IPR005540 (PFAM HB-other	1,455	5,014	4,946	8,092	9,603			0,948	0,015				up	
Solyc12g010420	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT5G14895.1)						PTHR33168:SF13 (PANTHER): PTHR	6,326	6,502	4,339	10,007	6,508					1,203	0,001			up
Solyc12g010430	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT3G01430.1)						mobidb-lite (MOBIDB_LITE): PTHR331	13,186	16,376	13,781	17,121	15,399									
Solyc12g010440	Glycerol-3-phosphate transporter family protein (AHRD V3.3 *** B9IML0_POPTR)		C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport			IPR011701 (PFAM): G3DSA:1.20.125(	35,762	26,750	8,304	18,386	12,034					1,143	0,000			up
Solyc12g010450	Protein phosphatase 2c, putative (AHRD V3.3 *** B9T2N5_RICCO)		F:GO:0004722: P:G(	F:protein serine/thr	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): IPR036457 (G3D	0,886	0,808	1,680	1,768	1,464									
Solyc12g010470	PLATZ transcription factor family protein (AHRD V3.3 *** A0A061GPE1_THECC)						IPR006734 (PFAM): PTHR31065:SF1	0,019	0,000	0,000	0,000	0,000									
Solyc12g010480	ADIPOR-like receptor (AHRD V3.3 *** W9QY38_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR004254 (PFAM): IPR004254 (PAN	0,313	0,364	0,168	0,123	0,116									
Solyc12g010500	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G47180.1)		P:GO:0016567: F:G(	P:protein ubiquitination: F:ligase activity: F:ubiquitin protein ligas			IPR001841 (PFAM): IPR013083 (G3D	0,061	0,122	0,046	0,069	0,023									
Solyc12g010510	Oxysterol-binding protein (AHRD V3.3 *** A9ZM29_SOYBN)						G3DSA:2.40.160.120 (GENE3D): IPR(	0,019	0,036	0,000	0,025	0,000									
Solyc12g010520	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *** B6U1I9_MAIZE)		F:GO:0003747: C:G(	F:translation release factor activity: C:cytoplasm: P:translationa			IPR029064 (G3DSA:3.30.1330.GENE	50,789	75,024	59,232	58,898	56,644	0,590	0,020					up		
Solyc12g010530	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *** AT5G35200.2)		F:GO:0005545: C:G(	F:1-phosphatidylinositol binding: C:clathrin-coated vesicle: F:cla			IPR011417 (PFAM): IPR008942 (G3D	0,000	0,000	0,000	0,022	0,000									
Solyc12g010540	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	UGlcAE1-like	C:GO:0016021: F:G(	C:integral compone	EC:5.1.3.12	UDP-glucuronate 5'-e	PR01713 (PRINTS): G3DSA:3.90.25.1	193,056	99,667	55,020	115,609	100,143	-0,928	0,000	0,861	0,004	1,072	0,000	down	up	up
Solyc12g010570	Tetraspanin family protein (AHRD V3.3 *** A0A072V357_MEDTR)		C:GO:0016021	C:integral component of membrane			IPR000301 (PRINTS): IPR018499 (PF	0,075	0,289	0,000	0,025	0,000									
Solyc12g010590	O-acyltransferase WSD1 (AHRD V3.3 *** A0A151TQI5_CAJCA)		F:GO:0004144: P:G(	F:diacylglycerol O-a	EC:2.3.1.2	Diacylglycerol O-acy	IPR009721 (PFAM): IPR004255 (PFA	3,760	4,199	0,000	0,000	0,000									
Solyc12g010600	RNA polymerase 2 second largest subunit 2	RPB2-2	F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR007644 (PFAM): IPR037034 (G3D	0,590	0,477	0,000	0,167	0,070									
Solyc12g010610	Copine (Calcium-dependent phospholipid-binding protein) family (AHRD V3.3 --* AT1G67800.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc12g010640	Aldolase-type TIM barrel family protein (AHRD V3.3 --* AT3G14130.4)						PTHR36811 (PANTHER)	9,581	8,296	11,402	11,777	10,611									
Solyc12g010650	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G07900.1)		F:GO:0003690: P:G(	F:double-stranded DNA binding: P:regulation of transcription, DN			IPR019333 (PFAM): IPR038538 (G3D	4,349	5,337	4,773	5,137	4,666									
Solyc12g010660	Disease resistance protein RGH4 (AHRD V3.3 *-* H6TDA8_9SOLN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:3.40.50.3	0,162	0,289	0,165	0,097	0,190									
Solyc12g010670	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G74990.1)		F:GO:0046872	F:metal ion binding			IPR018957 (PFAM): IPR013083 (G3D	0,463	0,615	0,710	0,658	0,989									
Solyc12g010680	Acyl-CoA N-acyltransferase (AHRD V3.3 *** A0A103Y831_CYNCS)		F:GO:0016740	F:transferase activity			IPR000182 (PFAM): G3DSA:3.40.630	4,579	4,911	6,787	6,324	6,248									
Solyc12g010690	Polyol monosaccharide transporter 3	PMT3	C:GO:0016021: F:G(	C:integral component of membrane: F:transmembrane transport			IPR003663 (PRINTS): IPR003663 (TI(	24,521	23,141	17,637	22,400	20,199									
Solyc12g010700	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061E4V2_THECC)		P:GO:0015031	P:protein transport			G3DSA:1.20.1260.60 (GENE3D): IPR(	0,037	0,018	0,000	0,000	0,000									
Solyc12g010710	LOW QUALITY:30S ribosomal protein S19, chloroplastic (AHRD V3.3 --* RR19_PINKO)						mobidb-lite (MOBIDB_LITE)	0,975	3,231	0,221	0,367	0,232									
Solyc12g010730	Plant/F9H3-4 protein (AHRD V3.3 *** A0A072VLR0_MEDTR)						IPR008507 (PFAM): mobidb-lite (MOB	43,347	53,311	69,606	60,322	63,078									
Solyc12g010740	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* C0LGQ2_ARATH)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	31,552	22,594	37,838	46,349	42,590									
Solyc12g010745	LRR receptor-like kinase (AHRD V3.3 *** A7UE73_SOLTU)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	160,370	127,464	196,101	222,696	229,189									
Solyc12g010750	Secretory carrier membrane protein (AHRD V3.3 *** B3TLU6_ELAGV)		P:GO:0015031: C:G(	P:protein transport; C:integral component of membrane			IPR007273 (PFAM): mobidb-lite (MOB	3,329	4,504	3,063	1,396	2,515					-1,110	0,004			down
Solyc12g010790	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)		F:GO:0003924: F:G(	F:GTPase activity:	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR001806 (PFA	75,831	60,252	37,586	46,357	41,535									
Solyc12g010800	BZIP family transcription factor (AHRD V3.3 *** G7ZUL8_MEDTR)		F:GO:0003700: P:G(	F:DNA-binding transcription factor activity: P:regulation of trans(			IPR004827 (PFAM bZIP	1,197	1,384	3,406	5,642	4,434									
Solyc12g010820	Late embryogenesis abundant protein-like (AHRD V3.3 *-* Q9LF88_ARATH)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,493	6,321	2,024	4,362	1,252									
Solyc12g010830	Pentatricopeptide (PPR) repeat protein (AHRD V3.3 --* A0A072VHT8_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	19,507	18,707	30,182	33,956	32,247									
Solyc12g010840	Ketol-acid reductoisomerase (AHRD V3.3 *** M1ADA6_SOLTU)		F:GO:0004455: P:G(	F:ketol-acid reductc	EC:1.1.1.86	Ketol-acid reductoisc	G3DSA:3.40.50.720 (GENE3D): IPR0(	149,311	149,489	84,414	75,886	97,296									
Solyc12g010860	tft8	tft8	F:GO:0019904	F:protein domain specific binding			IPR000308 (PRINTS): IPR036815 (G3	71,235	72,232	124,250	111,749	109,571									
Solyc12g010870	ATP synthase I-like protein		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR341	18,859	26,994	32,247	28,359	41,797									
Solyc12g010890	sequence-specific DNA binding transcription factor (AHRD V3.3 *** AT3G58630.2)		C:GO:0005634: F:G(	C:nucleus: F:sequence-specific DNA binding: F:transcription reg			PF13837 (PFAM): Trihelix	21,456	15,995	17,209	19,505	17,146									
Solyc12g010900	F-box protein (AHRD V3.3 *** T1RVG4_STRHE)		F:GO:0004842: C:G(	F:ubiquitin-protein transferase activity: C:nucleus: P:multicellula			IPR041567 (PFAM): IPR032675 (G3D	22,054	12,680	10,562	18,139	14,987	-0,771	0,020	0,503	0,019	0,782	0,000	down	up	up
Solyc12g010910	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G42690.1)		P:GO:0006629: F:G(	P:lipid metabolic pro	EC:3.1.1.32: EC:3.1.	Phospholipase A(1):	IPR002921 (PFAM): G3DSA:3.40.50.1	4,866	10,607	0,330	0,665	1,525									
Solyc12g010920	Oleosin (AHRD V3.3 *** K4DCH8_SOLLC)		C:GO:0012511: C:G(	C:monolayer-surrounded lipid storage body: C:integral compone			IPR000136 (PFAM): mobidb-lite (MOB	65,452	70,813	5,112	14,055	0,949									
Solyc12g010930	Ribosomal L5P family protein (AHRD V3.3 *** AT5G45775.2)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR031309 (PFAM): IPR031310 (PFA	120,758	123,950	82,166	71,435	75,827									
Solyc12g010940	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072V475_MEDTR)						IPR012881 (PFAM): PTHR33785:SF2	1,751	0,476	0,681	1,322	0,803	-1,828	0,001					down		
Solyc12g010950	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TLD5_MEDTR)		P:GO:0055114	P:oxidation-reduction process			IPR013149 (PFAM): G3DSA:3.40.50.7	42,868	77,905	47,824	58,900	48,898	0,889	0,002					up		
Solyc12g010960	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)		P:GO:0055114	P:oxidation-reduction process			IPR041694 (PFAM): G3DSA:3.40.50.7	2,580	3,374	0,253	0,191	0,234									
Solyc12g010980	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3	0,198	0,877	0,000	0,000	0,000									
Solyc12g010990	Nucleotide/sugar transporter family protein (AHRD V3.3 *-* AT1G06470.4)		P:GO:0055085	P:transmembrane transport			IPR013657 (PFAM): PTHR44827 (PAN	0,021	0,019	0,022	0,000	0,000									
Solyc12g010995	Nucleotide/sugar transporter family protein (AHRD V3.3 *-* AT1G06470.4)		C:GO:0005793: C:G(	C:endoplasmic reticulum-Golgi intermediate compartment: C:cis			IPR004853 (PFAM): PTHR44827 (PAN	0,021	0,000	0,000	0,000	0,000									
Solyc12g011000	Citrate synthase (AHRD V3.3 *** K4DCI6_SOLLC)		F:GO:0046912	F:transferase activity, transferring acyl groups, acyl groups con			IPR002020 (PRINTS): IPR016143 (G3	90,867	101,682	198,929	211,085	198,949									
Solyc12g011010	protodermal factor 1 (AHRD V3.3 *-* AT2G42840.1)		C:GO:0016021	C:integral component of membrane			PR01217 (PRINTS): mobidb-lite (MOB	5,826	9,033	0,050	0,178	0,000									
Solyc12g011020	Haloacid dehalogenase superfamily protein (AHRD V3.3 *** I7AYD7_PHAVU)		P:GO:0016311: F:G(	P:dephosphorylation; F:phosphatase activity			IPR006549 (TIGRFAM): IPR010021 (T	2,383	3,416	3,658	3,244	3,539									

Solyc12g011040	Lipoxygenase (AHRD V3.3 *** A0A0V0ISB6_SOLCH)	LOX10	F:GO:0016702; F:G(	F:oxidoreductase a	EC:1.13.11	Acting on single donc	IPR001246 (PRINTS): IPR013819 (PF	2,373	4,914	0,000	0,000	0,046									
Solyc12g011050	RNA binding protein, putative (AHRD V3.3 *** B9SEZ1_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	59,717	47,936	68,161	66,296	66,238									
Solyc12g011070	Vacuolar cation/proton exchanger, putative (AHRD V3.3 *** B9SEZ0_RICCO)		P:GO:0006816; F:G(	P:calcium ion transport; F:calcium:proton antiporter activity; C:i			G3DSA:1.20.1420.30 (GENE3D): G3D	0,040	0,140	0,050	0,000	0,046									
Solyc12g011080	vacuolar cation/proton exchanger (AHRD V3.3 --* AT1G55720.2)		P:GO:0006811; C:G(	P:ion transport; C:membrane			PTHR31503:SF34 (PANTHER); PTHR	0,021	0,039	0,000	0,047	0,023									
Solyc12g011090	cellulose synthase, putative (DUF1644) (AHRD V3.3 --* AT3G24740.6)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,099	0,284	0,050	0,048	0,024									
Solyc12g011100	glycerol-3-phosphate acyltransferase 3 (AHRD V3.3 --* AT4G01950.2)						mobidb-lite (MOBIDB_LITE)	0,040	0,078	0,000	0,000	0,000									
Solyc12g011130	Ras-related protein (AHRD V3.3 *** W9R1W6_9ROSA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): IPR005225 (TIGF	14,133	13,633	22,968	22,715	22,152									
Solyc12g011140	Subtilisin-like protease family protein (AHRD V3.3 *** B9IAW9_POPTR)		F:GO:0004252; P:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR015500 (PRINTS): IPR036852 (G3	1,499	1,023	0,122	0,025	0,071									
Solyc12g011160	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072V5U1_MEDTR)		F:GO:0003860	F:3-hydroxyisobutyi	EC:3.1.2.4	3-hydroxyisobutyryl-(	G3DSA:3.90.226.40 (GENE3D): IPR0	57,674	52,455	133,218	139,870	133,938									
Solyc12g011170	Phospholipase D (AHRD V3.3 *** M1AD93_SOLTU)		F:GO:0004630; F:G(	F:phospholipase D	EC:3.1.4.4	Phospholipase D	G3DSA:3.30.870.10 (GENE3D): IPR0	0,203	0,514	0,616	0,751	0,660									
Solyc12g011180	Transcription factor-related family protein (AHRD V3.3 *** B9IJ55_POPTR)		C:GO:0000127; P:G(	C:transcription factor TFIIIC complex; P:transcription initiation fr			IPR019136 (PFAM): IPR041499 (PFA	19,979	17,787	28,978	29,430	30,485									
Solyc12g011190	Plant regulator RWP-RK family protein (AHRD V3.3 *-* AT2G43500.9)						IPR003035 (PFAM Nin-like	9,131	9,303	9,093	10,532	9,803									
Solyc12g011200	WRKY transcription factor 28	WRKY28	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM WRKY	0,019	0,000	0,025	0,047	0,000									
Solyc12g011213	Subtilase family protein (AHRD V3.3 --* AT5G59130.4)							0,375	0,450	0,309	0,676	0,612									
Solyc12g011230	LOW QUALITY:FBD%2C F-box and Leucine Rich Repeat domains containing protein (AHRD V3.3 --* AT5G56560.2)							0,139	0,196	0,351	0,148	0,261									
Solyc12g011270	ethylene-responsive elongation factor EF-Ts precursor	er49	F:GO:0003746; F:G(	F:translation elongation factor activity; F:protein binding; P:trans			G3DSA:1.10.8.10 (GENE3D): IPR036	24,687	27,694	35,743	33,985	32,296									
Solyc12g011280	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4DCL4_SOLLC)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	14,114	91,234	3,026	8,252	13,964	2,719	0,000	2,198	0,000	1,446	0,000	up	up	up
Solyc12g011290	Kinesin-like protein (AHRD V3.3 *** M1AD89_SOLTU)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR036961 (G3	3,476	3,416	2,630	2,233	3,098									
Solyc12g011310	Glutathione S-transferase (AHRD V3.3 *** Q0PN10_9FABA)	GSTU53	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): G3D	8,176	4,684	244,686	226,765	260,198									
Solyc12g011320	Glutathione S-transferase (AHRD V3.3 *** D3Y4H6_BRUGY)	GSTU54	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:1.20.105	13,449	9,449	10,030	8,653	9,723									
Solyc12g011330	ethylene receptor 1	ETR1	F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS): IPR029016 (G3	32,066	28,817	41,448	42,422	35,660									
Solyc12g011340	RNA-binding protein, putative (AHRD V3.3 *** B9SVC9_RICCO)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	49,258	49,727	98,533	106,121	90,974									
Solyc12g011350	NB-ARC domain-containing disease resistance protein (AHRD V3.3 --* AT1G10920.4)							0,230	1,368	0,000	0,025	0,072									
Solyc12g011360	Interactor of constitutive active ROPs protein, putative (AHRD V3.3 *** A0A072V8T5_MEDTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,101	0,101	0,025	0,000	0,046									
Solyc12g011370	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RY28_RICCO)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR002293 (PFAM): G3DSA:1.20.174	5,747	7,685	3,768	4,336	3,566									
Solyc12g011390	LOW QUALITY:SNOWY COTYLEDON protein (DUF566) (AHRD V3.3 --* AT3G19570.4)		C:GO:0016021	C:integral component of membrane				0,000	0,043	0,000	0,000	0,000									
Solyc12g011400	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XLX2_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,571	3,408	3,804	3,376	3,514									
Solyc12g011410	LOW QUALITY:tRNA-splicing ligase (DUF239) (AHRD V3.3 --* AT5G56530.2)							2,386	2,069	0,065	0,025	0,165									
Solyc12g011420	Calcium-dependent lipid-binding domain protein (AHRD V3.3 *** A0A072VA30_MEDTR)		F:GO:0008289	F:lipid binding			IPR035892 (G3DSA:2.60.40.GENE3D	93,362	49,779	142,585	129,926	126,193	-0,881	0,000					down		
Solyc12g011430	Hydroxyacylglutathione hydrolase 3 (AHRD V3.3 *** F4HRK0_ARATH)		F:GO:0051213; P:G(	F:dioxygenase activity; P:oxidation-reduction process			IPR036866 (G3DSA:3.60.15.GENE3D	7,474	7,054	15,133	12,446	12,286									
Solyc12g011440	60S ribosomal protein L18a-like protein (AHRD V3.3 *** A0A199VD98_ANACO)		C:GO:0005840; C:G(	C:ribosome; C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	24,299	21,907	11,546	15,238	16,002									
Solyc12g011450	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1AG46_SOLTU)		P:GO:0009765; C:G(	P:photosynthesis, light harvesting; C:membrane			IPR023329 (G3DSA:1.10.3460.GENE	144,708	340,885	26,871	44,163	90,650	1,264	0,023	1,749	0,000	0,719	0,004	up	up	up
Solyc12g013470	Phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *-* B9RHQ1_RICCO)		F:GO:0016307; P:G(	F:phosphatidylinositol phosphate kinase activity; P:phosphatidy			IPR027483 (G3DSA:3.30.810.GENE3	0,000	0,043	0,025	0,000	0,023									
Solyc12g013490	LOW QUALITY:S5-locus F-box type-14 protein (AHRD V3.3 --* A0A076YHU5_PETIN)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,025	0,000									
Solyc12g013500	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT2G15630.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	26,872	18,811	44,470	41,647	41,358									
Solyc12g013510	Histone H2B (AHRD V3.3 *** K4DCN6_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti			IPR000558 (PRINTS): IPR009072 (G3	8,719	8,975	5,008	5,420	5,660									
Solyc12g013520	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_NYMAL)							1,071	1,429	0,477	0,529	0,587									
Solyc12g013525	Alkyl transferase (AHRD V3.3 --* A0A067FVT3_CITSI)							1,007	1,469	0,290	0,453	0,681									
Solyc12g013530	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 --* A0A0K1ZY18_9ASTR)						mobidb-lite (MOBIDB_LITE): mobidb-lit	34,059	24,997	34,776	30,356	32,441									
Solyc12g013540	GDSL-like lipase/acylhydrolase superfamily protein (AHRD V3.3 --* AT1G58520.7)						mobidb-lite (MOBIDB_LITE): mobidb-lit	28,189	32,409	29,463	26,561	29,300									
Solyc12g013550	1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase (AHRD V3.3 *** A0A0B0PDZ2_GOSAR)						mobidb-lite (MOBIDB_LITE): PTHR352	97,383	89,989	169,578	144,002	157,138									
Solyc12g013560	3(2),5-bisphosphate nucleotidase HAL2 (AHRD V3.3 *** A0A118JXE0_CYNCS)		P:GO:0006790; F:G(	P:sulfur compound r	EC:3.1.3.7; EC:3.1.3	3'(2'),5'-bisphosphate	IPR000760 (PFAM): G3DSA:3.30.540	3,051	2,817	6,228	6,298	5,489									
Solyc12g013570	Plant cadmium resistance 2, putative (AHRD V3.3 *** A0A061E1P7_THECC)		C:GO:0016021	C:integral component of membrane			IPR006461 (PFAM): IPR006461 (TIGF	0,059	0,142	0,050	0,050	0,024									
Solyc12g013580	Peptidyl-prolyl cis-trans isomerase, putative (AHRD V3.3 *** B9SW20_RICCO)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PFAM): IPR024936 (PAN	15,412	15,584	23,031	35,332	32,767			0,507	0,002	0,622	0,000		up	up
Solyc12g013590	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061F		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): G3DS	2,634	2,192	1,266	1,784	2,127									
Solyc12g013600	TPR and ankyrin repeat-containing protein 1 (AHRD V3.3 *** A0A0B2R102_GLYSO)		F:GO:0005515; F:G(	F:protein binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	5,562	5,292	3,675	4,355	4,342									
Solyc12g013610	LOW QUALITY:calmodulin-binding protein (DUF1645) (AHRD V3.3 *** AT2G15760.1)		C:GO:0005886	C:plasma membrane			IPR012442 (PFAM): PTHR33095 (PAN	6,188	2,286	0,025	0,073	0,116	-1,398	0,002					down		
Solyc12g013620	jasmonic acid 2	NAC098/JA2	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR003441 (PFAM NAC	9,549	17,867	63,533	66,614	48,358	0,928	0,010					up		
Solyc12g013630	ABC transporter G family member (AHRD V3.3 *** A0A0K9Q0M2_ZOSMR)	ABCG29	F:GO:0005524; C:G(	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR013525 (PFAM): G3DSA:3.40.50.3	0,000	0,062	0,000	0,000	0,000									
Solyc12g013640	ABC transporter G family member (AHRD V3.3 *** A0A0K9Q0M2_ZOSMR)	ABCG30	F:GO:0005524; C:G(	F:ATP binding; C:me	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): IPR013525 (PFA	0,058	0,018	0,025	0,356	0,046									
Solyc12g013650	Fiber protein Fb34 (AHRD V3.3 *** A0A0A0L071_CUCSA)		C:GO:0016021	C:integral component of membrane			IPR009606 (PFAM): PTHR31769 (PAN	2,253	2,042	2,153	2,447	2,636									
Solyc12g013660	ethylene-responsive transcription factor (AHRD V3.3 *-* AT5G07580.1)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	0,000	0,000	0,047	0,000	0,000									
Solyc12g013665	Mannan endo-1,4-beta-mannosidase 1 (AHRD V3.3 *** MAN1_SOLLC)		C:GO:0005576; F:G(	C:extracellular regic	EC:3.2.1.25; EC:3.2.	Beta-mannosidase; M	G3DSA:3.20.20.80 (GENE3D): PTHR3	0,000	0,019	0,022	0,022	0,071									
Solyc12g013690	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT5G05320.1)		F:GO:0071949	F:FAD binding			PR00420 (PRINTS): IPR036188 (G3D	24,553	40,973	1643,215	1775,332	1215,306									
Solyc12g013700	Stem-specific protein tsjt1, putative (AHRD V3.3 *** D6BRF0_JATCU)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; C:plasma membrane; C:plasmodesma			IPR024286 (PFAM): IPR029055 (G3D	0,545	0,820	27,453	49,982	24,378					0,867	0,012			up
Solyc12g013710	light dependent NADH:protochlorophyllide oxidoreductase 1	POR1	F:GO:0016630; P:G(	F:protochlorophyllid	EC:1.3.1.33	Protochlorophyllide re	IPR002347 (PRINTS): G3DSA:3.40.50	14,882	112,504	3,073	9,305	14,412	2,945	0,000	2,226	0,000	1,601	0,000	up	up	up
Solyc12g013720	LOW QUALITY:3-hydroxybenzoate 6-hydroxylase 1 (AHRD V3.3 *-* A0A0B2PUT8_GLYSO)		C:GO:0016021; F:G(	C:integral component of membrane; F:FAD binding			PTHR13789:SF185 (PANTHER): PTHR	0,021	0,082	0,349	0,246	0,096									
Solyc12g013730	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT3G24240.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR001611 (PFA	0,042	0,252	0,000	0,000	0,072									
Solyc12g013750	Mannan endo-1,4-beta-mannosidase 1 (AHRD V3.3 *-* MAN1_SOLLC)		C:GO:0005576; F:G(	C:extracellular regic	EC:3.2.1.25; EC:3.2.	Beta-mannosidase; M	G3DSA:3.20.20.80 (GENE3D): PTHR3	13,095	15,215	12,646	12,876	12,603									
Solyc12g013770	Mannan endo-1,4-beta-mannosidase 1 (AHRD V3.3 *** MAN1_SOLLC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001547 (PFAM): G3DSA:3.20.20.8	0,121	0,121	0,242	0,596	0,425									
Solyc12g013790	Nucleic acid binding protein, putative (AHRD V3.3 *-* B9SNN8_RICCO)						mobidb-lite (MOBIDB_LITE): mobidb-lit	12,056	12,382	18,465	16,438	17,810									
Solyc12g013800	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G42030.1)		F:GO:0046872	F:metal ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	18,550	18,111	17,201	15,798	18,144									
Solyc12g013810	Thioredoxin (AHRD V3.3 *** A0A103YK44_CYNCS)		P:GO:0006662; F:G(	P:glycerol ether metabolic process; F:protein disulfide oxidored			PR00421 (PRINTS): IPR005746 (TIGF	25,272	33,023	31,115	27,408	36,329									
Solyc12g013820	Ubiquitin conjugating enzyme, putative (AHRD V3.3 *** B9T0E4_RICCO)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ubiquitin conjugating enzyme activity			IPR000608 (PFAM): IPR016135 (G3D	18,476	28,694	18,670	32,756	18,073					0,816	0,002			up
Solyc12g013830	Metallothionein (AHRD V3.3 -** B8YM44_SOLNI)							0,000	0,018	0,709	1,240	1,196									
Solyc12g013840	SPA1-related 3 (AHRD V3.3 *** AT3G15354.3)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			IPR020472 (PRINTS): IPR001680 (PF	28,251	18,230	39,843	37,763	46,224									
Solyc12g013850	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** F4JIW2_ARATH		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:membrane			IPR003406 (PFAM): PTHR19297:SF7	0,000	0,000	0,025	0,000	0,000									
Solyc12g013860	Proton pump interactor 1 (AHRD V3.3 *** D5L6G0_SOLTU)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:plasma membrane; P:regulation of p			G3DSA:1.20.5.340 (GENE3D): mobidb	0,021	0,018	0,000	0,000	0,000									
Solyc12g013865	Proton pump interactor 1 (AHRD V3.3 *-* D5L6G0_SOLTU)		C:GO:0005783; C:G(	C:endoplasmic reticulum; C:plasma membrane; P:regulation of p			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc12g013870	RNA-binding S4 domain-containing protein (AHRD V3.3 *** AT1G53120.1)		F:GO:0003723	F:RNA binding			IPR012677 (G3DSA:3.30.70.GENE3D	17,410	16,311	24,049	24,883	25,341									
Solyc12g013880	origin recognition complex subunit 3 (AHRD V3.3 *** AT5G16690.1)		F:GO:0003677; C:G(	F:DNA binding; C:nuclear origin of replication recognition comple			IPR020795 (PFAM): IPR040855 (PFA	9,736	8,663	3,564	3,796	3,200									
Solyc12g013890	embryo defective 2737 (AHRD V3.3 *** AT5G53860.2)		C:GO:0009941; P:G(	C:chloroplast envelope; P:thylakoid membrane organization; P:r			PTHR36404 (PANTHER)	29,434	30,955	19,111	19,661	23,039									
Solyc12g013900	CT099 (AHRD V3.3 *** Q30GX0_SOLPI)		F:GO:0009055	F:electron transfer activity			PR01217 (PRINTS): IPR003245 (PFA	16,240	39,751	21,797	25,039	30,355	1,317	0,000	0,476	0,047			up	up	
Solyc12g013910	PRA1 family protein (AHRD V3.3 *** K4DCS6_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004895 (PFAM): IPR004895 (PAN	9,764	8,571	12,680	12,944	12,490									
Solyc12g013920	Protein yippee-like (AHRD V3.3 *** K4DCS7_SOLLC)		C:GO:0000151; F:G(	C:ubiquitin ligase complex; F:metal ion binding			IPR004910 (PFAM): IPR039058 (PAN	33,624	29,205	39,305	33,507	33,122									
Solyc12g013930	LOW QUALITY:cytochrome P450, family 82, subfamily C, polypeptide 4 (AHRD V3.3 --* AT4G31940.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc12g013950	Sec1 family domain-containing protein 2 (AHRD V3.3 *** W9RNR0_9ROSA)		P:GO:0006904	P:vesicle docking involved in exocytosis			IPR027482 (G3DSA:3.40.50.GENE3D	34,640	28,232	37,226	35,098	35,050									
Solyc12g013960	arginine N-methyltransferase, putative (DUF688) (AHRD V3.3 *** AT2G30990.5)						IPR007789 (PFAM): mobidb-lite (MOB	0,949	5,461	4,272	4,687	5,291	2,533	0,000					up		
Solyc12g013970	Protein kinase, putative (AHRD V3.3 *-* B9SRD1_RICCO),Pfam:PF14381		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PF14381 (PFAM): mobidb-lite (MOBID	4,188	3,637	1,423	2,007	1,556									
Solyc12g013990	Protein kinase, putative (AHRD V3.3 *-* B9SRD1_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): G3DSA:3.30.19	21,146	22,100	22,527	23,618	22,445									
Solyc12g014000	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118K6D3_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR011990 ((	2,850	2,020	2,710	3,304	3,201									
Solyc12g014010	Glycosyltransferase (AHRD V3.3 *** M1B8J3_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	0,192	0,381	0,289	0,472	0,655									
Solyc12g014020	Nucleic acid-binding, OB-fold-like protein (AHRD V3.3 *** G7J0F9_MEDTR)						G3DSA:2.40.50.140 (GENE3D): PTHR	5,412	3,473	2,732	2,623	2,535									
Solyc12g014030	LOW QUALITY:Glutamate receptor 3.6 (AHRD V3.3 --* W9RW17_9ROSA)							2,782	2,296	0,482	0,454	0,512									
Solyc12g014040	LOW QUALITY:Serine/Threonine-kinase pakA-like protein (AHRD V3.3 *-* AT3G15095.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	4,290	3,124	1,016	0,472	1,059									
Solyc12g014050	Zinc binding dehydrogenase, putative (AHRD V3.3 *** B9RX93_RICCO)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.90.180.10 (GENE3D): PF13	30,108	25,076	63,459	63,358	70,471									
Solyc12g014060	RNA exonuclease, putative (AHRD V3.3 *** B9RXA0_RICCO)		F:GO:0003676; P:G(	F:nucleic acid binding; P:rRNA processing; F:3'-5' exonuclease			IPR036397 (G3DSA:3.30.420.GENE3	19,578	21,034	18,023	16,422	16,698									
Solyc12g014070	RING/U-box superfamily protein (AHRD V3.3 *** AT1G53190.2)		F:GO:0016874; F:G(	F:ligase activity; F:metal ion binding			IPR001841 (PFAM): IPR013083 (G3D	31,835	25,306	45,729	44,712	42,955									
Solyc12g014080	Rab family GTPase (AHRD V3.3 *** D8RE14_SELML)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	PR00449 (PRINTS): G3DSA:3.40.50.3	24,600	24,274	24,037	24,898	21,359									
Solyc12g014090	TAF RNA polymerase I subunit A (AHRD V3.3 *** AT1G53200.1),Pfam:PF14929		F:GO:0005515	F:protein binding			IPR039495 (PFAM): IPR011990 (G3D	9,961	8,182	10,150	9,646	9,024									
Solyc12g014100	homogentisate 1,2-dioxygenase	hgo	F:GO:0004411; P:G(	F:homogentisate 1,	EC:1.13.11; EC:1.13	Acting on single donc	IPR014710 (G3DSA:2.60.120.GENE3	45,796	30,855	71,303	73,152	67,463	-0,543	0,041					down		
Solyc12g014110	sodium/calcium exchanger family protein / calcium-binding EF hand family protein (AHRD V3.3 *** AT1G5321		F:GO:0005509; C:G(	F:calcium ion binding; C:integral component of membrane; P:tra			G3DSA:1.20.58.1130 (GENE3D): IPR	19,147	15,743	20,643	19,749	18,020									
Solyc12g014120	Actin cytoskeleton-regulatory complex protein pan1, putative isoform 2 (AHRD V3.3 *** A0A061F841_THEC(		F:GO:0003700	F:DNA-binding transcription factor activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	22,139	24,438	10,868	9,068	11,326									
Solyc12g014130	SUN-like protein 33	SUN33	F:GO:0005515	F:protein binding			IPR000048 (PFAM): PTHR32295 (PAN	1,748	1,604	0,050	0,022	0,047									
Solyc12g014140	SlTCP3	TCP3	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR017887 (PFAM TCP	1,273	0,838	0,842	0,456	0,683									
Solyc12g014150	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G73170.3)		F:GO:0005524	F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0	4,193	4,912	4,120	4,397	5,330									
Solyc12g014160	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT1G73170.4)		F:GO:0005524	F:ATP binding			mobidb-lite (MOBIDB_LITE): IPR0340	2,232	2,547	1,182	1,676	2,369			0,998	0,040				up	
Solyc12g014170	Transcription factor GTE4 (AHRD V3.3 *** W9QS80_9ROSA)		F:GO:0005515	F:protein binding			IPR001487 (PRINTS): IPR001487 (PF	41,018	40,312	44,571	45,562	47,697									
Solyc12g014180	Malate dehydrogenase (AHRD V3.3 *** K4DCV3_SOLLC)		P:GO:0005975; P:G(	P:carbohydrate met	EC:1.1.1.37	Malate dehydrogenas	IPR001236 (PFAM): G3DSA:3.40.50.7	24,975	23,814	13,538	10,718	13,187									
Solyc12g014190	tRNA isopentenyltransferase (AHRD V3.3 *** A0A103Y4A0_CYNCS)		P:GO:0008033	P:tRNA processing			IPR018022 (TIGRFAM): IPR018022 (F	12,967	14,176	12,238	10,143	12,741									
Solyc12g014200	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT1G73140.1)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; P:xylan			IPR026057 (PFAM): IPR025846 (PFA	0,400	0,261	0,000	0,000	0,000									
Solyc12g014210	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT3G15010.2)		F:GO:0003676	F:nucleic acid binding			IPR012677 (G3DSA:3.30.70.GENE3D	71,586	76,663	109,038	98,804	100,932									
Solyc12g014220	muscle M-line assembly protein (AHRD V3.3 *-* AT1G53800.3)		F:GO:0003677	F:DNA binding			IPR003611 (PFAM): mobidb-lite (MOB	10,077	13,084	8,133	8,840	9,921									
Solyc12g014230	DAG protein (AHRD V3.3 *** A0A0K9PW98_ZOSMR)		P:GO:0016554	P:cytidine to uridine editing			mobidb-lite (MOBIDB_LITE): mobidb-lit	6,383	6,238	8,026	7,435	6,358									
Solyc12g014250	Phosphoenolpyruvate carboxylase (AHRD V3.3 *** CAPP_SOLTU)		P:GO:0006099; F:G(	P:tricarboxylic acid	EC:4.1.1.31; EC:4.1.	Phosphoenolpyruvate	IPR021135 (PRINTS): IPR021135 (PF	269,820	251,338	145,742	136,809	169,074									
Solyc12g014260	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)		C:GO:0005634; P:G(	C:nucleus; P:mRNA transcription; P:response to light stimulus			IPR006936 (PFAM): mobidb-lite (MOB	10,453	7,456	4,000	3,062	3,116									
Solyc12g014270	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (AHRD V3.3 *** PNAA_PRUDU)		F:GO:0000224; C:G(	F:peptide-N4-(N-ace	EC:3.5.1.52	Peptide-N(4)-(N-acet	IPR021102 (PFAM): IPR021102 (PAN	4,261	6,304	1,192	1,534	1,173									
Solyc12g014280	CRS1/YhbY (CRM) domain protein (AHRD V3.3 *** A0A072UMR2_MEDTR)		F:GO:0003723	F:RNA binding			IPR035920 (G3DSA:3.30.110.GENE3	12,902	13,419	11,009	12,429	12,897									
Solyc12g014290	multiprotein bridging factor 1c		F:GO:0043565	F:sequence-specific DNA binding			IPR013729 (PFAM): G3DSA:1.10.260	92,463	91,344	110,247	96,926	100,034									
Solyc12g014300	transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)		P:GO:0006351; F:G(	P:transcription, DNA-templated; F:sequence-specific DNA bindir			IPR025422 (PFAM): PTHR22952:SF1	0,058	0,039	0,000	0,000	0,000									
Solyc12g014310	pathogenesis-related family protein (AHRD V3.3 *** AT1G78780.5)						G3DSA:3.10.450.50 (GENE3D): PTHR	1,367	4,562	0,349	0,502	1,361	1,754	0,000					up		
Solyc12g014320	Anaphase-promoting complex subunit 6-like protein (AHRD V3.3 *** A0A0B0MY79_GOSAR)		F:GO:0005515	F:protein binding			PF13432 (PFAM): PF13424 (PFAM): I	8,733	7,278	3,782	3,185	3,895									
Solyc12g014330	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9STL7_RICCO)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM): IPR002885 (F	3,113	2,885	2,999	2,230	2,424									
Solyc12g014350	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:2.60.120.430 (GENE3D): IPR(	43,788	31,872	35,790	35,306	37,458									
Solyc12g014355	Leucine-rich repeat transmembrane protein kinase (AHRD V3.3 *-* AT1G53430.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	18,338	11,480	13,381	14,880	15,627									
Solyc12g014360	protein trichome birefringence-like 41		C:GO:0005794; F:G(	C:Golgi apparatus; F:O-acetyltransferase activity			IPR026057 (PFAM): IPR025846 (PFA	1,331	1,477	0,172	0,067	0,024									
Solyc12g014380	glucose-6-phosphate isomerase DQ451687		F:GO:0004347; P:G(	F:glucose-6-phosph	EC:5.3.1.9	Glucose-6-phosphate	IPR001672 (PRINTS): IPR001672 (PF	74,183	68,079	117,811	106,154	110,080									
Solyc12g014390	Non-LTR retroelement reverse transcriptase-like protein, related (AHRD V3.3 --* Q2HRL4_MEDTR)							0,358	0,316	0,245	0,407	0,328									
Solyc12g014393	phosphoenolpyruvate carboxylase 4 (AHRD V3.3 --* AT1G68750.1)							0,284	0,354	0,140	0,214	0,187									
Solyc12g014395	Ribosomal protein L13 family protein (AHRD V3.3 *** AT1G78630.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR036899 (G3DSA:3.90.1180.GENE	1,487	2,533	1,460	1,939	2,782			0,916	0,028				up	
Solyc12g014397	Cell differentiation protein RCD1 like (AHRD V3.3 *** A0A0B2NW74_GLYSO)						PF04078 (PFAM): IPR011989 (G3DS/	0,241	0,269	0,437	0,563	0,306									
Solyc12g014400	Cell differentiation protein RCD1 like (AHRD V3.3 *** A0A0B2NW74_GLYSO)		C:GO:0000932; P:G(	C:P-body; P:negative regulation of translation; C:CCR4-NOT co			PF04078 (PFAM): IPR011989 (G3DS/	7,328	6,052	8,109	8,230	8,382									
Solyc12g014410	Ribonuclease 3-like protein 2 (AHRD V3.3 *** A0A061F5X1_THECC)		F:GO:0004525; P:G(	F:ribonuclease III a	EC:3.1.3; EC:3.1.26;	Acting on ester bonds	G3DSA:3.30.160.20 (GENE3D): PF14	33,784	27,241	16,834	13,583	16,183									
Solyc12g014413	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G52210.3)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc12g014420	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SU04_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			G3DSA:3.20.20.80 (GENE3D): IPR00	3,549	2,534	0,863	1,225	1,107									
Solyc12g014430	Cellulose synthase-like protein (AHRD V3.3 *** L0ASV8_POPTO)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR029044 (G3DSA:3.90.550.GENE3	17,923	10,430	4,895	4,359	4,230									
Solyc12g014440	BNR/Asp-box repeat family protein (AHRD V3.3 *** AT5G57700.3)		C:GO:0016021	C:integral component of membrane			G3DSA:2.120.10.10 (GENE3D): IPR0	60,978	50,281	32,322	28,141	31,127									
Solyc12g014450	extracellular ligand-gated ion channel protein (DUF3537) (AHRD V3.3 *** AT3G20300.1)		C:GO:0016021	C:integral component of membrane			IPR021924 (PFAM): mobidb-lite (MOB	0,059	0,000	0,000	0,022	0,024									
Solyc12g014460	EH domain-containing protein 1 (AHRD V3.3 *** EHD1_ARATH)		F:GO:0005509; F:G(	F:calcium ion binding; F:protein binding; F:GTP binding			IPR040990 (PFAM): IPR022812 (PFA	38,643	35,173	24,236	19,629	24,948									
Solyc12g014470	GrpE protein homolog (AHRD V3.3 *** K4DCY2_SOLLC)		F:GO:0000774; P:G(	F:adenyl-nucleotide exchange factor activity; P:protein folding; I			IPR000740 (PRINTS): IPR009012 (G3	2,584	1,858	4,465	4,637	3,977									
Solyc12g014480	golgin family A protein (AHRD V3.3 *-* AT4G22320.2)						mobidb-lite (MOBIDB_LITE): PTHR345	7,898	3,995	6,719	5,374	5,610	-0,954	0,007					down		
Solyc12g014485	Cell wall-associated hydrolase (AHRD V3.3 *-* T2DPD7_PHAVU)		C:GO:0009507	C:chloroplast				0,242	0,180	0,546	0,167	0,189									
Solyc12g014490	Microtubule associated family protein (AHRD V3.3 *** B9GJD5_POPTR)		P:GO:0000226; F:G(	P:microtubule cytoskeleton organization; F:microtubule binding			PF03999 (PFAM): G3DSA:1.20.58.15	65,493	45,443	23,327	19,916	22,396									
Solyc12g014500	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (AHRD V3.3 *** B9GJG7_POPTR)		F:GO:0008168	F:methyltransferase activity			G3DSA:1.10.1200.220 (GENE3D): IPF	2,135	1,840	0,464	0,147	0,258									
Solyc12g014530	L-aspartate oxidase (AHRD V3.3 *** K4DCY8_SOLLC)		F:GO:0008734; P:G(	F:L-aspartate oxida	EC:1.4.3.16; EC:1.4.	L-aspartate oxidase;	IPR036188 (G3DSA:3.50.50.GENE3D	18,595	34,385	8,055	8,440	9,319	0,911	0,004					up		
Solyc12g014540	PHD finger family protein (AHRD V3.3 *** B9GJG6_POPTR)		F:GO:0003682	F:chromatin binding			IPR019787 (PFAM): IPR001025 (PFA	44,225	40,162	41,824	40,289	42,895									
Solyc12g014560	Cell division protein FtsZ-1-like protein (AHRD V3.3 *** W9RBJ2_9ROSA)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR003008 (PRINTS): IPR000158 (TI(	2,944	3,176	1,522	1,227	1,603									
Solyc12g014565	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHRD V3.3 --* AT5G42140.2)						mobidb-lite (MOBIDB_LITE)	0,021	0,117	0,097	0,022	0,166									
Solyc12g014570	Glycerophosphoryl diester phosphodiesterase, putative (AHRD V3.3 *** B9SSQ8_RICCO)		P:GO:0006629; F:G(	P:lipid metabolic process; F:phosphoric diester hydrolase activi			IPR030395 (PFAM): IPR017946 (G3D	15,858	18,075	1,560	2,265	2,113									
Solyc12g014580	Pollen allergen Ole e 6-like protein (AHRD V3.3 *** A0A075WG86_CAPAN)						IPR015333 (PFAM): IPR036466 (G3D	0,021	0,062	0,000	0,000	0,000									
Solyc12g014590	Pirin-like protein family (AHRD V3.3 *** A0A151SXI4_CAJCA)						IPR003829 (PFAM): IPR008778 (PFA	0,460	0,695	0,144	0,169	0,024									

Solyc12g014600	RNA-binding protein, putative (AHRD V3.3 *** Q1ENZ5_MUSAC)		F:GO:0003723	F:RNA binding			IPR000504 (PFAM); IPR012677 (G3D	41,020	46,262	38,717	34,099	36,255									
Solyc12g014610	WRKY transcription factor 20		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM WRKY	18,394	15,141	9,181	9,254	10,192									
Solyc12g014620	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *-* 14KD_DAUCA)						G3DSA:1.10.110.10 (GENE3D); IPR0:	0,059	0,060	0,338	0,072	0,190									
Solyc12g014630	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *-* A0A0B2S7U0_GLYSO)						IPR027923 (PFAM); G3DSA:1.10.110.	92,380	166,605	8,060	2,676	2,927			-1,459	0,011	-1,584	0,005		down	down
Solyc12g015630	transmembrane protein (AHRD V3.3 *** AT5G55570.1)		C:GO:0016021	C:integral component of membrane			IPR014900 (PFAM); PTHR36809 (PAN	7,657	9,740	2,437	3,385	5,036			1,028	0,002				up	
Solyc12g015640	Mitochondrial transcription termination factor family protein (AHRD V3.3 *** AT5G55580.1)		F:GO:0003690; P:G(	F:double-stranded DNA binding; P:regulation of transcription, DN			IPR038538 (G3DSA:1.25.70.GENE3D	11,646	11,039	12,575	13,889	17,330			0,457	0,028				up	
Solyc12g015650	U-box domain-containing protein 4 (AHRD V3.3 *** W9REK9_9ROSA)		F:GO:0005515	F:protein binding			IPR000225 (PFAM); IPR011989 (G3D	4,823	5,272	5,799	5,658	5,561									
Solyc12g015655	Heavy metal transport/detoxification protein (AHRD V3.3 *** A2Q5G7_MEDTR)		P:GO:0030001; F:G(	P:metal ion transport; F:metal ion binding			G3DSA:3.30.70.100 (GENE3D); PTHR	0,795	0,393	0,409	0,640	0,614									
Solyc12g015660	DNA damage response protein WSS1 (AHRD V3.3 *** W9QFU6_9ROSA)		P:GO:0006508; F:G(	P:proteolysis; F:metallopeptidase activity; F:metal ion binding			G3DSA:2.20.28.140 (GENE3D); IPR0	4,481	5,301	5,717	4,991	5,427									
Solyc12g015680	Protein TIC 20-v, chloroplastic (AHRD V3.3 *** TI205_ARATH)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:integral component of men			IPR005691 (PFAM); PTHR33510:SF5	6,962	8,258	9,795	10,037	10,923									
Solyc12g015690	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)		C:GO:0031224	C:intrinsic component of membrane			IPR036378 (G3DSA:2.30.180.GENE3	57,787	39,940	1,463	1,205	1,994									
Solyc12g015700	Nudix hydrolase (AHRD V3.3 *** A0A061GGI6_THECC)		F:GO:0016787	F:hydrolase activity			IPR020476 (PRINTS); IPR003293 (PF	0,219	0,124	0,000	0,025	0,000									
Solyc12g015710	S-adenosyl-L-methionine-dependent methyltransferase (AHRD V3.3 *** I0Z5M1_COCSC)		F:GO:0003723; P:G(	F:RNA binding; P:regulation of transcription, DNA-templated; P:r			IPR023267 (PRINTS); IPR023268 (PF	19,159	17,494	27,103	26,317	29,824									
Solyc12g015730	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JXI6_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	13,342	11,128	12,422	15,658	14,694									
Solyc12g015740	Transmembrane emp24 domain-containing protein (AHRD V3.3 *** A0A1D1Z3N9_9ARAE)		C:GO:0005783; C:G(	C:endoplasmic retic	EC:2.4.1.12	Cellulose synthase (U	IPR009038 (PFAM); IPR015720 (PAN	10,687	10,115	17,809	21,403	14,857									
Solyc12g015770	Cellulose synthase, putative (AHRD V3.3 *** B9S9W0_RICCO)		C:GO:0016020; F:G(	C:membrane; F:cell	EC:2.4.1.12	Cellulose synthase (U	IPR005150 (PFAM); IPR029044 (G3D	18,332	9,893	1,001	0,838	0,919									
Solyc12g015780	DNA-directed RNA polymerase family protein (AHRD V3.3 *** AT1G60850.4)		F:GO:0003899; P:G(	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA po	IPR011263 (PFAM); IPR011262 (PFA	19,517	20,835	19,065	16,839	17,435									
Solyc12g015790	Eukaryotic translation initiation factor 6 (AHRD V3.3 *** K4DD14_SOLLC)		P:GO:0042256; F:G(	P:mature ribosome assembly; F:ribosome binding			IPR002769 (TIGRFAM); IPR002769 (F	0,000	0,043	0,000	0,000	0,000									
Solyc12g015800	RING/U-box superfamily protein (AHRD V3.3 *** AT5G55970.2)		C:GO:0016021; F:G(	C:integral component of membrane; F:ligase activity			IPR001841 (PFAM); IPR013083 (G3D	2,198	1,644	0,186	0,048	0,237									
Solyc12g015820	SufE-like protein, chloroplastic (AHRD V3.3 *-* A0A0B0P063_GOSAR)						G3DSA:3.90.1010.10 (GENE3D); IPR(	4,962	4,734	10,925	10,984	10,543									
Solyc12g015830	BolA-like family protein (AHRD V3.3 *** B9N5N6_POPTR)						G3DSA:3.30.300.90 (GENE3D); IPR0(	9,428	8,255	18,882	16,907	18,702									
Solyc12g015840	LOW QUALITY:pleckstrin homology (PH) domain-containing protein (AHRD V3.3 --* AT4G17140.3)							0,159	0,178	0,434	0,362	0,590									
Solyc12g015850	LOW QUALITY:Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT5G55950.1)		F:GO:0005338; C:G(	F:nucleotide-sugar transmembrane transporter activity; C:Golgi			IPR004853 (PFAM); mobidb-lite (MOB	18,848	13,725	5,028	3,775	6,477									
Solyc12g015860	farnesyl pyrophosphate synthase	fps1	F:GO:0004161; F:G(	F:dimethylallyltranst	EC:2.5.1.1; EC:2.5.1	(2E,6E)-farnesyl diph	IPR000092 (PFAM); IPR008949 (G3D	58,598	62,191	73,869	81,595	62,213									
Solyc12g015870	calcineurin B-like protein		F:GO:0005509	F:calcium ion binding			PR00450 (PRINTS); G3DSA:1.10.238.	33,774	37,219	35,390	41,005	35,221									
Solyc12g015880	Heat shock protein 90-1	Hsp90-1	F:GO:0005524; P:G(	F:ATP binding; P:protein folding; F:unfolded protein binding			IPR020575 (PRINTS); IPR036890 (G3	54,440	40,816	32,393	33,105	28,798									
Solyc12g015890	LOW QUALITY:Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *-* B9RSS3_RICCO)		F:GO:0016787	F:hydrolase activity			IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,000	0,022	0,000									
Solyc12g015910	SufE-like protein, chloroplastic (AHRD V3.3 *** A0A0B0P063_GOSAR)						IPR003808 (PFAM); IPR002634 (PFA	29,114	28,402	69,134	60,750	71,240									
Solyc12g015970	GPI-anchored protein LORELEI (AHRD V3.3 *-* A0A151SVS2_CAJCA)		C:GO:0016021	C:integral component of membrane			IPR039307 (PANTHER); PTHR31533:	15,045	12,562	10,103	9,433	11,653									
Solyc12g015980	Protein kinase (AHRD V3.3 *** A0A0K9NJ18_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); PIRS	0,000	0,000	0,025	0,000	0,046									
Solyc12g016070	Kinase family protein (AHRD V3.3 *-* D7MB90_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,040	0,080	0,047	0,000	0,024									
Solyc12g016080	Serine/Threonine kinase family protein (AHRD V3.3 *-* A0A072U637_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PTHR23257 (PANTHER); PTHR23257	0,076	0,138	0,122	0,164	0,070									
Solyc12g016100	Protein kinase (AHRD V3.3 *** A0A0K9NJ18_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF); IPR001245 (F	0,000	0,019	0,000	0,000	0,000									
Solyc12g016110	Kinase family protein (AHRD V3.3 *-* D7MB90_ARALL)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	0,000	0,018	0,025	0,000	0,000									
Solyc12g016120	Protein kinase (AHRD V3.3 *-* A0A0K9NJ18_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:1.10.510.	0,000	0,018	0,025	0,000	0,000									
Solyc12g016140	Protein kinase (AHRD V3.3 *** A0A0K9NJ18_ZOSMR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); PIRS	0,019	0,019	0,000	0,000	0,000									
Solyc12g016155	Cytochrome f (AHRD V3.3 --* CYF_LEPVR)							0,000	0,000	0,022	0,000	0,000									
Solyc12g016190	High mobility group family (AHRD V3.3 *** A0A061F3D5_THECC)		F:GO:0003677	F:DNA binding			IPR036431 (G3DSA:1.10.150.GENE3	16,273	16,002	24,379	21,190	22,375									
Solyc12g016200	LOW QUALITY:autoinhibited Ca(2+)-ATPase 10 (AHRD V3.3 --* AT4G29900.2)						mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,023									
Solyc12g016203	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* A0A0R0J3F4_SOYBN)							0,000	0,000	0,000	0,025	0,000									
Solyc12g016207	cullin 3B (AHRD V3.3 --* AT1G69670.2)							0,222	0,114	0,240	0,433	0,263									
Solyc12g016210	tRNA dimethylallyltransferase (AHRD V3.3 *** A0A0B0PPC4_GOSAR)						G3DSA:3.40.50.300 (GENE3D); PTHR	10,898	11,151	10,814	9,737	10,986									
Solyc12g016217	ATP binding microtubule motor family protein (AHRD V3.3 --* AT5G66310.3)							0,294	0,138	0,366	0,601	0,562									
Solyc12g016220	Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)		F:GO:0043531	F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	28,385	20,322	14,729	12,908	14,838									
Solyc12g017230	modifier of snc1 (AHRD V3.3 --* AT4G24680.5)						mobidb-lite (MOBIDB_LITE); mobidb-lit	29,269	18,054	99,376	93,400	84,434	-0,669	0,010					down		
Solyc12g017240	xyloglucan endo-transglycosylase B1	txetb1	F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	IPR008264 (PRINTS); IPR000757 (PF	0,019	0,000	0,125	0,149	0,024									
Solyc12g017250	Photosystem II 10 kDa polypeptide family protein (AHRD V3.3 *** A9PH94_POPTR)		C:GO:0009654; P:G(	C:photosystem II oxygen evolving complex; P:photosynthesis			IPR006814 (PFAM); IPR006814 (PAN	38,530	27,583	329,080	298,888	291,631									
Solyc12g017260	Topoisomerase II-associated protein PAT1 (AHRD V3.3 *** A0A103YJG9_CYNCS)		P:GO:0000290	P:deadenylation-dependent decapping of nuclear-transcribed ml			mobidb-lite (MOBIDB_LITE); mobidb-lit	57,418	54,576	75,514	75,201	72,116									
Solyc12g017264	50S ribosomal protein L22, chloroplastic (AHRD V3.3 --* RK22_JASNU)						PTHR33144:SF8 (PANTHER); PTHR3:	0,618	0,444	0,727	0,809	0,761									
Solyc12g017268	Sec23/Sec24 protein transport family protein (AHRD V3.3 --* AT4G14160.2)							0,571	0,386	0,553	0,733	0,497									
Solyc12g017280	ARM repeat superfamily protein (AHRD V3.3 *** AT1G79190.1)		C:GO:0016021	C:integral component of membrane			PTHR18460 (PANTHER); IPR016024 (	31,082	25,401	58,573	64,518	57,613									
Solyc12g017290	60S ribosomal L9 (AHRD V3.3 *** A0A0B0N9J1_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR036789 (G3DSA:3.90.930.GENE3	0,000	0,000	0,022	0,000	0,000									
Solyc12g017310	Defective in cullin neddylation protein (AHRD V3.3 *** K4DD65_SOLLC)						G3DSA:1.10.238.10 (GENE3D); IPR0(	0,000	0,000	0,000	0,000	0,023									
Solyc12g017360	Carbohydrate-binding X8 domain superfamily protein, putative (AHRD V3.3 *** A0A061EJW7_THECC)		C:GO:0016020	C:membrane			PR01217 (PRINTS); IPR012946 (PFA	0,284	0,404	0,219	0,097	0,236									
Solyc12g017370	Myb family transcription factor APL (AHRD V3.3 *** V9LXI2_TOBAC)		F:GO:0003677	F:DNA binding			IPR025756 (PFAM G2-like	5,327	4,303	2,685	3,222	3,721									
Solyc12g017380	Organic cation/carnitine transporter (AHRD V3.3 *** A0A072TPM4_MEDTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR005828 (PFAM); G3DSA:1.20.125(	0,760	0,874	0,424	0,350	0,330									
Solyc12g017400	NAC domain-containing protein, putative (AHRD V3.3 *** B9S679_RICCO)	NAC099	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated; P:r			IPR003441 (PFAM NAC	0,021	0,000	0,000	0,000	0,000									
Solyc12g017410	Zinc finger transcription factor 76	C3H76	F:GO:0046872	F:metal ion binding			G3DSA:2.30.30.11 C3H	27,731	25,150	35,525	37,613	37,507									
Solyc12g017420	ABC transporter family protein (AHRD V3.3 *** AT1G54350.1)	ABCD2	F:GO:0005524; C:G(	F:ATP binding; C:inl	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR011527 (PFA	51,281	48,628	36,636	41,325	50,196			0,450	0,012				up	
Solyc12g017430	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *-* AT2G01600.1)		F:GO:0005543	F:phospholipid binding			IPR011417 (PFAM); IPR008942 (G3D	2,091	1,560	0,975	1,563	1,809									
Solyc12g017450	Ubiquitin-specific protease family C19 protein (AHRD V3.3 *** A0A072UHD8_MEDTR)		P:GO:0006508; F:G(	P:proteolysis; F:peptidase activity; C:integral component of mer			mobidb-lite (MOBIDB_LITE); mobidb-lit	54,716	47,947	32,107	30,140	29,501									
Solyc12g017460	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds			IPR001087 (PFAM); IPR036514 (G3D	7,725	18,989	0,860	0,421	0,494	1,324	0,001					up		
Solyc12g017470	3-phosphoinositide-dependent protein kinase-1 (AHRD V3.3 *** B9HBB3_POPTR)		P:GO:0015919	P:peroxisomal membrane transport			IPR034571 (PANTHER)	2,296	2,407	2,726	1,926	2,333									
Solyc12g017480	Leucine-rich repeat-containing protein (AHRD V3.3 *** A0A118K791_CYNCS)		F:GO:0005515	F:protein binding			IPR001611 (PFAM); IPR032675 (G3D	0,021	0,171	0,047	0,195	0,117									
Solyc12g017510	AT2G31890-like protein (AHRD V3.3 *** A0A0G4APR9_9ROSI)		F:GO:0003723; C:G(	F:RNA binding; C:chloroplast; C:plastid nucleoid; P:chloroplast r			G3DSA:3.40.960.10 (GENE3D); IPR0:	11,982	16,731	29,894	30,979	30,399									
Solyc12g017515	Late embryogenesis abundant protein Lea14 (AHRD V3.3 *** A0A0K9PIU3_ZOSMR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:cytosol; C:plasma membrane; P:response			G3DSA:2.60.40.1820 (GENE3D); IPR(	0,509	0,376	0,222	0,147	0,307									
Solyc12g017540	Ankyrin repeat protein SKIP35 (AHRD V3.3 *** SKI35_ARATH)						IPR036770 (G3DSA:1.25.40.GENE3D	13,937	12,644	22,938	19,962	21,295									
Solyc12g017570	Rab GDP dissociation inhibitor (AHRD V3.3 *** C0LSK7_NICBE)		F:GO:0005093; P:G(	F:Rab GDP-dissociation inhibitor activity; P:small GTPase medi			IPR018203 (PRINTS); IPR000806 (PF	159,460	152,714	175,809	168,734	164,311									
Solyc12g017610	LOW QUALITY:CW-type Zinc Finger (AHRD V3.3 *-* AT3G62900.3)		F:GO:0008270	F:zinc ion binding			IPR011124 (PFAM); G3DSA:3.30.40.1	0,261	0,366	0,099	0,169	0,235									
Solyc12g017630	Ribosomal RNA small subunit methyltransferase NEP1 (AHRD V3.3 *** A0A0B2PCU7_GLYSO)		F:GO:0008168	F:methyltransferase activity			IPR005304 (PFAM); IPR029026 (G3D	19,868	24,263	7,379	7,536	9,170									
Solyc12g017675	LOW QUALITY:Ribosomal RNA small subunit methyltransferase NEP1 (AHRD V3.3 *-* A0A0B2PCU7_GLYS		F:GO:0008168	F:methyltransferase activity			IPR029026 (G3DSA:3.40.1280.GENE	0,021	0,021	0,000	0,000	0,000									
Solyc12g017690	Queuine tRNA-ribosyltransferase accessory subunit 2 (AHRD V3.3 *** K4DD97_SOLLC)		P:GO:0006400; F:G(	P:tRNA modificatior	EC:2.4.2.29	tRNA-guanine(34) tra	IPR002616 (TIGRFAM); IPR036511 ((	8,906	8,616	8,882	8,218	8,697									
Solyc12g017700	ATP-dependent RNA helicase (AHRD V3.3 *** A0A0K9PGQ5_ZOSMR)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	IPR011709 (PFAM); IPR001650 (PFA	0,304	0,115	0,000	0,022	0,023									
Solyc12g017750	pentatricopeptide (PPR) repeat-containing protein (AHRD V3.3 --* AT1G62914.1)							0,000	0,000	0,025	0,101	0,047									
Solyc12g017800	NBS-LRR class disease resistance protein (AHRD V3.3 *-* G8E3T3_SESIN)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS); IPR002182 (PFA	0,042	0,062	0,049	0,000	0,000									
Solyc12g017820	Golgi to ER traffic 4 (AHRD V3.3 *** A0A0B0NU26_GOSAR)		F:GO:0005515	F:protein binding			IPR007317 (PFAM); IPR011990 (G3D	0,000	0,018	0,000	0,000	0,000									
Solyc12g017835	Brefeldin A-inhibited guanine nucleotide-exchange 2 (AHRD V3.3 *** A0A0B0NVS2_GOSAR)		F:GO:0005086; P:G(	F:ARF guanyl-nucleotide exchange factor activity; P:regulation (			IPR000904 (PFAM); IPR032629 (PFA	224,204	200,299	189,571	196,071	188,110									
Solyc12g017840	Adenine nucleotide alpha hydrolases-domain containing protein kinase (AHRD V3.3 *** F4IK85_ARATH)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation; C			IPR006016 (PFAM); IPR014729 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc12g017850	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT5G20700.1)						IPR007650 (PFAM); PTHR33059:SF4(	4,632	4,379	15,178	15,707	13,774									
Solyc12g017860	ATP-dependent RNA helicase DOB1 (AHRD V3.3 *** A0A0K9PZL4_ZOSMR)		F:GO:0003723; F:G(	F:RNA binding; F:RI	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.10.3380.30 (GENE3D); G3D	25,957	22,109	27,101	28,644	27,080									
Solyc12g017880	Auxin induced-like protein (AHRD V3.3 *** E0Z5V0_PICSI)		C:GO:0016021; P:G(	C:integral component of membrane; P:oxidation-reduction proce			IPR017214 (PIRSF); IPR005018 (PFA	0,153	0,311	0,137	0,095	0,024									
Solyc12g017910	Potassium transporter (AHRD V3.3 *** M1BTK3_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM); IPR003855 (TIGF	95,144	85,669	101,041	92,812	95,263									
Solyc12g017920	Poly(ADP-ribose) glycohydrolase 1 (AHRD V3.3 *** A0A151SD07_CAJCA)		F:GO:0004649; P:G(	F:poly(ADP-ribose)	EC:3.2.1.143	Poly(ADP-ribose) gly	IPR007724 (PFAM); mobidb-lite (MOB	4,083	3,850	5,554	5,403	5,559									
Solyc12g017923	Poly(ADP-ribose) glycohydrolase 1 (AHRD V3.3 *-* PARG1_ARATH)		F:GO:0004649; P:G(	F:poly(ADP-ribose)	EC:3.2.1.143	Poly(ADP-ribose) gly	IPR007724 (PFAM); PTHR12837:SF0	0,021	0,018	0,000	0,022	0,000									
Solyc12g017960	LOW QUALITY:disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 --* AT1G27180.8)						PTHR35485 (PANTHER); PTHR35485	1,606	4,228	0,190	0,100	0,376	1,415	0,023					up		
Solyc12g017970	LOW QUALITY:GPI-anchored adhesin-like protein (AHRD V3.3 *** AT2G43990.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,963	3,509	0,269	0,120	0,237									
Solyc12g018990	Inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** B9HGC2_POPTR)						IPR001910 (PFAM); IPR036452 (G3D	68,273	61,622	161,531	158,257	149,750									
Solyc12g019000	La-related protein 7 (AHRD V3.3 *** W9RF44_9ROSA)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprote			IPR002344 (PRINTS); IPR036388 (G3	29,389	33,900	47,918	44,111	45,244									
Solyc12g019010	2-phytyl-1,4-beta-naphthoquinone methyltransferase, chloroplastic (AHRD V3.3 *** K4DDC9_SOLLC)		P:GO:0042372; F:G(	P:phylloquinone biosynthetic process; F:2-phytyl-1,4-naphthoqu			IPR004033 (TIGRFAM); G3DSA:3.40.!	17,182	21,863	33,269	43,257	41,069					0,383	0,029			up
Solyc12g019060	Ankyrin repeat family protein (AHRD V3.3 *** AT2G31820.1)		F:GO:0005515	F:protein binding			IPR020683 (PFAM); PF13857 (PFAM)	22,011	16,621	16,881	15,393	16,116									
Solyc12g019070	Type II inositol 5-phosphatase, putative (AHRD V3.3 *-* B9SSY3_RICCO)		F:GO:0016787; P:G(	F:hydrolase activity; P:phosphatidylinositol dephosphorylation			mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,000	0,000	0,000	0,000									
Solyc12g019080	Type I inositol polyphosphate 5-phosphatase 12 (AHRD V3.3 *** IP5PC_ARATH)		F:GO:0005515	F:protein binding			IPR005135 (PFAM); IPR015943 (G3D	2,110	1,623	2,460	2,309	2,173									
Solyc12g019090	LOW QUALITY:Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151RA30_CAJCA)						IPR019557 (PFAM); mobidb-lite (MOB	0,040	0,000	0,000	0,000	0,047									
Solyc12g019095	Valyl-tRNA synthetase, putative (AHRD V3.3 *-* B9SYX1_RICCO)		F:GO:0004812; F:G(	F:aminoacyl-tRNA ligase activity; F:ATP binding; P:tRNA amino			IPR002300 (PFAM); G3DSA:1.10.730.	0,000	0,000	0,025	0,025	0,000									
Solyc12g019100	Valyl-tRNA synthetase, putative (AHRD V3.3 *** B9SYX1_RICCO)		F:GO:0002161; F:G(	F:aminoacyl-tRNA e	EC:3.1.1.1	Carboxylesterase	IPR009008 (G3DSA:3.90.740.GENE3	0,572	0,601	0,667	0,536	0,825									
Solyc12g019110	Valyl-tRNA synthetase (AHRD V3.3 *** A0A151SWL9_CAJCA)		F:GO:0002161; F:G(	F:aminoacyl-tRNA e	EC:6.1.1.9; EC:3.1.1	Valine--tRNA ligase;	IPR002303 (PRINTS); IPR014729 (G3	11,549	14,667	16,521	16,220	17,562									
Solyc12g019142	HAT family dimerisation domain containing protein (AHRD V3.3 *-* Q7XH61_ORYSJ)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM); mobidb-lite (MOB	0,040	0,000	0,000	0,000	0,000									
Solyc12g019144	RING/U-box superfamily protein (AHRD V3.3 *-* AT4G34040.1)		F:GO:0016874	F:ligase activity			IPR001841 (PFAM); IPR013083 (G3D	0,037	0,039	0,000	0,000	0,000									
Solyc12g019170	LOW QUALITY:Maturase K (AHRD V3.3 --* MATK_PINEG)						mobidb-lite (MOBIDB_LITE)	0,000	0,000	0,000	0,000	0,023									
Solyc12g019180	polygalacturonase 7	PG24-6 (TPG7)	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM); IPR012334 (G3D	0,094	0,188	0,148	0,254	0,023									
Solyc12g019230	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G59850.2)	PG24-7	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR012334 (G3DSA:2.160.20.GENE3	0,037	0,000	0,097	0,022	0,023									
Solyc12g019290	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SBF4_CYNCS)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	34,059	40,079	49,560	48,193	45,492									
Solyc12g019295	RING/U-box superfamily protein (AHRD V3.3 --* AT5G63760.3)						mobidb-lite (MOBIDB_LITE)	1,663	1,885	2,542	2,224	2,477									
Solyc12g019300	Acetolactate synthase small subunit (AHRD V3.3 *-* A0A151UBY0_CAJCA)		F:GO:0003984; P:G(	F:acetolactate synt	EC:2.2.1.6	Acetolactate synthas	IPR027271 (G3DSA:3.30.70.GENE3D	3,447	3,272	7,991	7,477	8,424									
Solyc12g019310	Acetolactate synthase, small subunit (AHRD V3.3 *** A0A118K2Y2_CYNCS)		F:GO:0003984; P:G(	F:acetolactate synt	EC:2.2.1.6	Acetolactate synthas	IPR027271 (G3DSA:3.30.70.GENE3D	12,546	13,093	31,680	27,731	31,430									
Solyc12g019320	Protein DETOXIFICATION (AHRD V3.3 *** K4DDF8_SOLLC)		P:GO:0006855; F:G(	P:drug transmembrane transport; F:drug transmembrane transpc			IPR002528 (PFAM); IPR002528 (TIGF	0,117	0,954	0,448	0,322	0,309									
Solyc12g019410	Integrin-linked protein kinase family (AHRD V3.3 *** AT2G43850.3)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			PIRSF000654 (PIRSF); IPR036770 ((	0,675	1,190	0,750	0,702	0,659									
Solyc12g019460	mitogen-activated protein kinase 1	mpk1	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); G3DS	27,838	26,279	16,415	14,379	16,970									
Solyc12g019470	Nonsense-mediated mRNA decay protein 2 isoform 2 (AHRD V3.3 *** A0A061EJP7_THECC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	15,761	16,433	19,316	17,324	16,975									
Solyc12g019480	Formin-like protein (AHRD V3.3 *** K4DDH4_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR015425 (PFAM); G3DSA:1.20.58.2	1,605	1,244	0,022	0,094	0,094									
Solyc12g019490	Acyl-CoA thioesterase, putative (AHRD V3.3 *** B9T2I4_RICCO)		P:GO:0006637; F:G(	P:acyl-CoA metabol	EC:3.1.2.2	Acyl-CoA hydrolase	G3DSA:3.10.129.10 (GENE3D); G3DS	11,423	11,700	8,929	9,917	10,026									
Solyc12g019540	membrane steroid binding protein 1 (AHRD V3.3 --* AT5G52240.2)							2,235	3,033	1,970	1,915	1,957									
Solyc12g019550	Lipase maturation factor 2 (AHRD V3.3 *** A0A1D1ZBR5_9ARAE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	3,112	10,923	0,804	2,040	2,302	1,836	0,016	1,515	0,000	1,346	0,004	up	up	up
Solyc12g019560	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	3,676	3,395	3,528	4,638	3,838									
Solyc12g019570	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y3_RICCO)		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PFAM); G3DSA:3.40.50.1	7,636	7,533	7,493	8,124	8,140									
Solyc12g019610	Kinesin-like protein (AHRD V3.3 *-* M1BMZ3_SOLTU)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	G3DSA:1.20.58.1980 (GENE3D); PTH	0,019	0,000	0,000	0,000	0,023									
Solyc12g019627	Cytochrome P450 (AHRD V3.3 *-* A0A103XIA9_CYNCS)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR001128 (PF	0,019	0,000	0,000	0,047	0,000									
Solyc12g019670	ESSS subunit of NADH:ubiquinone oxidoreductase (complex I) protein (AHRD V3.3 --* AT3G57785.1)							0,077	0,043	0,000	0,000	0,000									
Solyc12g019680	Cytochrome P450 family protein (AHRD V3.3 *** A0A061DTU0_THECC)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS); IPR002401 (PF	0,019	0,000	7,599	12,144	8,739									
Solyc12g019690	small basic intrinsic protein 1.1	SIP1.1	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS); IPR023271 (G3	28,293	19,629	25,098	23,797	24,906									
Solyc12g019700	Protein Ycf2 (AHRD V3.3 --* YCF2_CHLSC)							16,528	20,176	4,363	8,526	10,141			1,211	0,003	0,963	0,042		up	up
Solyc12g019705	E2F transcription factor 3 (AHRD V3.3 --* AT2G36010.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	2,938	2,663	1,863	2,691	2,513									
Solyc12g019740	Thioredoxin, putative (AHRD V3.3 *** B9SHJ2_RICCO)		P:GO:0045454	P:cell redox homeostasis			G3DSA:3.40.30.10 (GENE3D); IPR01:	52,820	43,928	43,237	37,458	46,747									
Solyc12g019750	Polypyrimidine tract-binding-like protein (AHRD V3.3 *** G7IBX9_MEDTR)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:mRNA processing			IPR021790 (PFAM); IPR012677 (G3D	56,824	51,005	64,701	56,751	60,661									
Solyc12g019760	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G04080.5)							0,037	0,000	0,000	0,000	0,000									
Solyc12g019860	CCR4-NOT transcription complex subunit 3 (AHRD V3.3 *** W9RL65_9ROSA)		C:GO:0005634; P:G(	C:nucleus; P:regulation of transcription, DNA-templated; C:CCR			IPR012270 (PIRSF); IPR038635 (G3D	89,627	90,569	151,286	145,673	144,085									
Solyc12g019870	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT2G33170.2		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR032675 (G3DSA:3.80.10.GENE3D	0,000	0,021	0,000	0,000	0,000									
Solyc12g019880	phosphatidylinositol- 4-phosphate 5-kinase 5 (AHRD V3.3 *** AT2G41210.1)		F:GO:0005524; F:G(	F:ATP binding; F:1-(	EC:2.7.1.68	1-phosphatidylinosito	IPR027483 (G3DSA:3.30.810.GENE3	0,000	0,000	0,000	0,022	0,000									
Solyc12g019885	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT1G74390.4)		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity; P:RNA phosphodiester bond hydrolysis				0,061	0,061	0,047	0,223	0,140									
Solyc12g019890	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SHH6_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR000490 (PFAM); G3DSA:3.20.20.8	16,540	17,071	13,977	18,013	18,194									
Solyc12g019930	LOW QUALITY:Myosin (AHRD V3.3 *-* W5ZSG9_MAIZE)		F:GO:0003774; F:G(	F:motor activity; F:/	EC:3.6.1.15	Nucleoside-triphosph	IPR036961 (G3DSA:3.40.850.GENE3	0,000	0,000	0,025	0,000	0,000									
Solyc12g019960	Telomerase activating protein Est1 (AHRD V3.3 *** A0A072UH06_MEDTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	60,569	67,318	68,782	78,631	74,980									
Solyc12g019970	LOW QUALITY:Serine/threonine-protein kinase SAPK7 (AHRD V3.3 --* A0A151S2E5_CAJCA)							3,146	4,440	3,625	4,131	3,982									
Solyc12g019975	Glycosyltransferase (AHRD V3.3 *-* K4D3V7_SOLLC)		F:GO:0035251	F:UDP-glucosyltransferase activity			G3DSA:3.40.50.2000 (GENE3D); PTH	12,975	11,946	15,448	16,922	16,352									
Solyc12g019980	Telomerase activating protein Est1 (AHRD V3.3 --* AT5G19400.5)						mobidb-lite (MOBIDB_LITE); PTHR156	10,679	14,139	13,215	13,715	13,213									
Solyc12g020000	Arginine/serine-rich coiled-coil 2 (AHRD V3.3 *** A0A0B0NVA2_GOSAR)						mobidb-lite (MOBIDB_LITE); mobidb-lit	90,182	88,801	117,088	117,661	109,489									
Solyc12g020030	LOW QUALITY:CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 1 (AHRD V3.3 *-* A0A061DL35		C:GO:0016021	C:integral component of membrane			PTHR22930 (PANTHER); PTHR22930	0,000	0,021	0,000	0,000	0,000									
Solyc12g020050	DNA-binding protein DQ117941		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	36,510	38,984	46,982	40,895	42,221									
Solyc12g020110	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding; F:zinc ion binding; F:hydrc			IPR013083 (G3DSA:3.30.40.GENE3D	6,376	5,632	2,294	1,603	2,350									
Solyc12g020120	Class III homeobox-leucine zipper protein (AHRD V3.3 *-* I0IUI3_9ASPA)		F:GO:0008289	F:lipid binding			IPR002913 (PFAM); SSF55961 (SUPE	1,599	1,863	0,618	0,400	0,872									
Solyc12g020130	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT3G07810.2)						PTHR33527:SF14 (PANTHER); PTHR:	0,019	0,099	0,000	0,000	0,000									

Solyc12g021130	Reticulon-like protein (AHRD V3.3 *** K4DDN2_SOLLC)		F:GO:0003854; P:G(	F:3-beta-hydroxy-de	EC:1.1.1.145	3-beta-hydroxy-Delta	IPR003388 (PFAM); IPR002225 (PFA	42,033	32,829	45,128	46,927	44,455									
Solyc12g021140	Sulfotransferase (AHRD V3.3 *** K4DDN3_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	0,420	0,146	0,000	0,000	0,000									
Solyc12g021150	Sulfotransferase (AHRD V3.3 *** K4DDN4_SOLLC)		F:GO:0008146	F:sulfotransferase activity			G3DSA:3.40.50.300 (GENE3D); IPR0(	1,062	0,439	0,000	0,025	0,000									
Solyc12g021160	LOW QUALITY:cysteine-rich RLK (RECEPTOR-like protein kinase) 29 (AHRD V3.3 --* AT4G21410.3)							1,785	1,800	1,554	1,303	1,642									
Solyc12g021170	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (AHRD V3.3 *** K4DDN6_SOLLC)		F:GO:0004174; P:G(	F:electron-transferr	EC:1.5.5.1	Electron-transferring-	PR00469 (PRINTS); IPR036188 (G3D	21,032	20,588	42,483	38,951	35,592									
Solyc12g021180	Dual specificity protein phosphatase, putative (AHRD V3.3 *** B9S842_RICCO)		P:GO:0006470; F:G(	P:protein dephosph	EC:3.1.3.16	Protein-serine/threor	IPR000340 (PFAM); PTHR10159:SF4(	8,226	7,233	11,062	11,963	11,428									
Solyc12g021190	Dual specificity protein phosphatase, putative (AHRD V3.3 *-* B9S842_RICCO)		F:GO:0004725; F:G(	F:protein tyrosine p	EC:3.1.3.16; EC:3.1.	Protein-serine/threor	IPR024950 (PANTHER); PTHR10159:	8,090	9,997	12,783	12,835	11,391									
Solyc12g021195	Mediator of RNA polymerase II transcription subunit 20-like protein (AHRD V3.3 *** A0A0U3C148_REHGL)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR013921 (PANTHER)	0,021	0,059	0,050	0,076	0,024									
Solyc12g021200	E3 ubiquitin protein ligase DRIP2 (AHRD V3.3 *-* M7ZYU9_TRIUA)		F:GO:0016874; F:G(	F:ligase activity; F:metal ion binding			G3DSA:3.10.20.90 (GENE3D); mobidb	0,000	0,018	0,000	0,000	0,000									
Solyc12g021210	E3 ubiquitin protein ligase DRIP2 (AHRD V3.3 *-* A0A1D1YJH4_9ARAE)		F:GO:0016874; F:G(	F:ligase activity; F:metal ion binding			G3DSA:3.10.20.90 (GENE3D); mobidb	0,000	0,058	0,000	0,000	0,000									
Solyc12g021230	DNA gyrase subunit B (AHRD V3.3 *** K4DDP2_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:3.6.1.3; EC:5.99.	Adenosinetriphospha	PR00418 (PRINTS); IPR000565 (PRIN	33,720	38,189	47,271	49,104	52,976									
Solyc12g021280	Kinase family protein (AHRD V3.3 *** B9HIY8_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); G3DS	24,395	25,208	29,699	30,520	34,212									
Solyc12g021310	WD40 repeat-containing protein (AHRD V3.3 *-* A0A103YG45_CYNCS)		F:GO:0005515; P:G(	F:protein binding; P:regulation of phosphatidylinositol 3-kinase a			IPR001680 (PFAM); IPR015943 (G3D	0,038	0,019	0,051	0,000	0,024									
Solyc12g021313	WD repeat-containing protein 91 (AHRD V3.3 *-* A0A1D1YYY7_9ARAE)		P:GO:0043551; P:G(	P:regulation of phosphatidylinositol 3-kinase activity; P:early en			IPR039724 (PANTHER)	6,387	5,716	10,663	11,879	11,276									
Solyc12g021317	WD40 repeat-containing protein (AHRD V3.3 *-* A0A103YG45_CYNCS)		F:GO:0005515; P:G(	F:protein binding; P:regulation of phosphatidylinositol 3-kinase a			IPR015943 (G3DSA:2.130.10.GENE3I	0,141	0,043	0,072	0,069	0,187									
Solyc12g021320	LOW QUALITY:FAR1-related sequence 3 (AHRD V3.3 --* AT2G27110.3)		C:GO:0005739; C:G(	C:mitochondrion; C:integral component of membrane				0,042	0,021	0,000	0,000	0,024									
Solyc12g021340	Rhodanese/Cell cycle control phosphatase superfamily protein (AHRD V3.3 *** AT4G24750.1)		C:GO:0009507	C:chloroplast			IPR001763 (PFAM); IPR036873 (G3D	35,417	43,897	36,719	36,345	45,891									
Solyc12g021360	Protein apaG (AHRD V3.3 *-* A0A151RPX9_CAJCA)		F:GO:0005515	F:protein binding			IPR001943 (PFAM); IPR001943 (PRC	9,995	13,510	7,405	7,528	12,495			0,749	0,001				up	
Solyc12g021365	Protein ApaG (AHRD V3.3 *** A0A1D1XPX2_9ARAE)						IPR007474 (PFAM); IPR036767 (G3D	9,064	12,096	6,710	5,966	10,632			0,658	0,021				up	
Solyc12g026400	Protease Do-like 9 (AHRD V3.3 *** W9S874_9ROSA)		F:GO:0004252; F:G(	F:serine-type endor	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS); PF13365 (PFAI	44,083	39,809	58,637	59,415	54,721									
Solyc12g026420	LOW QUALITY:YCF20-like protein (DUF565) (AHRD V3.3 --* AT3G56830.8)						mobidb-lite (MOBIDB_LITE); mobidb-lit	6,615	6,845	8,083	8,018	6,884									
Solyc12g026430	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** A0A072VA43_MEDTR)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR006043 (PFAM); mobidb-lite (MOB	42,574	41,227	56,799	57,343	55,891									
Solyc12g026470	Heat shock factor, putative (AHRD V3.3 --* Q25BL9_BRAOL)						mobidb-lite (MOBIDB_LITE)	0,854	1,168	1,291	0,855	0,946									
Solyc12g027540	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151RVI7_CAJCA)		F:GO:0005488	F:binding			PTHR44695 (PANTHER); cd09272 (CI	2,312	0,861	1,936	1,834	1,525	-1,377	0,009					down		
Solyc12g027550	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_LACSA)		C:GO:0009521; P:G(	C:photosystem; P:photosynthetic electron transport chain; F:chl			IPR000932 (PFAM); IPR000932 (PAN	0,135	0,419	0,251	0,247	0,377									
Solyc12g027580	exportin-4 protein (AHRD V3.3 *** AT3G04490.2)						IPR011989 (G3DSA:1.25.10.GENE3D	29,775	28,837	17,674	18,688	23,169									
Solyc12g027600	Exportin-4 (AHRD V3.3 *-* A0A0B0P4E4_GOSAR)						PTHR12596 (PANTHER); PTHR12596	0,000	0,021	0,000	0,000	0,000									
Solyc12g027630	LOW QUALITY:Glycosyl-phosphatidyl inositol-anchored, plant (AHRD V3.3 --* A0A103XTF9_CYNCS)							0,200	0,579	0,212	0,294	0,213									
Solyc12g027700	LOW QUALITY:Peroxisome biogenesis protein 2 (AHRD V3.3 *-* W9REG8_9ROSA)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:peroxisome; C:cytoso			PTHR45174 (PANTHER)	0,021	0,000	0,000	0,000	0,000									
Solyc12g027710	LOW QUALITY:Telomere-binding family protein (AHRD V3.3 *-* B9HPG4_POPTR)		F:GO:0003677	F:DNA binding			PTHR21717 (PANTHER); PTHR21717	0,000	0,000	0,022	0,000	0,000									
Solyc12g027720	LOW QUALITY:ATP synthase subunit b, chloroplastic (AHRD V3.3 *-* ATPF_NICTO)		F:GO:0005524; C:G(	F:ATP binding; C:ch	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR34264 (PANTHER); PTHR34264	0,019	0,057	0,050	0,051	0,024									
Solyc12g027740	Arginine/serine-rich coiled coil protein, putative (AHRD V3.3 *-* B9R8Z5_RICCO)		P:GO:0000380	P:alternative mRNA splicing, via spliceosome			mobidb-lite (MOBIDB_LITE); IPR0346(	12,771	13,033	18,033	15,823	15,075									
Solyc12g027750	Arginine/serine-rich coiled coil protein (AHRD V3.3 *-* G7JNS7_MEDTR)		P:GO:0000380	P:alternative mRNA splicing, via spliceosome			mobidb-lite (MOBIDB_LITE); mobidb-lit	10,321	10,865	13,857	12,564	13,442									
Solyc12g027753	Ribosomal protein S12 (AHRD V3.3 *-* A0A0C5G6K8_IPOBA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:2.40.50.140 (GENE3D); IPR0(	0,080	0,192	0,047	0,100	0,072									
Solyc12g027760	Serine/threonine-protein kinase (AHRD V3.3 --* N1QWT2_AEGTA)							1,030	1,213	1,165	1,278	1,585									
Solyc12g027770	Rhodanese-like domain-containing protein (AHRD V3.3 *** A0A118K4F8_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR022111 (PFAM); G3DSA:3.30.70.1	6,642	9,462	13,788	13,333	15,826									
Solyc12g027820	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_SILLA)		C:GO:0005739; C:G(	C:mitochondrion; C:	EC:1.6.99.5; EC:1.6.	Acting on NADH or NADPH; NADH dehydrogenase; NADH:ub		0,000	0,019	0,000	0,072	0,047									
Solyc12g027850	Cyclin-dependent kinase (AHRD V3.3 *** G7J2M4_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D); G3DS	37,147	32,901	63,516	62,478	59,247									
Solyc12g032920	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 --* A0A151RYX6_CAJCA)							0,745	0,223	0,173	0,000	0,000									
Solyc12g032930	CBS domain-containing protein (AHRD V3.3 *-* W9QLL8_9ROSA)		C:GO:0016021	C:integral component of membrane			G3DSA:3.10.580.10 (GENE3D); IPR0(	2,547	0,527	0,025	0,000	0,024									
Solyc12g032933	CBS domain-containing protein (AHRD V3.3 *** W9QLL8_9ROSA)		F:GO:0005515	F:protein binding			IPR000270 (PFAM); G3DSA:3.10.580	10,523	2,996	0,217	0,025	0,048	-1,786	0,001					down		
Solyc12g032937	lon protease 3 (AHRD V3.3 --* AT3G05780.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,135	0,083	0,000	0,000	0,000									
Solyc12g032950	CBS domain-containing protein (AHRD V3.3 *-* W9RJ31_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR000644 (PFAM); G3DSA:3.10.580	20,549	19,174	30,534	27,141	29,758									
Solyc12g032955	CBS domain-containing protein (AHRD V3.3 *** W9RJ31_9ROSA)		F:GO:0005515	F:protein binding			IPR000270 (PFAM); G3DSA:3.10.580	27,129	26,263	40,486	36,818	39,483									
Solyc12g032960	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_MAIZE)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM); IPR036408 (G3D	0,037	0,122	0,146	0,201	0,117									
Solyc12g032980	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLLC)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,059	0,288	0,322	0,742	0,286									
Solyc12g032990	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* A0A0A0PE77_9ROSI)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM); IPR036408 (G3D	0,000	0,039	0,025	0,172	0,024									
Solyc12g033000	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_PINKO)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,041	0,000	0,022	0,093									
Solyc12g033020	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* NU2C_BRANA)		F:GO:0008137; C:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM); PTHR45564 (PAN	0,000	0,018	0,000	0,076	0,047									
Solyc12g033030	50S ribosomal protein L23, chloroplastic (AHRD V3.3 *** RK23_ATRBE)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012677 (G3DSA:3.30.70.GENE3D	0,196	0,859	0,072	0,127	0,187									
Solyc12g033040	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_MORIN)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,058	0,036	0,025	0,149	0,118									
Solyc12g033050	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM); IPR036408 (G3D	0,040	0,275	0,025	0,321	0,117									
Solyc12g033060	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_SOLTU)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PFAM); IPR036408 (G3D	0,040	0,268	0,101	0,424	0,259									
Solyc12g033070	NADH dehydrogenase subunit (AHRD V3.3 *-* Q8HSC3_9SOLN)		F:GO:0008137; C:G(	F:NADH dehydroge	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR018393 (PRINTS); IPR001280 (PF	0,000	0,000	0,000	0,025	0,094									
Solyc12g033080	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic (AHRD V3.3 *-* A0A0X8IHH4_9GE		C:GO:0005886; F:G(	C:plasma membran	EC:1.6.99.5; EC:1.6.	Acting on NADH or N	IPR001750 (PFAM); PTHR45564 (PAN	0,000	0,018	0,000	0,025	0,000									
Solyc12g033090	50S ribosomal protein L23, chloroplastic (AHRD V3.3 *** RK23_ATRBE)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012677 (G3DSA:3.30.70.GENE3D	0,021	0,142	0,000	0,025	0,046									
Solyc12g035130	RNA helicase DEAD36	DEAD36	F:GO:0003676; F:G(	F:nucleic acid binding; F:protein binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D); IPR0(	3156,218	2517,692	1559,638	1409,204	1464,924									
Solyc12g035170	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HW10_POPTR)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	5,910	4,848	6,711	4,642	4,492									
Solyc12g035190	Anthranilate phosphoribosyltransferase (AHRD V3.3 *** W9SD31_9ROSA)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:2.4.2.18	Anthranilate phospho	IPR005940 (TIGRFAM); IPR000312 (F	3,560	3,137	3,493	4,095	1,829			-0,933	0,024				down	
Solyc12g035195	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G01320.3)							0,019	0,000	0,000	0,025	0,000									
Solyc12g035240	DNA-binding protein, putative (AHRD V3.3 *** A0A072U4W9_MEDTR)						IPR010820 (PFAM); mobidb-lite (MOB	48,165	37,959	68,261	66,261	64,130									
Solyc12g035250	Zinc finger transcription factor 77	C3H77	F:GO:0003676; F:G(	F:nucleic acid binding; F:metal ion binding			IPR000504 (PFAM); IPR012677 (G3D	27,643	23,390	31,404	30,453	29,262									
Solyc12g035270	LOW QUALITY:receptor like protein 34 (AHRD V3.3 --* AT3G11010.6)						mobidb-lite (MOBIDB_LITE)	0,000	0,021	0,000	0,000	0,000									
Solyc12g035280	LOW QUALITY:Photosystem II CP47 reaction center protein (AHRD V3.3 *-* PSBB_AETGR)		F:GO:0003676; C:G(	F:nucleic acid binding; C:photosystem I; P:photosynthetic electr			IPR000932 (PFAM); IPR012677 (G3D	0,000	0,081	0,025	0,125	0,047									
Solyc12g035360	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G14530.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS); IPR015943 (G3	12,382	11,947	16,372	15,722	15,778									
Solyc12g035400	WAT1-related protein (AHRD V3.3 *** K4DE01_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM); PTHR31218:SF1	0,000	0,000	0,000	0,000	0,024									
Solyc12g035420	Developmentally regulated GTP-binding protein, putative (AHRD V3.3 *-* B9S5S3_RICCO)		F:GO:0005525	F:GTP binding			mobidb-lite (MOBIDB_LITE); PTHR431	5,774	3,723	5,529	5,774	6,209									
Solyc12g035430	LOW QUALITY:Alpha-N-acetylglucosaminidase (AHRD V3.3 *-* Q9ZR45_TOBAC)		C:GO:0005773; P:G(	C:vacuole; P:embryo development ending in seed dormancy; P:			G3DSA:3.20.20.80 (GENE3D); IPR02	1,610	1,614	2,190	2,290	2,242									
Solyc12g035470	Beta-1,4-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061E8J3_THECC)		F:GO:0003830; P:G(	F:beta-1,4-mannos	EC:2.4.1.144	Beta-1,4-mannosyl-g	IPR006813 (PFAM); IPR006813 (PAN	6,403	5,409	8,938	9,720	8,549									
Solyc12g035475	Endoplasmic reticulum metallopeptidase 1 (AHRD V3.3 *-* W9S320_9ROSA)		C:GO:0016021	C:integral component of membrane			G3DSA:3.40.630.10 (GENE3D); PTHF	3,904	3,482	3,669	3,008	4,423									
Solyc12g035500	Endoplasmic reticulum metallopeptidase 1 (AHRD V3.3 *** W9S320_9ROSA)		C:GO:0016021	C:integral component of membrane			IPR007484 (PFAM); G3DSA:3.40.630	19,708	17,149	16,842	18,742	17,250									
Solyc12g035520	Calmodulin-binding transcription activator (AHRD V3.3 *-* A0A072TVD4_MEDTR)		F:GO:0005515	F:protein binding			IPR013783 (G3DS CAMTA	54,232	60,536	66,524	71,561	74,025									
Solyc12g035550	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM); IPR008896 (PAN	0,019	0,043	0,000	0,025	0,000									
Solyc12g035620	Holliday junction resolvase-like protein (AHRD V3.3 *-* A0A072UJ99_MEDTR)		P:GO:0006364	P:rRNA processing			IPR005227 (PANTHER); PTHR33317:	1,841	2,060	1,605	1,267	1,649									
Solyc12g035650	Nuclear pore complex protein Nup54 (AHRD V3.3 *** A0A0B2QWA7_GLYSO)		C:GO:0005643	C:nuclear pore			IPR025712 (PFAM); mobidb-lite (MOB	22,693	24,371	22,914	20,236	23,522									
Solyc12g035670	SAC3/GANP/Nin1/mts3/eIF-3 p25 family (AHRD V3.3 *** AT3G06290.3)		C:GO:0005737; P:G(	C:cytoplasm; P:poly(A)+ mRNA export from nucleus; C:nuclear r			G3DSA:1.25.40.990 (GENE3D); IPR0(	49,802	37,788	54,496	52,902	53,396									
Solyc12g035710	DUF21 domain-containing protein (AHRD V3.3 *** A0A0B2P5X7_GLYSO)		C:GO:0016021	C:integral component of membrane			IPR002550 (PFAM); mobidb-lite (MOB	0,915	1,165	0,118	0,295	0,260									
Solyc12g035740	LOW QUALITY:Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_ATRBE)		C:GO:0009522; P:G(	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PRINTS); IPR036408 (G3	0,000	0,000	0,000	0,022	0,000									
Solyc12g035760	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:G(	F:ATP binding; C:chloroplast			IPR008543 (PFAM); IPR008543 (PAN	0,000	0,021	0,000	0,000	0,000									
Solyc12g035790	Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007642 (PFAM); IPR014724 (G3D	0,000	0,043	0,000	0,025	0,023									
Solyc12g035826	Cytochrome c biogenesis C (AHRD V3.3 *-* V9PBU8_VACMA)		C:GO:0005739; F:G(	C:mitochondrion; F:heme transporter activity; P:heme transport; C:integral component of membrane; P:(				0,000	0,000	0,022	0,050	0,000									
Solyc12g035828	50S ribosomal protein L23, chloroplastic (AHRD V3.3 *** RK23_CITSI)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012678 (SUPERFAMILY)	0,000	0,000	0,000	0,025	0,000									
Solyc12g035860	30S ribosomal protein S11, chloroplastic (AHRD V3.3 *-* RR11_PLAOC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR001971 (PFAM); IPR036967 (G3D	0,000	0,064	0,000	0,025	0,000									
Solyc12g035870	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *** S8D4Z9_9LAMI)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007641 (PFAM); IPR007120 (PFA	0,019	0,021	0,022	0,050	0,024									
Solyc12g035875	30S ribosomal protein S3, chloroplastic (AHRD V3.3 --* RR3_ACOCL)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; C:ribosome; P:translation; C:chloroplast; C:plastid;				0,097	0,142	0,098	0,098	0,117									
Solyc12g035880	30S ribosomal protein S3, chloroplastic (AHRD V3.3 *-* RR3_SOLTU)		F:GO:0003723; F:G(	F:RNA binding; F:structural constituent of ribosome; P:translatio			IPR015946 (G3DSA:3.30.300.GENE3I	0,000	0,021	0,000	0,000	0,023									
Solyc12g035890	DNA-directed RNA polymerase subunit alpha (AHRD V3.3 *** RPOA_SOLBU)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:1.10.150.20 (GENE3D); IPR0	0,000	0,000	0,025	0,047	0,000									
Solyc12g035930	DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_SOLLC)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:3.90.1100.10 (GENE3D); IPR(	0,019	0,021	0,025	0,025	0,023									
Solyc12g036010	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLBU)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA polymerase		0,000	0,019	0,000	0,000	0,000									
Solyc12g036140	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *-* A0A072'	ABCC18	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR24223:SF251 (PANTHER); PTHF	1,485	1,426	1,108	1,409	1,252									
Solyc12g036143	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *-* A0A072UV66_MEDTR)		F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	0,556	0,723	0,504	0,497	0,586									
Solyc12g036150	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *-* A0A072'	ABCC17	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	0,037	0,000	0,000	0,000	0,024									
Solyc12g036160	ABC transporter family protein (AHRD V3.3 *** A0A097P9R5_HEVBR)	ABCC25	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR036640 (G3D	4,590	5,485	3,856	3,497	3,125									
Solyc12g036165	Pre-mRNA-splicing factor ATP-dependent RNA helicase (AHRD V3.3 *-* W9RS86_9ROSA)		P:GO:0000398; F:G(	P:mRNA splicing, vi	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE)	0,059	0,064	0,000	0,049	0,094									
Solyc12g036170	Photosynthetic NDH subcomplex B 4 (AHRD V3.3 *** A0A0F7GZK7_PELHO)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:photosynthetic electron tra			IPR034570 (PANTHER)	6,928	19,330	1,989	2,966	8,473	1,505	0,000	2,072	0,000			up	up	
Solyc12g036200	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** K4DE77_SOLLC)		F:GO:0003755	F:peptidyl-prolyl cis-	EC:5.2.1.8	Peptidylprolyl isomer	G3DSA:3.10.50.40 (GENE3D); PF136	113,675	117,064	203,331	175,826	180,269									
Solyc12g036220	APOLLO (AHRD V3.3 *** U5U566_9BRAS)		F:GO:0003676	F:nucleic acid binding			IPR036397 (G3DSA:3.30.420.GENE3I	14,425	13,765	15,563	16,876	15,874									
Solyc12g036250	HNH endonuclease family protein, expressed (AHRD V3.3 *** Q8LMG0_ORYSJ)		F:GO:0003676; F:G(	F:nucleic acid binding; F:endonuclease activity; C:integral comp			G3DSA:3.30.40.60 (GENE3D); PTHR3	21,267	19,226	20,018	15,971	19,262									
Solyc12g036280	LOW QUALITY:emp24/gp25L/p24 family/GOLD family protein (AHRD V3.3 --* AT3G29070.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc12g036285	cryptochrome 2 (AHRD V3.3 --* AT1G04400.2)							0,019	0,021	0,000	0,000	0,000									
Solyc12g036300	myosin heavy chain-like protein (AHRD V3.3 *** AT5G07890.5)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation			PTHR36390 (PANTHER)	13,688	13,106	15,421	14,092	13,479									
Solyc12g036310	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_CHLSC)							0,021	0,000	0,000	0,000	0,024									
Solyc12g036320	Kinase superfamily protein (AHRD V3.3 *** A0A061G213_THECC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR032872 (PFAM); PTHR33138 (PAN	0,241	0,512	0,000	0,147	0,023									
Solyc12g036325	Protein kinase family protein (AHRD V3.3 *** AT5G38210.3)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR032872 (PFAM); IPR000719 (PFA	1,696	3,902	0,554	0,727	0,987	1,217	0,030					up		
Solyc12g036340	Pentatricopeptide repeat (PPR-like) superfamily protein (AHRD V3.3 --* AT1G05670.3)							2,162	2,163	2,688	2,292	1,958									
Solyc12g036380	WRKY DNA-binding protein 31 (AHRD V3.3 --* AT4G22070.4)						G3DSA:1.20.5.170 (GENE3D)	0,078	0,096	0,069	0,047	0,165									
Solyc12g036390	Calmodulin binding protein-like, putative (AHRD V3.3 *** A0A061G202_THECC)		F:GO:0005516	F:calmodulin binding			IPR012416 (PFAM); IPR012416 (PAN	0,103	0,729	0,100	0,266	0,236									
Solyc12g036410	Elongation factor 1-alpha, putative (AHRD V3.3 *** B9SPP6_RICCO)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS); G3DSA:4.10.1(	19,427	19,175	18,840	18,015	18,377									
Solyc12g036415	SAUR-like auxin-responsive protein family (AHRD V3.3 --* AT3G09870.1)							8,348	10,344	9,187	25,284	12,717					1,466	0,000			up
Solyc12g036430	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G49770.1)		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	0,019	0,021	0,000	0,000	0,000									
Solyc12g036450	40S ribosomal protein S7 (AHRD V3.3 *-* A0A0B2Q5H6_GLYSO)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000554 (PFAM); IPR000554 (PAN	2,844	4,170	3,508	3,017	3,134									
Solyc12g036470	bHLH transcription factor 071		P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (PFAM bHLH	0,019	0,021	0,000	0,025	0,024									
Solyc12g036480	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	NAC100	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated			IPR036093 (G3DS NAC	0,000	0,000	0,000	0,050	0,000									
Solyc12g036490	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)		P:GO:0006629; F:G(	P:lipid metabolic prc	EC:3.1.1.32; EC:3.1.	Phospholipase A(1);	IPR002921 (PFAM); G3DSA:3.40.50.1	0,000	0,000	0,022	0,022	0,000									
Solyc12g036500	DUF1666 family protein (AHRD V3.3 *** G7KN40_MEDTR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR012870 (PFAM); mobidb-lite (MOB	3,144	2,678	1,036	1,398	1,414									
Solyc12g036520	Fatty acid desaturase (AHRD V3.3 *** E5D7U7_9GENT)		P:GO:0008152; C:G(	P:metabolic process; C:membrane			PTHR32100:SF16 (PANTHER); PTHR3	0,019	0,080	0,050	0,047	0,140									
Solyc12g036530	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103XHN5_CYNCS)		P:GO:0009451	P:RNA modification				0,297	0,333	0,265	0,213	0,281									
Solyc12g036550	Ycf1 (AHRD V3.3 *** A0A0U1ZFC2_SOLCI)		C:GO:0016021	C:integral component of membrane			IPR008896 (PFAM); mobidb-lite (MOB	0,000	0,128	0,046	0,101	0,046									
Solyc12g036650	translocase subunit seca (AHRD V3.3 *** AT1G68490.1)						PTHR33384 (PANTHER); PTHR33384	18,287	16,654	2,946	3,460	4,086									
Solyc12g036653	Tubulin beta chain (AHRD V3.3 *-* Q9ZRA7_WHEAT)		F:GO:0005200; F:G(	F:structural constituent of cytoskeleton; F:GTP binding; C:micro			IPR000217 (PRINTS); IPR036525 (G3	0,021	0,000	0,000	0,000	0,000									
Solyc12g036657	Tubulin beta chain (AHRD V3.3 *-* A0A0D3BFN8_BRAOL)		C:GO:0005874; P:G(	C:microtubule; P:microtubule-based process			IPR036525 (G3DSA:3.40.50.GENE3D	0,059	0,021	0,000	0,025	0,000									
Solyc12g036670	LOW QUALITY:Glutamate/malate translocator (AHRD V3.3 *-* Q8L7Z8_TOBAC)		F:GO:0005215; P:G(	F:transporter activity; P:sodium ion transport; C:integral compor			mobidb-lite (MOBIDB_LITE)	1,379	1,177	0,873	1,191	1,011									
Solyc12g036677	Cytochrome P450 (AHRD V3.3 *-* Q9AVQ2_SOLTU)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired do			IPR002401 (PRINTS); IPR001128 (PF	0,021	0,000	0,000	0,000	0,023									
Solyc12g036710	RNA polymerase subunit (AHRD V3.3 --* D3W5Z6_9SPER)		C:GO:0009507	C:chloroplast				0,019	0,000	0,025	0,000	0,024									
Solyc12g036720	LOW QUALITY:Maturase (AHRD V3.3 *-* B2VQ11_9SOLA)		F:GO:0005524; P:G(	F:ATP binding; P:mRNA processing; C:chloroplast			IPR024937 (PFAM); IPR008543 (PFA	0,038	0,043	0,075	0,076	0,047									
Solyc12g036727	NADH-ubiquinone oxidoreductase chain 5 (AHRD V3.3 --* NU5M_WHEAT)							0,176	0,337	0,410	0,849	0,592									
Solyc12g036740	protein VARIATION IN COMPOUND TRIGGERED ROOT growth protein (AHRD V3.3 --* AT5G46500.4)							0,161	0,099	0,298	0,099	0,305									
Solyc12g036790	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex subunit 10-B (AHRD V3.3 *** A0A199UZR1_ANACO)						IPR019377 (PFAM); mobidb-lite (MOB	93,214	96,454	109,324	82,651	97,326					-0,399	0,027			down
Solyc12g036793	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR001611 (PFA	10,453	6,835	2,699	3,293	5,348			0,975	0,048				up	
Solyc12g036797	G-type lectin S-receptor-like Serine/Threonine-kinase (AHRD V3.3 --* AT4G03230.8)							0,000	0,000	0,000	0,025	0,000									
Solyc12g036800	Receptor like protein (AHRD V3.3 *-* A2V882_TOBAC)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:kinase acti			IPR032675 (G3DSA:3.80.10.GENE3D	0,693	0,243	0,221	0,295	0,378									
Solyc12g036810	Kinesin-like protein (AHRD V3.3 *** S8DSZ5_9LAMI)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR036872 (G3	0,880	0,714	0,398	0,265	0,614									
Solyc12g036820	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT1G67235.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane				0,358	0,186	0,246	0,222	0,259									
Solyc12g036830	LOW QUALITY:Kinesin-like protein (AHRD V3.3 *-* K4C886_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR036961 (G3DSA:3.40.850.GENE3I	0,021	0,000	0,000	0,000	0,000									
Solyc12g036850	stress response NST1-like protein (AHRD V3.3 --* AT3G51650.4)							1,945	1,412	2,393	2,189	1,791									
Solyc12g036860	Retrotransposon protein (AHRD V3.3 *** B6THQ7_MAIZE)		C:GO:0016020	C:membrane			IPR027806 (PFAM); PTHR22930:SF1	0,019	0,000	0,000	0,025	0,000									
Solyc12g036870	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** G7LIE6_MEDTR)						IPR024752 (PFAM); mobidb-lite (MOB	0,019	0,018	0,000	0,025	0,000									
Solyc12g036900	LOW QUALITY:evolutionarily conserved C-terminal region 9 (AHRD V3.3 --* AT1G27960.3)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,021	0,019	0,000	0,000	0,000									
Solyc12g036910	LOW QUALITY:Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 --* AT1G60890.2)							0,019	0,000	0,000	0,000	0,000									
Solyc12g036915	Chloroplast fatty acid desaturase 8 (AHRD V3.3 --* C6T7L5_SOYBN)							0,692	0,511	0,775	0,646	0,779									
Solyc12g036920	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)							0,000	0,021	0,025	0,000	0,000									

Solyc12g036930	Bidirectional sugar transporter SWEET11 (AHRD V3.3 --* SWT11_ORYSI)							0,199	0,061	0,047	0,098	0,095									
Solyc12g036935	Squamosa promoter-binding-like protein 6 (AHRD V3.3 --* SPL6_ARATH)							0,237	0,122	0,047	0,073	0,117									
Solyc12g037930	zinc finger (Ran-binding) family protein (AHRD V3.3 --* AT5G17790.1)							3,770	2,765	0,025	0,050	0,024									
Solyc12g037940	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* RPOB_TOBAC)		F:GO:0003677: F:G(	F:DNA binding: F:DI	EC:2.7.7.6	DNA-directed RNA p(	IPR007641 (PFAM): IPR037033 (G3D	0,021	0,064	0,000	0,072	0,024									
Solyc12g037950	Protein PLANT CADMIUM RESISTANCE 2 (AHRD V3.3 *** A0A1D1Y359_9ARAE)		C:GO:0016021	C:integral component of membrane			IPR006461 (TIGRFAM): IPR006461 (I	0,000	0,021	0,000	0,000	0,024									
Solyc12g037960	LOW QUALITY:50S ribosomal L3 (AHRD V3.3 --* A0A0B0NXM6_GOSAR)							0,118	0,059	0,072	0,098	0,000									
Solyc12g037970	Peptidyl-tRNA hydrolase family protein (AHRD V3.3 *** AT1G18440.1)		F:GO:0004045	F:aminoacyl-tRNA I	EC:3.1.1.29: EC:3.1.	Aminoacyl-tRNA hydr	IPR001328 (TIGRFAM): IPR001328 (I	12,272	14,957	39,819	36,340	37,449									
Solyc12g037980	Actin-related family protein (AHRD V3.3 *** B9I2R4_POPTR)						IPR004000 (PRINTS): G3DSA:3.90.64	59,365	63,952	88,383	85,832	85,389									
Solyc12g038080	LOW QUALITY:Photosystem II CP43 reaction center protein (AHRD V3.3 *-* PSBC_SOLTU)		C:GO:0009521: P:G(	C:photosystem: P:photosynthetic electron transport chain: F:chl			IPR000932 (PFAM): PTHR33180:SF4	0,160	0,227	0,277	0,568	0,639									
Solyc12g038090	LOW QUALITY:membrane-anchored ubiquitin-fold protein 1 precursor (AHRD V3.3 --* AT3G01050.5)						mobidb-lite (MOBIDB_LITE)	0,218	0,219	0,090	0,197	0,211									
Solyc12g038100	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A0B2RG95		C:GO:0000943	C:retrotransposon nucleocapsid			PF14223 (PFAM): mobidb-lite (MOBID	0,000	0,019	0,025	0,000	0,000									
Solyc12g038140	LOW QUALITY:Rho guanine nucleotide exchange factor (AHRD V3.3 *-* AT1G49290.1)						PTHR33527 (PANTHER): PTHR33527	0,000	0,019	0,025	0,000	0,024									
Solyc12g038160	Lipase family protein (AHRD V3.3 *** B9I2Q8_POPTR)		P:GO:0006629	P:lipid metabolic process			IPR006693 (PFAM): IPR029058 (G3D	46,179	37,600	15,452	13,158	15,641									
Solyc12g038200	Replication factor-A-like protein (AHRD V3.3 *** G7JG68_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	0,058	0,116	0,186	0,145	0,096									
Solyc12g038230	LOW QUALITY:Calcium-dependent protein kinase 25 (AHRD V3.3 --* CDPKP_ARATH)		P:GO:0006486: C:G(	P:protein glycosylation: C:integral component of membrane: F:transferase activity, transferring glycosyl				0,000	0,000	0,072	0,000	0,000									
Solyc12g038240	LOW QUALITY:hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --* AT5G09530.1)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc12g038250	Extensin-like protein Ext1 (AHRD V3.3 *** Q8VWM5_SOLLC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,000	0,000	0,000	0,000									
Solyc12g038340	Translation initiation factor eIF-2B subunit delta (AHRD V3.3 *** W9S6A9_9ROSA)		P:GO:0044237	P:cellular metabolic process			IPR000649 (PFAM): G3DSA:3.40.50.1	45,516	36,617	40,005	41,235	41,291									
Solyc12g038350	UDP-glucose 6-dehydrogenase 1 (AHRD V3.3 --* UGDH1_SOYBN)							0,454	0,255	0,000	0,145	0,000									
Solyc12g038360	LOW QUALITY:Bidirectional sugar transporter SWEET4 (AHRD V3.3 --* SWET4_ORYSJ)							0,895	0,443	0,124	0,166	0,188									
Solyc12g038370	Single-stranded DNA-binding protein (AHRD V3.3 *** A0A0K9PNM3_ZOSMR)		F:GO:0003697	F:single-stranded DNA binding			G3DSA:2.40.50.140 (GENE3D): IPR0(	11,569	11,620	15,559	13,337	14,996									
Solyc12g038400	Acetyl-coenzyme A synthetase (AHRD V3.3 *** A0A151TDT7_CAJCA)		F:GO:0003824	F:catalytic activity			G3DSA:3.30.300.30 (GENE3D): G3DS	76,301	76,002	58,434	53,407	59,059									
Solyc12g038420	BTB and TAZ domain protein 5 (AHRD V3.3 --* AT4G37610.1)							3,117	3,829	1,350	1,942	1,934									
Solyc12g038423	SPX domain-containing family protein (AHRD V3.3 *-* B9GW54_POPTR)		C:GO:0016020: C:G(	C:membrane: C:integral component of membrane: P:transmemb			PTHR23510:SF21 (PANTHER): PTHR:	0,000	0,021	0,025	0,025	0,070									
Solyc12g038430	Kinesin-like calmodulin-binding protein like (AHRD V3.3 *-* A0A0B2PXL0_GLYSO)						IPR004252 (PFAM): mobidb-lite (MOB	9,219	10,551	10,499	11,994	11,806									
Solyc12g038450	Ethylene-responsive transcription factor, putative (AHRD V3.3 *-* B9RVV2_RICCO)		F:GO:0003677: F:G(	F:DNA binding: F:DNA-binding transcription factor activity: P:rec			IPR001471 (PRIN' ERF	5,410	3,152	0,344	0,047	0,023									
Solyc12g038455	Dead box ATP-dependent RNA helicase, putative (AHRD V3.3 *-* B9RDP2_RICCO)		F:GO:0000166: F:G(	F:nucleotide binding; F:hydrolase activity			IPR001650 (PFAM): G3DSA:3.40.50.3	0,980	1,469	1,365	1,370	1,179									
Solyc12g038460	LOW QUALITY:RNA-binding pno1 (AHRD V3.3 *-* A0A0B0PEE6_GOSAR)		F:GO:0003723	F:RNA binding			IPR036612 (G3DSA:3.30.1370.GENE:	0,081	0,061	0,025	0,000	0,000									
Solyc12g038490	Dentin sialophosphoprotein-related, putative (AHRD V3.3 *** A0A061FY91_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	48,878	40,036	48,563	48,066	50,335									
Solyc12g038510	MADS-box transcription factor (AHRD V3.3 *** G5DFD9_MALDO)		F:GO:0000977: F:G(	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN' MIKC_MADS	4,064	4,886	3,935	3,924	3,886									
Solyc12g038520	Squamosa promoter binding protein 6c		F:GO:0003677: C:G(	F:DNA binding; C:nucleus; F:metal ion binding			PTHR31251 (PAN' SBP	7,753	6,604	2,678	3,302	3,449									
Solyc12g038540	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G60940.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	12,513	12,888	19,140	18,603	17,211									
Solyc12g038570	Clathrin assembly family protein (AHRD V3.3 *-* B9IKX9_POPTR)		F:GO:0000149: F:G(	F:SNARE binding: F:1-phosphatidylinositol binding: F:phosphatidylinositol-4,5-bisphosphate binding: C:p				2,566	2,257	2,178	2,502	2,514									
Solyc12g038580	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *-* B9S8D6_RICCO)		F:GO:0003824: F:G(	F:catalytic activity: F:alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity: F:trehalose-ph(				1,774	1,675	1,997	1,490	2,073									
Solyc12g038590	Rhomboid-like protein (AHRD V3.3 *** K4DEK8_SOLLC)		F:GO:0004252: C:G(	F:serine-type endo;	EC:3.4.21	Acting on peptide bo;	IPR035952 (G3DSA:1.20.1540.GENE:	4,448	4,579	6,195	6,759	6,382									
Solyc12g038600	Rhomboid-like protein (AHRD V3.3 *** K4DEK9_SOLLC)		F:GO:0004252: C:G(	F:serine-type endo;	EC:3.4.21	Acting on peptide bo;	IPR022764 (PFAM): PTHR43731:SF5	4,714	4,612	6,675	5,119	5,523									
Solyc12g038630	BSD domain-containing protein (AHRD V3.3 *** AT1G26300.1)						IPR005607 (PFAM): IPR035925 (G3D	35,044	37,026	27,011	24,857	26,386									
Solyc12g038640	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT4G32670.2)							0,042	0,101	0,025	0,050	0,023									
Solyc12g038645	FAR1-related sequence protein, putative (AHRD V3.3 --* A0A072TEZ3_MEDTR)							0,000	0,000	0,050	0,069	0,024									
Solyc12g038650	Protein Ycf2 (AHRD V3.3 --* YCF2_LOTJA)							0,000	0,000	0,000	0,000	0,024									
Solyc12g038653	FAR1-related sequence 5 (AHRD V3.3 *-* AT4G38180.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018289 (PFAM): IPR031052 (PAN	0,000	0,000	0,072	0,149	0,118									
Solyc12g038657	Protein FAR1-RELATED SEQUENCE 5 (AHRD V3.3 *** A0A151RKW8_CAJCA)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR004330 (PFAM): IPR031052 (PAN	0,000	0,000	0,000	0,000	0,071									
Solyc12g038660	LOW QUALITY:Regulator of chromosome condensation (RCC1) family protein (AHRD V3.3 --* AT5G08710.2)							0,000	0,021	0,193	0,269	0,213									
Solyc12g038670	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G15740.1)		C:GO:0005737: P:G(	C:cytoplasm: P:fucose metabolic process: C:integral componen			IPR024709 (PIRSF): IPR019378 (PFA	32,319	27,196	19,856	21,886	21,631									
Solyc12g038680	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)						IPR004146 (PFAM): PTHR13871:SF8:	0,000	0,021	0,000	0,000	0,000									
Solyc12g038690	LOW QUALITY:Ethylene receptor homolog (AHRD V3.3 *-* Q9XET9_SOLLC)		F:GO:0000155: F:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	PTHR44764 (PANTHER)	0,000	0,000	0,025	0,000	0,000									
Solyc12g038700	LOW QUALITY:Extensin repeat-containing protein (AHRD V3.3 *-* A0A103YFZ1_CYNCS)		F:GO:0005199: P:G(	F:structural constituent of cell wall: P:plant-type cell wall organiz			PR01217 (PRINTS): PF01190 (PFAM)	0,080	0,214	0,100	0,025	0,000									
Solyc12g038720	LOW QUALITY:Phosphoglycolate phosphatase (AHRD V3.3 --* M5WGH1_PRUPE)		C:GO:0005739	C:mitochondrion				0,000	0,000	0,000	0,022	0,024									
Solyc12g038805	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0S2I9Z9_MOMCH)		F:GO:0016301: P:G(	F:kinase activity; P:phosphorylation			PTHR44012:SF2 (PANTHER): PTHR4	0,157	0,085	0,534	0,119	0,822									
Solyc12g038810	Protein kinase (AHRD V3.3 --* Q9M7J5_ELYEL)		F:GO:0000166: F:G(	F:nucleotide binding: F:translation release factor activity: F:protein kinase activity: F:protein serine/thre				0,361	0,194	0,799	0,214	0,564									
Solyc12g038820	HAD-superfamily hydrolase, subfamily IIA (AHRD V3.3 *** A0A0K9P0R8_ZOSMR)						IPR006356 (TIGRFAM): IPR023214 ((	18,663	16,228	17,883	14,269	15,706									
Solyc12g038843	electron transfer flavoprotein beta (AHRD V3.3 --* AT5G43430.2)							0,196	0,095	0,100	0,000	0,188									
Solyc12g038910	R8 resistance protein (AHRD V3.3 *-* A0A191UMR5_SOLDE)		F:GO:0043531	F:ADP binding				0,019	0,018	0,000	0,000	0,023									
Solyc12g038920	serine/threonine protein kinase 3 (AHRD V3.3 *** AT5G08160.1)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			G3DSA:3.30.200.20 (GENE3D): IPR0(	31,469	32,738	12,999	13,582	15,629									
Solyc12g038970	EMB1873 protein (AHRD V3.3 *** A0A097PRP8_SOLLC)		F:GO:0004668: P:G(	F:protein-arginine d	EC:3.5.3.12: EC:3.5.	Agmatine deiminase:	IPR007466 (PFAM): IPR007466 (PAN	47,006	41,104	67,680	50,617	52,146			-0,379	0,028	-0,416	0,012		down	down
Solyc12g038980	H/ACA ribonucleoprotein complex subunit 2-like protein (AHRD V3.3 *** A0A0B2QAW4_GLYSO)		F:GO:0003723: C:G(	F:RNA binding; C:nucleolus			IPR018492 (PRINTS): IPR002415 (PF	45,132	46,814	38,753	32,564	34,134									
Solyc12g039000	Ribosomal protein S3 (AHRD V3.3 *-* A0A075VXF7_CAPAN)		F:GO:0003723: F:G(	F:RNA binding: F:structural constituent of ribosome: C:mitochon			PTHR35928 (PANTHER)	0,000	0,000	0,000	0,025	0,023									
Solyc12g039030	LOW QUALITY:Photosystem II protein D1 (AHRD V3.3 *-* PSBA_CUSOB)		P:GO:0009772: F:G(	P:photosynthetic electron transport in photosystem II: F:electro			IPR036854 (G3DSA:1.20.85.GENE3D	0,294	0,478	0,443	0,708	1,423									
Solyc12g039040	LOW QUALITY:Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *-* A0A103XZP5_CYNCS)						PF05664 (PFAM): PTHR31280:SF15 (	0,021	0,078	0,000	0,000	0,000									
Solyc12g039070	Strictosidine synthase (AHRD V3.3 *** G8E0P6_CAMAC)		P:GO:0009058: F:G(	P:biosynthetic proc	EC:4.3.3.2	Strictosidine synthas	IPR018119 (PFAM): IPR011042 (G3D	0,019	0,018	0,000	0,000	0,000									
Solyc12g039080	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *-* AT2G37050.3)		F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR024788 (PFAM): PTHR27003 (PAN	14,803	10,997	19,114	18,082	17,184									
Solyc12g039100	ACT domain-containing protein (AHRD V3.3 *-* A0A103XT27_CYNCS)		P:GO:0009735	P:response to cytokinin			IPR040217 (PANTHER): PTHR31096::	4,580	2,662	4,808	5,664	4,713									
Solyc12g039120	40S ribosomal protein S19-like (AHRD V3.3 *** Q2VCJ6_SOLTU)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR038111 (G3DSA:1.10.10.GENE3D	208,641	235,963	144,840	122,325	132,986									
Solyc12g039170	LOW QUALITY:potassium transporter 2 (AHRD V3.3 --* AT2G40540.5)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,217	0,234	0,022	0,164	0,163									
Solyc12g039180	Diacylglycerol kinase (AHRD V3.3 *** K4DER4_SOLLC)		F:GO:0003951: F:G(	F:NAD+ kinase acti	EC:2.7.1.23: EC:2.7.	NAD(+) kinase: Diac	IPR002219 (PFAM): IPR001206 (PFA	74,328	68,442	73,801	65,303	65,781									
Solyc12g040320	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT5G07910.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	1,003	1,132	0,888	1,084	0,659									
Solyc12g040330	LOW QUALITY:Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *-* B9SZC0_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,000	0,000	0,000	0,000	0,023									
Solyc12g040340	LOW QUALITY:Zinc finger CCCH domain-containing 27-like protein (AHRD V3.3 *-* A0A0B0PXQ4_GOSAR)		F:GO:0046872	F:metal ion binding			PTHR36886:SF4 (PANTHER): PTHR3(	0,040	0,000	0,000	0,000	0,000									
Solyc12g040360	RING/U-box superfamily protein (AHRD V3.3 --* AT1G73760.1)		F:GO:0008270: P:G(	F:zinc ion binding: P:protein ubiquitination: F:ubiquitin protein lig			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,022	0,000									
Solyc12g040390	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G73760.1)		F:GO:0008270: P:G(	F:zinc ion binding: P:protein ubiquitination: F:ubiquitin protein lig			IPR013083 (G3DSA:3.30.40.GENE3D	1,399	1,298	1,377	0,952	1,107									
Solyc12g040450	Ubiquitin-protein ligase, putative (AHRD V3.3 --* G7JLF9_MEDTR)							0,972	0,653	0,512	0,941	0,447									
Solyc12g040460	transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT3G18215.1)		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31168:SF1	10,882	7,280	6,236	6,055	5,414									
Solyc12g040470	non-specific phospholipase C2 (AHRD V3.3 --* AT2G26870.1)							0,259	0,362	0,022	0,000	0,000									
Solyc12g040480	Peroxin-3 (AHRD V3.3 *-* A0A103Y8T9_CYNCS)		C:GO:0005779: P:G(	C:integral component of peroxisomal membrane: P:peroxisome			IPR006966 (PFAM): IPR006966 (PAN	3,266	3,578	3,844	3,681	3,719									
Solyc12g040490	LOW QUALITY:Elongation factor 1-alpha (AHRD V3.3 --* EF1A2_HORVU)							0,288	0,134	0,000	0,050	0,072									
Solyc12g040500	peroxin 3 (AHRD V3.3 *** AT1G48635.1)		C:GO:0005779: P:G(	C:integral component of peroxisomal membrane: P:peroxisome			IPR006966 (PFAM): IPR006966 (PAN	4,970	5,647	5,658	6,148	6,078									
Solyc12g040510	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G18080.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	40,184	43,151	32,373	33,634	32,553									
Solyc12g040520	Katanin p60 ATPase-containing subunit A1 (AHRD V3.3 *** K4DEU6_SOLLC)		F:GO:0005509: F:G(	F:calcium ion bindin	EC:3.6.1.3: EC:3.6.1	Adenosinetriphospha	G3DSA:1.10.8.60 (GENE3D): IPR015	0,299	0,349	0,097	0,266	0,116									
Solyc12g040570	6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *-* A0A0K1P904_SOLCH)		F:GO:0004616: F:G(	F:phosphogluconate	EC:1.1.1.44	Phosphogluconate de	IPR006183 (PRINTS): G3DSA:3.40.50	0,532	0,274	0,429	0,365	0,306									
Solyc12g040580	6-phosphogluconate dehydrogenase, decarboxylating (AHRD V3.3 *-* K4BNC2_SOLLC)		F:GO:0004616: P:G(	F:phosphogluconate	EC:1.1.1.44	Phosphogluconate de	IPR013328 (G3DSA:1.10.1040.GENE:	0,324	0,180	0,362	0,200	0,142									
Solyc12g040640	Beta-glucosidase, putative (AHRD V3.3 *** B9T4F7_RICCO)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			IPR001360 (PRINTS): IPR001360 (PF	46,614	26,535	0,376	0,000	0,350									
Solyc12g040680	mitogen-activated protein kinase 16	mapk16	F:GO:0004672: F:G(	F:protein kinase activity: F:ATP binding: P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510	128,521	188,039	61,633	61,961	80,811									
Solyc12g040685	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 --* A0A072VFP8_MEDTR)							0,915	0,475	1,490	1,970	1,225									
Solyc12g040690	fatty acid hydroxylase 2 (AHRD V3.3 --* AT4G20870.2)							0,000	0,019	0,000	0,072	0,023									
Solyc12g040695	Calcium-dependent phosphotriesterase superfamily protein (AHRD V3.3 --* AT3G59530.3)							0,996	1,086	1,986	3,281	2,851									
Solyc12g040700	Sucrose synthase (AHRD V3.3 *-* M1B219_SOLTU)		P:GO:0005985: F:G(	P:sucrose metaboli	EC:2.4.1.13	Sucrose synthase	IPR000368 (PFAM): G3DSA:1.20.120	0,182	0,116	0,603	0,869	0,687									
Solyc12g040740	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding			IPR001611 (PFAM): IPR032675 (G3D	0,019	0,099	0,050	0,000	0,048									
Solyc12g040760	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *-* A0A061GE38_THECC)		F:GO:0004842: P:G(	F:ubiquitin-protein transferase activity; P:protein ubiquitination			IPR013083 (G3DSA:3.30.40.GENE3D	0,000	0,000	0,000	0,000	0,023									
Solyc12g040790	Phosphoethanolamine N-methyltransferase (AHRD V3.3 *** A0A075BJJ7_LYCBA)		F:GO:0000234: P:G(	F:phosphoethanolai	EC:2.1.1.13	Phosphoethanolamin	PF13489 (PFAM): G3DSA:3.40.50.15(	1,628	3,823	0,144	0,047	0,117									
Solyc12g040800	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT3G17980.1)						IPR000008 (PFAM): PTHR23180:SF3	12,507	20,731	5,466	4,716	6,793	0,755	0,012					up		
Solyc12g040810	Geranylgeranyl transferase type-2 subunit beta (AHRD V3.3 *** A0A0B2SUM0_GLYSO)		F:GO:0004663: P:G(	F:Rab geranylgerar	EC:2.5.1.6	Protein geranylgeran	G3DSA:1.50.10.20 (GENE3D): IPR00	37,383	35,125	42,409	41,558	40,327									
Solyc12g040860	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** A0A061FDC8_THECC)		F:GO:0004553: P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds: P:carb			IPR012946 (PFAM): IPR000490 (PFA	2,262	2,961	0,000	0,000	0,000									
Solyc12g040870	Nudix hydrolase (AHRD V3.3 *** A0A061E9N4_THECC)		F:GO:0016787	F:hydrolase activity			G3DSA:3.90.79.10 (GENE3D): IPR00(	0,176	0,591	0,294	0,311	0,304									
Solyc12g041870	Glutamine synthetase (AHRD V3.3 *** K4DEY2_SOLLC)		F:GO:0004356: P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetas	IPR008146 (PFAM): G3DSA:3.30.590	0,492	1,240	0,173	0,831	0,069									
Solyc12g041875	Glutamine synthetase (AHRD V3.3 *-* K4DEY2_SOLLC)		F:GO:0004356: P:G(	F:glutamate-ammon	EC:6.3.1.2	Glutamine synthetas	IPR036651 (G3DSA:3.10.20.GENE3D	0,211	0,315	0,099	0,151	0,000									
Solyc12g041880	Protein NEOXANTHIN-DEFICIENT 1 (AHRD V3.3 *** NDX1_SOLLC)		P:GO:0016123	P:xanthophyll biosynthetic process			IPR023375 (G3DSA:2.40.400.GENE3I	2,951	3,495	2,184	2,263	2,472									
Solyc12g041890	Non-structural maintenance of chromosome element 4 (AHRD V3.3 *** A0A1D1XPL1_9ARAE)		C:GO:0005634: P:G(	C:nucleus; P:DNA repair; C:Smc5-Smc6 complex			IPR014854 (PFAM): IPR027786 (PAN	0,615	0,576	0,284	0,359	0,329									
Solyc12g041950	O-methyltransferase (AHRD V3.3 *-* G4XGX0_VITVI)	ASMT13	F:GO:0008171	F:O-methyltransferase activity			IPR001077 (PFAM): G3DSA:3.40.50.1	0,677	1,839	0,094	0,385	0,308	1,457	0,030					up		
Solyc12g041955	Serine/Threonine-kinase ATM-like protein (AHRD V3.3 --* AT3G48190.3)							0,040	0,021	0,025	0,045	0,070									
Solyc12g041960	O-methyltransferase (AHRD V3.3 *** A0A1B4Z3W3_9ROSA)	ASMT14	F:GO:0008171: F:G(	F:O-methyltransferase activity; F:protein dimerization activity			G3DSA:3.40.50.150 (GENE3D): IPR0	0,021	0,021	0,000	0,000	0,000									
Solyc12g041980	Protein BREAST CANCER SUSCEPTIBILITY 1 like (AHRD V3.3 *** A0A0B2P4B4_GLYSO)		P:GO:0006281	P:DNA repair			IPR036420 (G3DSA:3.40.50.GENE3D	8,877	14,597	12,976	11,613	13,430	0,741	0,027					up		
Solyc12g042000	Protein BREAST CANCER SUSCEPTIBILITY 1 like (AHRD V3.3 *-* A0A0B2PNV8_GLYSO)		P:GO:0006281	P:DNA repair			PF13771 (PFAM): IPR013083 (G3DS/	0,162	0,143	0,318	0,168	0,188									
Solyc12g042010	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *** B9TBR8_RICCO)		F:GO:0046983	F:protein dimerization activity			IPR036638 (G3DS bHLH	6,486	4,824	1,464	0,732	1,246									
Solyc12g042060	ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B, chloroplastic (AHRD V3.3 *-* CLPAB		P:GO:0019538	P:protein metabolic process			IPR036628 (G3DSA:1.10.1780.GENE:	156,353	176,291	285,361	276,070	332,283									
Solyc12g042065	Chloroplast ATP-dependent Clp protease chaperone protein (AHRD V3.3 *** A0A088F8F4_NICBE)		F:GO:0005515: F:G(	F:protein binding; F:ATP binding			IPR001270 (PRINTS): IPR001943 (PF	365,140	460,635	678,681	647,624	782,947									
Solyc12g042070	Auxin Response Factor 2B	ARF2b					ARF	11,857	10,726	8,755	8,632	8,679									
Solyc12g042073	L-cysteine desulfhydrase 1 (AHRD V3.3 --* AT5G28030.5)							12,840	13,133	10,118	9,243	9,346									
Solyc12g042075	Auxin response factor (AHRD V3.3 *** K4DF01_SOLLC)		F:GO:0005515	F:protein binding			IPR033389 (PFAM): G3DSA:3.10.20.9	62,063	57,278	46,986	45,848	46,806									
Solyc12g042077	Auxin response factor (AHRD V3.3 *** K4DF01_SOLLC)		F:GO:0003677: C:G(	F:DNA binding: C:nucleus: P:regulation of transcription, DNA-ter			G3DSA:2.30.30.1040 (GENE3D): IPR(	56,461	44,034	38,473	41,567	39,995									
Solyc12g042080	40s ribosomal protein S11 (AHRD V3.3 *** K7XKQ3_SOLTU)		F:GO:0003735: C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000266 (PRINTS): IPR000266 (PF	521,695	493,454	263,846	240,472	243,453									
Solyc12g042100	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 --* AT1G43770.3)							0,042	0,160	0,046	0,194	0,118									
Solyc12g042110	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* B4FWF2_MAIZE)		F:GO:0003677	F:DNA binding			G3DSA:2.40.50.140 (GENE3D)	1,069	1,312	0,430	0,786	1,147									
Solyc12g042113	Cytochrome P450 family protein, expressed (AHRD V3.3 --* Q851G2_ORYSJ)		P:GO:0009987	P:cellular process				0,061	0,000	0,000	0,000	0,024									
Solyc12g042117	Transmembrane protein, putative (AHRD V3.3 *-* G7K2H5_MEDTR)		C:GO:0016021	C:integral component of membrane			PTHR31414:SF6 (PANTHER): IPR040	0,854	0,840	0,235	0,434	0,304									
Solyc12g042120	potassium transporter 2 (AHRD V3.3 --* AT2G40540.5)							0,888	1,235	0,340	0,386	0,988									
Solyc12g042170	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *-* G5DWI4_SILLA)		F:GO:0005096: F:G(	F:GTPase activator activity; F:protein binding			IPR001164 (PRINTS): IPR038508 (G3	11,884	13,730	2,896	2,310	2,858									
Solyc12g042173	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *-* G5DWI4_SILLA)		F:GO:0005096: C:G(	F:GTPase activator activity: C:cytoplasm: P:positive regulation			IPR011993 (G3DSA:2.30.29.GENE3D	3,032	2,665	0,712	0,684	0,794									
Solyc12g042177	ADP-ribosylation factor GTPase-activating protein (AHRD V3.3 *-* G5DWI4_SILLA),Pfam:PF16746		F:GO:0005096: C:G(	F:GTPase activator activity: C:cytoplasm: P:positive regulation			IPR027267 (G3DSA:1.20.1270.GENE:	3,494	3,418	0,944	0,814	1,075									
Solyc12g042200	Transducin/WD40 repeat protein (AHRD V3.3 *** G7J399_MEDTR)		F:GO:0005515: P:G(	F:protein binding; P:positive regulation of TOR signaling			IPR001680 (PFAM): IPR015943 (G3D	12,371	10,593	13,548	14,729	15,303									
Solyc12g042230	ATP synthase subunit beta, chloroplastic (AHRD V3.3 *** ATPB_SOLBU)		P:GO:0015986	P:ATP synthesis coupled proton transport			IPR024034 (G3DSA:1.10.1140.GENE:	0,276	0,670	0,097	0,322	0,141									
Solyc12g042240	Peptide transporter (AHRD V3.3 *-* W9SG60_9ROSA)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	4,387	4,494	1,579	1,578	1,246									
Solyc12g042250	Peptide transporter, putative (AHRD V3.3 *** B9S7C1_RICCO)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			IPR000109 (PFAM): IPR000109 (PAN	5,849	6,705	1,635	1,971	2,824									
Solyc12g042260	Peptide transporter (AHRD V3.3 *-* W9SG60_9ROSA)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			G3DSA:1.20.1250.20 (GENE3D): IPR(	0,019	0,018	0,000	0,000	0,024									
Solyc12g042300	Peptide transporter (AHRD V3.3 *** W9SG60_9ROSA)		C:GO:0016020: F:G(	C:membrane: F:transmembrane transporter activity: P:transmen			IPR000109 (PFAM): PTHR11654:SF1:	0,950	0,931	0,071	0,198	0,212									
Solyc12g042340	JHL07K02.14 protein, putative (AHRD V3.3 *** A0A061FYU9_THECC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,363	0,274	0,122	0,098	0,118									
Solyc12g042350	LOW QUALITY:alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G03140.2)		F:GO:0046872	F:metal ion binding			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,058	0,021	0,022	0,025	0,000									
Solyc12g042360	Exostosin family protein (AHRD V3.3 *** AT5G61840.1)		P:GO:0006486: F:G(	P:protein glycosylation: F:transferase activity, transferring glyco			IPR040911 (PFAM): IPR004263 (PAN	41,725	46,863	30,366	29,811	32,131									
Solyc12g042370	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G51030.1)		P:GO:0055114	P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	0,000	0,037	0,225	0,097	0,142									
Solyc12g042380	Stress up-regulated Nod 19 (AHRD V3.3 *** A0A118K3L3_CYNCS)		C:GO:0016021	C:integral component of membrane			IPR011692 (PFAM): IPR011692 (PAN	197,718	161,683	194,061	206,343	205,433									
Solyc12g042390	LOW QUALITY:Werner Syndrome-like exonuclease (AHRD V3.3 *** W9SHV7_9ROSA)		F:GO:0003676: P:G(	F:nucleic acid binding: P:nucleobase-containing compound meta			IPR002562 (PFAM): IPR036397 (G3D	0,372	0,523	0,000	0,000	0,047									
Solyc12g042400	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UJF3_ANACO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	0,879	0,885	0,759	0,945	0,872									
Solyc12g042430	Inositol polyphosphate multikinase (AHRD V3.3 *** K4DF36_SOLLC)		F:GO:0016301: P:G(	F:kinase activity; P:inositol phosphate biosynthetic process			IPR038286 (G3DSA:1.10.510.GENE3I	10,602	16,156	7,360	6,650	7,277	0,633	0,046					up		
Solyc12g042440	FRIGIDA-like protein, putative (AHRD V3.3 *** A0A061G6R8_THECC)		P:GO:0009908: P:G(	P:flower development; P:cell differentiation			IPR012474 (PFAM): mobidb-lite (MOB	36,597	30,055	44,420	40,727	44,704									
Solyc12g042460	4-coumarate--CoA ligase-like	4CL-like	F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.40.50.1	0,813	1,458	0,424	0,170	0,235									
Solyc12g042470	NAD(P)H-dependent oxidoreductase (AHRD V3.3 *** B6SZK3_MAIZE)		F:GO:0016491: P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR020471 (PRINTS): IPR036812 (G3	10,158	16,606	2,100	3,016	4,991	0,736	0,037	1,234	0,015			up	up	
Solyc12g042480	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506: F:G(	F:iron ion binding: F:oxidoreductase activity, acting on paired do			IPR001128 (PRINTS): IPR002401 (PF	6,328	10,178	24,926	29,553	37,379									
Solyc12g042483	Myb/SANT-like DNA-binding domain protein (AHRD V3.3 *** A0A072VX43_MEDTR)		C:GO:0016020	C:membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,049	0,000									
Solyc12g042500	Gibberellin-regulated family protein (AHRD V3.3 *** AT5G59845.1)						IPR003854 (PFAM): mobidb-lite (MOB	74,260	52,446	10,930	9,888	10,704									
Solyc12g042520	Gibberellin-regulated family protein (AHRD V3.3 *** AT2G39540.1)						IPR003854 (PFAM): PTHR23201:SF1(	0,021	0,000	0,000	0,025	0,000									
Solyc12g042530	phosphatidylinositol-glycan biosynthesis class F-like protein (AHRD V3.3 *** AT1G16040.1)		C:GO:0005789: P:G(	C:endoplasmic reticulum membrane: P:GPI anchor biosynthetic			IPR009580 (PFAM): PTHR43157 (PAN	2,483	3,269	5,853	8,720	7,811					0,579	0,042			up
Solyc12g042550	Importin subunit alpha (AHRD V3.3 --* IMA_SOLLC)							1,516	1,331	0,165	0,051	0,070									

Solyc12g042560	Heat shock protein 70 (AHRD V3.3 *-* V5K655_CAPAN)		F:GO:0005524; C:G(	F:ATP binding; C:ce	EC:1.3.1.74; EC:3.6.	2-alkenal reductase (	G3DSA:3.30.30.30 (GENE3D): IPR01:	0,137	0,327	0,025	0,047	0,024									
Solyc12g042570	Protein phosphatase 2C family protein (AHRD V3.3 *** AT4G31860.1)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM): mobidb-lite (MOB	15,878	16,937	13,455	13,525	15,270									
Solyc12g042580	Blue copper-like protein (AHRD V3.3 *** B8Y8A0_GOSHI)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,370	0,548	0,000	0,000	0,000									
Solyc12g042590	WRKY transcription factor 43	WRKY43	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR003657 (PFAM WRKY	0,000	0,121	0,000	0,075	0,023									
Solyc12g042600	Glycosyltransferase (AHRD V3.3 *** K4DF51_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,303	1,203	0,149	0,025	0,093									
Solyc12g042610	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151SA73_CAJCA)						IPR019557 (PFAM): PTHR44194 (PAN	0,121	0,079	0,000	0,000	0,000									
Solyc12g042650	40S ribosomal protein S12 (AHRD V3.3 *** M1CSI4_SOLTU)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR000530 (PRINTS): IPR004038 (PF	118,083	133,728	96,370	84,819	93,089									
Solyc12g042700	tyrosine sulfotransferase-like protein (AHRD V3.3 *** AT4G22000.1)						PTHR36781 (PANTHER)	12,432	12,484	9,936	9,428	9,912									
Solyc12g042710	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT1G56540.2)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,159	0,112	0,000	0,000	0,000									
Solyc12g042715	actin filament bundling protein P-115-ABP protein (AHRD V3.3 --* AT5G57320.2)						mobidb-lite (MOBIDB_LITE)	0,420	0,323	0,298	0,266	0,564									
Solyc12g042720	tyrosine sulfotransferase-like protein (AHRD V3.3 *** AT4G22000.1)						PTHR36781 (PANTHER)	24,202	22,947	26,675	23,379	26,071									
Solyc12g042730	LOW QUALITY:VQ motif-containing protein (AHRD V3.3 *** AT1G80450.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR008889 (PFAM): mobidb-lite (MOB	0,152	0,103	0,050	0,072	0,119									
Solyc12g042740	54-kD signal recognition particle	srp	F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000897 (PFAM): G3DSA:1.20.120	38,512	38,115	43,484	39,006	38,342									
Solyc12g042760	Leucine-rich repeat receptor-like protein kinase family protein, putative (AHRD V3.3 *-* A0A061E290_THEC		F:GO:0005515	F:protein binding			PR00019 (PRINTS): IPR032675 (G3D	0,401	0,323	0,000	0,050	0,047									
Solyc12g042770	post-illumination chlorophyll fluorescence increase (AHRD V3.3 *** AT3G15840.1)		C:GO:0009570; C:G(	C:chloroplast stroma; C:thylakoid; P:chlororespiration			IPR008972 (G3DSA:2.60.40.GENE3D	49,544	79,327	67,793	70,862	115,506	0,705	0,003	0,766	0,000			up	up	
Solyc12g042780	Blue copper protein, putative (AHRD V3.3 *** B9RV67_RICCO)		F:GO:0009055	F:electron transfer activity			IPR003245 (PFAM): IPR008972 (G3D	0,040	0,000	0,000	0,000	0,000									
Solyc12g042800	dsRNA-binding domain-like superfamily protein (AHRD V3.3 --* AT1G09700.1)							8,264	6,369	5,915	6,798	5,100									
Solyc12g042830	Small heat-shock protein, putative (AHRD V3.3 *** B9RV59_RICCO)	Hsp9.0	P:GO:0009408; P:G(	P:response to heat; P:response to high light intensity; P:respon			IPR008978 (G3DSA:2.60.40.GENE3D	35,079	26,286	255,891	319,352	281,332									
Solyc12g042840	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)		F:GO:0016740; F:G(	F:transferase activity; F:lyase activity			IPR004360 (PFAM): IPR029068 (G3D	0,021	0,000	0,000	0,099	0,023									
Solyc12g042860	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TG49_CAJCA)		C:GO:0000943	C:retrotransposon nucleocapsid			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,482	2,027	2,649	1,780	2,048									
Solyc12g042880	DUF1644 family protein (AHRD V3.3 *-* G7LIM9_MEDTR)						IPR012866 (PFAM): mobidb-lite (MOB	0,743	0,748	0,804	1,271	1,414									
Solyc12g042890	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A0B0PZC3_GOSAR)		F:GO:0016787	F:hydrolase activity			IPR003140 (PFAM): IPR029058 (G3D	9,566	6,117	4,745	2,405	5,247					-0,969	0,014			down
Solyc12g042900	Cytochrome c oxidase subunit 5b (AHRD V3.3 *** Q1EMP4_PLAMJ)		F:GO:0004129; C:G(	F:cytochrome-c oxi	EC:1.9.3.1	Cytochrome-c oxidas	IPR036972 (G3DSA:2.60.11.GENE3D	58,610	88,853	77,052	71,922	74,418	0,627	0,023					up		
Solyc12g042910	Cryptochrome-1 (AHRD V3.3 *** A0A151SGR1_CAJCA)		F:GO:0003914; P:G(	F:DNA (6-4) photol	EC:4.1.99; EC:4.1.9!	Carbon-carbon lyase	IPR006050 (PFAM): G3DSA:1.10.579	7,515	7,772	22,361	21,148	29,730									
Solyc12g042920	Cytochrome c1, heme protein (AHRD V3.3 *** G7KN99_MEDTR)		F:GO:0009055; F:G(	F:electron transfer activity; F:heme binding			IPR002326 (PRINTS): G3DSA:1.20.5.	26,423	35,644	44,346	41,403	49,774									
Solyc12g042930	choice-of-anchor C domain protein, putative (Protein of unknown function, DUF642) (AHRD V3.3 *** AT4G32460.2)						IPR006946 (PFAM): IPR008979 (G3D	0,021	0,078	0,022	0,072	0,024									
Solyc12g042950	Plastidic ATP/ADP-transporter (AHRD V3.3 *** TLC1_SOLTU)		F:GO:0005471; P:G(	F:ATP:ADP antiporter activity; P:nucleotide transport; C:integral			IPR004667 (TIGRFAM): IPR004667 (F	207,402	234,048	139,749	123,806	135,588									
Solyc12g042960	LOW QUALITY:PII, uridylyltransferase (DUF2921) (AHRD V3.3 *** AT1G52780.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR021319 (PFAM): PTHR33389:SF4	0,493	0,399	0,753	0,611	0,660									
Solyc12g042980	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** A0A061G9S7_THECC)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR026992 (PFAM): IPR027443 (G3D	0,019	0,000	0,047	0,388	0,093									
Solyc12g042990	CASC3/barentsz eIF4AIII-binding protein (AHRD V3.3 *** A0A072UG99_MEDTR)						IPR018545 (PFAM): mobidb-lite (MOB	43,341	42,766	53,438	56,179	54,068									
Solyc12g043000	Coatomer subunit beta-like protein (AHRD V3.3 *** A0A072VC11_MEDTR)		F:GO:0005198; F:G(	F:structural molecule activity; F:protein binding; P:intracellular p			IPR020472 (PRINTS): G3DSA:1.25.4(	144,092	148,616	173,507	167,749	165,322									
Solyc12g043005	Coatomer subunit beta-like protein (AHRD V3.3 *-* A0A072UH84_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3	5,919	5,860	6,566	8,840	6,915									
Solyc12g043020	Dihydroxy-acid dehydratase (AHRD V3.3 *** A0A1D1YZH9_9ARAE)		F:GO:0004160; P:G(	F:dihydroxy-acid de	EC:4.2.1.9	Dihydroxy-acid dehy	G3DSA:3.50.30.80 (GENE3D): IPR00	174,433	173,629	209,632	174,239	186,126									
Solyc12g043030	Sulfate transporter, putative (AHRD V3.3 *** B9SQC2_RICCO)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;			IPR001902 (TIGRFAM): IPR011547 (F	6,396	5,526	3,111	3,200	2,762									
Solyc12g043050	Protein SYS1 (AHRD V3.3 *** A0A1D1YDQ4_9ARAE)		C:GO:0005802; C:G(	C:trans-Golgi network; C:cytosol; P:Golgi to endosome transpor			IPR019185 (PFAM): PTHR12952:SF0	15,190	19,950	14,857	15,194	15,656									
Solyc12g043070	E3 ubiquitin-protein ligase SHPRH (AHRD V3.3 *-* A0A151U027_CAJCA)		F:GO:0005524; F:G(	F:ATP binding; F:ligase activity; F:metal ion binding			mobidb-lite (MOBIDB_LITE)	0,137	0,299	0,096	0,315	0,234									
Solyc12g043090	Transcription factor, putative (AHRD V3.3 *-* B9SQC7_RICCO)		C:GO:0005634; F:G(	C:nucleus; F:sequence-specific DNA binding; F:transcription rec			G3DSA:1.10.10.6(Trihelix	55,727	53,066	59,323	58,754	59,558									
Solyc12g043100	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151RWM8_CAJCA)		F:GO:0005515	F:protein binding			IPR002885 (PFAM): IPR002885 (PFA	7,661	5,541	5,982	6,226	6,377									
Solyc12g043110	LETSW12	tsw12	F:GO:0005524; C:G(	F:ATP binding; C:nucleus; C:cytosol			IPR013126 (PRINTS): IPR029048 (G3	294,727	245,105	331,778	311,593	319,192									
Solyc12g043120	Heat shock 70 kDa protein, putative (AHRD V3.3 *** B9SQC9_RICCO)		F:GO:0005524; C:G(	F:ATP binding; C:nucleus; C:cytosol			IPR013126 (PRINTS): G3DSA:3.30.3(	103,430	107,627	177,265	182,444	182,835									
Solyc12g043150	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061GBK3_THECC)		P:GO:0015031	P:protein transport			IPR005061 (PFAM): G3DSA:1.20.126	0,569	0,361	0,068	0,050	0,047									
Solyc12g043160	WAT1-related protein (AHRD V3.3 --* A0A061DIG6_THECC)							0,098	0,055	0,087	0,241	0,187									
Solyc12g044180	CC-NBS-LRR disease resistance protein (AHRD V3.3 *** A0A067XSU8_CICAR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	0,000	0,021	0,000	0,000	0,023									
Solyc12g044190	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072U106_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR032675 (G3D	25,299	15,409	16,951	17,630	20,623	-0,686	0,020					down		
Solyc12g044200	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072VNI6_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): G3DSA:1.10.8.43	57,484	49,365	30,420	25,200	26,189									
Solyc12g044220	Phox-associated domain,Phox-like,Sorting nexin isoform 1 (AHRD V3.3 *** A0A061GBL5_THECC)		F:GO:0035091	F:phosphatidylinositol binding			IPR001683 (PFAM): IPR003114 (PFA	82,784	67,104	86,806	89,493	90,363									
Solyc12g044230	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)		C:GO:0016021	C:integral component of membrane			IPR002781 (PFAM): PTHR14255:SF6	11,931	20,933	12,912	15,390	12,204	0,836	0,002					up		
Solyc12g044240	Dynein light chain family protein (AHRD V3.3 *** B9GXB1_POPTR)		P:GO:0007017; C:G(	P:microtubule-based process; C:dynein complex			IPR037177 (G3DSA:3.30.740.GENE3	16,113	16,146	12,135	14,371	10,890									
Solyc12g044250	Glyoxylate reductase (AHRD V3.3 *** A0A0B0MTB0_GOSAR)		F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			IPR006140 (PFAM): G3DSA:3.40.50.7	4,429	8,735	3,233	3,837	3,422	1,005	0,030					up		
Solyc12g044260	Glyoxylate reductase (AHRD V3.3 *** A0A1D1YDH1_9ARAE)	HPPR2	F:GO:0016616; F:G(	F:oxidoreductase activity, acting on the CH-OH group of donors			IPR006140 (PFAM): IPR006139 (PFA	0,410	2,097	0,167	0,146	0,985	2,333	0,000					up		
Solyc12g044270	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 *** AT1G52240.1)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			IPR005512 (PFAM): G3DSA:1.20.58.1	0,084	0,132	0,143	0,356	0,189									
Solyc12g044280	Photosystem I reaction center subunit VI (AHRD V3.3 *** B7FN63_MEDTR)		C:GO:0009538; P:G(	C:photosystem I reaction center; P:photosynthesis			IPR023833 (TIGRFAM): IPR004928 (F	5,591	37,225	1,486	2,551	7,346	2,761	0,000	2,279	0,000			up	up	
Solyc12g044290	Malonate--CoA ligase (AHRD V3.3 *-* AAE13_ARATH)		F:GO:0003824	F:catalytic activity			IPR020459 (PRINTS): G3DSA:3.40.5(	43,849	37,049	27,416	25,079	28,433									
Solyc12g044300	Malonate--CoA ligase (AHRD V3.3 *** A0A0B2P973_GLYSO)		F:GO:0003824	F:catalytic activity			IPR000873 (PFAM): G3DSA:3.30.300	87,164	80,003	51,357	43,486	49,214									
Solyc12g044310	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR000109 (PFAM): PTHR11654:SF1	1,542	1,454	0,069	0,025	0,047									
Solyc12g044320	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G50390.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	0,587	0,466	0,050	0,025	0,046									
Solyc12g044330	tonoplast intrinsic protein 2.1	TIP2.1	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport			IPR000425 (PRINTS): IPR023271 (G3	4,237	6,887	0,022	0,219	0,164									
Solyc12g044340	Coiled-coil domain-containing protein 111 like (AHRD V3.3 *** A0A0B2SDU5_GLYSO)						PF03121 (PFAM): PTHR31399 (PANT	6,297	6,312	3,760	3,723	4,548									
Solyc12g044360	DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 --* RPOC2_IPOPU)						mobidb-lite (MOBIDB_LITE)	0,177	0,019	0,097	0,172	0,165									
Solyc12g044370	Zinc phosphodiesterase ELAC protein 2 (AHRD V3.3 *** A0A0B2RKZ7_GLYSO)		P:GO:0008033	P:tRNA processing			IPR001279 (PFAM): IPR027794 (PFA	18,241	16,520	11,332	11,323	12,001									
Solyc12g044380	Cytochrome c oxidase assembly COX19 (AHRD V3.3 *** A0A0B0NX67_GOSAR)						mobidb-lite (MOBIDB_LITE): PTHR211	3,159	3,293	3,369	3,011	3,426									
Solyc12g044390	ethylene-responsive transcription factor (AHRD V3.3 *-* AT5G07580.1)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec			IPR001471 (PRIN ERF	1,391	0,566	0,284	0,217	0,211									
Solyc12g044400	ATP-dependent zinc metalloprotease FtsH (AHRD V3.3 *** W9R6A6_9ROSA)		F:GO:0004222; F:G(	F:metalloendopeptic	EC:3.4.24	Acting on peptide bor	G3DSA:1.10.8.60 (GENE3D): G3DSA:	56,761	58,040	79,259	80,560	85,513									
Solyc12g044410	Homeobox leucine-zipper protein (AHRD V3.3 *** Q76CL1_ZINVI)		F:GO:0003677; F:G(	F:DNA binding; F:lipid binding			IPR001356 (PFAM HD-ZIP	76,067	51,452	20,448	22,091	35,400			0,788	0,001				up	
Solyc12g044420	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)						IPR008480 (PFAM): PTHR33265:SF8	1,942	1,890	0,874	0,747	1,342									
Solyc12g044450	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)		C:GO:0005794; C:G(	C:Golgi apparatus; C:integral component of membrane; F:O-ace			IPR025846 (PFAM): IPR026057 (PFA	5,254	3,222	0,995	0,641	0,871									
Solyc12g044520	Glutathione S-transferase (AHRD V3.3 *** A0A096XCA4_BETPN)	GSTL4	F:GO:0005515	F:protein binding			PF13410 (PFAM): IPR004045 (PFAM)	1,733	1,456	0,025	0,050	0,000									
Solyc12g044530	Glutathione S-transferase (AHRD V3.3 *** A0A096XCA4_BETPN)	GSTL5	F:GO:0005515	F:protein binding			IPR004045 (PFAM): G3DSA:3.40.30.1	0,112	0,173	0,000	0,000	0,000									
Solyc12g044535	Protein phosphatase 2C family protein (AHRD V3.3 *-* AT4G16580.1)		C:GO:0000139; F:G(	C:Golgi membrane; F:transferase activity, transferring glycosyl			PTHR12320:SF16 (PANTHER): IPR03	0,000	0,018	0,025	0,000	0,023									
Solyc12g044540	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *-* A0A061E4Z7_THECC)		F:GO:0046983	F:protein dimerization activity			IPR008906 (PFAM): PTHR23272 (PAN	0,000	0,000	0,000	0,000	0,023									
Solyc12g044600	NADP-malic enzyme	me1	F:GO:0004471; F:G(	F:malate dehydrog	EC:1.1.1.38; EC:1.1.	Malate dehydrogenas	IPR001891 (PRINTS): IPR012301 (PF	1359,505	1210,891	1260,202	1147,038	1311,389									
Solyc12g044610	Myb transcription factor (AHRD V3.3 *** B1Q4U5_BRUGY)		F:GO:0003677; F:G(	F:DNA binding; F:zinc ion binding			G3DSA:1.10.10.6(MYB_related	4,875	4,697	1,591	2,019	3,339			1,052	0,014				up	
Solyc12g044620	Hemerythrin (AHRD V3.3 *-* A0A1D1XH40_9ARAE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	1,158	1,297	0,502	0,418	0,847									
Solyc12g044630	Profilin (AHRD V3.3 *** M1CJS2_SOLTU)		F:GO:0003785; C:G(	F:actin monomer binding; C:cytoskeleton; C:cell cortex; P:seque			IPR005455 (PRINTS): IPR005455 (PF	5,755	6,855	1,903	1,204	1,841									
Solyc12g044640	Mediator of RNA polymerase II transcription subunit 6 (AHRD V3.3 *** A0A0S2LKL8_REHGL)		F:GO:0003712; P:G(	F:transcription coregulator activity; P:regulation of transcription			IPR016820 (PIRSF): IPR038566 (G3D	38,453	27,957	45,639	45,450	42,827									
Solyc12g044650	pleiotropic drug resistance 13 (AHRD V3.3 --* AT4G15215.9)							0,000	0,018	0,000	0,000	0,000									
Solyc12g044653	F-box family protein (AHRD V3.3 *-* B9GFH4_POPTR)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,000	0,000	0,000	0,000									
Solyc12g044655	Tryptophan aminotransferase-related protein 4 (AHRD V3.3 --* TAR4_ARATH)							0,000	0,019	0,000	0,000	0,000									
Solyc12g044680	LOW QUALITY:Geranylgeranyl pyrophosphate synthase 9, chloroplastic (AHRD V3.3 --* GGPP9_ARATH)							1,968	0,964	2,097	2,636	1,646									
Solyc12g044690	Lysine--tRNA ligase (AHRD V3.3 *-* M1CK13_SOLTU)		F:GO:0000049; F:G(	F:tRNA binding; F:ly	EC:6.1.1.6	Lysine--tRNA ligase	G3DSA:3.30.930.10 (GENE3D): PTHF	0,000	0,137	0,143	0,025	0,023									
Solyc12g044700	F-box protein, putative (AHRD V3.3 *-* A2Q1T0_MEDTR)						IPR032675 (G3DSA:3.80.10.GENE3D	9,055	10,958	10,941	10,004	9,534									
Solyc12g044710	LOW QUALITY:Extensin-like protein Ext1 (AHRD V3.3 *** Q8VWM5_SOLLC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,000	0,000									
Solyc12g044720	60S ribosomal L28-like protein (AHRD V3.3 *** G7IUL4_MEDTR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.390.110 (GENE3D): IPR(	494,357	500,800	244,266	244,696	242,987									
Solyc12g044730	Ribosomal protein S8 (AHRD V3.3 *** A0A124SDM5_CYNCS)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.1490.10 (GENE3D): IPR(	2,716	3,518	1,243	1,333	2,067									
Solyc12g044733	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 --*		F:GO:0003676; F:G(	F:nucleic acid binding; F:RNA-DNA hybrid ribonuclease activity;			IPR026960 (PFAM)	0,082	0,018	0,050	0,000	0,046									
Solyc12g044737	LOW QUALITY:Ribonuclease H-like protein (AHRD V3.3 --* A0A061GHK1_THECC)		F:GO:0003676; F:G(	F:nucleic acid bindi	EC:3.1.3; EC:3.1.26;	Acting on ester bond	IPR036397 (G3DSA:3.30.420.GENE3	0,021	0,019	0,000	0,000	0,046									
Solyc12g044740	ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** AT3G21280.1)		F:GO:0005515; P:G(	F:protein binding; P	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR000626 (PFAM): IPR001394 (PFA	137,471	136,965	250,386	252,477	242,186									
Solyc12g044760	Hyp O-arabinosyltransferase-like protein (AHRD V3.3 *** AT5G13500.3)						PTHR31485 (PANTHER): PTHR31485	0,806	1,390	0,658	0,607	0,421									
Solyc12g044780	LOW QUALITY:F-box family protein (AHRD V3.3 *** AT5G49610.1)		F:GO:0005515	F:protein binding			IPR001810 (PFAM): G3DSA:1.20.128	0,079	0,000	0,000	0,000	0,000									
Solyc12g044800	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B (AHRD V3.3 *** K4DFG5_SOLLC)		C:GO:0000159; F:G(	C:protein phosphatase type 2A complex; F:protein binding; F:pr			IPR000009 (PRINTS): IPR001680 (PF	46,589	41,502	56,630	56,488	51,614									
Solyc12g044820	ABC transporter-like family-protein (AHRD V3.3 *** A0A072TLE5_MEDTR)	ABCC12	F:GO:0005524; C:G(	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): G3DSA:3.40.50.3	28,707	35,794	0,675	1,612	2,345			1,779	0,001				up	
Solyc12g044840	Kinase family protein (AHRD V3.3 *** U5GQI1_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,395	0,548	0,100	0,147	0,070									
Solyc12g044850	WAS/WASL-interacting family protein (AHRD V3.3 *** AT1G55160.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR343	2,889	2,591	1,757	1,851	2,120									
Solyc12g044860	ethylene-responsive RNA helicase	er68	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): G3DS	52,367	56,586	66,365	65,511	66,412									
Solyc12g044880	ss-galactosidase, clone tEG1B	teg1b	F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001944 (PRINTS): G3DSA:3.20.2(	33,498	25,500	42,085	48,045	34,945									
Solyc12g044890	Transmembrane 9 superfamily member (AHRD V3.3 *** M1D790_SOLTU)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): IPR004240 (PAN	2,823	1,692	1,508	1,601	1,525									
Solyc12g044900	Protein ROOT HAIR DEFECTIVE 3 homolog (AHRD V3.3 *** K4DFH4_SOLLC)		F:GO:0005525	F:GTP binding			IPR008803 (PFAM): G3DSA:3.40.50.3	3,030	4,119	1,769	1,313	1,320									
Solyc12g044910	copz2 nonclathrin coat protein zeta2-COP	copz2	P:GO:0006890; C:G(	P:retrograde vesicle-mediated transport, Golgi to endoplasmic r			G3DSA:3.30.450.60 (GENE3D): IPR0	20,420	20,949	14,368	15,536	12,783									
Solyc12g044920	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IZF4_SOLCH)		F:GO:0000287; F:G(	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	PR00119 (PRINTS): IPR006539 (TIGF	5,874	3,892	1,429	1,674	1,909									
Solyc12g044930	F-box family protein (AHRD V3.3 *** AT2G02240.1)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): G3DSA:1.20.128	11,625	11,285	8,341	7,371	8,729									
Solyc12g044940	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G55310.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	42,462	85,398	37,567	35,708	47,021	1,033	0,008					up		
Solyc12g044950	lipid desaturase	cevi19	P:GO:0006629; F:G(	P:lipid metabolic pro	EC:1.14.19	Acting on paired don	IPR005804 (PFAM): IPR021863 (PFA	1,894	1,516	3,301	4,314	19,392			2,542	0,018				up	
Solyc12g044983	Cytochrome P450 family protein (AHRD V3.3 *** B9HFV6_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d			IPR002401 (PRINTS): IPR036396 (G3	0,278	0,362	1,445	2,027	6,984									
Solyc12g044987	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d			IPR002401 (PRINTS): IPR001128 (PF	21,664	19,177	10,797	8,937	9,008									
Solyc12g045020	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired d			IPR001128 (PRINTS): IPR002401 (PF	0,125	0,754	0,121	0,428	1,318									
Solyc12g045030	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G55310.1)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS): IPR002347 (PF	15,191	64,062	5,758	9,360	22,274	2,094	0,004	1,947	0,000			up	up	
Solyc12g049030	Fatty acid desaturase (AHRD V3.3 *** B3SP99_CAPAN)		P:GO:0006629; F:G(	P:lipid metabolic pro	EC:1.14.19	Acting on paired don	IPR021863 (PFAM): IPR005804 (PFA	0,000	0,580	2,874	8,704	17,906			2,628	0,033				up	
Solyc12g049090	Extensin-like protein Ext1 (AHRD V3.3 *-* Q8VWM5_SOLLC)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,021	0,000	0,000	0,000									
Solyc12g049100	WD40 repeat-like protein (AHRD V3.3 *** I0YVP9_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	0,360	0,192	0,000	0,025	0,000									
Solyc12g049130	ABC transporter family protein (AHRD V3.3 *-* AT3G28415.1)	ABCB28	F:GO:0005524; F:G(	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0(	0,000	0,018	0,000	0,000	0,000									
Solyc12g049190	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)		F:GO:0005515	F:protein binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,037	0,076	0,000	0,000	0,000									
Solyc12g049210	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 *** G7IS34_MEDTR)						IPR021899 (PFAM): mobidb-lite (MOB	0,021	0,175	0,000	0,000	0,000									
Solyc12g049220	Mitochondrial import inner membrane translocase subunit tim23 (AHRD V3.3 *** A0A0K9Q5U7_ZOSMR)		C:GO:0005744; F:G(	C:TIM23 mitochondrial import inner membrane translocase com			PF02466 (PFAM): PTHR15371 (PANT	32,172	36,558	34,453	29,767	30,168									
Solyc12g049230	dentin sialophosphoprotein, putative (DUF1296) (AHRD V3.3 *** AT3G13990.2)		F:GO:0005515	F:protein binding			IPR009719 (PFAM): mobidb-lite (MOB	41,273	43,203	69,364	73,372	65,807									
Solyc12g049250	alpha-L-arabinofuranosidase 1 (AHRD V3.3 --* AT3G10740.4)							0,395	0,081	0,025	0,000	0,000									
Solyc12g049270	Developmentally regulated GTP binding family protein (AHRD V3.3 *** B9GWB7_POPTR)		F:GO:0005525	F:GTP binding			IPR006073 (PRINTS): G3DSA:3.40.5(	68,369	53,545	129,446	107,899	112,344									
Solyc12g049280	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061GJI8_THECC)		C:GO:0009507	C:chloroplast			IPR016040 (PFAM): G3DSA:3.40.50.7	2,888	4,171	7,604	6,495	8,580									
Solyc12g049290	ELF4-like protein (AHRD V3.3 *** C6ZKI0_SOLLC)		P:GO:0042753	P:positive regulation of circadian rhythm			IPR009741 (PFAM): G3DSA:1.20.58.3	0,082	0,208	0,194	0,073	0,187									
Solyc12g049300	R2R3MYB transcription factor 54	R2R3MYB54	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,464	0,353	1,002	0,664	0,948									
Solyc12g049310	Ubiquitin-like protein ATG12 (AHRD V3.3 *** K4DFL1_SOLLC)		P:GO:0000045; C:G(	P:autophagosome assembly; C:cytoplasm			IPR007242 (PFAM): G3DSA:3.10.20.9	7,480	6,526	11,975	13,515	10,899									
Solyc12g049320	Nodulation signaling pathway 1-like protein (AHRD V3.3 *** A0MSK8_NICBE)	GRAS	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:hormor			IPR005202 (PFAM GRAS	0,100	0,116	1,144	1,313	1,372									
Solyc12g049330	E3 Ubiquitin ligase (AHRD V3.3 *** A0A118JUQ6_CYNCS)		F:GO:0004842; P:G(	F:ubiquitin-protein transferase activity; P:organelle organization			PF13920 (PFAM): IPR013083 (G3DS/	8,542	8,168	10,271	10,744	10,300									
Solyc12g049340	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4BB98_SOLLC)		P:GO:0006633; C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a			IPR016039 (G3DSA:3.40.47.GENE3D	0,137	0,154	0,143	0,094	0,142									
Solyc12g049350	R2R3MYB transcription factor 11	R2R3MYB11	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,197	0,596	0,661	0,736	0,541									
Solyc12g049360	Kinase family protein (AHRD V3.3 *** U5GAR5_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): G3DS	0,019	0,270	0,000	0,000	0,000									
Solyc12g049370	Nucleoside diphosphate kinase (AHRD V3.3 *** K4DFL7_SOLLC)		F:GO:0004550; P:G(	F:nucleoside diphos	EC:2.7.4.6	Nucleoside-diphosph	IPR001564 (PRINTS): IPR034907 (PF	10,887	10,200	8,768	9,816	9,299									
Solyc12g049390	Lung seven transmembrane receptor family protein (AHRD V3.3 *** AT1G72480.1)		C:GO:0016021	C:integral component of membrane			IPR009637 (PFAM): mobidb-lite (MOB	34,279	27,232	7,491	6,848	8,411									
Solyc12g049400	Jasmonate-zim-domain protein (AHRD V3.3 *** A0A167V6B0_CAMSI)		C:GO:0005634; P:G(	C:nucleus; P:response to wounding; P:regulation of defense res			IPR010399 (PFAM): IPR018467 (PFA	1,889	8,070	0,593	0,345	0,329	2,115	0,000					up		
Solyc12g049410	nuclear pore complex protein (AHRD V3.3 *** AT3G14120.2)		C:GO:0005643; F:G(	C:nuclear pore; F:structural constituent of nuclear pore			G3DSA:1.10.3450.20 (GENE3D): IPR(	56,321	50,516	50,895	49,557	49,826									
Solyc12g049420	25, vesicle transport protein (AHRD V3.3 *** A0A1D1XNZ8_9ARAE)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			G3DSA:3.30.450.50 (GENE3D): IPR0	17,961	17,981	16,620	16,286	13,013									
Solyc12g049425	Adenylyl cyclase (AHRD V3.3 *-* C5MTW3_NICBE)		C:GO:0005747; P:G(	C:mitochondrial respiratory chain complex I; P:respiratory electron transport chain				0,000	0,000	0,025	0,000	0,000									
Solyc12g049430	Peptidyl-prolyl cis-trans isomerase-like protein (AHRD V3.3 *** A0A072U025_MEDTR)		P:GO:0000413; F:G(	P:protein peptidyl-p	EC:5.2.1.8	Peptidylprolyl isomer	IPR002130 (PRINTS): IPR012677 (G3	0,040	0,021	0,000	0,047	0,023									
Solyc12g049443	Actin-related family protein (AHRD V3.3 *-* B9GHK1_POPTR)						IPR025558 (PFAM): G3DSA:3.90.640	0,139	0,096	0,022	0,098	0,187									
Solyc12g049460	Actin-related family protein (AHRD V3.3 *-* B9GHK1_POPTR)		F:GO:0003677; F:G(	F:DNA binding; F:endonuclease activity; P:DNA repair; P:nuclei			G3DSA:3.90.640.10 (GENE3D): SSF5	0,139	0,179	0,047	0,092	0,189									
Solyc12g049470	Actin-related family protein (AHRD V3.3 *-* B9GHK1_POPTR)						G3DSA:3.30.420.40 (GENE3D): IPR0(	0,508	0,623	0,215	0,366	0,352									
Solyc12g049480	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT4G37380.1)							0,252	0,329	0,165	0,314	0,402									
Solyc12g049483	Ulp1 protease family, C-terminal catalytic domain containing protein (AHRD V3.3 *-* Q60D46_SOLDE)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			IPR003653 (PFAM): G3DSA:3.40.395	0,000	0,021	0,000	0,000	0,000									
Solyc12g049500	DUF936 family protein (AHRD V3.3 *** A0A072THZ7_MEDTR)						IPR010341 (PFAM): mobidb-lite (MOB	0,121	0,314	0,047	0,120	0,023									
Solyc12g049505	Clathrin adaptor complex small chain family protein (AHRD V3.3 --* AT4G35410.2)							0,241	0,346	0,044	0,047	0,000									
Solyc12g049510	Erect panicle 2 protein (AHRD V3.3 *-* I2AW42_9POAL)						mobidb-lite (MOBIDB_LITE): mobidb-lit	17,622	13,822	3,516	2,929	4,239									
Solyc12g049520	COP1-interacting-like protein (AHRD V3.3 *-* G7L8C6_MEDTR)						PTHR31008 (PANTHER): PTHR31008	3,026	1,800	0,695	0,735	0,564									

Solyc12g049530	Phosphoinositide phosphatase family protein (AHRD V3.3 *-* B9GXR7_POPTR)		P:GO:0007033; P:G(	P:vacuole organization; P:phosphatidylinositol-3-phosphate bios	mobidb-lite (MOBIDB_LITE); IPR0302	5,478	5,970	5,568	5,045	5,506									
Solyc12g049540	Phosphoinositide phosphatase family protein (AHRD V3.3 *** AT3G14205.1)		P:GO:0007033; P:G(	P:vacuole organization; P:phosphatidylinositol-3-phosphate bios	IPR002013 (PFAM); mobidb-lite (MOB	25,437	20,668	20,833	21,111	22,449									
Solyc12g049550	GDSL esterase/lipase 5 (AHRD V3.3 *** GLIP5_ARATH)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR001087 (PFAM); IPR036514 (G3D	0,193	0,322	0,284	0,773	0,520									
Solyc12g049560	Ethylene-responsive transcription factor (AHRD V3.3 *** I6MBV0_JATCU)	ERF.E5	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRINT_ERF	33,636	27,626	48,573	39,043	39,734									
Solyc12g049570	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** AT3G43240.1)		F:GO:0003677; P:G(	F:DNA binding; P:cellular metabolic process	G3DSA:1.20.120.1070 (GENE3D); IPI	76,467	76,560	112,157	110,254	106,818									
Solyc12g049580	translation initiation factor eIF-2B subunit alpha (AHRD V3.3 *** AT1G53880.1)		P:GO:0044237	P:cellular metabolic process	G3DSA:1.20.120.1070 (GENE3D); G3	0,844	0,788	1,025	0,806	0,965									
Solyc12g049590	1-phosphatidylinositol-3-phosphate 5-kinase (AHRD V3.3 *** W9R271_9ROSA)		F:GO:0005524; F:G(	F:ATP binding; F:phosphatidylinositol phosphate kinase activity;	IPR002423 (PFAM); IPR013083 (G3D	31,988	22,682	33,319	39,784	34,323									
Solyc12g049610	LOW QUALITY:aspartic proteinase A1 (AHRD V3.3 --* AT1G11910.2)					0,042	0,000	0,000	0,000	0,000									
Solyc12g049613	Glycosyltransferase (AHRD V3.3 --* M1CLQ4_SOLTU)				mobidb-lite (MOBIDB_LITE)	6,687	4,886	5,587	5,266	5,413									
Solyc12g049617	Glycosyltransferase (AHRD V3.3 *-* A0A0V0I634_SOLCH)		F:GO:0008194; C:G(	F:UDP-glycosyltransferase activity; C:integral component of me	G3DSA:3.40.50.2000 (GENE3D); PTH	6,772	6,033	4,875	6,257	4,236									
Solyc12g055690	UDP-galactose/UDP-glucose transporter 1 (AHRD V3.3 --* UTR1_ARATH)					0,000	0,000	0,000	0,000	0,047									
Solyc12g055710	RING/U-box superfamily protein (AHRD V3.3 *** AT1G72310.1)		C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40.GENE3D	3,165	3,823	0,115	0,188	0,210									
Solyc12g055720	Ovule receptor-like kinase 28 (AHRD V3.3 *** A4GWX5_SOLCH)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR013210 (PFAM); G3DSA:1.10.510	118,611	102,169	81,086	77,393	81,340									
Solyc12g055730	Lipase (AHRD V3.3 *** Q5S8F1_RICCO)		P:GO:0006629	P:lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	0,000	0,021	8,275	20,079	2,678			-1,624	0,024				down	
Solyc12g055740	Serine/threonine-protein phosphatase (AHRD V3.3 *** G7L9Y4_MEDTR)		P:GO:0006506; F:G(	P:GPI anchor biosynthetic process; F:hydrolase activity	IPR004843 (PFAM); IPR029052 (G3D	22,625	21,511	19,240	20,114	20,610									
Solyc12g055750	vacuolar cation/proton exchanger (AHRD V3.3 *** AT1G55720.2)		C:GO:0000275; P:G(	C:mitochondrial pro EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR004798 (TIGRFAM); IPR006721 (F	37,041	73,124	30,022	29,555	32,800	1,004	0,025					up		
Solyc12g055760	ATP synthase subunit epsilon, mitochondrial (AHRD V3.3 *** ATP5E_IPOBA)		C:GO:0000275; P:G(	C:mitochondrial pro EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR006721 (PFAM); IPR036742 (G3D	9,186	8,625	12,689	11,436	12,712									
Solyc12g055770	LOW QUALITY:Exocyst complex exo70-like protein (AHRD V3.3 *** G7I5R5_MEDTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis	G3DSA:1.20.1280.170 (GENE3D); IPI	0,021	0,037	0,000	0,045	0,023									
Solyc12g055780	RNA-binding KH domain-containing protein (AHRD V3.3 *** AT1G51580.1)		F:GO:0003723	F:RNA binding	G3DSA:3.30.310.210 (GENE3D); IPR(	54,484	51,377	59,033	53,004	54,568									
Solyc12g055800	vacuolar H+-ATPase A1 subunit isoform		F:GO:0005524; P:G(	F:ATP binding; P:A1 EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR031686 (PFAM); G3DSA:2.40.50.1	1012,819	840,718	920,396	823,170	823,672									
Solyc12g055810	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G57480.1)		F:GO:0005524	F:ATP binding	IPR003959 (PFAM); G3DSA:3.40.50.3	6,769	3,080	0,196	0,431	0,354									
Solyc12g055820	cinnamyl-alcohol dehydrogenase (AHRD V3.3 *** AT1G72680.1)		P:GO:0055114	P:oxidation-reduction process	IPR013149 (PFAM); IPR013154 (PFA	17,641	17,180	22,558	20,367	22,297									
Solyc12g055830	Soluble inorganic pyrophosphatase (AHRD V3.3 *** A0T3E7_SOLTU)		F:GO:0000287; F:G(	F:magnesium ion bi EC:3.6.1.1 Inorganic diphosphat	IPR036649 (G3DSA:3.90.80.GENE3D	155,879	164,020	103,125	103,379	102,982									
Solyc12g055840	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RYW1_RICCO)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	G3DSA:3.20.20.80 (GENE3D); IPR00	115,577	77,509	7,439	6,222	8,966									
Solyc12g055850	NC domain-containing protein-like protein (AHRD V3.3 *** AT4G00905.1)				IPR007053 (PFAM); mobidb-lite (MOB	8,609	7,878	7,158	6,056	8,203									
Solyc12g055855	ORMDL family protein (AHRD V3.3 *** AT5G42000.1)		C:GO:0005789; C:G(	C:endoplasmic reticulum membrane; C:integral component of m	IPR007203 (PIRSF); IPR007203 (PFA	18,059	20,476	25,767	27,329	26,804									
Solyc12g055870	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4DFR8_SOLLC)		C:GO:0016021	C:integral component of membrane	G3DSA:1.20.1280.290 (GENE3D); IPI	0,117	0,315	0,123	0,151	0,046									
Solyc12g055910	RING/U-box protein (AHRD V3.3 *** A0A072TWI2_MEDTR)		F:GO:0046872	F:metal ion binding	IPR013083 (G3DSA:3.30.40.GENE3D	27,083	20,713	22,023	21,914	24,329									
Solyc12g055920	Calcineurin B, putative (AHRD V3.3 *** B9RCU6_RICCO)		F:GO:0005509	F:calcium ion binding	PR00450 (PRINTS); G3DSA:1.10.238	0,040	0,000	0,000	0,000	0,024									
Solyc12g055930	UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU)		F:GO:0003978; P:G(	F:UDP-glucose 4-e EC:5.1.3.2 UDP-glucose 4-epim	IPR016040 (PFAM); G3DSA:3.90.25.1	14,347	21,928	24,604	28,826	22,103									
Solyc12g055940	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT1G64430.2)		F:GO:0005515	F:protein binding	IPR011990 (G3DSA:1.25.40.GENE3D	28,351	32,870	22,199	23,722	34,782			0,643	0,000				up	
Solyc12g055950	Pleckstrin-like (PH) domain protein (AHRD V3.3 *** A0A072TVL4_MEDTR)				IPR011993 (G3DSA:2.30.29.GENE3D	7,165	5,481	10,686	9,911	8,493									
Solyc12g055970	Endoglucanase (AHRD V3.3 *** Q93WY9_TOBAC)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001701 (PFAM); IPR012341 (G3D	2,108	7,549	0,090	0,047	0,165	1,866	0,002					up		
Solyc12g055990	Abscisic acid receptor PYL9-like protein (AHRD V3.3 *** V5L1G0_SOLNI)		F:GO:0004864; C:G(	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR023393 (G3DSA:3.30.530.GENE3	18,645	15,844	26,907	27,563	24,569									
Solyc12g056000	Cysteine protease, putative (AHRD V3.3 *** B9SBS8_RICCO)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS); G3DSA:3.90.70	0,155	0,018	0,000	0,022	0,047									
Solyc12g056030	ribosome biogenesis protein (AHRD V3.3 *** AT2G01640.2),Pfam:PF15341		P:GO:0000462; C:G(	P:maturation of SSU-rRNA from tricistronic rRNA transcript (SSI	IPR028160 (PFAM); mobidb-lite (MOB	17,888	16,446	29,053	28,483	27,318									
Solyc12g056040	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 --* AT1G04540.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,061	0,094	0,025	0,000	0,000									
Solyc12g056080	Crooked neck protein, putative (AHRD V3.3 *** B9RCP3_RICCO)		F:GO:0005515; P:G(	F:protein binding; P:RNA processing	IPR003107 (PFAM); IPR011990 (G3D	68,225	62,315	83,959	80,739	77,354									
Solyc12g056090	Cox19-like CHCH family protein (AHRD V3.3 *-* AT4G23760.1)		C:GO:0016021	C:integral component of membrane	IPR010625 (PFAM); G3DSA:1.10.287	4,338	4,855	5,015	5,352	4,521									
Solyc12g056100	Ubiquitin conjugating enzyme E2-like (AHRD V3.3 *** Q38JG8_SOLTU)		F:GO:0004839; F:G(	F:ubiquitin activatin EC:6.2.1.45 E1 ubiquitin-activatin	IPR016135 (G3DSA:3.10.110.GENE3	546,525	434,945	683,778	532,258	580,039					-0,358	0,043			down
Solyc12g056110	V-type proton ATPase subunit E (AHRD V3.3 *** VATE_CITLI)		P:GO:0015991; C:G(	P:ATP hydrolysis cc EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR038495 (G3DSA:3.30.2320.GENE	53,275	47,462	43,961	38,647	43,073									
Solyc12g056130	BTB/POZ domain-containing family protein (AHRD V3.3 *** B9I8T4_POPTR)		F:GO:0005515	F:protein binding	G3DSA:3.30.710.10 (GENE3D); IPR(	13,561	11,512	14,881	14,140	15,149									
Solyc12g056150	Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase form (AHRD V3.3 *** A0A1D1Y4A8_9ARAE)				IPR005079 (PFAM); G3DSA:3.60.60.1	1,592	2,716	1,411	1,884	2,003									
Solyc12g056160	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)		P:GO:0006812; F:G(	P:cation transport; F:solute:proton antiporter activity; C:integral	IPR006153 (PFAM); IPR038770 (G3D	3,406	6,524	3,238	4,861	6,389			0,970	0,011				up	
Solyc12g056170	Chromosome segregation in meiosis 3 (AHRD V3.3 *** A0A0B0NSU0_GOSAR)				mobidb-lite (MOBIDB_LITE); mobidb-lit	11,782	12,927	14,129	12,841	12,875									
Solyc12g056180	Sl 1-aminocyclopropane-1-carboxylate synthase	ACS13	F:GO:0003824; P:G(	F:catalytic activity; P:biosynthetic process; F:pyridoxal phospha	PR00753 (PRINTS); IPR004839 (PFA	0,145	0,122	0,044	0,022	0,000									
Solyc12g056190	Nuclear transport factor 2 (NTF2) family protein (AHRD V3.3 *** AT5G41470.1)		C:GO:0016021	C:integral component of membrane	G3DSA:3.10.450.50 (GENE3D); PTHR	0,120	0,094	0,000	0,050	0,070									
Solyc12g056200	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT4G11350.1)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:integral component	IPR006740 (PFAM); G3DSA:3.90.550	31,068	17,655	0,184	0,100	0,096									
Solyc12g056210	PLAC8 family protein (AHRD V3.3 *** AT1G63830.3)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	79,964	107,662	75,285	82,292	80,518									
Solyc12g056220	plasma membrane intrinsic protein 1.3	PIP1.3	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS); IPR023271 (G3	246,998	223,346	50,648	56,431	68,180									
Solyc12g056230	glutathione peroxidase like encoding 2	gpxle2	F:GO:0004602; P:G(	F:glutathione peroxi EC:1.11.1.9; EC:1.1 Glutathione peroxida	IPR000889 (PRINTS); G3DSA:3.40.30	66,196	69,378	89,719	81,834	84,279									
Solyc12g056240	Glutathione peroxidase (AHRD V3.3 *** K4DFV5_SOLLC)	GPX	F:GO:0004602; P:G(	F:glutathione peroxi EC:1.11.1.9; EC:1.1 Glutathione peroxida	IPR000889 (PRINTS); IPR000889 (PI	8,730	9,274	6,466	5,337	6,412									
Solyc12g056250	Glutathione S-transferase (AHRD V3.3 *** Q9M558_EUPES)	GSTT4	F:GO:0005515	F:protein binding	G3DSA:1.20.1050.10 (GENE3D); G3D	50,273	56,242	54,189	56,759	49,846									
Solyc12g056260	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9RCA5_RICCO)		P:GO:0006486; F:G(	P:protein glycosylation; F:transferase activity, transferring glycc	IPR040911 (PFAM); IPR004263 (PAN	0,000	0,000	0,000	0,000	0,024									
Solyc12g056270	Phosphopantothenoylcysteine decarboxylase (AHRD V3.3 *** W9RGR9_9ROSA)		F:GO:0003824	F:catalytic activity	IPR003382 (PFAM); IPR036551 (G3D	0,590	0,724	0,735	1,021	0,707									
Solyc12g056280	Transmembrane protein, putative (AHRD V3.3 *-* G7J9T6_MEDTR)		C:GO:0005743; F:G(	C:mitochondrial inn EC:1.1.2; EC:1.1.2.2 Acting on diphenols and related substances as donors; Quinc		9,125	9,036	14,751	16,754	14,488									
Solyc12g056290	Transmembrane protein, putative (AHRD V3.3 *-* G7J9T6_MEDTR)		C:GO:0005743; F:G(	C:mitochondrial inn EC:1.1.2; EC:1.1.2.2 Acting on diphenols and related substances as donors; Quinc		4,162	3,765	4,931	5,840	4,502									
Solyc12g056295	LOW QUALITY:RNA-directed DNA polymerase (reverse transcriptase)-related family protein (AHRD V3.3 *-* AT3G24255.3)				IPR026960 (PFAM)	0,481	0,558	0,512	0,416	0,659									
Solyc12g056300	Receptor kinase, putative (AHRD V3.3 *** B9RC93_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D); IPR0	10,996	7,979	5,526	5,328	5,577									
Solyc12g056330	LOW QUALITY:UPSTREAM OF FLC protein (DUF966) (AHRD V3.3 --* AT5G10150.4)					0,059	0,062	0,212	0,025	0,023									
Solyc12g056340	RNA helicase DEAD38		F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D); IPR0	16,550	17,521	18,622	15,547	16,449									
Solyc12g056350	Stress responsive alpha-beta barrel domain protein (AHRD V3.3 *** AT2G32500.2)				G3DSA:3.30.70.100 (GENE3D); IPR0	1,819	3,195	0,233	0,509	0,470									
Solyc12g056355	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 --* AT1G53000.2)					0,040	0,041	0,000	0,025	0,023									
Solyc12g056360	Thaumatin-like protein (AHRD V3.3 *** TLP_ACTDE)				IPR001938 (PRINTS); IPR037176 (G3	4,842	16,594	1,327	2,377	3,157	1,795	0,046	1,257	0,005			up	up	
Solyc12g056380	Thaumatin-like protein (AHRD V3.3 *** TLP_ACTDE)				IPR001938 (PRINTS); IPR037176 (G3	0,063	0,039	0,000	0,022	0,094									
Solyc12g056390	Thaumatin-like protein (AHRD V3.3 *** Q5DJS5_TOBAC)		C:GO:0005773; P:G(	C:vacuole; P:defense response; P:response to biotic stimulus	IPR001938 (PRINTS); IPR001938 (PF	1,316	1,804	2,309	2,233	1,577									
Solyc12g056400	RING/U-box superfamily protein (AHRD V3.3 *** AT3G61180.1)		C:GO:0005774; F:G(	C:vacuolar membrane; F:zinc ion binding; C:integral component	IPR013083 (G3DSA:3.30.40.GENE3D	17,327	12,004	19,497	26,801	17,890					0,463	0,035			up
Solyc12g056410	F-box protein PP2-A13 (AHRD V3.3 *** P2A13_ARATH)		F:GO:0005515	F:protein binding	IPR025886 (PFAM); PTHR31960:SF2	30,757	35,789	55,365	55,251	52,736									
Solyc12g056420	Membrane bound O-acyl transferase family protein (AHRD V3.3 *** B9GW66_POPTR)		C:GO:0016021; F:G(	C:integral component of membrane; F:transferase activity, trans	IPR004299 (PFAM); PTHR13906 (PAI	0,000	0,000	0,047	0,025	0,048									
Solyc12g056440	SPX domain-containing family protein (AHRD V3.3 *** B9GW54_POPTR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	IPR011701 (PFAM); mobidb-lite (MOB	18,245	15,981	33,331	38,275	30,486									
Solyc12g056450	Hydroxymethylglutaryl-CoA synthase (AHRD V3.3 *** HMCS_ARATH)		F:GO:0004421; P:G(	F:hydroxymethylglut EC:2.3.3.1 Hydroxymethylglutary	IPR010122 (TIGRFAM); IPR016039 ((	6,431	6,566	9,714	7,128	8,314									
Solyc12g056480	STAY-GREEN-like protein (AHRD V3.3 *** AT4G11910.1)		F:GO:0005515; C:G(	F:protein binding; C:chloroplast; P:chlorophyll catabolic process	IPR024438 (PFAM); mobidb-lite (MOB	0,042	0,139	0,097	0,141	0,047									
Solyc12g056490	WD40 repeat-containing protein (AHRD V3.3 *** A0A103XFY3_CYNCS)		F:GO:0005515; F:G(	F:protein binding; F:anaphase-promoting complex binding; F:ubi	IPR015943 (G3DSA:2.130.10.GENE3	1,001	1,086	0,971	1,294	1,110									
Solyc12g056510	Trihelix transcription factor GT-2 (AHRD V3.3 *** A0A0B2SAG9_GLYSO)		F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati	G3DSA:1.10.10.6(Trihelix	54,671	31,010	33,455	25,357	27,622	-0,789	0,014			-0,397	0,017	down		down
Solyc12g056520	Exocyst complex component, putative (AHRD V3.3 *-* B9T2G4_RICCO)		C:GO:0000145; P:G(	C:exocyst; P:Golgi to plasma membrane transport	mobidb-lite (MOBIDB_LITE); mobidb-lit	3,251	3,281	4,106	4,272	3,661									
Solyc12g056523	Exocyst complex component, putative (AHRD V3.3 *-* B9T2G4_RICCO)		P:GO:0016192	P:vesicle-mediated transport		0,619	0,689	0,877	1,258	0,963									
Solyc12g056525	Exocyst complex component Sec5 family protein (AHRD V3.3 *-* B9GTJ6_POPTR)		C:GO:0000145; P:G(	C:exocyst; P:Golgi to plasma membrane transport	IPR029175 (PANTHER)	1,755	1,256	1,245	1,400	1,505									
Solyc12g056527	Exocyst complex component, putative (AHRD V3.3 *-* B9T2G4_RICCO)		C:GO:0000145; P:G(	C:exocyst; P:Golgi to plasma membrane transport	mobidb-lite (MOBIDB_LITE); mobidb-lit	2,718	1,841	2,158	2,285	2,549									
Solyc12g056530	Fructose-1,6-bisphosphatase (AHRD V3.3 *** A0A068JD95_TOBAC)		P:GO:0005975; F:G(	P:carbohydrate met EC:3.1.3.23; EC:3.1 Sugar-phosphatase;	IPR028343 (PRINTS); G3DSA:3.30.54	71,943	67,879	214,323	219,668	196,090									
Solyc12g056540	Histone H3 (AHRD V3.3 *** K4DFY5_SOLLC)		C:GO:0000786; F:G(	C:nucleosome; F:DNA binding; F:protein heterodimerization acti	IPR000164 (PRINTS); IPR007125 (PF	2,213	2,879	0,647	0,337	0,399									
Solyc12g056550	LOW QUALITY:Plant/F1M20-13 protein (AHRD V3.3 *** G7IBZ7_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR008511 (PFAM); PTHR31509 (PAI	29,642	18,987	11,301	18,310	13,934	-0,617	0,022			0,695	0,002	down		up
Solyc12g056560	Heat shock family protein (AHRD V3.3 *-* B9GTI4_POPTR)	Hsp27.2	C:GO:0016021	C:integral component of membrane	IPR002068 (PFAM); IPR008978 (G3D	8,956	6,290	2,061	2,731	2,467									
Solyc12g056570	UPF0496 protein (AHRD V3.3 *** A0A0B2QAE4_GLYSO)		C:GO:0016021	C:integral component of membrane	IPR007749 (PFAM); PTHR31113:SF4	0,098	0,079	0,025	0,000	0,000									
Solyc12g056580	Cellulose synthase (AHRD V3.3 *** M1AQH6_SOLTU)		C:GO:0016020; F:G(	C:membrane; F:cell EC:2.4.1.12 Cellulose synthase (I	IPR029044 (G3DSA:3.90.550.GENE3	199,831	163,414	34,873	28,198	55,693									
Solyc12g056590	Ethylene Response Factor D.2	ERF.D2	F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN_ERF	7,892	18,622	9,510	9,532	7,104	1,261	0,010					up		
Solyc12g056600	short-chain dehydrogenase-reductase,Pfam:PF13561		F:GO:0004022; P:G(	F:alcohol dehydrog EC:1.1.1.1 Alcohol dehydrogena	IPR002347 (PRINTS); IPR002347 (PF	0,140	0,897	26,496	67,161	21,628					1,345	0,000			up
Solyc12g056610	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561		F:GO:0004022; P:G(	F:alcohol dehydrog EC:1.1.1.1 Alcohol dehydrogena	IPR002347 (PRINTS); PF13561 (PFAI	0,000	0,000	0,166	0,124	0,047									
Solyc12g056620	Photosystem II 22 kDa, chloroplastic (AHRD V3.3 *** A0A0B0NSB2_GOSAR)		C:GO:0009535; P:G(	C:chloroplast thylakoid membrane; P:response to light intensity	IPR023329 (G3DSA:1.10.3460.GENE	0,160	0,390	0,509	0,938	1,627			1,657	0,001				up	
Solyc12g056625	Plant neutral invertase family protein (AHRD V3.3 --* AT4G34860.3)					1,336	1,119	1,283	1,570	1,722									
Solyc12g056630	Holocarboxylase synthetase (AHRD V3.3 *** B3TM33_ELAGV)				IPR016549 (PIRSF); mobidb-lite (MOE	14,131	13,815	31,688	34,933	31,301									
Solyc12g056640	Transporter-related family protein (AHRD V3.3 *** B9H7W1_POPTR)		F:GO:0005338; P:G(	F:nucleotide-sugar transmembrane transporter activity; P:nucle	IPR004853 (PFAM); mobidb-lite (MOB	41,054	53,181	36,588	39,752	33,280									
Solyc12g056650	GIGANTEA (AHRD V3.3 *** F2Z6M2_IPONI)		P:GO:2000028	P:regulation of photoperiodism, flowering	IPR026211 (PRINTS); mobidb-lite (MC	194,356	166,855	194,335	186,715	235,921									
Solyc12g056660	Mitochondrial carrier protein, putative (AHRD V3.3 *** B9SW87_RICCO)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpc	IPR002067 (PRINTS); IPR018108 (PF	10,521	9,110	7,216	5,900	6,594									
Solyc12g056670	LOW QUALITY:Superoxide dismutase [Cu-Zn] (AHRD V3.3 --* SODC_SOYBN)					0,159	0,174	0,046	0,193	0,118									
Solyc12g056673	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SA73_CAJCA)				IPR019557 (PFAM); PTHR44194 (PAI	0,080	0,018	0,047	0,000	0,118									
Solyc12g056690	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *** A0A151RU32_CAJCA)				IPR019557 (PFAM); PTHR44194 (PAI	2,714	5,175	1,953	0,530	6,748			1,785	0,003				up	
Solyc12g056710	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT1G52340.1),Pfam:PF13561		F:GO:0004022; P:G(	F:alcohol dehydrog EC:1.1.1.1 Alcohol dehydrogena	IPR002347 (PRINTS); IPR002347 (PF	0,000	0,000	0,000	0,075	0,023									
Solyc12g056720	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4DG03_SOLLC)		P:GO:0006633; C:G(	P:fatty acid biosynthetic process; C:membrane; F:transferase a	IPR013747 (PFAM); IPR012392 (PIRS	0,000	0,000	0,074	0,025	0,000									
Solyc12g056730	LRR receptor-like kinase (AHRD V3.3 *** A0A072VNN3_MEDTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	PR00019 (PRINTS); IPR013210 (PFA	0,076	0,064	0,093	0,097	0,165									
Solyc12g056740	RNA helicase DEAD39	DEAD39	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding	IPR011545 (PFAM); G3DSA:3.40.50.3	48,445	54,258	67,668	58,854	65,364									
Solyc12g056750	WRKY transcription factor 61	WRKY61	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR036576 (G3DS_WRKY	0,000	0,062	0,000	0,000	0,094									
Solyc12g056760	Eukaryotic translation initiation factor 3 subunit C (AHRD V3.3 *** A0A1D1ZH74_9ARAE)		C:GO:0016021	C:integral component of membrane	PTHR35475:SF1 (PANTHER); PTHR3	2,011	1,308	0,589	0,828	0,542									
Solyc12g056770	F-actin capping protein beta subunit (AHRD V3.3 *** A0A072VNL1_MEDTR)		C:GO:0008290; P:G(	C:F-actin capping protein complex; P:barbed-end actin filament	IPR001698 (PRINTS); IPR001698 (PF	17,283	17,797	10,645	8,959	10,402									
Solyc12g056780	HSP20-like chaperones superfamily protein (AHRD V3.3 *** A0A061FJ96_THECC)		C:GO:0005634; C:G(	C:nucleus; C:cytosol; P:protein folding; F:chaperone binding; P:	IPR008978 (G3DSA:2.60.40.GENE3D	25,926	16,845	64,516	58,550	53,328	-0,595	0,041					down		
Solyc12g056790	NAC Transcription Factor	NAC101	F:GO:0003677; P:G(	F:DNA binding; P:regulation of transcription, DNA-templated	IPR036093 (G3DS_NAC	104,962	100,231	55,379	77,925	74,378			0,422	0,035	0,494	0,003		up	up
Solyc12g056800	Oxidoreductase family protein (AHRD V3.3 *** A0A061FK19_THECC)		F:GO:0016491	F:oxidoreductase activity	G3DSA:3.40.50.720 (GENE3D); G3DS	21,753	26,366	12,017	9,333	13,752									
Solyc12g056810	Cytochrome P450, putative (AHRD V3.3 *** B9SMA4_RICCO)		F:GO:0005506; F:G(	F:iron ion binding; F:oxidoreductase activity, acting on paired dc	IPR002401 (PRINTS); IPR001128 (PF	0,000	0,000	0,022	0,000	0,024									
Solyc12g056820	Laccase (AHRD V3.3 *** A0A022RU64_ERYGU)		F:GO:0005507; P:G(	F:copper ion bindin EC:1.1.3; EC:1.1.3.2 Acting on diphenols a	IPR017761 (TIGRFAM); IPR008972 ((	0,175	0,158	0,000	0,000	0,000									
Solyc12g056830	ATP synthase delta-subunit protein (AHRD V3.3 *** A0A061F8S8_THECC)		P:GO:0015986; F:G(	P:ATP synthesis co EC:3.6.1.3; EC:3.6.1 Adenosinetriphospha	IPR000711 (PRINTS); IPR000711 (PF	79,803	175,364	48,705	61,965	127,932	1,164	0,001	1,389	0,000			up	up	
Solyc12g056840	phosphopantothenate-cysteine ligase-like protein (AHRD V3.3 *** AT5G02080.7)		F:GO:0016874	F:ligase activity	IPR035929 (G3DSA:3.40.50.GENE3D	19,411	19,328	23,710	24,180	24,512									
Solyc12g056850	Chaperone protein DnaJ (AHRD V3.3 *** W9SH24_9ROSA)		C:GO:0009507	C:chloroplast	IPR001623 (PRINTS); IPR001623 (PF	1,360	1,773	6,061	7,182	6,722									
Solyc12g056855	2OG-Fe(II) oxygenase (AHRD V3.3 *-* Q2HV29_MEDTR)				IPR007021 (PFAM); mobidb-lite (MOB	0,040	0,079	0,072	0,045	0,000									
Solyc12g056860	bZIP transcription factor family protein (AHRD V3.3 *** AT1G77920.1)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans	IPR025422 (PFAN_bZIP	22,702	22,877	27,486	26,623	26,985									
Solyc12g056880	oxidoreductase%2C 2OG-Fe(II) oxygenase family protein (AHRD V3.3 *-* AT2G22260.5)		F:GO:0008168; F:G(	F:methyltransferase activity; F:oxidoreductase activity; P:methylation; F:dioxygenase activity; P:oxidati		0,040	0,138	0,046	0,025	0,140									
Solyc12g056900	Membrane-anchored ubiquitin-fold protein (AHRD V3.3 *** A0A0K9NMY0_ZOSMR)		F:GO:0005515	F:protein binding	IPR017000 (PIRSF); G3DSA:3.10.20.!	20,912	21,617	25,723	24,642	21,130									
Solyc12g056910	zinc finger CCCH domain protein (AHRD V3.3 *** AT1G22140.3)				IPR032378 (PFAM); mobidb-lite (MOB	9,837	9,139	13,067	12,886	10,316									
Solyc12g056920	Sulfate transporter, putative (AHRD V3.3 *** B9RJF7_RICCO)		F:GO:0008271; P:G(	F:secondary active sulfate transmembrane transporter activity;	IPR002645 (PFAM); IPR011547 (PFA	0,019	0,094	0,025	0,000	0,000									
Solyc12g056930	sulfate transporter 2	LeST1-2	C:GO:0005886; F:G(	C:plasma membrane; F:secondary active sulfate transmembran	IPR001902 (TIGRFAM); IPR011547 (F	25,100	18,006	6,884	3,199	5,254					-1,103	0,034			down
Solyc12g056940	Acetyl-CoA carboxylase family protein (AHRD V3.3 *** B9GUK0_POPTR)		F:GO:0003989; F:G(	F:acetyl-CoA carbo EC:6.4.1.2 Acetyl-CoA carboxyla	IPR005479 (PFAM); IPR005481 (PFA	133,061	91,139	316,445	370,464	339,681									
Solyc12g056950	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT1G78020.1)				IPR007650 (PFAM); mobidb-lite (MOB	7,650	5,196	15,864	10,740	11,334									
Solyc12g056960	Glucan 1,3-beta-glucosidase (AHRD V3.3 *** A0A151TZN5_CAJCA)		F:GO:0004553; P:G(	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb	IPR001547 (PFAM); G3DSA:2.80.10.5	1,192	0,765	1,174	2,096	1,364									
Solyc12g056980	Ethylene-responsive element binding-factor (AHRD V3.3 *** K9UTK3_JATCU)		F:GO:0003677; F:G(	F:DNA binding; F:DNA-binding transcription factor activity; P:rec	IPR001471 (PRIN_ERF	2,629	4,025	1,204	0,726	1,341									
Solyc12g056990	LOW QUALITY:nucleolar GTP-binding protein (AHRD V3.3 *** AT1G78110.1)				mobidb-lite (MOBIDB_LITE); mobidb-lit	0,277	0,461	0,265	0,241	0,237									
Solyc12g056995	tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *** AT5G65160.1)		F:GO:0005515	F:protein binding	PF13414 (PFAM); IPR019734 (PFAMI	5,031	4,079	5,840	5,669	5,717									
Solyc12g057000	VQ motif-containing protein (AHRD V3.3 *-* A0A061FH18_THECC)		F:GO:0016301; P:G(	F:kinase activity; P:phosphorylation	IPR039609 (PANTHER); PTHR33179:	1,811	2,279	0,499	0,761	0,726									
Solyc12g057010	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport	G3DSA:1.20.1250.20 (GENE3D); IPR	0,216	0,118	0,000	0,025	0,000									
Solyc12g057020	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)				IPR005181 (PFAM); IPR036514 (G3D	0,136	0,213	0,000	0,000	0,000									
Solyc12g057040	cryptochrome 1b	cry1b	P:GO:0009785; F:G(	P:blue light signaling pathway; F:blue light photoreceptor activity	IPR002081 (PRINTS); G3DSA:1.25.40	63,296	44,653	10,558	11,323	21,204			0,999	0,006				up	
Solyc12g057050	NOD26-like intrinsic protein 3.2	NIP3.2	F:GO:0015267; C:G(	F:channel activity; C:membrane; P:transmembrane transport	IPR000425 (PRINTS); IPR023271 (G3	0,019	0,000	0,000	0,022	0,000									
Solyc12g057060	Glycosyltransferase (AHRD V3.3 *** M1AG38_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR	0,735	1,031	0,262	0,406	0,774									
Solyc12g057070	Glycosyltransferase (AHRD V3.3 *** Q589Y2_TOBAC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR	0,000	0,000	0,000	0,025	0,000									
Solyc12g057075	Purine permease-like protein (AHRD V3.3 *-* G7J4H5_MEDTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane	PF16913 (PFAM); PTHR31376:SF8 (F	0,202	0,199	0,100	0,025	0,164									
Solyc12g057077	Zinc-finger domain of monoamine-oxidase A repressor R1 protein (AHRD V3.3 --* AT5G38690.2)					0,080	0,057	0,000	0,000	0,023									
Solyc12g057080	Glycosyltransferase (AHRD V3.3 *** Q589Y2_TOBAC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D); IPR	0,000	0,000	0,000	0,075	0,000									
Solyc12g057100	Purine permease (AHRD V3.3 *** G7KBC7_MEDTR)		F:GO:0005215; C:G(	F:transporter activity; C:integral component of membrane	PF16913 (PFAM); PTHR31376:SF8 (F	0,021	0,097	0,025	0,000	0,000									
Solyc12g057110	14-3-3 protein		F:GO:0019904	F:protein domain specific binding	IPR000308 (PRINTS); IPR036815 (G3	55,509	68,864	12,125	12,904	14,007									
Solyc12g057120	Subunit VIb of cytochrome c oxidase (AHRD V1 *-*- C4R7U6_PICPG)		C:GO:0005739	C:mitochondrion	IPR003213 (PFAM); IPR036549 (G3D	56,863	54,518	60,935	68,937	62,212									
Solyc12g057130	Protein FAM91A1 (AHRD V3.3 *** A0A0B2QR44_GLYSO)				IPR028097 (PFAM); IPR028091 (PFA	0,061	0,176	0,025	0,025	0,118									
Solyc12g057140	Arabinogalactan protein (AHRD V3.3 *** A0A140JWN5_TOBAC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	9,139	11,548	4,266	5,588	6,776									
Solyc12g057150	transmembrane protein (AHRD V3.3 --* AT2G46550.3)				mobidb-lite (MOBIDB_LITE)	71,599	36,965	18,685	55,931	42,961			1,196	0,000	1,581	0,000		up	up
Solyc12g057160	Arabinogalactan protein (AHRD V3.3 *** A0A140JWN5_TOBAC)		C:GO:0016021	C:integral component of membrane	mobidb-lite (MOBIDB_LITE); mobidb-lit	52,316	14,636	18,863	79,119	51,305	-1,815	0,000	1,439	0,000	2,068	0,000	down	up	up

Solyc12g062160	LOW QUALITY:DUF1645 family protein (AHRD V3.3 -** A0A072V162_MEDTR)						PTHR33095:SF23 (PANTHER): PTHR:	0,767	0,830	0,384	0,173	0,307									
Solyc12g062200	LOW QUALITY:Ferredoxin--NADP reductase, chloroplastic (AHRD V3.3 --* FENR_CHLRE)						mobidb-lite (MOBIDB_LITE): mobidb-lit	10,595	15,263	11,190	16,951	14,295					0,601	0,008			up
Solyc12g062220	LOW QUALITY:DUF1645 family protein (AHRD V3.3 *** A0A072V162_MEDTR)						IPR012442 (PFAM): PTHR33095:SF2:	0,000	0,000	0,000	0,000	0,024									
Solyc12g062250	like SEX4 1 (AHRD V3.3 *** AT3G01510.1)		F:GO:0005515; P:GO	F:protein binding; P:starch catabolic process			IPR013783 (G3DSA:2.60.40.GENE3D	22,377	22,528	22,890	17,660	28,682									
Solyc12g062260	5'-AMP-activated protein kinase subunit beta-2 (AHRD V3.3 *-* A0A1D1ZJL7_9ARAE)		P:GO:0005983	P:starch catabolic process			IPR013783 (G3DSA:2.60.40.GENE3D	0,019	0,000	0,000	0,022	0,000									
Solyc12g062280	MAP kinase kinase kinase 86	MAPKKK86	F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PRINTS): G3DSA:1.10.51	41,792	44,828	55,378	58,337	59,730									
Solyc12g062290	Protease Do-like 9 (AHRD V3.3 *** W9SJ69_9ROSA)		F:GO:0004252; F:GO	F:serine-type endo	EC:3.4.21	Acting on peptide bor	IPR001940 (PRINTS): G3DSA:2.30.42	50,794	39,174	32,425	24,940	23,587			-0,463	0,008	-0,376	0,034		down	down
Solyc12g062295	Gag-pro-like protein (AHRD V3.3 *-* A0A061E733_THECC)		F:GO:0003676	F:nucleic acid binding			IPR000467 (PFAM): mobidb-lite (MOB	0,000	0,021	0,022	0,000	0,000									
Solyc12g062340	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G44840.1)							2,047	2,003	1,255	1,128	1,257									
Solyc12g062343	Transmembrane 9 superfamily member (AHRD V3.3 *-* K4C7L1_SOLLC)		C:GO:0016021	C:integral component of membrane			IPR004240 (PFAM): PTHR10766:SF4	0,868	0,879	0,663	0,575	0,281									
Solyc12g062450	LOW QUALITY:DNA repair metallo-beta-lactamase family protein (AHRD V3.3 --* AT3G26680.3)		C:GO:0005739	C:mitochondrion				0,019	0,062	0,025	0,000	0,000									
Solyc12g062480	conserved telomere maintenance component 1 (AHRD V3.3 *** AT4G09680.4)		P:GO:0000723	P:telomere maintenance			IPR028262 (PFAM): PTHR14865 (PAN	18,282	15,467	16,237	15,730	16,233									
Solyc12g062490	LOW QUALITY:Enhancer of mRNA-decapping protein 4 (AHRD V3.3 *-* W9QQU0_9ROSA)		C:GO:0000932; P:GO	C:P-body; P:deadenylation-independent decapping of nuclear-tr			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,019	0,000	0,025	0,046									
Solyc12g062510	LOW QUALITY:Phospholipid-transporting ATPase (AHRD V3.3 *-* A0A0V0IZF0_SOLCH)		F:GO:0000287; F:GO	F:magnesium ion bi	EC:3.6.1.3; EC:3.6.3	Adenosinetriphospha	IPR006539 (PANTHER): PTHR24092:	0,442	0,499	0,339	0,143	0,213									
Solyc12g062520	AP-2 complex subunit mu (AHRD V3.3 *-* AP2M_ARATH)		P:GO:0006886; P:GO	P:intracellular protein transport; P:vesicle-mediated transport; C			G3DSA:2.60.40.1170 (GENE3D): IPR	0,019	0,085	0,168	0,100	0,046									
Solyc12g062530	ATP synthase beta subunit (AHRD V3.3 *-* H6X0W0_9ASTE)		P:GO:0046034; P:GO	P:ATP metabolic process; P:proton transmembrane transport			G3DSA:2.40.10.170 (GENE3D): G3DS	0,000	0,078	0,072	0,025	0,047									
Solyc12g062540	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *** RBL_HYDFO)		F:GO:0000287; F:GO	F:magnesium ion bi	EC:4.1.1.39	Ribulose-bisphospha	IPR017443 (PFAM): IPR036376 (G3D	0,000	0,043	0,101	0,201	0,094									
Solyc12g062550	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_NICPH)		F:GO:0000287	F:magnesium ion binding			IPR000685 (PFAM): IPR036376 (G3D	0,075	0,167	0,171	0,299	0,306									
Solyc12g062560	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_CLAXA)		F:GO:0000287	F:magnesium ion binding			IPR036376 (G3DSA:3.20.20.GENE3D	0,021	0,043	0,025	0,075	0,000									
Solyc12g062570	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0K1ZCY4_9LAMI)		F:GO:0016740	F:transferase activity			SSF64484 (SUPERFAMILY)	0,000	0,000	0,000	0,050	0,000									
Solyc12g062580	DNA-directed RNA polymerase subunit (AHRD V3.3 *-* A0A0C5CGC5_9ROSI)		F:GO:0003899; C:GO	F:DNA-directed 5'-3	EC:2.7.7.6	DNA-directed RNA pc	G3DSA:2.40.40.20 (GENE3D): SSF64	0,000	0,000	0,000	0,025	0,000									
Solyc12g062585	Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V3.3 *-* PSAA_SOLBU)		C:GO:0009522; P:GO	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,000	0,000	0,025	0,000									
Solyc12g062590	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_PIPCE)		C:GO:0009522; P:GO	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,000	0,072	0,000	0,000									
Solyc12g062595	30S ribosomal protein S2, chloroplastic (AHRD V3.3 *-* RR2_SOLLC)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:translation; C:small ribos			IPR001865 (PRINTS): IPR001865 (PF	0,021	0,037	0,000	0,025	0,024									
Solyc12g062600	Photosystem I P700 chlorophyll A apoprotein (AHRD V3.3 *-* C7U1N4_9ASPA)		C:GO:0009522; P:GO	C:photosystem I; P:photosynthesis; C:integral component of me			IPR001280 (PRINTS): IPR001280 (PF	0,019	0,000	0,000	0,025	0,000									
Solyc12g062610	Photosystem I P700 chlorophyll a apoprotein A2 (AHRD V3.3 *-* PSAB_CITSI)		C:GO:0009522; P:GO	C:photosystem I; P:photosynthesis; C:integral component of me			IPR036408 (G3DSA:1.20.1130.GENE	0,000	0,018	0,000	0,000	0,000									
Solyc12g062680	HNH endonuclease (AHRD V3.3 *-* A0A103YC95_CYNCS)		F:GO:0003676; F:GO	F:nucleic acid binding; F:endonuclease activity; P:nucleic acid phosphodiester bond hydrolysis				0,000	0,043	0,000	0,000	0,000									
Solyc12g062690	transmembrane protein (AHRD V3.3 --* AT3G47510.1)						PTHR33474:SF2 (PANTHER): PTHR3:	2,016	1,523	0,430	0,173	0,567									
Solyc12g062720	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151SLA5_CAJCA)		F:GO:0005515; F:GO	F:protein binding; F:zinc ion binding			IPR002885 (PFAM): IPR002885 (PFA	0,000	0,000	0,000	0,025	0,000									
Solyc12g062733	Tropomyosin GRF zinc finger protein (AHRD V3.3 *** A0A191UMP7_SOLDE)		F:GO:0008270	F:zinc ion binding			IPR010666 (PFAM): PTHR33248 (PAN	0,000	0,019	0,000	0,000	0,000									
Solyc12g062800	SCAR family protein (AHRD V3.3 --* AT2G34150.5)							0,379	0,898	0,000	0,000	0,070									
Solyc12g062810	LOW QUALITY:glucose-6-phosphate/phosphate translocator 2 (AHRD V3.3 --* AT1G61800.2)							0,000	0,000	0,000	0,101	0,024									
Solyc12g062840	LOW QUALITY:abscisic acid responsive elements-binding factor 2 (AHRD V3.3 --* AT1G45249.9)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): PTHR332	0,021	0,000	0,000	0,000	0,000									
Solyc12g062860	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT5G14680.1)		F:GO:0016208	F:AMP binding			IPR006015 (PRINTS): IPR006016 (PF	66,068	65,621	167,210	145,893	156,712									
Solyc12g062870	Kinase family protein (AHRD V3.3 *** D7M6L5_ARALL)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM): G3DSA:1.10.510.	137,000	143,263	209,107	227,458	204,018									
Solyc12g062930	Transcription elongation factor-related family protein (AHRD V3.3 *** B9H8S4_POPTR)		C:GO:0005634	C:nucleus			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,021	0,062	0,149	0,100	0,071									
Solyc12g062940	Exostosin-like (AHRD V3.3 *** Q2HVN7_MEDTR)		P:GO:0006486; F:GO	P:protein glycosylation; F:transferase activity, transferring glycc			IPR040911 (PFAM): mobidb-lite (MOB	0,000	0,037	0,000	0,000	0,000									
Solyc12g063050	RNA polymerase II C-terminal domain phosphatase-like 3, putative (AHRD V3.3 *** A0A061E5T0_THECC)		F:GO:0008420; P:GO	F:RNA polymerase	EC:3.1.3.16	Protein-serine/threor	IPR004274 (PFAM): IPR001357 (PFA	188,690	169,849	163,688	163,591	162,050									
Solyc12g068070	Filament-like plant protein (AHRD V3.3 *** G7J2M7_MEDTR)		F:GO:0030674; C:GO	F:protein binding, bridging; C:cytoplasmic vesicle; P:regulation c			IPR008587 (PFAM): mobidb-lite (MOB	62,647	39,827	42,718	35,104	40,661	-0,625	0,010					down		
Solyc12g070080	Fatty acid amide hydrolase (AHRD V3.3 *** A0A172CJD2_POPTO)		F:GO:0004040	F:amidase activity	EC:3.5.1.4	Amidase	IPR023631 (PFAM): IPR036928 (G3D	3,813	4,865	24,454	31,551	36,202			0,565	0,005				up	
Solyc12g070100	Mediator of RNA polymerase II transcription subunit 25 (AHRD V3.3 *** A0A0B0PNK0_GOSAR)		C:GO:0016592; C:GO	C:mediator complex; C:nuclear transcription factor complex; P:p			IPR021419 (PFAM): mobidb-lite (MOB	37,967	36,356	60,208	61,112	57,353									
Solyc12g070113	CTP synthase (AHRD V3.3 *-* K4BA89_SOLLC)		F:GO:0000166; F:GO	F:nucleotide binding	EC:6.3.4.2	CTP synthase (glutamine hydrolyzing)		5,357	4,280	7,439	8,721	8,084									
Solyc12g070117	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *-* AT1G06645.1)		F:GO:0046872; F:GO	F:metal ion binding; F:dioxygenase activity; P:oxidation-reductic			IPR027443 (G3DSA:2.60.120.GENE3I	4,889	4,840	13,378	12,376	10,640									
Solyc12g070120	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein (AHRD V3.3 --* AT1G60240.1)							0,120	0,164	0,862	1,074	0,777									
Solyc12g070152	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28620.3)							0,295	0,359	0,266	0,338	0,329									
Solyc12g070156	LOW QUALITY:GRF zinc finger family protein (AHRD V3.3 -** Q2R399_ORYSJ)		F:GO:0008270	F:zinc ion binding			IPR010666 (PFAM)	0,000	0,000	0,044	0,000	0,000									
Solyc12g070200	potassium transporter 2 (AHRD V3.3 --* AT2G40540.5)		F:GO:0003743; P:GO	F:translation initiation factor activity; P:translational initiation			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,042	0,136	0,000	0,025	0,000									
Solyc12g070220	LOW QUALITY:Protein Ycf2 (AHRD V3.3 *-* YCF2_SOLLC)		F:GO:0005524; C:GO	F:ATP binding; C:chloroplast			IPR008543 (PANTHER)	0,019	0,021	0,025	0,050	0,024									
Solyc12g070270	ABC transporter B family protein (AHRD V3.3 *** G7JYX3_MEDTR)		F:GO:0005524; C:GO	F:ATP binding; C:int	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	11,105	11,793	10,278	11,991	13,462									
Solyc12g070280	Abc transporter, putative (AHRD V3.3 *-* B9SPK8_RICCO)	ABCB29	F:GO:0005524; F:GO	F:ATP binding; F:AT	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D): IPR0	12,792	15,388	12,448	13,102	15,080									
Solyc12g076320	Pachytene checkpoint protein 2 like (AHRD V3.3 *-* A0A0B2QCF2_GLYSO)		F:GO:0005524; C:GO	F:ATP binding; C:nu	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR23077 (PANTHER): PTHR23077	4,448	5,095	4,374	4,143	4,664									
Solyc12g076340	P-loop containing nucleoside triphosphate hydrolases superfamily protein isoform 1 (AHRD V3.3 *-* A0A061		F:GO:0005524	F:ATP binding			IPR003959 (PFAM): G3DSA:3.40.50.3	1,092	0,894	0,951	0,679	0,684									
Solyc12g076350	Pachytene checkpoint protein 2-like protein (AHRD V3.3 *-* W9RJB1_9ROSA)		F:GO:0005524; C:GO	F:ATP binding; C:nu	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	mobidb-lite (MOBIDB_LITE): mobidb-lit	3,896	3,449	3,322	3,852	3,864									
Solyc12g077370	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1BPG2_SOLTU)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,057	0,019	0,000	0,000	0,000									
Solyc12g077380	LOW QUALITY:ABC-2 type transporter family protein (AHRD V3.3 --* AT2G37360.1)							0,057	0,039	0,025	0,022	0,000									
Solyc12g077390	Protein kinase (AHRD V3.3 *** C6ZRQ9_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	0,236	0,057	0,000	0,025	0,000									
Solyc12g077420	Zinc finger family protein (AHRD V3.3 *-* B9GY13_POPTR)		F:GO:0003676; F:GO	F:nucleic acid binding; F:DNA binding; C:nucleus; P:regulation o			mobidb-lite (MOBIDB_LITE): PTHR232	3,160	2,863	3,143	3,099	3,490									
Solyc12g077430	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *-* B9GY13_POPTR)		F:GO:0003677; C:GO	F:DNA binding; C:nucleus; P:regulation of transcription, DNA-templated; C:integral component of membr				0,080	0,076	0,118	0,075	0,142									
Solyc12g077440	Zinc finger family protein (AHRD V3.3 *-* B9GY13_POPTR)		F:GO:0003676; F:GO	F:nucleic acid binding; F:DNA binding; C:nucleus; P:regulation of transcription, DNA-templated; C:membi				0,278	0,213	0,320	0,481	0,590									
Solyc12g077460	WD-40 repeat family protein / beige-like protein (AHRD V3.3 --* AT2G45540.6)							1,367	1,302	2,057	2,176	2,193									
Solyc12g077463	pre-mRNA cleavage complex 2 Pcf11-like protein (AHRD V3.3 --* AT2G36480.2)							0,060	0,036	0,000	0,125	0,047									
Solyc12g077467	Zinc finger family protein (AHRD V3.3 *-* B9GY13_POPTR)		F:GO:0003677	F:DNA binding			PTHR23215 (PANTHER): IPR003656 (	0,038	0,075	0,047	0,000	0,000									
Solyc12g077540	Trihelix transcription factor GT-1 (AHRD V3.3 *** TGT1_ARATH)		F:GO:0003677	F:DNA binding			PF13837 (PFAM): Trihelix	5,919	4,930	7,157	7,460	6,997									
Solyc12g077541	Trihelix transcription factor GT-1 (AHRD V3.3 *-* A0A0B2QWD1_GLYSO)						PTHR45169 (PANTHER)	1,264	1,537	2,259	2,217	2,216									
Solyc12g077548	Pleiotropic drug resistance ABC transporter (AHRD V3.3 --* W0TUG3_ACAMN)		F:GO:0000166; F:GO	F:nucleotide binding; F:ATP binding; C:plasma membrane; C:membrane; C:integral component of membr				0,118	0,217	0,072	0,097	0,143									
Solyc12g077590	Peptidyl-tRNA hydrolase 2 (AHRD V3.3 *** B4FSD3_MAIZE)		F:GO:0004045	F:aminoacyl-tRNA h	EC:3.1.1.29; EC:3.1.	Aminoacyl-tRNA hydr	IPR023476 (G3DSA:3.40.1490.GENE	23,429	22,187	27,766	26,768	27,976									
Solyc12g077630	LOW QUALITY:NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --* AT1G09500.1)							0,000	0,019	0,000	0,050	0,000									
Solyc12g077650	30S ribosomal protein S12, chloroplastic (AHRD V3.3 *** RR12_HELAN)		F:GO:0003735; P:GO	F:structural constituent of ribosome; P:translation; C:small ribos			IPR006032 (PRINTS): IPR006032 (PII	0,040	0,246	0,071	0,226	0,237									
Solyc12g077660	Protein SET (AHRD V3.3 *-* A0A0B0PFE9_GOSAR)		C:GO:0005634; P:GO	C:nucleus; P:nucleosome assembly			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,518	1,286	0,933	1,181	1,128									
Solyc12g077680	Protein SET (AHRD V3.3 *-* A0A0B2QEX3_GLYSO)		C:GO:0005634; P:GO	C:nucleus; P:nucleosome assembly			IPR037231 (SUPERFAMILY)	0,139	0,081	0,097	0,025	0,094									
Solyc12g082710	SPX domain-containing family protein (AHRD V3.3 *-* B9GW54_POPTR)		C:GO:0016020; C:GO	C:membrane; C:integral component of membrane; P:transmemb			PTHR23510:SF21 (PANTHER): PTHR:	0,000	0,000	0,050	0,050	0,023									
Solyc12g082720	En/Spm-like transposon protein (AHRD V3.3 --* Q9ZUQ3_ARATH)						PTHR33499:SF1 (PANTHER): PTHR3:	1,615	0,880	2,474	3,898	1,737									
Solyc12g082730	Kinesin-like calmodulin-binding protein like (AHRD V3.3 *-* A0A0B2PXL0_GLYSO)		F:GO:0003777; F:GO	F:microtubule motor	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	PTHR33499:SF1 (PANTHER): PTHR3:	2,336	1,457	3,351	4,892	2,308									
Solyc12g087790	arginine/serine-rich zinc knuckle-containing protein 33 (AHRD V3.3 --* AT2G37340.1)						mobidb-lite (MOBIDB_LITE)	125,832	41,374	42,723	151,962	94,329	-1,582	0,000	1,140	0,000	1,833	0,000	down	up	up
Solyc12g087810	MADS-box transcription factor (AHRD V3.3 *** F1T119_9ERIC)		F:GO:0003700; C:GO	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR002487 (PFAM): PTHR11945:SF2	18,328	15,454	24,352	24,225	24,642									
Solyc12g087830	MADS-box transcription factor (AHRD V3.3 *** F1T119_9ERIC)		F:GO:0000977; F:GO	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRIN MIKC_MADS	37,037	35,446	48,759	55,994	48,974									
Solyc12g087840	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FG67_THECC)		C:GO:0016021; P:GO	C:integral component of membrane; P:protein ubiquitination			IPR013083 (G3DSA:3.30.40.GENE3D	0,063	0,182	2,098	2,549	1,674									
Solyc12g087850	Basic helix-loop-helix transcription factor (AHRD V3.3 *-* A0A0H3YB55_SALMI)		F:GO:0046983	F:protein dimerization activity			PTHR11969 (PAN bHLH	0,019	0,000	0,000	0,000	0,000									
Solyc12g087860	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FLH6_THECC)		C:GO:0016021	C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	0,161	0,399	0,022	0,050	0,047									
Solyc12g087870	Purine permease-like protein (AHRD V3.3 *** G7J4H5_MEDTR)		F:GO:0005215; C:GO	F:transporter activity; C:integral component of membrane			PF16913 (PFAM): PTHR31376:SF1 (F	0,098	0,060	0,116	0,045	0,164									
Solyc12g087890	Transcription factor protein (AHRD V3.3 *** A0A0B0PPY8_GOSAR)		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	41,540	36,086	10,254	8,953	10,942									
Solyc12g087893	Conserved peptide upstream open reading frame 37 (AHRD V3.3 *** B3H738_ARATH)						PTHR35281 (PANTHER): PTHR35281	8,403	7,579	1,774	2,129	2,092									
Solyc12g087900	cyclinD2_1	CycD2_1	C:GO:0005634	C:nucleus			IPR039361 (PIRSF): G3DSA:1.10.472	0,567	0,197	0,000	0,000	0,000									
Solyc12g087920	Receptor-like protein kinase (AHRD V3.3 *** C6F1T6_SOYBN)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR038408 (G3DSA:3.30.430.GENE3I	0,000	0,000	0,000	0,000	0,023									
Solyc12g087940	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061FET5_THECC)		F:GO:0004190; P:GO	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	IPR032799 (PFAM): IPR032861 (PFA	1,370	1,736	0,075	0,000	0,000									
Solyc12g087950	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7J554_MEDTR)		F:GO:0003680	F:AT DNA binding			G3DSA:3.30.1330.80 (GENE3D): IPR(	9,530	22,290	5,503	4,753	5,711	1,251	0,000					up		
Solyc12g087960	Ribosomal RNA small subunit methyltransferase A (AHRD V3.3 *** A0A0B0NTG7_GOSAR)						mobidb-lite (MOBIDB_LITE): PTHR344	10,648	7,914	15,047	18,133	14,377									
Solyc12g087970	Myb family transcription factor family protein (AHRD V3.3 *** B9GN48_POPTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB_related	23,694	18,596	20,447	17,920	18,802									
Solyc12g087980	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061FEX2_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR003480 (PFAM): IPR023213 (G3D	9,353	7,386	2,443	1,763	2,378									
Solyc12g087990	Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 *** G7JYE9_MEDTR)		P:GO:0000398; P:GO	P:mRNA splicing, via spliceosome; P:production of miRNAs invc			IPR028265 (PFAM): mobidb-lite (MOB	6,745	7,957	8,580	8,015	7,463									
Solyc12g088010	Golgi-body localization protein domain isoform 4 (AHRD V3.3 *** A0A061FEK5_THECC)		C:GO:0016021	C:integral component of membrane			IPR019441 (PFAM): IPR019443 (PFA	1,957	1,984	0,773	1,000	1,243									
Solyc12g088020	farnesylcysteine lyase (AHRD V3.3 *** AT5G63910.1)		F:GO:0001735; P:GO	F:prenylcysteine ox	EC:1.8.3.5	Prenylcysteine oxida	PF13450 (PFAM): IPR017046 (PIRSF	7,249	10,217	15,322	17,966	15,631									
Solyc12g088030	Transcription initiation factor IIA subunit 2 (AHRD V3.3 *** K4DGM4_SOLLC)		C:GO:0005672; P:GO	C:transcription factor TFIIA complex; P:transcription initiation fro			IPR015871 (PFAM): IPR015872 (PFA	22,880	22,574	18,828	16,925	16,094									
Solyc12g088040	Kinase, putative (AHRD V3.3 *** A0A061FTR2_THECC)		F:GO:0004672; F:GO	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0	1,010	1,586	0,638	0,922	0,971									
Solyc12g088050	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09890.4)		F:GO:0003824; P:GO	F:catalytic activity; P:carbohydrate metabolic process; F:carbol			IPR029411 (PFAM): IPR010325 (PFA	7,259	9,439	3,603	3,852	3,214									
Solyc12g088060	TRAF-type zinc finger domain-containing 1 (AHRD V3.3 *** A0A0B0MEE8_GOSAR)		F:GO:0008270	F:zinc ion binding			IPR013083 (G3DSA:3.30.40.GENE3D	0,038	0,019	0,125	0,048	0,118									
Solyc12g088070	TRAF-type zinc finger domain-containing 1 (AHRD V3.3 *** A0A0B0MEE8_GOSAR)		F:GO:0008270; C:GO	F:zinc ion binding; C:integral component of membrane			IPR013083 (G3DSA:3.30.40.GENE3D	6,842	5,214	7,709	7,545	7,317									
Solyc12g088090	MADS-box transcription factor (AHRD V3.3 *** G7IS85_MEDTR)		F:GO:0000977; F:GO	F:RNA polymerase II regulatory region sequence-specific DNA I			IPR002100 (PRINTS): IPR002487 (PF	0,058	0,140	0,000	0,025	0,143									
Solyc12g088140	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,138	0,096	0,094	0,025	0,165									
Solyc12g088160	Phosphoenolpyruvate carboxykinase (AHRD V3.3 *** Q94LX8_FLATR)		F:GO:0004612; F:GO	F:phosphoenolpyru	EC:4.1.1.49; EC:4.1.	Phosphoenolpyruvate	IPR001272 (PIRSF): G3DSA:2.170.8.	0,258	0,256	0,140	0,313	0,350									
Solyc12g088170	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,063	2,899	0,022	0,000	0,023	5,409	0,000					up		
Solyc12g088180	Tubulin alpha chain (AHRD V3.3 *** Q2XPX0_SOLTU)		F:GO:0005200; F:GO	F:structural constituent of cytoskeleton; F:GTP binding; C:micro			IPR002452 (PRINTS): IPR037103 (G3	0,121	0,059	0,000	0,094	0,048									
Solyc12g088190	Amino acid permease (AHRD V3.3 *** A0A0K9P9F3_ZOSMR)		C:GO:0005886; F:GO	C:plasma membrane; F:acidic amino acid transmembrane transı			IPR013057 (PFAM): PTHR22950:SF2	0,738	0,998	0,916	2,510	2,110			1,194	0,035	1,451	0,002		up	up
Solyc12g088200	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *** K4DGP1_SOLLC)		F:GO:0000287; F:GO	F:magnesium ion bi	EC:2.7.1.134; EC:2.1	Inositol-tetrakisphosı	G3DSA:3.40.50.11370 (GENE3D): G3	3,996	4,669	4,518	5,546	4,356									
Solyc12g088210	Inositol-tetrakisphosphate 1-kinase (AHRD V3.3 *-* K4DGP1_SOLLC)		F:GO:0004553; P:GO	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carb			IPR001000 (PRINTS): IPR003305 (PF	42,364	30,813	49,443	60,518	52,061									
Solyc12g088220	SlBCAT1	BCAT1	F:GO:0004084; P:GO	F:branched-chain-a	EC:2.6.1.42	Branched-chain-amir	IPR001544 (PFAM): G3DSA:3.30.470.	1,241	0,508	547,768	840,728	386,852			-0,504	0,043	0,621	0,014		down	up
Solyc12g088230	mitochondrial malate dehydrogenase	mmdh	C:GO:0016020	C:membrane			IPR032880 (PFAM): IPR027815 (PFA	63,101	57,277	136,170	164,206	125,158									
Solyc12g088240	Cellulose synthase-like protein (AHRD V3.3 *** L0ASJ1_POPTO)		C:GO:0016021; F:GO	C:integral component of membrane; F:transferase activity			PF13641 (PFAM): IPR029044 (G3DS/	2,104	2,807	14,042	14,602	17,265									
Solyc12g088250	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)		F:GO:0004185; P:GO	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS): IPR001563 (PF	0,358	2,122	0,050	0,075	0,284	2,567	0,000					up		
Solyc12g088290	Transducin/WD-like repeat-protein (AHRD V3.3 *** G7LGL1_MEDTR)		F:GO:0005515	F:protein binding			IPR015943 (G3DSA:2.130.10.GENE3I	58,886	54,002	64,118	71,336	59,333									
Solyc12g088300	At4g33800-like protein (AHRD V3.3 *** A0A068F620_BRANA)		P:GO:0009690	P:cytokinin metabolic process			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,120	0,181	0,143	0,142	0,236									
Solyc12g088310	FAD/NAD(P)-binding oxidoreductase (AHRD V3.3 --* AT1G15140.3)		P:GO:0009690	P:cytokinin metabolic process				14,575	11,421	26,956	23,843	22,499									
Solyc12g088320	Transcription factor LIM		F:GO:0046872	F:metal ion binding			IPR001781 (PFAM): G3DSA:2.10.110.	0,709	1,792	0,386	0,170	0,519	1,354	0,035					up		
Solyc12g088340	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G27840.1)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	31,960	32,351	30,863	31,202	31,952									
Solyc12g088350	heat shock protein HSP20/alpha crystallin family protein (AHRD V3.3 --* AT4G16545.1)							0,042	0,000	0,025	0,050	0,000									
Solyc12g088360	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PK99_ZOSMR)		F:GO:0005515	F:protein binding			IPR000225 (PFAM): IPR011989 (G3D	22,198	14,256	17,950	51,769	28,566			0,665	0,003	1,528	0,000		up	up
Solyc12g088370	Interferon-related developmental regulator family protein (AHRD V3.3 *** B9IBS1_POPTR)						IPR006921 (PFAM): IPR007701 (PFA	7,924	8,393	18,448	24,915	20,306									
Solyc12g088380	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT2G14760.1		F:GO:0046983	F:protein dimerization activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,048									
Solyc12g088390	Zinc-finger protein (AHRD V3.3 *** Q40899_PETHY)		F:GO:0003676	F:nucleic acid binding			PF13912 (PFAM): C2H2	4,450	2,283	0,263	1,303	0,467									
Solyc12g088400	Zinc-finger protein (AHRD V3.3 *-* Q40899_PETHY)		F:GO:0003677	F:DNA binding				3,038	0,927	0,091	0,359	0,186	-1,676	0,009					down		
Solyc12g088410	Glycosyl hydrolase family 35 protein, putative (AHRD V3.3 *** A0A061FGE0_THECC)		C:GO:0016021	C:integral component of membrane			mobidb-lite (MOBIDB_LITE): mobidb-lit	0,873	0,669	1,190	1,726	1,271									
Solyc12g088420	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT5G43140.1)		C:GO:0016021	C:integral component of membrane			IPR007248 (PFAM): PTHR11266:SF4	3,819	3,178	19,162	23,599	19,481									
Solyc12g088430	LOW QUALITY:transmembrane protein (AHRD V3.3 *** AT1G75810.1)		C:GO:0016021	C:integral component of membrane			PTHR37714 (PANTHER)	10,197	5,785	1,306	0,995	1,174									
Solyc12g088440	Syntaxin-61-like protein (AHRD V3.3 *** A0A0B0PXY6_GOSAR)		C:GO:0016020; P:GO	C:membrane; P:Golgi vesicle transport			IPR015260 (PFAM): G3DSA:1.20.58.9	18,714	18,836	23,057	20,330	21,030									
Solyc12g088450	C5orf35 (AHRD V3.3 *** AT5G23200.1)						G3DSA:2.170.270.10 (GENE3D): mob	8,370	5,644	13,923	13,464	12,355									
Solyc12g088460	Cytochrome P450, putative (AHRD V3.3 *** A0A061FMR1_THECC)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	8,612	7,856	408,406	452,700	510,332									
Solyc12g088470	cyclin A3_4	CycA3_4	C:GO:0005634	C:nucleus			IPR006671 (PFAM): G3DSA:1.10.472	0,770	0,763	0,552	0,310	0,379									
Solyc12g088480	Zinc-finger domain of monoamine-oxidase A repressor R1 (AHRD V3.3 *-* AT2G23530.1)		P:GO:0006355	P:regulation of transcription, DNA-templated			IPR018866 (PFAM): mobidb-lite (MOB	12,424	10,191	10,244	8,183	9,154									
Solyc12g088500	cyclin A3_5	CycA3_5	C:GO:0005634	C:nucleus			IPR004367 (PFAM): IPR006671 (PFA	0,198	0,392	0,119	0,117	0,023									
Solyc12g088510	Cytochrome P450, putative (AHRD V3.3 *** A0A061FMR1_THECC)		F:GO:0005506; F:GO	F:iron ion binding; F:oxidoreductase activity, acting on paired dc			IPR001128 (PRINTS): IPR002401 (PF	0,000	0,019	0,125	0,050	0,141									
Solyc12g088520	cyclin A3_3	CycA3_3	C:GO:0005634	C:nucleus			IPR039361 (PIRSF): IPR006671 (PFA	0,526	0,691	0,216	0,220	0,118									
Solyc12g088530	cyclin A3.1	CycA3_1	C:GO:0005634	C:nucleus			G3DSA:1.10.472.10 (GENE3D): IPR0	11,906	9,239	1,822	1,067	1,466									
Solyc12g088540	WD40 repeat-like protein (AHRD V3.3 *** I0YVP9_COCSC)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR015943 (G3	0,000	0,076	0,000	0,000	0,000									
Solyc12g088620	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 *** A0A0K9NVB9_ZOSMR)		F:GO:0005515	F:protein binding			IPR020472 (PRINTS): IPR001680 (PF	0,000	0,043	0,000	0,000	0,000									
Solyc12g088640	Carbohydrate esterase plant-like protein (AHRD V3.3 *** G7J707_MEDTR)						IPR036514 (G3DSA:3.40.50.GENE3D	0,316	0,200	0,101	0,045	0,048									
Solyc12g088650	cyclinD3_2	CycD3_2	C:GO:0005634	C:nucleus			IPR004367 (PFAM): G3DSA:1.10.472.	2,131	2,020	0,659	0,747	0,817									
Solyc12g088660	Mannose-P-dolichol utilization defect 1 protein (AHRD V3.3 *** AT4G07390.2)		C:GO:0016021	C:integral component of membrane			G3DSA:1.20.1280.290 (GENE3D): IPF	12,682	11,877	16,606	17,672	16,527									
Solyc12g088670	cysteine protease CYP1	c14	P:GO:0006508; F:GO	P:proteolysis; F:cysteine-type peptidase activity			IPR000668 (PRINTS): G3DSA:3.90.70	30,922	23,837	42,256	34,301	46,572									
Solyc12g088680	Ubiquitin-conjugating enzyme (AHRD V3.3 *** B7FGV0_MEDTR)		F:GO:0019789	F:SUMO transferase activity			IPR016135 (G3DSA:3.10.110.GENE3I	3,333	2,636	7,765	6,809	4,763			-0,707	0,014				down	
Solyc12g088690	Glycosyltransferase (AHRD V3.3 *** M1DJX3_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,658	1,150	0,189	0,139	0,496									
Solyc12g088700	Glycosyltransferase (AHRD V3.3 *** M1B8Y5_SOLTU)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	8,383	14,324	1,198	1,320	4,478			1,872	0,000				up	

Solyc12g088720	Polyadenylate-binding protein (AHRD V3.3 *** K4DGU3_SOLLC)		F:GO:0003723	F:RNA binding	IPR000504 (PFAM): IPR012677 (G3D	424,402	450,327	388,428	356,059	365,576									
Solyc12g088730	50S ribosomal L4 (AHRD V3.3 *** A0A0B0Q1P8_GOSAR)		F:GO:0003735: C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	IPR013005 (TIGRFAM): IPR023574 ((	22,054	25,915	40,636	39,604	37,487									
Solyc12g088740	RING/U-box superfamily protein (AHRD V3.3 *** AT5G42940.2)		P:GO:0016567: F:GC	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga:	IPR013083 (G3DSA:3.30.40.GENE3D	31,872	27,648	41,496	40,413	35,993									
Solyc12g088750	Kinase family protein (AHRD V3.3 *** B9ICA0_POPTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR000719 (PFAM): PIRSF000615 (P	19,071	13,529	6,732	4,933	7,666									
Solyc12g088760	Subtilisin-like protease (AHRD V3.3 *** W9SHY0_9ROSA)		F:GO:0004252: P:GC	F:serine-type endo; EC:3.4.21 Acting on peptide bor	IPR015500 (PRINTS): G3DSA:2.60.4C	0,040	0,021	0,202	0,136	0,140									
Solyc12g088800	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)		P:GO:0006629	P:lipid metabolic process	IPR029058 (G3DSA:3.40.50.GENE3D	0,509	0,628	0,115	0,167	0,214									
Solyc12g088810	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (AHRD V3.3 *-* AT1G30550.2)		P:GO:0001510: F:GC	P:RNA methylation; F:protein binding; F:methyltransferase activ	IPR019012 (PFAM): G3DSA:2.20.70.1	11,611	9,602	13,888	13,975	13,297									
Solyc12g088820	Protein kinase family protein (AHRD V3.3 *** AT5G09890.1)		F:GO:0004674: F:GC	F:protein serine/thr EC:2.7.11 Transferring phospho	IPR017892 (PFAM): IPR000719 (PFA	5,634	4,089	1,864	1,435	2,631									
Solyc12g088830	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (AHRD V3.3 *** WEB1_ARATH)		C:GO:0005829: P:GC	C:cytosol; P:chloroplast avoidance movement; P:chloroplast ac	IPR008545 (PFAM): mobidb-lite (MOB	6,633	7,746	7,656	9,468	11,344			0,565	0,025				up	
Solyc12g088840	LOW QUALITY:Calcium-binding EF-hand family protein, putative (AHRD V3.3 *** A0A061FAV4_THECC)		F:GO:0005509	F:calcium ion binding	G3DSA:1.10.238.10 (GENE3D): IPR0(	2,666	3,026	2,018	3,560	3,368					0,823	0,035			up
Solyc12g088870	PHD finger transcription factor (AHRD V3.3 --* AT5G58610.9)					0,019	0,000	0,000	0,022	0,024									
Solyc12g088880	NAD(P)-binding rossmann-fold protein (AHRD V3.3 *** G7J6B7_MEDTR)		F:GO:0003824: F:GC	F:catalytic activity; F:coenzyme binding	G3DSA:3.40.50.720 (GENE3D): IPR0(	3,722	4,095	1,970	1,718	1,994									
Solyc12g088890	DnaJ domain containing protein (AHRD V3.3 *** B6TXC7_MAIZE)		C:GO:0016021: F:GC	C:integral component of membrane; F:metal ion binding	IPR001623 (PRINTS): IPR036671 (G3	1,561	1,696	1,607	1,995	1,339									
Solyc12g088895	BnaA10g05150D protein (AHRD V3.3 *** A0A078EZZ4_BRANA)				PTHR36324 (PANTHER)	0,079	0,138	0,223	0,220	0,190									
Solyc12g088900	succinate dehydrogenase 5 (AHRD V3.3 *** AT1G47420.1)				IPR025397 (PFAM): IPR025397 (PAN	14,930	16,083	17,641	16,181	15,579									
Solyc12g088910	Sulfotransferase (AHRD V3.3 *** A0A0D2S823_GOSRA)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.50.300 (GENE3D): PTHF	5,631	8,161	0,598	0,315	0,729									
Solyc12g088920	Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 *** AT4G11800.1)		F:GO:0016787	F:hydrolase activity	IPR004843 (PFAM): mobidb-lite (MOB	15,200	15,918	17,114	22,222	20,357									
Solyc12g088930	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G42680.2)				IPR006460 (TIGRFAM): IPR006460 (F	0,281	0,575	0,115	0,025	0,000									
Solyc12g088940	MAP kinase kinase kinase 87	MAPKKK87	F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	8,013	11,533	2,777	3,332	5,171									
Solyc12g088950	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *-* A0A0K9PTR8_ZOSMR)				PR01217 (PRINTS): IPR013210 (PFA	0,000	0,000	0,169	0,025	0,000									
Solyc12g088960	Lipid transfer-like protein (AHRD V3.3 -** J9U4R0_ARALP)					21,248	23,074	34,139	34,318	29,888									
Solyc12g088980	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G26490.1)		F:GO:0005515	F:protein binding	IPR020472 (PRINTS): IPR015943 (G3	0,019	0,000	0,000	0,000	0,000									
Solyc12g088990	exocyst complex component sec3A (AHRD V3.3 *** AT1G47550.1)		C:GO:0000145: P:GC	C:exocyst; P:exocytosis	IPR019160 (PFAM): IPR028258 (PFA	75,432	66,970	64,598	64,519	63,074									
Solyc12g089000	RING/U-box superfamily protein (AHRD V3.3 *** AT4G34370.1)		F:GO:0004842: P:GC	F:ubiquitin-protein transferase activity; P:protein ubiquitination	IPR002867 (PFAM): G3DSA:1.20.120	51,311	46,508	95,893	101,514	86,183									
Solyc12g089010	ATP-dependent RNA helicase, putative (AHRD V3.3 *** B9SMB4_RICCO)		F:GO:0004386	F:helicase activity EC:3.6.1.15 Nucleoside-triphosph	IPR007502 (PFAM): IPR018647 (PFA	3,495	3,456	2,043	1,901	1,929									
Solyc12g089020	Kinase family protein (AHRD V3.3 *** B9H5Z0_POPTR)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PFAM): G3DSA:3.30.200	2,946	3,748	2,142	2,267	2,026									
Solyc12g089030	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** AT2G18600.2)		F:GO:0005524: F:GC	F:ATP binding; F:NEDD8 transferase activity; P:protein neddyla	IPR000608 (PFAM): IPR016135 (G3D	29,239	35,280	31,204	28,773	30,250									
Solyc12g089040	mature anther-specific protein LAT61	lat61	F:GO:0003700: P:GC	F:DNA-binding transcription factor activity; P:transcription, DNA	IPR008540 (PFAM): BES1	146,979	113,443	74,306	94,403	89,477									
Solyc12g089050	LOW QUALITY:MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** G7K4		F:GO:0005515: C:GC	F:protein binding; C:integral component of membrane; P:sterol c	IPR032805 (PFAM): PTHR31595 (PAN	0,061	0,135	0,000	0,000	0,000									
Solyc12g089060	PPPDE putative thiol peptidase-like protein				G3DSA:3.90.1720.30 (GENE3D): IPR(	13,650	11,344	8,184	6,876	7,538									
Solyc12g089065	30S ribosomal protein S4, chloroplastic (AHRD V3.3 --* RR4_STIHE)					0,057	0,200	0,072	0,072	0,048									
Solyc12g089080	Glycosyltransferase (AHRD V3.3 *** M1A2F8_SOLTU)		F:GO:0003824: C:GC	F:catalytic activity; C:membrane	IPR005069 (PFAM): PTHR10994:SF1	0,038	0,000	0,000	0,000	0,000									
Solyc12g089090	Protein phosphatase 2c, putative (AHRD V3.3 *** B9R7R1_RICCO)		F:GO:0003824	F:catalytic activity	IPR036457 (G3DSA:3.60.40.GENE3D	22,393	26,892	30,435	27,003	26,381									
Solyc12g089100	Outer envelope pore protein 24B, chloroplastic (AHRD V3.3 *** OP24B_ARATH)		F:GO:0022843: P:GC	F:voltage-gated cation channel activity; P:regulation of ion trans	PTHR35284:SF1 (PANTHER): IPR034	2,088	2,008	1,063	1,315	1,480									
Solyc12g089130	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G75170.2)		F:GO:0008526: P:GC	F:phosphatidylinositol transporter activity; P:phospholipid trans	IPR011074 (PFAM): IPR036865 (G3D	10,483	10,914	23,427	21,542	18,088									
Solyc12g089140	Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** AT1G75180.3)		F:GO:0004617: P:GC	F:phosphoglycerate EC:1.1.1.95 Phosphoglycerate de	PTHR42938 (PANTHER): PTHR42938	254,256	186,428	205,785	218,273	212,736									
Solyc12g089147	4-hydroxy-3-methylbut-2-enyl diphosphate synthase (AHRD V3.3 --* AT5G60600.2)				mobidb-lite (MOBIDB_LITE)	6,056	3,959	4,238	5,508	5,589									
Solyc12g089150	Syntaxin protein (AHRD V3.3 *** G7K3H9_MEDTR)		C:GO:0016020: P:GC	C:membrane; P:Golgi vesicle transport	G3DSA:1.20.5.110 (GENE3D): G3DS/	45,799	42,283	51,639	47,459	45,868									
Solyc12g089160	Lrr receptor protein kinase, putative (AHRD V3.3 *** B9R7U7_RICCO)		F:GO:0004672: F:GC	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc	IPR032675 (G3DSA:3.80.10.GENE3D	44,462	32,469	24,151	27,215	32,806			0,437	0,025				up	
Solyc12g089170	Myb family transcription factor family protein (AHRD V3.3 *** A9PAX0_POPTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(MYB_related	1,359	0,609	0,000	0,000	0,000									
Solyc12g089180	Sugar facilitator protein 6	SFP6	C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport	IPR003663 (PRINTS): IPR005828 (PF	18,608	18,256	32,943	40,826	41,571									
Solyc12g089190	Myb family transcription factor family protein (AHRD V3.3 *** B9H0R6_POPTR)		F:GO:0003677	F:DNA binding	G3DSA:1.10.10.6(MYB_related	0,000	0,000	0,000	0,000	0,024									
Solyc12g089195	Proteasome subunit alpha type (AHRD V3.3 *-* M1B931_SOLTU)		F:GO:0004298: C:GC	F:threonine-type en EC:3.4.25 Acting on peptide bonds (peptidases)		1,475	1,244	1,473	1,517	1,720									
Solyc12g089200	Peptidyl-prolyl cis-trans isomerase-like protein (AHRD V3.3 *** A0A072U025_MEDTR)		P:GO:0000413: F:GC	P:protein peptidyl-p EC:5.2.1.8 Peptidylprolyl isomer	IPR000504 (PFAM): IPR012677 (G3D	0,163	0,018	0,075	0,097	0,024									
Solyc12g089210	Ornithine carbamoyltransferase (AHRD V3.3 *** K4BVE0_SOLLC)		F:GO:0004585: P:GC	F:ornithine carbamc EC:2.1.3.3 Ornithine carbamoylt	IPR006130 (PRINTS): IPR002292 (PF	11,180	13,716	165,721	106,574	177,853					-0,633	0,028			down
Solyc12g089220	Bifunctional nuclease 1 (AHRD V3.3 *** BBD1_ARATH)		F:GO:0004518	F:nuclease activity	IPR003729 (PFAM): IPR036104 (G3D	8,806	10,072	101,770	87,294	96,682									
Solyc12g089230	Peptide transporter (AHRD V3.3 *** A0A072V2Y9_MEDTR)		C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport	IPR006634 (PFAM): G3DSA:1.20.125	0,205	0,272	0,075	0,141	0,093									
Solyc12g089240	Zinc finger, B-box (AHRD V3.3 *** A0A103XBE6_CYNCS)	BBX20	F:GO:0008270	F:zinc ion binding	G3DSA:3.30.40.2(DBB	25,347	23,934	109,773	98,343	109,181									
Solyc12g089250	LOW QUALITY:Glyoxal oxidase-related protein (AHRD V3.3 *** A0A061FD00_THECC)				IPR013783 (G3DSA:2.60.40.GENE3D	0,927	0,543	0,049	0,300	0,023									
Solyc12g089260	Zinc finger transcription factor 80	C3H80	F:GO:0046872	F:metal ion binding	mobidb-lite (MOBIDB_LITE): mobidb-lit	8,839	11,329	13,117	12,399	12,792									
Solyc12g089280	5'-3' exoribonuclease 3 (AHRD V3.3 *** AT1G75660.1)		F:GO:0003676: F:GC	F:nucleic acid bindi EC:3.1.13; EC:3.1.1! Acting on ester bonds	G3DSA:3.40.50.12390 (GENE3D): IPF	36,541	35,971	28,283	31,904	28,279									
Solyc12g089290	HVA22-like protein (AHRD V3.3 *** K4DH00_SOLLC)		C:GO:0016020	C:membrane	IPR004345 (PFAM): mobidb-lite (MOB	3,511	3,278	3,855	4,515	4,264									
Solyc12g089293	Initiation factor eIF-4 gamma, MA3 (AHRD V3.3 --* AT4G30680.1)					0,040	0,076	0,254	0,849	0,607									
Solyc12g089295	DWNN domain, a CCHC-type zinc finger (AHRD V3.3 --* AT5G47430.5)					0,157	0,057	0,277	0,925	0,703									
Solyc12g089297	methyltransferase 1 (AHRD V3.3 --* AT5G49160.2)					0,000	0,000	0,000	0,265	0,070									
Solyc12g089300	Gibberellin-regulated protein 2 (AHRD V3.3 *-* B6TLZ8_MAIZE)				IPR003854 (PFAM): PTHR23201:SF2	19,054	21,168	61,316	66,916	67,046									
Solyc12g089310	Tubulin beta chain (AHRD V3.3 *** A0A0V0ICK0_SOLCH)		F:GO:0003924: F:GC	F:GTPase activity; EC:3.6.1.15 Nucleoside-triphosph	IPR000217 (PRINTS): IPR002453 (PF	0,211	0,161	0,000	0,000	0,000									
Solyc12g089320	Transcription elongation factor family protein, putative isoform 1 (AHRD V3.3 *** A0A061FCJ0_THECC)		C:GO:0005634	C:nucleus	mobidb-lite (MOBIDB_LITE): mobidb-lit	28,209	29,969	35,181	35,484	32,262									
Solyc12g089325	Casparian strip membrane protein 2 (AHRD V3.3 --* CASP2_SORBI)					0,099	0,075	0,122	0,216	0,141									
Solyc12g089330	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G20080.5)		F:GO:0008289	F:lipid binding	IPR000008 (PRINTS): IPR035892 (G3	0,059	0,057	0,025	0,025	0,023									
Solyc12g089340	Vacuolar protein sorting-associated protein 35 (AHRD V3.3 *** K4DH05_SOLLC)		P:GO:0015031: C:GC	P:protein transport; C:retromer, cargo-selective complex; P:retr	G3DSA:1.25.40.660 (GENE3D): IPR0(	49,881	42,991	102,527	105,399	93,938									
Solyc12g089350	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SN40_GLYSO)		F:GO:0016788	F:hydrolase activity, acting on ester bonds	IPR036514 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,022	0,097	0,000									
Solyc12g089380	expansin 8	EXPA8	C:GO:0005576: P:GC	C:extracellular region; P:plant-type cell wall organization	IPR007118 (PRINTS): IPR002963 (PF	0,000	0,000	0,000	0,025	0,000									
Solyc12g094380	Thioredoxin superfamily protein (AHRD V3.3 *** A0A061FEH2_THECC)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.30.10 (GENE3D): PTHR:	13,552	14,125	35,178	36,388	40,653									
Solyc12g094390	LOW QUALITY:Syringolide-induced protein 14-1-1 (AHRD V3.3 *** T2DNU1_PHAVU)				mobidb-lite (MOBIDB_LITE): IPR0387	0,659	10,950	0,166	0,310	0,544	4,070	0,000					up		
Solyc12g094400	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.1)		F:GO:0005215: C:GC	F:transporter activity; C:integral component of membrane; P:tra	IPR001958 (PRINTS): G3DSA:1.20.12	0,157	0,346	0,473	0,496	0,821									
Solyc12g094410	MAP kinase kinase kinase 88	MAPKKK88	F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR001245 (PRINTS): G3DSA:1.10.51	0,000	0,036	0,000	0,000	0,000									
Solyc12g094420	Mechanosensitive ion channel family protein (AHRD V3.3 *** AT2G17010.1)		C:GO:0016020: P:GC	C:membrane; P:transmembrane transport	IPR016688 (PIRSF): IPR006685 (PFA	11,735	10,509	31,173	34,916	26,308									
Solyc12g094430	Glutathione S-transferase (AHRD V3.3 *** C7F8A3_ARAHY)	GSTF5	F:GO:0005515	F:protein binding	G3DSA:3.40.30.10 (GENE3D): IPR0(	33,480	41,096	63,417	61,617	69,245									
Solyc12g094440	High mobility group family (AHRD V3.3 *** E5GCD0_CUCME)		F:GO:0003677	F:DNA binding	IPR001606 (PFAM): IPR036431 (G3D	3,414	2,119	0,000	0,000	0,000									
Solyc12g094450	Enoyl-CoA hydratase 2, peroxisomal (AHRD V3.3 *** ECH2_ARATH)		C:GO:0005777: P:GC	C:peroxisome; P:fatty acid beta-oxidation, unsaturated, even nu	G3DSA:3.10.129.10 (GENE3D): IPR0(	28,586	29,804	28,377	29,721	35,780									
Solyc12g094460	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2RKV6_GLYSO)		F:GO:0005507: F:GC	F:copper ion binding; F:oxidoreductase activity; P:oxidation-red	IPR011706 (PFAM): IPR008972 (G3D	0,161	0,440	0,044	0,591	0,442									
Solyc12g094480	Pantothenate synthetase (AHRD V3.3 *** A0A1D1ZM39_9ARAE)		C:GO:0005739: C:GC	C:mitochondrion; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR363	3,297	2,496	1,451	1,655	1,521									
Solyc12g094490	Pre-mRNA cleavage complex 2 Pcf11 (AHRD V3.3 *** A0A0B0PJQ4_GOSAR)		F:GO:0000993: F:GC	F:RNA polymerase II complex binding; F:mRNA binding; C:cytop	IPR006903 (PFAM): IPR008942 (G3D	59,626	36,609	55,896	51,189	48,157	-0,676	0,023					down		
Solyc12g094500	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9R8J1_RICCO)		P:GO:0055114	P:oxidation-reduction process	G3DSA:3.90.180.10 (GENE3D): IPR0	38,256	36,364	36,106	31,179	35,563									
Solyc12g094510	NADH-ubiquinone oxidoreductase chain (AHRD V3.3 *** AT1G20460.1)		C:GO:0016021	C:integral component of membrane	PTHR34936:SF1 (PANTHER): PTHR3	5,064	6,706	6,173	5,265	5,651									
Solyc12g094520	4-coumarate--CoA ligase family protein (AHRD V3.3 *** B9H5E9_POPTR)	4CL	F:GO:0003824	F:catalytic activity	IPR025110 (PFAM): G3DSA:3.30.300	47,275	89,385	77,019	75,332	69,765	0,944	0,005					up		
Solyc12g094530	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** A0A072VS58_MEDTR)				IPR004320 (PFAM): PTHR33070 (PAN	0,000	0,039	0,000	0,000	0,000									
Solyc12g094550	At1g76250 (AHRD V3.3 *** Q8GX25_ARATH)		C:GO:0016021	C:integral component of membrane	PTHR35112 (PANTHER)	25,937	27,209	51,710	52,884	46,139									
Solyc12g094560	E3 ubiquitin-protein ligase-like protein (AHRD V3.3 *** A0A1B1LUK2_VITPS)		F:GO:0004842: F:GC	F:ubiquitin-protein transferase activity; F:protein binding	G3DSA:3.10.20.90 (GENE3D): G3DS/	0,000	0,018	0,025	0,000	0,000									
Solyc12g094580	AT hook motif DNA-binding family protein (AHRD V3.3 --* AT5G46640.1)					3,750	3,709	3,195	3,208	3,620									
Solyc12g094585	inactive purple acid phosphatase-like protein (AHRD V3.3 *-* AT1G42430.1)				mobidb-lite (MOBIDB_LITE): mobidb-lit	0,000	0,000	0,000	0,000	0,024									
Solyc12g094590	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G76270.1)		P:GO:0006004: C:GC	P:fucose metabolic process; C:integral component of membrane	IPR024709 (PIRSF): IPR019378 (PFA	23,253	21,870	33,074	30,953	32,652									
Solyc12g094600	cyclinB2_5	CycB2_5	C:GO:0005634	C:nucleus	G3DSA:1.10.472.10 (GENE3D): IPR0(	0,216	0,239	0,025	0,025	0,095									
Solyc12g094610	U-box domain-containing 15-like protein (AHRD V3.3 *** A0A0B0PZ68_GOSAR)		F:GO:0004842: F:GC	F:ubiquitin-protein transferase activity; F:protein binding; P:cell	IPR003613 (PFAM): IPR000225 (PFA	0,059	0,018	1,403	1,584	2,182									
Solyc12g094615	Ring/U-Box superfamily protein (AHRD V3.3 --* AT2G27950.3)					0,000	0,018	0,119	0,244	0,164									
Solyc12g094620	catalase	cat1	F:GO:0004096: P:GC	F:catalase activity; EC:1.11.1.7; EC:1.1 Peroxidase; Catalas	IPR018028 (PRINTS): IPR010582 (PF	1122,549	982,592	6016,255	6951,243	6405,394									
Solyc12g094630	Chloroplast inner membrane localized protein (AHRD V3.3 *** Q9C7S3_ARATH)		C:GO:0005739: C:GC	C:mitochondrion; C:chloroplast thylakoid membrane; C:chlorople	mobidb-lite (MOBIDB_LITE): mobidb-lit	64,955	85,517	104,533	109,489	124,610									
Solyc12g094640	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4DH36_SOLLC)		P:GO:0006006: F:GC	P:glucose metabolic process; F:oxidoreductase activity, acting	IPR020831 (PRINTS): IPR020828 (PF	4,257	17,906	0,436	0,411	1,736	2,094	0,000					up		
Solyc12g094650	DUF594 family protein (AHRD V3.3 *** A0A072VN99_MEDTR)		C:GO:0016021	C:integral component of membrane	IPR007658 (PFAM): IPR025315 (PFA	1,366	5,932	0,284	0,637	0,752	2,138	0,000					up		
Solyc12g094660	Disease resistance protein (AHRD V3.3 *** A0A103YE14_CYNCS)		F:GO:0043531	F:ADP binding	PR00364 (PRINTS): IPR002182 (PFA	20,102	21,800	8,944	8,473	9,970									
Solyc12g094680	Protein kinase (AHRD V3.3 *** S8D6E4_9LAMI)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): PIRS	0,019	0,000	0,000	0,000	0,023									
Solyc12g094690	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FF49_THECC)		C:GO:0016021	C:integral component of membrane	IPR013083 (G3DSA:3.30.40.GENE3D	0,611	0,731	0,430	0,222	0,141									
Solyc12g094700	Cysteine protease, putative (AHRD V3.3 *** B9R8S7_RICCO)		P:GO:0006508: F:GC	P:proteolysis; F:cysteine-type peptidase activity	IPR000668 (PRINTS): IPR000668 (PF	0,363	0,691	0,072	0,000	0,000									
Solyc12g094710	AT hook motif DNA-binding family protein (AHRD V3.3 *** AT2G33620.4)		F:GO:0003680	F:AT DNA binding	G3DSA:3.30.1330.80 (GENE3D): IPR(	37,040	38,742	48,696	43,796	43,621									
Solyc12g094720	Photosystem II reaction center PsbP family protein (AHRD V3.3 *** AT1G76450.1)		F:GO:0005509: C:GC	F:calcium ion binding; C:photosystem II oxygen evolving comple	IPR002683 (PFAM): IPR016123 (G3D	2,215	7,072	0,950	1,082	2,463	1,693	0,000	1,350	0,003			up	up	
Solyc12g094730	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *** AT1G76510.4)		F:GO:0003677: C:GC	F:DNA binding; C:nucleus	IPR002068 (PFAM): IPR008978 (G3D	3,320	6,329	5,253	4,350	7,108									
Solyc12g095740	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *-* AT1G76510.4)		F:GO:0003677: C:GC	F:DNA binding; C:nucleus	IPR008978 (G3DSA:2.60.40.GENE3D	0,019	0,000	0,000	0,000	0,000									
Solyc12g095750	Auxin efflux carrier family protein, putative (AHRD V3.3 *** A0A061FMX0_THECC)		C:GO:0016021: P:GC	C:integral component of membrane; P:transmembrane transport	IPR004776 (PFAM): PTHR31651:SF6	0,376	0,211	0,338	0,462	0,404									
Solyc12g095760	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (AHRD \ PFK1		F:GO:0003872: F:GC	F:6-phosphofructok EC:2.7.1.9; EC:2.7.1 Diphosphate--fructos	G3DSA:3.40.50.450 (GENE3D): IPR0	172,984	151,159	83,262	57,182	71,540									
Solyc12g095770	UPF0047 protein YbjQ (AHRD V3.3 *** A0A199VB71_ANACO)		C:GO:0009507	C:chloroplast	IPR035917 (G3DSA:2.60.120.GENE3	25,258	29,401	30,924	29,194	32,393									
Solyc12g095780	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT1G76660.1)		C:GO:0005886	C:plasma membrane	mobidb-lite (MOBIDB_LITE): mobidb-lit	2,891	2,075	1,195	1,072	1,293									
Solyc12g095790	nucleotide-sugar transporter family protein		F:GO:0005459: C:GC	F:UDP-galactose transmembrane transporter activity; C:Golgi a	IPR004853 (PFAM): mobidb-lite (MOB	43,620	43,714	39,302	41,850	38,649									
Solyc12g095800	DnaJ protein family-like (AHRD V3.3 *** Q7F1J8_ORYSJ)				IPR001623 (PRINTS): IPR036869 (G3	39,522	37,548	37,458	39,613	34,641									
Solyc12g095810	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)		C:GO:0016020: F:GC	C:membrane; F:transmembrane transporter activity; P:transmer	IPR000109 (PFAM): PTHR11654:SF1	1,875	1,646	1,966	2,465	1,648									
Solyc12g095820	Thioredoxin-related transmembrane protein 2 (AHRD V3.3 *** A0A151QPU7_CAJCA)		C:GO:0016021	C:integral component of membrane	G3DSA:3.40.30.10 (GENE3D): IPR03(	7,571	5,325	6,041	6,251	6,266									
Solyc12g095830	Protein kinase family protein (AHRD V3.3 *** AT2G25760.1)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): IPR0(	140,816	124,070	170,436	153,217	162,002									
Solyc12g095840	ATP-dependent protease La (LON) domain protein		P:GO:0016567: C:GC	P:protein ubiquitination; C:Cul4A-RING E3 ubiquitin ligase comp	IPR003111 (PFAM): G3DSA:2.170.15	21,175	18,832	29,576	23,761	26,742									
Solyc12g095850	Tryptophan-tRNA ligase (AHRD V3.3 *** A0A072V216_MEDTR)		F:GO:0004830: F:GC	F:tryptophan-tRNA l EC:6.1.1.2 Tryptophan--tRNA lig	IPR002306 (PRINTS): G3DSA:1.10.24	5,940	6,157	0,972	1,162	1,978			0,998	0,048				up	
Solyc12g095860	LEY17226 cyclin-dependent protein kinase 2A-2	cdc2a2	F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:3.30.200.20 (GENE3D): PIRS	36,440	38,741	38,264	37,193	37,812									
Solyc12g095870	Protein kinase (AHRD V3.3 *** A0A059LJJ8_9CHLO)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	G3DSA:1.10.510.10 (GENE3D): G3DS	4,388	3,630	5,330	3,843	3,182			-0,750	0,018				down	
Solyc12g095880	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** A0A0V0IM90_SOLCH)		F:GO:0003872: F:GC	F:6-phosphofructok EC:2.7.1.11 6-phosphofructokinas	IPR022953 (PRINTS): G3DSA:3.40.5C	37,020	39,722	96,754	97,931	95,120									
Solyc12g095890	Poly(A) polymerase (AHRD V3.3 *** A0A0B2Q923_GLYSO)		F:GO:0003723: F:GC	F:RNA binding; F:pc EC:2.7.7.19 Polynucleotide aden:	G3DSA:1.10.1410.10 (GENE3D): G3D	74,163	71,828	62,833	59,636	64,294									
Solyc12g095900	EARLY FLOWERING 3 (AHRD V3.3 *** A0A088PY80_9ROSI)		P:GO:2000028	P:regulation of photoperiodism, flowering	mobidb-lite (MOBIDB_LITE): mobidb-lit	28,292	27,641	32,289	32,541	34,854									
Solyc12g095910	cysteine protease	cysp	P:GO:0006508: F:GC	P:proteolysis; F:peptidase activity	IPR001096 (PRINTS): G3DSA:1.10.13	157,535	126,219	275,090	264,395	241,671									
Solyc12g095920	BRISC and BRCA1-A complex member 1 (AHRD V3.3 *** A0A0B0NV34_GOSAR)		P:GO:0045739: C:GC	P:positive regulation of DNA repair; C:BRCA1-A complex; C:BR	IPR036465 (G3DSA:3.40.50.GENE3D	38,294	29,417	20,770	16,616	19,466									
Solyc12g095930	Serine hydroxymethyltransferase (AHRD V3.3 *** M1CVE4_SOLTU)		F:GO:0004372: P:GC	F:glycine hydroxym EC:2.1.2.1 Glycine hydroxymeth	IPR015422 (G3DSA:3.90.1150.GENE	33,208	37,103	23,299	21,200	24,681									
Solyc12g095940	LOW QUALITY:DUF1764 domain protein (AHRD V3.3 *** A0A072UNS8_MEDTR)				IPR013885 (PFAM): mobidb-lite (MOB	8,701	10,456	8,090	6,727	7,132									
Solyc12g095960	Far upstream element-binding protein 2 (AHRD V3.3 *** W9R3G4_9ROSA)		F:GO:0003723	F:RNA binding	IPR036612 (G3DSA:3.30.1370.GENE	576,790	489,086	392,275	366,592	387,601									
Solyc12g095970	Abscisic acid receptor (AHRD V3.3 *** G7IB92_MEDTR)		F:GO:0004864: C:GC	F:protein phosphatase inhibitor activity; C:nucleus; C:cytoplasm	IPR023393 (G3DSA:3.30.530.GENE3	0,194	0,041	0,000	0,000	0,000									
Solyc12g095980	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0005886: C:GC	C:plasma membrane; C:integral component of membrane	mobidb-lite (MOBIDB_LITE): PTHR312	14,506	17,868	2,112	1,712	1,429									
Solyc12g095990	RNA helicase DEAD40	DEAD40	F:GO:0003676: F:GC	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): IPR0	355,752	413,154	383,040	379,047	366,293									
Solyc12g096000	RNA helicase DEAD41	DEAD41	F:GO:0003676: F:GC	F:nucleic acid binding; F:ATP binding	G3DSA:3.40.50.300 (GENE3D): IPR0	244,792	239,839	277,003	273,360	267,331									
Solyc12g096010	protein kinase family protein (AHRD V3.3 *** AT5G26150.2)		F:GO:0004672: F:GC	F:protein kinase activity; F:ATP binding; P:protein phosphorylati	IPR006016 (PFAM): IPR000719 (PFA	13,104	8,894	4,970	4,221	4,284									
Solyc12g096020	Protein phosphatase 2c (AHRD V3.3 *** F8WL78_CITUN)		F:GO:0004722: P:GC	F:protein serine/thr EC:3.1.3.16 Protein-serine/threor	IPR036457 (G3DSA:3.60.40.GENE3D	60,205	55,445	54,599	51,589	50,990									
Solyc12g096030	LOW QUALITY:Mitochondrial carrier protein (AHRD V3.3 *** F8WLA3_CITUN)		F:GO:0022857: P:GC	F:transmembrane transporter activity; P:transmembrane transpo	IPR002067 (PRINTS): IPR018108 (PF	10,128	9,915	9,663	5,646	7,013					-0,772	0,001			down
Solyc12g096040	PHD finger alfin-like protein (AHRD V3.3 *** A0A072V846_MEDTR)		P:GO:0006355: F:GC	P:regulation of transcription, DNA-templated; F:histone binding	IPR019787 (PFAM): IPR013083 (G3D	15,178	13,939	15,276	13,446	14,586									
Solyc12g096050	Pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein (AHRD \		F:GO:0008289	F:lipid binding	IPR002913 (PFAM): IPR009769 (PFA	30,259	27,021	43,061	45,904	41,906									
Solyc12g096060	MOB kinase activator-like 1A (AHRD V3.3 *** MOB1A_ARATH)		C:GO:0005634: C:GC	C:nucleus; C:early endosome; C:trans-Golgi network; C:plasma	IPR005301 (PFAM): IPR036703 (G3D	14,758	16,715	35,360	39,548	33,294									
Solyc12g096070	Growth-regulating factor (AHRD V3.3 *** A0A072TW62_MEDTR)		F:GO:0005524: C:GC	F:ATP binding; C:nucleus; P:regulation of transcription, DNA-tem	IPR014978 (PFAM): GRF	3,864	4,862	14,953	14,567	12,961									
Solyc12g096080	Glycosyltransferase (AHRD V3.3 *** B2CZL6_PILOF)		F:GO:0016758	F:transferase activity, transferring hexosyl groups	G3DSA:3.40.50.2000 (GENE3D): G3D	1,802	3,563	0,273	1,103	0,000									
Solyc12g096090	Cadmium induced protein AS8 (AHRD V3.3 *** A9PH05_POPTR)		C:GO:0016021	C:integral component of membrane	IPR037735 (PANTHER): PS51257 (PF	6,177	6,331	11,149	10,393	10,698									
Solyc12g096100	Protein PAM68, chloroplastic (AHRD V3.3 *** PAM68_ARATH)		C:GO:0009507: C:GC	C:chloroplast; C:integral component of membrane	IPR021855 (PFAM): mobidb-lite (MOB	2,884	5,873	1,122	1,477	3,424	1,054	0,028	1,578	0,001			up	up	
Solyc12g096110	BREVIS RADIX	BRX			IPR013591 (PFAM): mobidb-lite (MOB	0,021	0,218	0,000	0,000	0,000									
Solyc12g096120	Ubiquitin-fold modifier 1 (AHRD V3.3 *** K4DH85_SOLLC)		C:GO:0005634: C:GC	C:nucleus; C:cytoplasm; P:protein K69-linked ufmylation	IPR005375 (PFAM): G3DSA:3.10.20.9	33,542	32,349	59,206	51,106	53,657									
Solyc12g096130	ARABIDILLO-1 (AHRD V3.3 --* AT2G44900.2)					1,115	0,922	0,594	0,807	0,688									
Solyc12g096140	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061E1M4_THECC)		F:GO:0005515	F:protein binding	IPR002885 (PFAM): IPR002885 (PFA	18,574	18,345	18,795	21,849	19,280									
Solyc12g096150	60S ribosomal protein L13 (AHRD V3.3 *** K4DH88_SOLLC)		F:GO:0003735: C:GC	F:structural constituent of ribosome; C:ribosome; P:translation	IPR001380 (PFAM): IPR001380 (PAN	68,442	84,458	84,552	76,983	75,842									
Solyc12g096160	WAT1-related protein (AHRD V3.3 *** K4DH89_SOLLC)		C:GO:0016021: F:GC	C:integral component of membrane; F:transmembrane transport	IPR000620 (PFAM): IPR030184 (PAN	18,525	16,714	22,473	21,888	22,063									
Solyc12g096170	Embryo defective 3006, putative isoform 2 (AHRD V3.3 *** A0A061G7I3_THECC)		C:GO:0000818	C:nuclear MIS12/MIND complex	IPR007128 (PFAM): IPR007128 (PAN	2,237	2,162	1,366	0,556	1,055									
Solyc12g096180	LOW QUALITY:Late embryogenesis abundant (LEA)hydroxyproline-rich glycoprotein family (AHRD V3.3 ***		C:GO:0016021	C:integral component of membrane	PTHR31852 (PANTHER): PTHR31852	0,061	0,057	0,000	0,000	0,000									

Solyc12g096190	Tryptophan synthase-related (AHRD V3.3 *** A0A0A9M6W8_ARUDO)		P:GO:0000162; F:G(	P:tryptophan biosyr	EC:4.2.1.2	Tryptophan synthase	IPR006316 (TIGRFAM): IPR006316 (F	216,379	192,532	216,011	176,978	231,779									
Solyc12g096200	R2R3MYB transcription factor 6	R2R3MYB6	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.6(MYB	0,042	0,021	0,000	0,000	0,000									
Solyc12g096210	F-box/RNI-like superfamily protein (AHRD V3.3 --* AT1G06630.9)							0,360	0,339	0,359	0,168	0,258									
Solyc12g096220	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9S1Q7_RICCO)		F:GO:0005089	F:Rho guanyl-nucleotide exchange factor activity			IPR023106 (G3DSA:1.10.15.GENE3D	643,852	665,536	392,740	372,454	387,633									
Solyc12g096230	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT1G31600.4)		F:GO:0003676; F:G(	F:nucleic acid binding; F:oxidoreductase activity; P:oxidation-re			IPR012677 (G3DSA:3.30.70.GENE3D	4,472	4,860	5,770	6,744	5,751									
Solyc12g096250	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061DGL0_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,513	0,463	0,912	0,945	0,638									
Solyc12g096260	LOW QUALITY:Ankyrin repeat family protein (AHRD V3.3 *** AT5G07840.1)		F:GO:0005515	F:protein binding			IPR002110 (PRINTS): PF13637 (PFAI	0,140	0,250	0,292	0,364	0,471									
Solyc12g096270	Heterotrimeric G-protein gamma subunit 2 (AHRD V3.3 *** A0A077EPA9_CAPAN)		C:GO:0005886; P:G(	C:plasma membrane; P:G protein-coupled receptor signaling pat			mobidb-lite (MOBIDB_LITE): PTHR351	7,628	7,424	8,061	10,073	7,430									
Solyc12g096280	endonuclease V family protein (AHRD V3.3 *** AT4G31150.4)		F:GO:0004519; P:G(	F:endonuclease activity; P:DNA repair			IPR007581 (PFAM): G3DSA:3.30.217(	6,626	6,388	8,053	7,416	7,631									
Solyc12g096290	exocyst complex component sec15A (AHRD V3.3 *** AT3G56640.1)		C:GO:0000145; P:G(	C:exocyst; P:vesicle docking involved in exocytosis			G3DSA:1.20.58.670 (GENE3D): IPR0(	14,248	18,487	12,622	10,337	11,054									
Solyc12g096300	40S ribosomal protein S6 (AHRD V3.3 *** K4DHA3_SOLLC)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			IPR014401 (PIRSF): IPR001377 (PFA	245,569	276,776	251,612	195,455	216,405									
Solyc12g096310	plant/protein (Protein of unknown function, DUF599) (AHRD V3.3 *** AT5G10580.4)		C:GO:0016021	C:integral component of membrane			IPR006747 (PFAM): PTHR31881:SF6	11,002	9,503	67,813	59,426	53,939									
Solyc12g096320	Gamma-glutamylcyclotransferase (AHRD V3.3 *** K4DHA5_SOLLC)		F:GO:0003839; P:G(	F:gamma-glutamylc	EC:4.3.2.9	Gamma-glutamylcycl	IPR006840 (PFAM): G3DSA:3.10.490	1,232	1,266	1,838	1,523	1,838									
Solyc12g096330	methyltransferase (AHRD V3.3 *** AT5G10620.2)		P:GO:0006364; F:G(	P:rRNA processing; F:methyltransferase activity			IPR003742 (PIRSF): IPR029026 (G3I	6,447	6,953	7,092	6,127	7,306									
Solyc12g096340	UDP-sugar transporter, putative (AHRD V3.3 *** B9RNP8_RICCO)		F:GO:0005459; F:G(	F:UDP-galactose transmembrane transporter activity; F:UDP-gl			IPR004853 (PFAM): PTHR44748 (PAN	59,309	55,670	63,739	74,658	63,345									
Solyc12g096350	WRKY transcription factor 10	WRKY10	F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of trans			IPR018872 (PFAM WRKY	14,939	49,221	6,463	4,427	7,636	1,744	0,000					up		
Solyc12g096370	Exocyst complex exo70-like protein (AHRD V3.3 *** G7I5R5_MEDTR)		C:GO:0000145; P:G(	C:exocyst; P:exocytosis			G3DSA:1.20.1280.170 (GENE3D): IPF	18,594	15,754	13,319	13,585	14,056									
Solyc12g096380	Cationic amino acid transporter (AHRD V3.3 *** S8D7Y4_9LAMI)		C:GO:0016020; F:G(	C:membrane; F:transmembrane transporter activity; P:transmen			IPR002293 (PFAM): G3DSA:1.20.174(	0,000	0,000	0,000	0,025	0,000									
Solyc12g096390	Peptidyl-tRNA hydrolase II (PTH2) family protein (AHRD V3.3 *** AT5G10700.1)		F:GO:0004045	F:aminoacyl-tRNA h	EC:3.1.1.29; EC:3.1.	Aminoacyl-tRNA hydr	IPR002833 (PFAM): IPR023476 (G3D	9,527	10,418	10,649	12,532	12,040									
Solyc12g096400	Calmodulin-binding family protein (AHRD V3.3 *** B9NA01_POPTR)		F:GO:0005516	F:calmodulin binding			IPR012417 (PFAM): mobidb-lite (MOB	0,859	1,026	0,223	0,457	0,542									
Solyc12g096420	RING/U-box superfamily protein (AHRD V3.3 *** AT5G10650.2)		P:GO:0016567; F:G(	P:protein ubiquitination; F:ligase activity; F:ubiquitin protein liga			IPR001841 (PFAM): IPR013083 (G3D	38,657	34,089	83,174	73,552	73,808									
Solyc12g096430	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** D7MB42_ARALL)		P:GO:0016579; F:G(	P:protein deubiquiti	EC:3.4.19.12	Ubiquitinyl hydrolase	IPR001394 (PFAM): G3DSA:3.90.70.1	1,911	1,240	2,495	2,707	2,733									
Solyc12g096450	Zinc finger protein (AHRD V3.3 *** W9SHD6_9ROSA)		F:GO:0003676; F:G(	F:nucleic acid binding; F:zinc ion binding; C:cytosolic large ribos			IPR041661 (PFAM): IPR022755 (PFA	19,621	20,780	33,730	32,009	30,612									
Solyc12g096460	DUF1644 family protein (AHRD V3.3 *** A0A072VDU4_MEDTR)						IPR013083 (G3DSA:3.30.40.GENE3D	12,666	13,839	17,486	16,449	16,999									
Solyc12g096470	Transcription factor, putative (AHRD V3.3 *** B9RNR0_RICCO)		C:GO:0005634; P:G(	C:nucleus; P:DNA-templated transcription, initiation			IPR003923 (PRINTS): IPR003923 (PF	20,658	21,758	37,232	36,938	35,524									
Solyc12g096480	Glutamine dumper 4, putative (AHRD V3.3 *** A0A061GHE4_THECC)		P:GO:0080143	P:regulation of amino acid export			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,184	0,767	2,535	2,389	1,769									
Solyc12g096490	Glutamine dumper 4, putative (AHRD V3.3 *** A0A061GHE4_THECC)		P:GO:0080143	P:regulation of amino acid export			mobidb-lite (MOBIDB_LITE): mobidb-lit	1,162	0,713	0,343	0,267	0,401									
Solyc12g096500	CONSTANS-like protein (AHRD V3.3 *** Q0MQL9_SOLTU)	BBX5	F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR010402 (PFAM CO-like	71,773	70,656	12,054	6,840	12,755					-0,815	0,013			down
Solyc12g096520	Peroxidase (AHRD V3.3 *** K4DHC6_SOLLC)		F:GO:0004601; P:G(	F:peroxidase activi	EC:1.11.1.7	Peroxidase	IPR000823 (PRINTS): IPR002016 (PF	61,425	60,800	93,301	87,848	90,975									
Solyc12g096540	40S ribosomal protein S10-like (AHRD V3.3 *** Q2XPV4_SOLTU)		P:GO:0000028; F:G(	P:ribosomal small subunit assembly; F:structural constituent of r			IPR005326 (PFAM): IPR036388 (G3D	220,861	234,134	189,315	161,335	179,437									
Solyc12g096550	Pheophorbide a oxygenase (AHRD V3.3 *** A0A103XQM0_CYNCS)		F:GO:0010277; F:G(	F:chlorophyllide a o	EC:1.13.12; EC:1.14	Acting on single donc	IPR017941 (PFAM): IPR013626 (PFA	65,137	75,172	91,446	95,830	129,630			0,500	0,004				up	
Solyc12g096560	Apyrase-like protein (AHRD V3.3 *** A0MWC2_TOBAC)		F:GO:0016787	F:hydrolase activity			G3DSA:3.30.420.150 (GENE3D): IPR(	253,654	213,051	164,750	132,939	142,136									
Solyc12g096570	ARGOS (AHRD V3.3 *** C7SFP7_SOLLC)		P:GO:0046622	P:positive regulation of organ growth			PTHR36023:SF3 (PANTHER): IPR037	0,647	4,781	5,209	6,031	1,715	2,890	0,001	-1,602	0,005			up	down	
Solyc12g096580	Potassium transporter (AHRD V3.3 *** M1BTK3_SOLTU)		F:GO:0015079; C:G(	F:potassium ion transmembrane transporter activity; C:membrai			IPR003855 (PFAM): IPR003855 (TIGF	26,790	19,889	34,170	40,763	38,615									
Solyc12g096590	6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** K4DHD2_SOLLC)		F:GO:0000906; P:G(	F:6,7-dimethyl-8-rib	EC:2.5.1.78	6,7-dimethyl-8-ribityll	IPR002180 (PFAM): IPR036467 (G3D	9,014	11,396	6,956	7,919	8,560									
Solyc12g096600	Poly(ADP-ribose) glycohydrolase, putative (AHRD V3.3 *-* B9T530_RICCO)		F:GO:0004649; P:G(	F:poly(ADP-ribose)	EC:3.2.1.143	Poly(ADP-ribose) gly	IPR007724 (PFAM): PTHR12837:SF0	1,171	1,180	1,191	0,831	1,251									
Solyc12g096610	Poly(ADP-ribose) glycohydrolase 1 (AHRD V3.3 *** W9RGD8_9ROSA)		F:GO:0004649; P:G(	F:poly(ADP-ribose)	EC:3.2.1.143	Poly(ADP-ribose) gly	IPR007724 (PFAM): mobidb-lite (MOB	1,840	2,165	2,188	2,672	2,894									
Solyc12g096630	Inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** B9HGC2_POPTR)		C:GO:0005829; P:G(	C:cytosol; P:purine	EC:3.2.2.1	Purine nucleosidase	IPR036452 (G3DSA:3.90.245.GENE3I	0,591	1,508	0,216	0,173	0,449	1,358	0,042					up		
Solyc12g096640	Lupus La protein (AHRD V3.3 *** A0A103Y0S5_CYNCS)		F:GO:0003723; C:G(	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprote			IPR002344 (PRINTS): IPR006630 (PF	0,019	0,000	0,739	0,169	0,071									
Solyc12g096650	Vacuolar protein sorting-associated protein 20 homolog 1 (AHRD V3.3 *** VP201_ARATH)		P:GO:0007034	P:vacuolar transport			IPR005024 (PFAM): G3DSA:1.10.287	20,870	16,674	27,481	30,802	28,389									
Solyc12g096660	Type II inositol 5-phosphatase, putative (AHRD V3.3 *** B9RM01_RICCO)		F:GO:0005515	F:protein binding			IPR036691 (G3DSA:3.60.10.GENE3D	1,689	1,919	3,096	2,218	4,560									
Solyc12g096670	Ankyrin repeat family protein (AHRD V3.3 *** AT2G31820.1)		F:GO:0005515	F:protein binding			IPR020683 (PFAM): IPR036770 (G3D	44,566	32,809	90,072	100,159	83,943									
Solyc12g096680	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT2G03880.1)		F:GO:0005515; F:G(	F:protein binding; F:zinc ion binding			IPR011990 (G3DSA:1.25.40.GENE3D	2,451	2,599	5,136	4,562	3,957									
Solyc12g096690	Cytosolic Fe-S cluster assembly factor NBP35 (AHRD V3.3 *** K4DHE2_SOLLC)		P:GO:0016226; F:G(	P:iron-sulfur cluster assembly; F:4 iron, 4 sulfur cluster binding			IPR033756 (PFAM): mobidb-lite (MOB	29,639	38,662	44,835	43,000	39,648									
Solyc12g096700	60S ribosomal L9 (AHRD V3.3 *** A0A0B0N9P7_GOSAR)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR036789 (G3DSA:3.90.930.GENE3I	190,068	214,225	140,678	141,494	130,443									
Solyc12g096710	Receptor-like kinase (AHRD V3.3 *** D4QD70_DIACA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:3.30.200	10,107	17,098	19,074	31,361	33,328			0,803	0,004	0,719	0,003		up	up
Solyc12g096720	Receptor-like kinase (AHRD V3.3 *-* D4QD70_DIACA)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001245 (PFAM): G3DSA:1.10.510	0,513	0,843	0,968	1,843	1,838									
Solyc12g096730	polygalacturonase TPG6	PG24-3(TAPG6)	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	2,639	0,622	0,096	0,022	0,117									
Solyc12g096740	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT2G43870.1)	PG24-1(TAPG5)	F:GO:0004650; P:G(	F:polygalacturonase	EC:3.2.1.15	Polygalacturonase	IPR000743 (PFAM): IPR012334 (G3D	0,000	0,000	0,000	0,025	0,000									
Solyc12g096760	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)		P:GO:0055114	P:oxidation-reduction process			G3DSA:3.40.50.720 (GENE3D): IPR0	129,851	108,384	119,698	110,556	125,762									
Solyc12g096770	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	1,663	8,381	0,244	0,394	0,636	2,356	0,000					up		
Solyc12g096780	Zinc binding dehydrogenase, putative (AHRD V3.3 *** B9SW66_RICCO)		P:GO:0055114	P:oxidation-reduction process			IPR013154 (PFAM): G3DSA:3.90.180	0,000	0,037	0,000	0,000	0,000									
Solyc12g096790	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC)		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,000	0,036	0,000	0,000	0,000									
Solyc12g096800	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC		F:GO:0016747	F:transferase activity, transferring acyl groups other than aminc			IPR023213 (G3DSA:3.30.559.GENE3I	0,258	0,410	0,022	0,125	0,094									
Solyc12g096810	LETM1 and EF-hand domain-containing protein 1 (AHRD V3.3 *** A0A061EI71_THECC)		F:GO:0005509; F:G(	F:calcium ion binding; F:ribosome binding			G3DSA:1.10.238.10 (GENE3D): IPR0	14,634	12,580	15,356	12,906	11,877									
Solyc12g096820	Glycosyltransferase (AHRD V3.3 *** K4DHF5_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	3,102	5,614	0,452	0,583	1,310									
Solyc12g096830	Glycosyltransferase (AHRD V3.3 *** K4DHF6_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	10,344	12,295	10,790	12,645	14,348									
Solyc12g096860	thioesterase superfamily protein		P:GO:0006637; F:G(	P:acyl-CoA metabol	EC:3.1.2.2	Acyl-CoA hydrolase	G3DSA:3.10.129.10 (GENE3D): G3DS	2,950	2,421	0,096	0,076	0,399									
Solyc12g096870	Glycosyltransferase (AHRD V3.3 *** Q0PI14_VITLA)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): G3D	21,229	17,408	0,339	0,388	0,561									
Solyc12g096880	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 *-* AT3G44670.2)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction			IPR000157 (PFAM): IPR035897 (G3D	1,134	4,601	0,171	0,445	0,739	2,035	0,006					up		
Solyc12g096890	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)		P:GO:0007165	P:signal transduction			IPR025886 (PFAM): PTHR32278:SF2	3,030	10,183	0,246	0,916	1,157	1,767	0,002					up		
Solyc12g096900	Disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G72840.3)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction			IPR000157 (PFAM): IPR035897 (G3D	20,520	31,952	1,091	0,958	1,762	0,665	0,037					up		
Solyc12g096910	LOW QUALITY:DNA-directed RNA polymerase subunit beta'' (AHRD V3.3 *-* RPOC2_SOLBU)		F:GO:0003677; F:G(	F:DNA binding; F:DI	EC:2.7.7.6	DNA-directed RNA pc	IPR007081 (PFAM): PTHR19376:SF4	0,019	0,106	0,025	0,075	0,070									
Solyc12g096920	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** G7IID2_MEDTR)		F:GO:0043531	F:ADP binding			PR00364 (PRINTS): IPR002182 (PFA	8,190	6,081	0,243	0,696	0,866									
Solyc12g096930	Caleosin (AHRD V3.3 *** S8C3C9_9LAMI)		F:GO:0004497; F:G(	F:monooxygenase activity; F:calcium ion binding; C:integral cor			IPR007736 (PFAM): PTHR31495:SF6	27,530	22,079	1,820	5,006	0,324									
Solyc12g096940	CCT motif protein (AHRD V3.3 *** A0A072VLD7_MEDTR)		F:GO:0005515	F:protein binding			IPR010402 (PFAM): mobidb-lite (MOB	2,693	2,669	0,644	0,124	0,401									
Solyc12g096950	TLD-domain containing nucleolar protein, putative isoform 1 (AHRD V3.3 *** A0A061ENH1_THECC)						IPR006571 (PFAM): mobidb-lite (MOB	0,573	0,887	0,225	0,458	0,330									
Solyc12g096960	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)		P:GO:0006952	P:defense response			IPR024949 (PRINTS): IPR023393 (G3	0,000	0,194	0,000	0,049	0,117									
Solyc12g096980	auxin-regulated IAA11	IAA11	F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:regulation of transcription, DNA-t			IPR033389 (PFAM): G3DSA:3.10.20.9	0,136	0,216	0,000	0,000	0,000									
Solyc12g096990	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A0K9P7F6_ZOSMR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	IPR003105 (PFAM): G3DSA:2.170.27(	12,378	13,038	11,278	8,594	11,254									
Solyc12g097000	TIR-NBS-LRR class disease resistance protein (AHRD V3.3 *-* A2I7Q5_9ROSI)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction			IPR000157 (PFAM): IPR035897 (G3D	2,971	21,245	2,609	3,499	3,412	2,863	0,000					up		
Solyc12g097010	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)		P:GO:0007165; F:G(	P:signal transduction; F:ADP binding			IPR032675 (G3DSA:3.80.10.GENE3D	0,462	0,652	0,050	0,198	0,072									
Solyc12g097020	TIR-NBS-LRR class disease resistance protein (AHRD V3.3 *** A2I7Q5_9ROSI)		F:GO:0005515; P:G(	F:protein binding; P:signal transduction; F:ADP binding			PR00364 (PRINTS): IPR035897 (G3D	0,261	0,993	0,000	0,092	0,048									
Solyc12g097030	Carboxyl-terminal-processing protease (AHRD V3.3 *** A0A0B0NIC9_GOSAR)		F:GO:0005515; P:G(	F:protein binding; P:proteolysis; F:serine-type peptidase activity			G3DSA:3.90.226.10 (GENE3D): G3DS	12,104	13,799	11,632	12,109	13,250									
Solyc12g097050	Late embryogenesis-abundant protein (AHRD V3.3 --* Q5G1J3_ISATI)						mobidb-lite (MOBIDB_LITE): mobidb-lit	0,019	0,021	0,000	0,048	0,046									
Solyc12g097060	LOW QUALITY:UPF0329 protein ECU01_0100/ECU01_1510/ECU08_0030, putative isoform 2 (AHRD V3.3 *** A0A061ELC2_THECC)						PTHR37226 (PANTHER)	0,105	0,106	0,025	0,025	0,024									
Solyc12g097070	Heavy meromyosin-like protein, putative (AHRD V3.3 *-* A0A072VST2_MEDTR)						PTHR19306 (PANTHER): PTHR19306	6,833	5,708	7,575	8,713	6,743									
Solyc12g097075	plant self-incompatibility protein S1 family protein (AHRD V3.3 --* AT3G44170.1)							0,943	0,513	0,762	1,071	0,941									
Solyc12g097080	Glutathione s-transferase, putative (AHRD V3.3 *** B9RWR5_RICCO)	GSTU56	F:GO:0005515	F:protein binding			G3DSA:1.20.1050.10 (GENE3D): IPR(	0,021	0,000	0,051	0,022	0,000									
Solyc12g098090	Chalcone synthase (AHRD V3.3 *** CHSY_CATRO)	CHS	P:GO:0009058; F:G(	P:biosynthetic process; F:transferase activity, transferring acyl			IPR016039 (G3DSA:3.40.47.GENE3D	0,000	0,000	0,047	0,000	0,024									
Solyc12g098100	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4DHI4_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM): IPR032675 (G3D	0,040	0,058	0,022	0,000	0,000									
Solyc12g098110	LOW QUALITY:Self-incompatibility S1 family protein (AHRD V3.3 *** Q9LIQ2_ARATH)		C:GO:0016021	C:integral component of membrane			IPR010264 (PFAM): PTHR31232:SF8	0,157	0,097	0,000	0,000	0,000									
Solyc12g098130	Glucose-6-phosphate isomerase, cytosolic 1 (AHRD V3.3 --* G6PI1_CLARO)						PTHR34463:SF2 (PANTHER): PTHR3	5,499	7,319	0,716	3,059	0,393									
Solyc12g098150	Aldo/keto reductase (AHRD V3.3 *** A0A103Y0I1_CYNCS)		F:GO:0047681; P:G(	F:aryl-alcohol dehy	EC:1.1.1.91	Aryl-alcohol dehydroc	IPR005399 (PRINTS): IPR023210 (PF	50,981	53,889	79,910	79,609	83,743									
Solyc12g098160	Always early, putative (AHRD V3.3 *** B9RT24_RICCO)		F:GO:0003677; P:G(	F:DNA binding; P:transcription, DNA-templated; C:transcriptiona			IPR033471 (PFAM): G3DSA:1.20.58.1	29,364	27,879	22,763	24,179	25,335									
Solyc12g098180	Vesicle-associated membrane protein, putative (AHRD V3.3 *** B9RWK6_RICCO)		C:GO:0016021; P:G(	C:integral component of membrane; P:vesicle-mediated transpo			IPR001388 (PRINTS): G3DSA:1.20.5.	0,101	0,160	0,165	0,169	0,191									
Solyc12g098190	F-box family protein (AHRD V3.3 *** AT2G02240.1)		F:GO:0005515	F:protein binding			IPR025886 (PFAM): G3DSA:1.20.128(	16,832	17,365	29,089	21,431	22,244					-0,437	0,017			down
Solyc12g098210	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG52	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM): IPR013525 (PFA	0,040	0,058	0,000	0,000	0,000									
Solyc12g098220	RNA-binding protein (AHRD V3.3 *-* AT4G13690.1)						PTHR38382 (PANTHER)	1,840	1,869	1,294	1,828	1,394									
Solyc12g098230	Unknown protein (AHRD V3.3)		C:GO:0016021	C:integral component of membrane				4,143	2,789	0,050	0,076	0,117									
Solyc12g098240	Unknown protein (AHRD V3.3)		C:GO:0016021	C:integral component of membrane				0,082	0,018	0,000	0,000	0,000									
Solyc12g098310	Cyclin dependent kinase inhibitor, putative (AHRD V3.3 *** A0A061EJV9_THECC)		F:GO:0004861; C:G(	F:cyclin-dependent protein serine/threonine kinase inhibitor acti			IPR003175 (PIRSF): IPR003175 (PFA	21,149	19,401	19,153	17,770	17,234									
Solyc12g098320	Cytochrome b5 (AHRD V3.3 *** CYB5_TOBAC)		C:GO:0016021; F:G(	C:integral component of membrane; F:heme binding; C:intracellu			IPR001199 (PRINTS): IPR001199 (PF	0,140	0,212	0,312	0,149	0,261									
Solyc12g098330	60S ribosomal protein L13a-like protein (AHRD V3.3 *** Q3HRW1_SOLTU)		F:GO:0003735; P:G(	F:structural constituent of ribosome; P:translation; C:large ribos			IPR036899 (G3DSA:3.90.1180.GENE	71,100	85,722	78,389	62,144	65,451									
Solyc12g098340	Pectinesterase (AHRD V3.3 *** K4DHK8_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM): IPR012334 (G3D	35,338	16,630	15,520	10,183	10,720	-1,056	0,000			-0,607	0,012	down		down
Solyc12g098350	Translation initiation factor IF-1, chloroplastic (AHRD V3.3 *** IF1C_SOLLC)		F:GO:0003743; P:G(	F:translation initiation factor activity; P:translational initiation			G3DSA:2.40.50.140 (GENE3D): IPR0(	10,812	16,123	24,639	25,915	30,422									
Solyc12g098360	Photosystem II D2 protein (AHRD V3.3 --* PSBD_CHLAT)		C:GO:0005739; F:G(	C:mitochondrion; F:methyltransferase activity; P:methylation			IPR003788 (PFAM): IPR038375 (G3D	5,060	5,148	6,039	5,487	4,805									
Solyc12g098370	Myb family transcription factor APL (AHRD V3.3 *** A0A0B0NIP7_GOSAR)		F:GO:0003677	F:DNA binding			IPR006447 (TIGRI G2-like	18,122	14,698	6,222	4,492	5,307									
Solyc12g098380	zein-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *-* AT4G13630.2)		C:GO:0016021	C:integral component of membrane			IPR007656 (PFAM): mobidb-lite (MOB	34,176	30,344	27,472	28,883	29,023									
Solyc12g098390	Ankyrin repeat-containing protein, putative (AHRD V3.3 *** B9RWH7_RICCO)		F:GO:0005515	F:protein binding			IPR020683 (PFAM): IPR036770 (G3D	1,154	0,912	0,297	0,451	0,331									
Solyc12g098400	O-fucosyltransferase family protein (AHRD V3.3 *** AT1G76270.1)		P:GO:0006004; C:G(	P:fucose metabolic process; C:integral component of membrane			IPR019378 (PFAM): IPR024709 (PIRS	0,224	0,276	0,047	0,100	0,141									
Solyc12g098420	Actin-related protein 2/3 complex subunit 4 (AHRD V3.3 *-* K4DHL6_SOLLC)		F:GO:0005515; C:G(	F:protein binding; C:Arp2/3 protein complex; P:Arp2/3 complex-r			G3DSA:1.20.58.2190 (GENE3D): IPR(	58,630	62,154	80,760	75,604	78,337									
Solyc12g098430	Actin-related protein 2/3 complex subunit 4 (AHRD V3.3 *** K4DHL6_SOLLC)		C:GO:0005885; P:G(	C:Arp2/3 protein complex; P:Arp2/3 complex-mediated actin nuc			IPR008384 (PFAM): IPR034666 (G3D	0,353	0,274	0,401	0,463	0,404									
Solyc12g098440	RPM1-interacting protein 4 (AHRD V3.3 *** A0A1D1XMJ4_9ARAE)		C:GO:0005886; P:G(	C:plasma membrane; P:defense response signaling pathway, re			IPR008700 (PFAM): mobidb-lite (MOB	33,754	39,554	33,203	33,418	32,848									
Solyc12g098450	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)		F:GO:0015095; P:G(	F:magnesium ion transmembrane transporter activity; P:magnes			IPR008521 (PFAM): PTHR12570:SF2(	0,290	0,439	0,072	0,123	0,094									
Solyc12g098460	AP2/B3 transcription factor family protein (AHRD V3.3 *-* AT1G50680.1)		F:GO:0003677	F:DNA binding			IPR015300 (G3DS B3	0,019	0,000	0,000	0,000	0,000									
Solyc12g098465	myb-like protein X (AHRD V3.3 *-* AT5G48610.5)		F:GO:0004386	F:helicase activity			mobidb-lite (MOBIDB_LITE): mobidb-lit	2,538	1,966	2,467	2,440	2,115									
Solyc12g098470	Electron transport complex protein rnfC, putative isoform 1 (AHRD V3.3 *** A0A061EJK1_THECC)		F:GO:0004386	F:helicase activity	EC:3.6.1.15	Nucleoside-triphosph	mobidb-lite (MOBIDB_LITE): mobidb-lit	0,909	0,801	0,801	0,628	0,685									
Solyc12g098480	LOW QUALITY:UDP-glucuronate 4-epimerase 6 (AHRD V3.3 *-* W9QTQ1_9ROSA)		C:GO:0016021	C:integral component of membrane				0,021	0,060	0,000	0,000	0,000									
Solyc12g098490	Serine hydroxymethyltransferase (AHRD V3.3 *** M1A0B7_SOLTU)		F:GO:0004372; P:G(	F:glycine hydroxym	EC:2.1.2.1	Glycine hydroxymeth	IPR001085 (PIRSF): IPR015421 (G3I	12,571	13,617	3,548	2,215	3,954									
Solyc12g098500	Adenosylhomocysteinase (AHRD V3.3 *** K4DHM3_SOLLC)		F:GO:0004013; P:G(	F:adenosylhomocys	EC:3.3.1.1	Adenosylhomocystei	IPR000043 (PFAM): IPR000043 (TIGF	16,488	17,152	28,780	25,537	34,096									
Solyc12g098510	Rapid alkalinization factor 1 (AHRD V3.3 *** Q6TF29_SOLCH)		C:GO:0016020	C:membrane			IPR008801 (PFAM): PTHR33136:SF1(	7,417	4,143	1,989	2,099	2,375									
Solyc12g098520	SolycHsfA5	HSF-09	F:GO:0003700; C:G(	F:DNA-binding transcription factor activity; C:nucleus; P:regulati			IPR000232 (PRIN HSF	53,978	42,555	60,000	57,731	54,225									
Solyc12g098530	Histidine protein methyltransferase (AHRD V3.3 *** A0A199W6C5_ANACO)		F:GO:0008168; P:G(	F:methyltransferase activity; P:methylation			IPR019410 (PFAM): G3DSA:3.40.50.1	11,496	9,164	11,348	10,231	9,684									
Solyc12g098540	Apyrase (AHRD V3.3 *** APY_SOLTU)		F:GO:0016787	F:hydrolase activity			IPR000407 (PFAM): G3DSA:3.30.420	2,120	3,659	0,448	0,374	0,284									
Solyc12g098570	Receptor-like kinase (AHRD V3.3 *** C0SW32_SOYBN)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:prc			IPR013210 (PFAM): G3DSA:3.30.200	73,823	67,378	38,416	35,878	54,094									
Solyc12g098580	Glycosyltransferase (AHRD V3.3 *** K4DHN1_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,320	1,186	0,692	1,044	2,448									
Solyc12g098590	Glycosyltransferase (AHRD V3.3 *** K4DHN2_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			G3DSA:3.40.50.2000 (GENE3D): IPR(	0,019	2,030	0,000	0,000	0,046	6,113	0,000					up		
Solyc12g098600	Glycosyltransferase (AHRD V3.3 *** K4DHN3_SOLLC)		F:GO:0016758	F:transferase activity, transferring hexosyl groups			IPR002213 (PFAM): G3DSA:3.40.50.2	29,123	39,385	3,888	4,301	10,450			1,416	0,015				up	
Solyc12g098610	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4DHN4_SOLLC)		F:GO:0004553; C:G(	F:hydrolase activity	EC:2.4.1.27	Xyloglucan:xyloglucos	G3DSA:2.60.120.200 (GENE3D): IPR(	0,493	0,667	0,736	3,750	1,729					2,354	0,000			up
Solyc12g098615	Cysteine proteinase inhibitor (AHRD V3.3 *** A0A075FB34_TOBAC)		F:GO:0004869	F:cysteine-type endopeptidase inhibitor activity			G3DSA:3.10.450.10 (GENE3D): IPR0(	0,135	0,255	0,099	0,176	0,000									
Solyc12g098620	bHLH transcription factor 072	ARANCIO	P:GO:0006355; F:G(	P:regulation of transcription, DNA-templated; F:protein dimerizat			IPR011598 (PFAM bHLH	0,021	0,062	2,594	6,190	2,027					1,262	0,020			up
Solyc12g098630	phragmoplast-associated kinesin-related protein (AHRD V3.3 *** AT3G23670.1)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS): IPR001752 (PF	2,810	2,212	1,851	2,025	2,243									
Solyc12g098640	Cycloeucalenol cycloisomerase (AHRD V3.3 *-* CCI1_ARATH)		F:GO:0047793	F:cycloeucalenol cy	EC:5.5.1.9	Cycloeucalenol cyclo	IPR020532 (PANTHER): IPR020532 (I	36,117	38,006	26,083	24,427	28,045									
Solyc12g098660	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G19850.1)	PPHL2	F:GO:0005094; C:G(	F:Rho GDP-dissociation inhibitor activity; C:cytoplasm			IPR000073 (PRINTS): IPR029058 (G3	3,328	3,797	3,165	2,622	4,443									
Solyc12g098670	Signal peptide peptidase-like protein (AHRD V3.3 *-* A0A072U6J0_MEDTR)		F:GO:0004190; C:G(	F:aspartic-type end	EC:3.4.23	Acting on peptide bor	G3DSA:3.50.30.30 (GENE3D): IPR00	24,418	19,911	27,791	28,527	25,544									
Solyc12g098675	Eukaryotic translation initiation factor 3 subunit H (AHRD V3.3 *** K4DHP1_SOLLC)		F:GO:0003743; F:G(	F:translation initiati	EC:3.4.23	Acting on peptide bor	IPR000555 (PFAM): IPR007369 (PFA	390,136	328,032	219,361	184,122	190,717									
Solyc12g098680	Galactose oxidase/kelch repeat superfamily protein (AHRD V3.3 --* AT2G36360.4)							0,061	0,000	0,000	0,047	0,023									
Solyc12g098690	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT5G56190.6)		F:GO:0005515	F:protein binding			IPR001680 (PFAM): IPR015943 (G3D	63,630	54,878	60,942	59,331	53,675									
Solyc12g098700	RNA helicase DEAD42	DEAD42	F:GO:0003676; F:G(	F:nucleic acid binding; F:ATP binding			G3DSA:3.40.50.300 (GENE3D): IPR0(	83,242	68,010	122,477	127,195	110,348									
Solyc12g098710	15-cis-zeta-carotene isomerase (AHRD V3.3 *** A0A0A7DVN8_LYCBA)	ZISO	C:GO:0009507; C:G(	C:chloroplast; C:integral component of membrane; P:carotene b			G3DSA:1.20.120.1630 (GENE3D): IPF	48,471	46,077	942,221	1535,947	816,777									
Solyc12g098720	Vacuolar ATPase subunit e-like (AHRD V3.3 *** Q8GUB2_MESCR)		F:GO:0015078; P:G(	F:proton transmembrane transporter activity; P:ATP hydrolysis (			IPR008389 (PFAM): PTHR12263:SF3	10,604	10,950	19,497	17,151	15,147									
Solyc12g098730	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G31690.1)		P:GO:0006629	P:lipid metabolic process			IPR002921 (PFAM): G3DSA:3.40.50.1	0,037	0,104	0,000	0,000	0,000									
Solyc12g098740	Clathrin interactor EPSIN 2 (AHRD V3.3 *** EPN2_ARATH)						IPR013809 (PFAM): IPR008942 (G3D	419,952	403,349	196,814	167,208	190,234									
Solyc12g098753	Pollen protein Ole E I-like protein (AHRD V3.3 *-* A0A072VSY6_MEDTR)		F:GO:0005199; P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			PR01217 (PRINTS): PF01190 (PFAM)	0,640	0,916	0,337	0,337	0,706									
Solyc12g098757	Extensin-like protein (AHRD V3.3 *-* Q7DLZ6_VIGUN)		F:GO:0005199; P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			PR01217 (PRINTS): IPR006706 (PFA	0,447	0,528	0,509	0,593	0,991									
Solyc12g098770	strictosidine synthase-like 3 (AHRD V3.3 --* AT1G08470.1)							0,000	0,021	0,000	0,073	0,000									
Solyc12g098780		0	F:GO:0005199; P:G(	F:structural constituent of cell wall; P:plant-type cell wall organiz			PR01217 (PRINTS): IPR006706 (PFA	0,019	0,000	0,025	0,025	0,024									
Solyc12g098810	Chitinase family protein (AHRD V3.3 *** AT1G05850.2)		F:GO:0004568; P:G(	F:chitinase activity;	EC:3.2.1.14	Chitinase	G3DSA:3.30.20.10 (GENE3D): IPR01(	80,578	36,342	88,518	58,640	68,006	-1,120	0,000			-0,591	0,000	down		down
Solyc12g098820	Protein kinase superfamily protein (AHRD V3.3 *** AT3G59350.6)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D): IPR0(	58,423	60,608	57,939	58,369	58,605									
Solyc12g098830	Cytosolic purine 5-nucleotidase, putative (AHRD V3.3 *** B9S015_RICCO)		F:GO:0008253; C:G(	F:5'-nucleotidase ac	EC:3.1.3.5; EC:3.1.3	5'-nucleotidase; Nucl	IPR023214 (G3DSA:3.40.50.GENE3D	67,155	78,996	135,521	133,029	128,682									

Solyc12g098840	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	ABCB16	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	7,849	5,585	2,416	4,914	3,511					1,022	0,026			up
Solyc12g098850	ethylene-forming enzyme	efe	F:GO:0010181; F:G(	F:FMN binding; F:oxidoreductase activity, acting on NAD(P)H; F			G3DSA:3.40.30.10 (GENE3D); mobidb	75,063	75,950	50,864	75,606	56,361					0,576	0,030			up
Solyc12g098860	chromatin remodeling factor18 (AHRD V3.3 *** AT1G48310.1)		F:GO:0005524	F:ATP binding			IPR000330 (PFAM); IPR001650 (PFA	19,543	13,242	12,427	13,105	13,934									
Solyc12g098870	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	ABCB17	F:GO:0005524; C:G(	F:ATP binding; C:in	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR036640 (G3DSA:1.20.1560.GENE	0,000	0,039	0,000	0,000	0,000									
Solyc12g098890	50S ribosomal protein L18 (AHRD V3.3 *** W9QXJ8_9ROSA)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation			G3DSA:3.30.420.100 (GENE3D); IPR(	14,018	28,364	10,792	12,436	18,258	1,044	0,000	0,757	0,000			up	up	
Solyc12g098900	Late embryogenesis abundant protein (AHRD V3.3 *** J7F2C7_CAMSI)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			G3DSA:1.20.120.20 (GENE3D); mobic	1,235	2,399	2,141	6,211	1,142									
Solyc12g098910	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4DHR4_SOLLC)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR001772 (PFAM); G3DSA:3.30.200.	0,824	1,434	0,340	0,477	0,308									
Solyc12g098920	RelA-SpoT like protein RSH4 (AHRD V3.3 *** Q84LE6_TOBAC)		F:GO:0005509; P:G(	F:calcium ion binding; P:guanosine tetraphosphate metabolic pr			IPR002048 (PFAM); G3DSA:1.10.238.	21,610	16,915	27,325	26,511	32,680									
Solyc12g098930	pyruvate dehydrogenase kinase (AHRD V3.3 *** AT3G06483.1)		F:GO:0004672	F:protein kinase activity			IPR036890 (G3DSA:3.30.565.GENE3I	0,098	0,039	0,000	0,000	0,047									
Solyc12g098940	Ubiquitin, putative (AHRD V3.3 *** B9RN74_RICCO)		F:GO:0003735; F:G(	F:structural constituent of ribosome; F:protein binding; C:ribosoı			IPR019956 (PRINTS); IPR002906 (PF	355,623	368,325	295,106	278,643	280,142									
Solyc12g098950	Novel plant snare, putative (AHRD V3.3 *** B9S000_RICCO)		F:GO:0000149; F:G(	F:SNARE binding; F:SNAP receptor activity; C:endoplasmic reti			IPR005606 (PFAM); G3DSA:1.20.5.11	71,673	60,730	46,989	46,873	45,991									
Solyc12g098960	Kinase family protein (AHRD V3.3 *** B9N417_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			G3DSA:1.10.510.10 (GENE3D); IPR0(	16,639	26,660	4,020	3,133	4,294	0,708	0,006					up		
Solyc12g098980	Pto kinase interactor 1	PTI1	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			PIRSF000654 (PIRSF); G3DSA:1.10.5	42,469	42,823	63,702	68,594	56,514									
Solyc12g098990	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RZZ6_RICCO)		F:GO:0005515	F:protein binding			IPR011990 (G3DSA:1.25.40.GENE3D	11,382	13,223	10,300	10,103	10,315									
Solyc12g099000	S-adenosylmethionine synthase (AHRD V3.3 *** M1A0F3_SOLTU)		F:GO:0004478; F:G(	F:methionine adeno	EC:2.5.1.6	Methionine adenosyl	IPR022629 (PFAM); G3DSA:3.30.300.	353,511	431,864	236,186	218,748	227,097									
Solyc12g099010	protein serine/threonine kinase (AHRD V3.3 *** AT5G18525.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:1.10.510.10 (GENE3D); IPR0(	19,087	16,357	31,466	36,726	30,971									
Solyc12g099020	Serine/threonine kinases,protein tyrosine kinases,ATP binding,protein kinases isoform 2 (AHRD V3.3 *-* A0A061EPA7_THECC)							1,725	1,017	1,703	2,307	1,862									
Solyc12g099030	Ubiquitin, putative (AHRD V3.3 *** B9RN74_RICCO)		F:GO:0003735; F:G(	F:structural constituent of ribosome; F:protein binding; C:ribosoı			IPR019956 (PRINTS); IPR002906 (PF	201,918	205,674	197,932	176,804	178,764									
Solyc12g099040	LOW QUALITY:NBS-LRR resistance protein (AHRD V3.3 *** M9SZF2_COCNU)						IPR032675 (G3DSA:3.80.10.GENE3D	0,021	0,039	0,022	0,000	0,000									
Solyc12g099060	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* A0A124SEN1_CYNCS)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane; F:ADP bindin			IPR041118 (PFAM); G3DSA:3.40.50.3	0,000	0,000	0,025	0,000	0,000									
Solyc12g099070	Inositol transporter 3	INT3	C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR003663 (PRINTS); IPR003663 (TI(	0,040	0,019	0,000	0,025	0,024									
Solyc12g099080	ADP-ribosylation factor (AHRD V3.3 *** ARF_VIGUN)		F:GO:0005525	F:GTP binding			IPR006689 (PRINTS); IPR006689 (PF	215,105	161,023	167,628	160,200	152,481									
Solyc12g099090	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *-* AT3G13460.4)		F:GO:0003723	F:RNA binding			G3DSA:3.10.590.10 (GENE3D); IPR0(	49,042	50,359	75,887	82,203	75,520									
Solyc12g099100	Dihydrolipoyl dehydrogenase (AHRD V3.3 *** K4DHT1_SOLLC)		F:GO:0004148; F:G(	F:dihydrolipoyl dehy	EC:1.8.1.4	Dihydrolipoyl dehydro	PR00411 (PRINTS); PR00368 (PRINT	65,829	88,294	75,209	70,453	75,186									
Solyc12g099110	30S ribosomal protein S1		F:GO:0003676	F:nucleic acid binding			IPR003029 (PFAM); G3DSA:2.40.50.1	22,228	24,949	63,680	56,934	53,826									
Solyc12g099120	Abscisic acid induced MYB1	R2R3MYB78	F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 MYB	0,371	0,934	0,144	0,430	0,093									
Solyc12g099130	R2R3MYB transcription factor 108	R2R3MYB108	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,019	0,064	0,000	0,000	0,000									
Solyc12g099140	R2R3MYB transcription factor 45	R2R3MYB45	F:GO:0003677	F:DNA binding			IPR001005 (PFAM MYB	0,119	0,445	0,690	0,788	0,449									
Solyc12g099160	serine carboxypeptidase family protein		F:GO:0004185; P:G(	F:serine-type carbo	EC:3.4.21; EC:3.4.1(	Acting on peptide bor	IPR001563 (PRINTS); IPR001563 (PF	19,384	43,308	30,591	30,866	31,013	1,186	0,000					up		
Solyc12g099170	F-box family protein (AHRD V3.3 *** AT5G49610.1)		F:GO:0005515	F:protein binding			IPR001810 (PFAM); IPR017451 (TIGF	4,416	4,280	5,044	4,241	4,750									
Solyc12g099175	F-box protein (AHRD V3.3 --* A0A0B2QYH5_GLYSO)							3,282	4,448	5,568	3,957	4,467									
Solyc12g099180	Poly(A) polymerase, putative (AHRD V3.3 *** B9RZU0_RICCO)		F:GO:0003723; F:G(	F:RNA binding; F:pc	EC:2.7.7.19	Polynucleotide adeny	G3DSA:3.30.70.590 (GENE3D); G3DS	0,926	1,175	2,026	2,950	2,949									
Solyc12g099190	LOW QUALITY:Invertase inhibitor (AHRD V3.3 *** C1KBP2_SOLTU)		F:GO:0004857; P:G(	F:enzyme inhibitor activity; P:negative regulation of catalytic ac			IPR006501 (PFAM); IPR035513 (G3D	8,235	6,789	4,282	3,163	4,713									
Solyc12g099200	Invertase inhibitor (AHRD V3.3 *** I1VR17_SOLTU)		F:GO:0004857; P:G(	F:enzyme inhibitor activity; P:negative regulation of catalytic ac			IPR035513 (G3DSA:1.20.140.GENE3I	35,007	20,063	29,768	39,977	26,035	-0,775	0,002					down		
Solyc12g099210	Invertase inhibitor (AHRD V3.3 *** I1VR17_SOLTU)		F:GO:0004857; P:G(	F:enzyme inhibitor activity; P:negative regulation of catalytic ac			IPR006501 (TIGRFAM); IPR006501 (F	0,000	0,000	0,050	0,102	0,046									
Solyc12g099230	Pectinesterase (AHRD V3.3 *** K4DHU4_SOLLC)		F:GO:0030599; P:G(	F:pectinesterase ac	EC:3.1.1.11; EC:3.1.	Pectinesterase; Cart	IPR000070 (PFAM); IPR012334 (G3D	0,021	0,000	0,000	0,000	0,000									
Solyc12g099240	Huntingtin-interacting protein K (AHRD V3.3 *** A0A0B2Q4F2_GLYSO)		C:GO:0005829	C:cytosol			PTHR31184 (PANTHER); IPR038922 (	12,075	11,682	16,320	13,754	14,729									
Solyc12g099250	MAP kinase kinase kinase 89	MAPKKK89	F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:regulation of transcri			IPR001245 (PRINTS); IPR000014 (TI(	19,760	18,433	4,979	5,493	6,886									
Solyc12g099260	ATP-citrate synthase, putative (AHRD V3.3 *** B9RZR0_RICCO)		F:GO:0046912	F:transferase activity, transferring acyl groups, acyl groups con			IPR016102 (G3DSA:3.40.50.GENE3D	36,317	40,554	13,381	8,725	11,640									
Solyc12g099270	4Fe-4S ferredoxin, iron-sulfur binding (AHRD V3.3 *** A2Q2W7_MEDTR)						IPR017896 (PFAM); G3DSA:3.30.70.2	58,557	63,165	57,617	60,232	73,405									
Solyc12g099280	Pre-mRNA polyadenylation factor Fip1 (AHRD V3.3 *-* A0A103XT69_CYNCS)		C:GO:0005847; P:G(	C:mRNA cleavage and polyadenylation specificity factor comple			IPR007854 (PFAM); mobidb-lite (MOB	20,750	16,123	9,833	8,900	9,279									
Solyc12g099290	Aldehyde dehydrogenase (AHRD V3.3 *** M1A0H0_SOLTU)		F:GO:0016620; P:G(	F:oxidoreductase activity, acting on the aldehyde or oxo group (			IPR016162 (G3DSA:3.40.605.GENE3I	10,558	10,715	6,778	5,909	6,641									
Solyc12g099300	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G50150.1)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR004158 (PFAM); PTHR31549:SF3	0,000	0,019	0,000	0,000	0,023									
Solyc12g099310	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** B9HIP6_POPTR)		C:GO:0005783; P:G(	C:endoplasmic reticulum; P:ubiquitin-dependent protein catabol			IPR016135 (G3DSA:3.10.110.GENE3I	78,300	97,219	204,558	226,278	181,158									
Solyc12g099320	Serine/threonine-protein phosphatase 4 regulatory subunit 3 (AHRD V3.3 *** A0A0B2PYQ7_GLYSO)						IPR011993 (G3DSA:2.30.29.GENE3D	39,206	34,990	46,026	49,089	46,555									
Solyc12g099330	Unknown protein (AHRD V3.3)							86,471	94,070	66,312	58,907	60,445									
Solyc12g099340	calmodulin-binding transcription activator (AHRD V3.3 *** AT3G16940.3)		F:GO:0005515	F:protein binding			G3DSA:1.20.5.190 CAMTA	39,828	32,095	74,310	82,063	71,796									
Solyc12g099345	calmodulin-binding transcription activator (AHRD V3.3 *-* AT3G16940.2)		F:GO:0003677	F:DNA binding			IPR005559 (PFAM); PTHR23335 (PAN	4,363	2,590	8,031	8,536	7,666									
Solyc12g099350	LOW QUALITY:Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha (AHRD V3.3 --* PFPA_RICCO)						mobidb-lite (MOBIDB_LITE); mobidb-lit	1,752	1,065	1,296	0,569	0,706									
Solyc12g099360	CoA ligase (AHRD V3.3 *** A0A0K9PM15_ZOSMR)		F:GO:0003824	F:catalytic activity			G3DSA:3.40.50.12780 (GENE3D); G3	152,127	112,183	619,017	524,962	611,971									
Solyc12g099370	GATA transcription factor, putative (AHRD V3.3 *** B9RZK8_RICCO)		F:GO:0003700; P:G(	F:DNA-binding transcription factor activity; P:regulation of transo			IPR013088 (G3DS GATA	8,711	12,792	4,329	3,608	4,422									
Solyc12g099390	Dehydration-induced 19-like protein (AHRD V3.3 *** E3T7S4_GOSHI)						IPR008598 (PFAM); IPR027935 (PFA	60,634	57,197	34,766	32,418	34,132									
Solyc12g099400	BnaA03g42290D protein (AHRD V3.3 *** A0A078DNK4_BRANA)		C:GO:0005829; C:G(	C:cytosol; C:chloroplast stroma			PTHR35748 (PANTHER)	11,071	17,085	16,164	15,814	14,205	0,652	0,036					up		
Solyc12g099420	condensin-2 complex subunit H2-like protein (AHRD V3.3 *** AT3G16730.1)		P:GO:0030261	P:chromosome condensation			IPR009378 (PFAM); IPR031737 (PFA	18,558	18,056	15,000	13,534	14,032									
Solyc12g099430	Epoxide hydrolase (AHRD V3.3 *** A0A072UTA2_MEDTR)		F:GO:0003824	F:catalytic activity			IPR000639 (PRINTS); IPR000073 (PF	234,822	177,028	55,938	35,514	66,049									
Solyc12g099440	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)		F:GO:0003857; P:G(	F:3-hydroxyacyl-Co	EC:1.1.1.35	3-hydroxyacyl-CoA d	G3DSA:3.40.50.720 (GENE3D); IPR0(	324,894	286,031	787,954	783,845	759,697									
Solyc12g099450	vitellogenin-like protein (AHRD V3.3 *** AT3G06868.1)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,697	0,842	0,072	0,022	0,023									
Solyc12g099470	eukaryotic translation initiation factor 2 gamma subunit (AHRD V3.3 *** AT1G04170.2)		F:GO:0003924; F:G(	F:GTPase activity;	EC:3.6.1.15	Nucleoside-triphosph	IPR000795 (PRINTS); IPR015256 (PF	47,893	54,838	54,594	49,341	50,283									
Solyc12g099490	7-dehydrocholesterol reductase (AHRD V3.3 *-* A0A0B2RUL0_GLYSO)		C:GO:0005730; C:G(	C:nucleolus; C:integral component of membrane; F:oxidoreducta			IPR013865 (PFAM); mobidb-lite (MOB	48,847	53,540	46,028	40,517	36,894									
Solyc12g099500	oxidoreductase/transition metal ion-binding protein (AHRD V3.3 --* AT2G31940.1)		C:GO:0016021	C:integral component of membrane			PTHR33306:SF1 (PANTHER); PTHR3:	85,253	68,218	18,564	29,471	26,044					0,666	0,017			up
Solyc12g099510	Chaperone protein dnaJ, putative (AHRD V3.3 *-* B9RT65_RICCO)		C:GO:0016021	C:integral component of membrane			IPR001623 (PRINTS); IPR036869 (G3	42,940	45,857	65,342	62,352	58,119									
Solyc12g099515	Condensin-2 complex subunit D3 (AHRD V3.3 *** A0A0B0NYG8_GOSAR)		P:GO:0007076	P:mitotic chromosome condensation			IPR011989 (G3DSA:1.25.10.GENE3D	6,983	7,068	4,685	4,447	4,252									
Solyc12g099520	Universal stress protein A-like protein (AHRD V3.3 *** A0A1D1ZLE5_9ARAE)						IPR014729 (G3DSA:3.40.50.GENE3D	0,000	0,000	0,025	0,000	0,000									
Solyc12g099530	Ubiquitin-like-specific protease ESD4 (AHRD V3.3 *** A0A0B0MXS6_GOSAR)		P:GO:0006508; F:G(	P:proteolysis; F:cysteine-type peptidase activity			G3DSA:3.40.395.10 (GENE3D); IPR0(	25,310	27,456	28,593	26,873	25,766									
Solyc12g099540	Kinesin-like protein (AHRD V3.3 *** K4DHX5_SOLLC)		F:GO:0003777; F:G(	F:microtubule motor	EC:3.6.1.15	Nucleoside-triphosph	IPR001752 (PRINTS); IPR001752 (PF	1,324	1,607	0,459	0,723	0,517									
Solyc12g099560	Protein arginine n-methyltransferase, putative (AHRD V3.3 *** B9RT51_RICCO)		P:GO:0006479; F:G(	P:protein methylation; F:methyltransferase activity			G3DSA:2.70.160.11 (GENE3D); PF06	12,970	14,209	4,629	4,738	5,433									
Solyc12g099570	meiotically up-regulated protein (AHRD V3.3 --* AT5G66930.2)							12,395	14,252	12,710	15,605	13,695									
Solyc12g099580	WAT1-related protein (AHRD V3.3 *** K4DHX9_SOLLC)		C:GO:0016021; F:G(	C:integral component of membrane; F:transmembrane transport			IPR000620 (PFAM); mobidb-lite (MOB	0,105	0,043	0,094	0,076	0,118									
Solyc12g099590	LOW QUALITY:BnaCnng45880D protein (AHRD V3.3 *** A0A078JHJ1_BRANA)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,405	0,511	0,075	0,075	0,141									
Solyc12g099600	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G16560.4)		F:GO:0004722; P:G(	F:protein serine/thre	EC:3.1.3.16	Protein-serine/threor	IPR001932 (PFAM); IPR036457 (G3D	28,226	23,995	22,698	22,526	21,035									
Solyc12g099620	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JVA8_CYNCS)		F:GO:0005515	F:protein binding			IPR002885 (TIGRFAM); IPR002885 (F	1,087	1,029	1,240	1,223	1,063									
Solyc12g099630	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G48970.1)		F:GO:0022857; P:G(	F:transmembrane transporter activity; P:transmembrane transpo			IPR002067 (PRINTS); IPR018108 (PF	2,701	2,788	1,836	1,601	2,307									
Solyc12g099650	Photosystem II 5 kDa protein (AHRD V3.3 *** K7WNW4_SOLTU)		C:GO:0016020; C:G(	C:membrane; C:integral component of membrane			IPR040296 (PANTHER); IPR040296 (I	53,444	138,693	24,342	35,011	67,470	1,405	0,001	1,467	0,000			up	up	
Solyc12g099660	Glucosidase 2 subunit beta (AHRD V3.3 *** A0A0B2SD07_GLYSO)		F:GO:0005515; P:G(	F:protein binding; P:N-glycan processing			G3DSA:4.10.400.10 (GENE3D); IPR0:	113,833	99,723	138,468	129,561	126,190									
Solyc12g099670	LOW QUALITY:Histidine kinase CKI1 (AHRD V3.3 *-* W9RM17_9ROSA)		P:GO:0000160	P:phosphorelay signal transduction system			G3DSA:3.40.50.2300 (GENE3D); IPR(	0,021	0,039	0,000	0,000	0,000									
Solyc12g099700	Lipoyl synthase, chloroplastic (AHRD V3.3 *** K4DHZ1_SOLLC)		P:GO:0009107; C:G(	P:lipoate biosynthet	EC:2.8.1.8	Lipoyl synthase	IPR013785 (G3DSA:3.20.20.GENE3D	24,993	28,366	47,904	50,139	46,949									
Solyc12g099710	Reactive oxygen species modulator 1 (AHRD V3.3 *** A0A118K4V8_CYNCS)		C:GO:0005744; C:G(	C:TIM23 mitochondrial import inner membrane translocase com			IPR018450 (PFAM); PTHR28525:SF3	13,410	14,744	25,058	22,690	21,210									
Solyc12g099720	Histidine kinase 1 (AHRD V3.3 *** A0A072VZ96_MEDTR)		F:GO:0000155; P:G(	F:phosphorelay ser	EC:2.7.13.3	Histidine kinase	IPR004358 (PRINTS); G3DSA:3.40.50	0,042	0,000	0,000	0,047	0,000									
Solyc12g099730	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT1G01570.2)		F:GO:0008375; C:G(	F:acetylglucosaminyltransferase activity; C:integral component			G3DSA:3.90.550.50 (GENE3D); IPR0(	0,078	0,097	0,000	0,000	0,000									
Solyc12g099740	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein (AHF		F:GO:0046872	F:metal ion binding			IPR000408 (PRINTS); IPR001849 (PF	55,321	39,543	40,169	42,409	39,453									
Solyc12g099760	Homeobox leucine zipper protein (AHRD V3.3 *** G7K365_MEDTR)		F:GO:0003677	F:DNA binding			G3DSA:1.10.10.60 HB-other	35,470	33,162	64,996	70,953	60,030									
Solyc12g099770	Mitochondria fission 1 (AHRD V3.3 *** A0A0B0PYJ7_GOSAR)		P:GO:0000266; F:G(	P:mitochondrial fission; F:protein binding			IPR016543 (PIRSF); IPR011990 (G3D	81,515	113,038	83,418	80,539	78,762									
Solyc12g099780	RPM1-interacting protein 4 (RIN4) family protein (AHRD V3.3 *-* AT5G19473.1)						IPR008700 (PFAM); mobidb-lite (MOB	0,704	1,305	0,642	0,823	1,201									
Solyc12g099790	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9SJ93_RICCO)		F:GO:0004672; F:G(	F:protein kinase activity; F:calcium ion binding; F:ATP binding; F			IPR000719 (PFAM); G3DSA:1.10.238.	0,804	1,302	1,801	1,634	1,340									
Solyc12g099800	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** M1A0K1_SOLTU)		F:GO:0003755	F:peptidyl-prolyl cis-	EC:5.2.1.8	Peptidylprolyl isomer:	IPR036873 (G3DSA:3.40.250.GENE3I	10,887	17,080	26,133	27,720	28,240	0,679	0,020					up		
Solyc12g099810	Crt (AHRD V3.3 *** A0A0B0NUB3_GOSAR)		C:GO:0016021	C:integral component of membrane			IPR013936 (PFAM); PTHR31326:SF3	2,931	3,854	34,541	40,678	31,887									
Solyc12g099820	Signal recognition particle 9 kDa protein (AHRD V3.3 *** M1A0K6_SOLTU)		P:GO:0006614; F:G(	P:SRP-dependent cotranslational protein targeting to membrane			IPR009018 (G3DSA:3.30.720.GENE3I	9,991	9,940	12,369	13,157	12,871									
Solyc12g099830	Kinase family protein (AHRD V3.3 *** B9GKI2_POPTR)		F:GO:0004672; F:G(	F:protein kinase activity; F:protein binding; F:ATP binding; P:pro			G3DSA:1.10.510.10 (GENE3D); IPR0(	17,337	16,237	2,957	3,410	4,061									
Solyc12g099860	Mitochondrial GTPase 1 (AHRD V3.3 *** A0A1D1XTV6_9ARAE)		F:GO:0005525	F:GTP binding			IPR006073 (PFAM); G3DSA:3.40.50.3	2,241	2,116	1,933	2,223	2,258									
Solyc12g099870	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding			IPR013210 (PFAM); IPR032675 (G3D	0,000	0,021	0,000	0,000	0,000									
Solyc12g099880	LOW QUALITY:Leucine-rich receptor-like kinase family protein, putative (AHRD V3.3 *-* G7KZT3_MEDTR)		C:GO:0016020	C:membrane			IPR013210 (PFAM); IPR032675 (G3D	0,000	0,098	0,000	0,000	0,000									
Solyc12g099890	Protein SDA1 like (AHRD V3.3 *** A0A0B2SJ94_GLYSO)		P:GO:0000055; P:G(	P:ribosomal large subunit export from nucleus; P:actin cytoskele			IPR012977 (PFAM); IPR007949 (PFA	45,171	50,824	45,885	44,515	45,115									
Solyc12g099900	SCL3 (scarecrow-like 3)	GRAS/SCL3	F:GO:0003712; C:G(	F:transcription coregulator activity; C:nucleus			IPR005202 (PFAM GRAS	13,967	15,014	22,761	19,435	26,157									
Solyc12g099910	chromatin remodeling 5 (AHRD V3.3 *** AT2G13370.3)		F:GO:0005524	F:ATP binding			G3DSA:1.10.10.60 (GENE3D); G3DS/	116,724	98,508	143,436	163,290	156,774									
Solyc12g099920	Required to maintain repression 2 (AHRD V3.3 *-* I6XGM5_MAIZE)						mobidb-lite (MOBIDB_LITE); mobidb-lit	29,616	24,077	42,300	44,148	38,601									
Solyc12g099930	alanine:glyoxylate aminotransferase (AHRD V3.3 *** AT2G13360.3)		F:GO:0003824	F:catalytic activity			IPR024169 (PIRSF); IPR000192 (PFA	107,073	177,385	15,536	20,174	47,107			1,594	0,000				up	
Solyc12g099940	Acyl-CoA N-acyltransferase (AHRD V3.3 *** A0A103YFJ4_CYNCS)						G3DSA:3.40.630.30 (GENE3D); IPR0(	10,576	10,176	14,960	17,800	16,420									
Solyc12g099950	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.2)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR001611 (PFA	0,000	0,000	0,025	0,025	0,000									
Solyc12g099960	LOW QUALITY:Ribosomal-like protein, putative (AHRD V3.3 *** I3RZK0_MEDTR)		C:GO:0009535; C:G(	C:chloroplast thylakoid membrane; C:chloroplast envelope			mobidb-lite (MOBIDB_LITE); mobidb-lit	9,317	10,207	2,744	2,153	3,401									
Solyc12g099970	SNF1 kinase complex anchoring protein	gal83	F:GO:0005515	F:protein binding			IPR006828 (PFAM); IPR013783 (G3D	26,381	27,919	23,248	31,210	31,568			0,439	0,016	0,428	0,016		up	up
Solyc12g099980	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G08850.1)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR032675 (G3D	0,300	0,427	0,380	0,525	1,104									
Solyc12g099990	Calmodulin 5	CaM5	F:GO:0005509	F:calcium ion binding			IPR002048 (PFAM); G3DSA:1.10.238.	61,932	69,906	90,938	86,490	85,275									
Solyc12g099995	U-box domain-containing protein 4 (AHRD V3.3 *-* W9QMI4_9ROSA)		F:GO:0004842; C:G(	F:ubiquitin-protein transferase activity; C:nucleus; C:cytoplasm;			PTHR23315:SF119 (PANTHER); PTHI	4,639	6,182	6,948	6,679	6,504									
Solyc12g100000	U-box domain-containing 4-like protein (AHRD V3.3 *** A0A0B0PVU4_GOSAR)		F:GO:0004842; F:G(	F:ubiquitin-protein transferase activity; F:protein binding; P:prot			IPR003613 (PFAM); IPR000225 (PFA	28,953	34,834	40,310	38,884	39,460									
Solyc12g100010	Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)		F:GO:0005515; C:G(	F:protein binding; C:nucleus; P:ubiquitin-dependent protein catal			PR00019 (PRINTS); IPR018121 (PFA	0,079	0,749	0,071	0,069	0,662									
Solyc12g100030	LOW QUALITY:Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A097BR55_GOSBA)		F:GO:0005515	F:protein binding			PR00019 (PRINTS); IPR032675 (G3D	3,032	2,440	0,025	0,117	0,141									
Solyc12g100040	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *** B9RIA5_RICCO)						G3DSA:1.10.10.60 Trihelix	15,111	16,766	13,692	11,522	12,328									
Solyc12g100050	MSF1-like family protein (AHRD V3.3 *** AT5G13070.1)		C:GO:0005758	C:mitochondrial intermembrane space			IPR006797 (PFAM); IPR037365 (PAN	20,469	19,663	20,025	16,791	19,233									
Solyc12g100060	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *-* A0A0K9NMC5_ZOSM		F:GO:0008270	F:zinc ion binding			IPR000058 (PFAM); IPR035896 (G3D	455,048	382,029	198,707	184,517	205,262									
Solyc12g100070	HemK methyltransferase family member 2 (AHRD V3.3 *** A0A0B2RUZ4_GLYSO)		F:GO:0008168	F:methyltransferase activity			G3DSA:3.40.50.150 (GENE3D); IPR0(	6,472	5,088	8,403	9,205	7,778									
Solyc12g100080	Extensin-like protein Ext1 (AHRD V3.3 *** Q8VWM5_SOLLC)						mobidb-lite (MOBIDB_LITE); mobidb-lit	0,000	0,000	0,025	0,000	0,000									
Solyc12g100120	DUF1680 domain protein (AHRD V3.3 *** G7JCI1_MEDTR)		P:GO:0046373; F:G(	P:L-arabinose meta	EC:3.2.1.55	Non-reducing end alp	G3DSA:2.80.10.50 (GENE3D); IPR01:	123,630	62,762	50,923	36,824	47,367	-0,950	0,002			-0,466	0,039	down		down
Solyc12g100130	Phosphate transporter (AHRD V3.3 *** A0A0A1G5X8_MANES)		C:GO:0016021; P:G(	C:integral component of membrane; P:transmembrane transport			IPR011701 (PFAM); G3DSA:1.20.125	19,904	21,520	15,328	16,086	15,230									
Solyc12g100140	Basic helix-loop-helix (BHLH) DNA-binding superfamily (AHRD V3.3 *-* A0A0K9PC85_ZOSMR)		F:GO:0046983	F:protein dimerization activity			IPR011598 (PFAM bHLH	22,943	21,468	3,654	2,754	3,733									
Solyc12g100150	LOB domain-containing protein, putative (AHRD V3.3 *** B9RI26_RICCO)						IPR004883 (PFAM LBD	0,019	0,082	0,000	0,025	0,000									
Solyc12g100160	Ribosomal protein L6 family (AHRD V3.3 *** AT1G05190.1)		F:GO:0003735; C:G(	F:structural constituent of ribosome; C:ribosome; P:translation;			IPR019906 (PRINTS); IPR036789 (G3	20,292	31,901	26,433	24,248	32,403	0,680	0,009					up		
Solyc12g100170	LOW QUALITY:2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POP		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3I	0,040	0,043	0,172	0,285	0,214									
Solyc12g100180	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG53	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	IPR003439 (PFAM); IPR003439 (PFA	0,300	0,347	0,661	0,611	0,687									
Solyc12g100190	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	ABCG54	F:GO:0005524; C:G(	F:ATP binding; C:m	EC:3.6.1.3; EC:3.6.1	Adenosinetriphospha	G3DSA:3.40.50.300 (GENE3D); IPR0	0,058	0,041	0,025	0,025	0,046									
Solyc12g100200	UPF0061 protein (AHRD V3.3 *** A0A199W512_ANACO)						IPR003846 (PFAM); IPR003846 (PAN	33,573	31,879	36,289	31,295	31,818									
Solyc12g100220	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G55290.2)		F:GO:0016491; P:G(	F:oxidoreductase activity; P:oxidation-reduction process			IPR002347 (PRINTS); IPR002347 (PF	0,096	0,083	0,218	0,243	0,287									
Solyc12g100230	Fatty acid desaturase (AHRD V3.3 *** E5D7U7_9GENT)		P:GO:0006629; F:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR005804 (PFAM); IPR021863 (PFA	0,000	0,018	0,000	0,025	0,024									
Solyc12g100240	Fatty acid desaturase (AHRD V3.3 *-* B3SP99_CAPAN)		P:GO:0006629; C:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	PTHR32100 (PANTHER); PTHR32100	0,000	0,000	0,025	0,120	0,259									
Solyc12g100250	Fatty acid desaturase (AHRD V3.3 *** E5D7U7_9GENT)		P:GO:0006629; F:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	IPR021863 (PFAM); IPR005804 (PFA	0,078	0,774	2,393	4,278	15,224			2,657	0,015				up	
Solyc12g100260	Fatty acid desaturase (AHRD V3.3 *-* B3SP99_CAPAN)		P:GO:0006629; C:G(	P:lipid metabolic prc	EC:1.14.19	Acting on paired donc	PTHR32100 (PANTHER); PTHR32100	0,000	0,039	0,049	0,022	0,306									
Solyc12g100270	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT1G02205.2)		F:GO:0005506; P:G(	F:iron ion binding; P:lipid biosynthetic process; F:oxidoreductas			IPR006694 (PFAM); IPR021940 (PFA	0,056	0,118	3,423	2,970	15,767			2,193	0,033				up	
Solyc12g100290	Histone-lysine N-methyltransferase (AHRD V3.3 *** A0A072UKT3_MEDTR)		F:GO:0005515; C:G(	F:protein binding; C	EC:2.1.1.43	Histone-lysine N-met	G3DSA:2.170.270.10 (GENE3D); IPR(	3,585	5,563	3,481	3,347	3,551									
Solyc12g100300	Metal tolerance protein (AHRD V3.3 *** D7RJ71_CARPA)		P:GO:0006812; F:G(	P:cation transport; F:cation transmembrane transporter activity;			IPR002524 (TIGRFAM); IPR002524 (F	0,198	0,227	0,599	0,539	0,424									
Solyc12g100310	Protein kinase family protein (AHRD V3.3 *** AT3G13670.1)		F:GO:0004672; F:G(	F:protein kinase activity; F:ATP binding; P:protein phosphorylati			IPR000719 (PFAM); G3DSA:1.10.510.	58,980	48,967	70,232	59,712	56,170									
Solyc12g100320	BnaC08g32810D protein (AHRD V3.3 *-* A0A078CII9_BRANA)		C:GO:0009536	C:plastid			PTHR36773 (PANTHER)	11,923	11,772	16,381	14,387	15,117									
Solyc12g100330	cytosine-5 DNA methyltransferase3L	MET3L	F:GO:0003682; F:G(	F:chromatin binding; F:methyltransferase activity			IPR001525 (PRINTS); G3DSA:3.90.12	82,272	71,032	39,088	30,638	33,215									
Solyc12g100350	calpain-type cysteine protease family (AHRD V3.3 *-* AT1G55350.6)		F:GO:0004198; P:G(	F:calcium-depender	EC:3.4.22	Acting on peptide bonds (peptidases)		6,384	4,634	5,290	7,266	5,890									
Solyc12g100353	calpain-type cysteine protease family (AHRD V3.3 *** AT1G55350.6)		F:GO:0004198; C:G(	F:calcium-depender	EC:3.4.22	Acting on peptide bor	IPR022684 (PRINTS); G3DSA:3.90.70	0,021	0,000	0,000	0,000	0,000									

Table S3. Gene set enrichment analysis.
Gene Set Enrichment Analysis (GSEA, FDR < 0.25) performed with differentially expressed genes list as test-set and tomato genome as reference-set (Sol Genomics Networks ITAG3.2 annotation). Refer to Subramanian *et al.* (2005) PNAS 102: 15555-15560 for detailed information of GSEA analysis.

[a] GO terms IDs, names and categories annotated using the Blast2GO software.

[b] Gene set size associated with the GO ID and name.

[c] Normalized Enrichment Score.

[d] False Discovery Rate (estimated probability that the gene set and the corresponding NES represents a false positive).
[e] Differentially expressed genes list used for analysis according to the Table S2. Sample abbreviations: WT - wild-type; L1 - PPC2::PHYB2^{OE} line #1; L6 - PPC2::PHYB2^{Y252H} line #6; MG - mature green fruit stage; BK - breaker fruit stage.

GO Id[a]	GO Name[a]	GO Category[a]	Size[b]	NES[c]	FDR q-val[d]	Comparison[e]
GO:0015979	photosynthesis	BIOLOGICAL_PROCESS	77	4,679679	0	L6BKxWTBK
GO:0015979	photosynthesis	BIOLOGICAL_PROCESS	68	4,189261	0	L6MGxWTMG
GO:0009579	thylakoid	CELLULAR_COMPONENT	68	2,501036	0,00203933	L6BKxWTBK
GO:0009579	thylakoid	CELLULAR_COMPONENT	61	3,005177	2,69E-04	L6MGxWTMG
GO:0044436	thylakoid part	CELLULAR_COMPONENT	61	2,727169	4,65E-04	L6BKxWTBK
GO:0034357	photosynthetic membrane	CELLULAR_COMPONENT	59	2,738933	5,23E-04	L6BKxWTBK
GO:0006091	generation of precursor metabolites and energy	BIOLOGICAL_PROCESS	58	3,683217	0	L6BKxWTBK
GO:0044436	thylakoid part	CELLULAR_COMPONENT	53	2,923209	2,24E-04	L6MGxWTMG
GO:0034357	photosynthetic membrane	CELLULAR_COMPONENT	51	2,847976	3,15E-04	L6MGxWTMG
GO:0006091	generation of precursor metabolites and energy	BIOLOGICAL_PROCESS	48	3,123878	0	L6MGxWTMG
GO:0019684	photosynthesis, light reaction	BIOLOGICAL_PROCESS	44	4,144851	0	L6BKxWTBK
GO:0042651	thylakoid membrane	CELLULAR_COMPONENT	44	1,850557	0,08838679	L6BKxWTBK
GO:0098796	membrane protein complex	CELLULAR_COMPONENT	40	2,817269	2,80E-04	L6MGxWTMG
GO:0044435	plastid part	CELLULAR_COMPONENT	40	2,03832	0,043893	L6MGxWTMG
GO:0044434	chloroplast part	CELLULAR_COMPONENT	40	2,037349	0,040516615	L6MGxWTMG
GO:0051186	cofactor metabolic process	BIOLOGICAL_PROCESS	38	-1,67435	0,10818667	L6MGxWTMG
GO:0098796	membrane protein complex	CELLULAR_COMPONENT	37	3,70806	0	L6BKxWTBK
GO:0019684	photosynthesis, light reaction	BIOLOGICAL_PROCESS	36	3,285279	0	L6MGxWTMG
GO:0042651	thylakoid membrane	CELLULAR_COMPONENT	36	2,13931	0,025304984	L6MGxWTMG

GO:0017144	drug metabolic process	BIOLOGICAL_PROCESS	36	1,497669	0,20102523	L6MGxWTMG
GO:0015075	ion transmembrane transporter activity	MOLECULAR_FUNCTION	33	1,86091	0,087970115	L6MGxWTMG
GO:0015318	inorganic molecular entity transmembrane transporter activity	MOLECULAR_FUNCTION	33	1,397603	0,23040488	L6MGxWTMG
GO:0044283	small molecule biosynthetic process	BIOLOGICAL_PROCESS	32	1,414459	0,22396883	L6MGxWTMG
GO:0043565	sequence-specific DNA binding	MOLECULAR_FUNCTION	32	1,450992	0,24044909	L1BKxWTBK
GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	31	-2,24148	0,10051815	L6MGxWTMG
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MOLECULAR_FUNCTION	29	1,745025	0,111070536	L6MGxWTMG
GO:0031984	organelle subcompartment	CELLULAR_COMPONENT	29	-1,70446	0,14948925	L6MGxWTMG
GO:0051188	cofactor biosynthetic process	BIOLOGICAL_PROCESS	28	1,466166	0,20601648	L6MGxWTMG
GO:0005506	iron ion binding	MOLECULAR_FUNCTION	28	1,440521	0,21480791	L6MGxWTMG
GO:0009521	photosystem	CELLULAR_COMPONENT	28	3,256517	0	L6BKxWTBK
GO:0071554	cell wall organization or biogenesis	BIOLOGICAL_PROCESS	28	-1,35623	0,24104658	L1BKxWTBK
GO:0009765	photosynthesis, light harvesting	BIOLOGICAL_PROCESS	27	3,477768	0	L6MGxWTMG
GO:0009521	photosystem	CELLULAR_COMPONENT	27	2,863435	3,60E-04	L6MGxWTMG
GO:0031976	plastid thylakoid	CELLULAR_COMPONENT	27	2,014584	0,04407236	L6MGxWTMG
GO:0009534	chloroplast thylakoid	CELLULAR_COMPONENT	27	1,994737	0,04431257	L6MGxWTMG
GO:0019752	carboxylic acid metabolic process	BIOLOGICAL_PROCESS	27	-1,57301	0,121337615	L1BKxWTBK
GO:0043436	oxoacid metabolic process	BIOLOGICAL_PROCESS	27	-1,54923	0,12988822	L1BKxWTBK
GO:0017144	drug metabolic process	BIOLOGICAL_PROCESS	26	1,574355	0,120327234	L6BKxWTBK
GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	26	-1,9306	0,14606166	L6BKxWTBK
GO:0044283	small molecule biosynthetic process	BIOLOGICAL_PROCESS	26	-1,77121	0,0577837	L1BKxWTBK
GO:0055086	nucleobase-containing small molecule metabolic process	BIOLOGICAL_PROCESS	25	1,670424	0,14672741	L6MGxWTMG
GO:0009765	photosynthesis, light harvesting	BIOLOGICAL_PROCESS	25	3,96763	0	L6BKxWTBK
GO:0070647	protein modification by small protein conjugation or removal	BIOLOGICAL_PROCESS	23	-2,01235	0,06638006	L6MGxWTMG
GO:0032446	protein modification by small protein conjugation	BIOLOGICAL_PROCESS	23	-1,97172	0,073694125	L6MGxWTMG
GO:0016567	protein ubiquitination	BIOLOGICAL_PROCESS	23	-1,95728	0,070720784	L6MGxWTMG

GO:0055035	plastid thylakoid membrane	CELLULAR_COMPONENT	23	1,84579	0,086167865	L6MGxWTMG
GO:0009535	chloroplast thylakoid membrane	CELLULAR_COMPONENT	23	1,798751	0,09526602	L6MGxWTMG
GO:0015979	photosynthesis	BIOLOGICAL_PROCESS	23	1,706712	0,13564523	L1BKxWTBK
GO:0006753	nucleoside phosphate metabolic process	BIOLOGICAL_PROCESS	22	1,694013	0,139537	L6MGxWTMG
GO:0009117	nucleotide metabolic process	BIOLOGICAL_PROCESS	22	1,678533	0,14539367	L6MGxWTMG
GO:0004842	ubiquitin-protein transferase activity	MOLECULAR_FUNCTION	22	-1,53761	0,17685795	L6MGxWTMG
GO:0019787	ubiquitin-like protein transferase activity	MOLECULAR_FUNCTION	22	-1,5105	0,19308701	L6MGxWTMG
GO:0015075	ion transmembrane transporter activity	MOLECULAR_FUNCTION	22	1,434863	0,19358832	L6BKxWTBK
GO:0015318	inorganic molecular entity transmembrane transporter activity	MOLECULAR_FUNCTION	22	1,412444	0,2046398	L6BKxWTBK
GO:0044262	cellular carbohydrate metabolic process	BIOLOGICAL_PROCESS	22	1,535978	0,20479344	L1BKxWTBK
GO:0005576	extracellular region	CELLULAR_COMPONENT	21	-1,91844	0,07896406	L6MGxWTMG
GO:0016798	hydrolase activity, acting on glycosyl bonds	MOLECULAR_FUNCTION	21	-1,58391	0,15414685	L6MGxWTMG
GO:0016746	transferase activity, transferring acyl groups	MOLECULAR_FUNCTION	21	1,36424	0,24907295	L6MGxWTMG
GO:0005509	calcium ion binding	MOLECULAR_FUNCTION	21	1,677551	0,14519414	L1BKxWTBK
GO:0071554	cell wall organization or biogenesis	BIOLOGICAL_PROCESS	20	-2,22137	0,03713258	L6MGxWTMG
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	MOLECULAR_FUNCTION	20	-1,68191	0,119410135	L6MGxWTMG
GO:0006732	coenzyme metabolic process	BIOLOGICAL_PROCESS	20	1,362865	0,24684763	L6MGxWTMG
GO:0034220	ion transmembrane transport	BIOLOGICAL_PROCESS	19	1,857902	0,08464132	L6MGxWTMG
GO:1901293	nucleoside phosphate biosynthetic process	BIOLOGICAL_PROCESS	19	1,833173	0,08440339	L6MGxWTMG
GO:0009165	nucleotide biosynthetic process	BIOLOGICAL_PROCESS	19	1,823155	0,086036764	L6MGxWTMG
GO:0019693	ribose phosphate metabolic process	BIOLOGICAL_PROCESS	19	1,56221	0,18363242	L6MGxWTMG
GO:0006952	defense response	BIOLOGICAL_PROCESS	18	2,000111	0,04577427	L6MGxWTMG
GO:0006457	protein folding	BIOLOGICAL_PROCESS	18	-1,697	0,12904412	L6MGxWTMG
GO:0072521	purine-containing compound metabolic process	BIOLOGICAL_PROCESS	18	1,522453	0,20049456	L6MGxWTMG
GO:0009259	ribonucleotide metabolic process	BIOLOGICAL_PROCESS	18	1,515096	0,20280473	L6MGxWTMG
GO:0016853	isomerase activity	MOLECULAR_FUNCTION	18	1,509617	0,19533181	L6MGxWTMG
GO:1902494	catalytic complex	CELLULAR_COMPONENT	18	1,360627	0,24580768	L6MGxWTMG

GO:1902494	catalytic complex	CELLULAR_COMPONENT	18	1,699441	0,09042747	L6BKxWTBK
GO:0046527	glucosyltransferase activity	MOLECULAR_FUNCTION	18	1,656009	0,14986497	L1BKxWTBK
GO:0006163	purine nucleotide metabolic process	BIOLOGICAL_PROCESS	17	1,480449	0,2008073	L6MGxWTMG
GO:0009150	purine ribonucleotide metabolic process	BIOLOGICAL_PROCESS	17	1,473395	0,20311946	L6MGxWTMG
GO:0031967	organelle envelope	CELLULAR_COMPONENT	17	1,448358	0,2148572	L6MGxWTMG
GO:0051704	multi-organism process	BIOLOGICAL_PROCESS	17	1,445288	0,21386574	L6MGxWTMG
GO:0031975	envelope	CELLULAR_COMPONENT	17	1,424744	0,22211754	L6MGxWTMG
GO:0044042	glucan metabolic process	BIOLOGICAL_PROCESS	17	1,752834	0,13044246	L1BKxWTBK
GO:0005976	polysaccharide metabolic process	BIOLOGICAL_PROCESS	17	1,727471	0,13380888	L1BKxWTBK
GO:0044264	cellular polysaccharide metabolic process	BIOLOGICAL_PROCESS	17	1,761617	0,14162165	L1BKxWTBK
GO:0044036	cell wall macromolecule metabolic process	BIOLOGICAL_PROCESS	17	1,433098	0,2360498	L1BKxWTBK
GO:0009142	nucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	16	1,613153	0,18695419	L6MGxWTMG
GO:0046390	ribose phosphate biosynthetic process	BIOLOGICAL_PROCESS	16	1,603411	0,19079845	L6MGxWTMG
GO:0009199	ribonucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	16	1,589402	0,19158545	L6MGxWTMG
GO:0009141	nucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	16	1,587445	0,18775922	L6MGxWTMG
GO:0009260	ribonucleotide biosynthetic process	BIOLOGICAL_PROCESS	16	1,581805	0,18704873	L6MGxWTMG
GO:0009201	ribonucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	16	1,567863	0,18936922	L6MGxWTMG
GO:0009523	photosystem II	CELLULAR_COMPONENT	16	2,226281	0,012531978	L6BKxWTBK
GO:0022804	active transmembrane transporter activity	MOLECULAR_FUNCTION	16	1,815432	0,08584975	L6BKxWTBK
GO:0005509	calcium ion binding	MOLECULAR_FUNCTION	16	1,56825	0,121268444	L6BKxWTBK
GO:0006073	cellular glucan metabolic process	BIOLOGICAL_PROCESS	16	1,541295	0,21355666	L1BKxWTBK
GO:0019787	ubiquitin-like protein transferase activity	MOLECULAR_FUNCTION	16	1,598238	0,17250265	L1BKxWTBK
GO:0004842	ubiquitin-protein transferase activity	MOLECULAR_FUNCTION	16	1,607955	0,17609163	L1BKxWTBK
GO:0098772	molecular function regulator	MOLECULAR_FUNCTION	16	-1,97174	0,027105559	L1BKxWTBK
GO:0016874	ligase activity	MOLECULAR_FUNCTION	16	-1,68453	0,07625332	L1BKxWTBK
GO:0033013	tetrapyrrole metabolic process	BIOLOGICAL_PROCESS	15	-1,6757	0,11217307	L6MGxWTMG
GO:0009523	photosystem II	CELLULAR_COMPONENT	15	1,65973	0,15098944	L6MGxWTMG

GO:0044262	cellular carbohydrate metabolic process	BIOLOGICAL_PROCESS	15	-1,55656	0,16757084	L6MGxWTMG
GO:0009145	purine nucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	15	1,537266	0,1965348	L6MGxWTMG
GO:0009152	purine ribonucleotide biosynthetic process	BIOLOGICAL_PROCESS	15	1,534852	0,1940865	L6MGxWTMG
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	15	1,513736	0,19978057	L6MGxWTMG
GO:0006164	purine nucleotide biosynthetic process	BIOLOGICAL_PROCESS	15	1,512677	0,19653516	L6MGxWTMG
GO:0072522	purine-containing compound biosynthetic process	BIOLOGICAL_PROCESS	15	1,496483	0,19807974	L6MGxWTMG
GO:0009144	purine nucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	15	1,489636	0,20030689	L6MGxWTMG
GO:0009205	purine ribonucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	15	1,48241	0,2029491	L6MGxWTMG
GO:0022900	electron transport chain	BIOLOGICAL_PROCESS	15	1,832339	0,08226793	L6BKxWTBK
GO:1990204	oxidoreductase complex	CELLULAR_COMPONENT	15	2,226067	0,011487647	L6BKxWTBK
GO:0032446	protein modification by small protein conjugation	BIOLOGICAL_PROCESS	15	1,493854	0,21956886	L1BKxWTBK
GO:0016567	protein ubiquitination	BIOLOGICAL_PROCESS	15	1,47399	0,22857139	L1BKxWTBK
GO:0022607	cellular component assembly	BIOLOGICAL_PROCESS	15	-1,93349	0,028930502	L1BKxWTBK
GO:0033014	tetrapyrrole biosynthetic process	BIOLOGICAL_PROCESS	14	-1,67156	0,105466135	L6MGxWTMG
GO:1990204	oxidoreductase complex	CELLULAR_COMPONENT	14	1,580582	0,18356597	L6MGxWTMG
GO:0006754	ATP biosynthetic process	BIOLOGICAL_PROCESS	14	1,428365	0,22221072	L6MGxWTMG
GO:0046034	ATP metabolic process	BIOLOGICAL_PROCESS	14	1,418036	0,22469063	L6MGxWTMG
GO:0022414	reproductive process	BIOLOGICAL_PROCESS	14	1,532333	0,13728338	L6BKxWTBK
GO:0000003	reproduction	BIOLOGICAL_PROCESS	14	1,502485	0,15397623	L6BKxWTBK
GO:0019684	photosynthesis, light reaction	BIOLOGICAL_PROCESS	14	2,061392	0,18653482	L1BKxWTBK
GO:0017144	drug metabolic process	BIOLOGICAL_PROCESS	14	-2,47202	0,0028802	L1BKxWTBK
GO:0042737	drug catabolic process	BIOLOGICAL_PROCESS	14	-2,47821	0,0043203	L1BKxWTBK
GO:0006520	cellular amino acid metabolic process	BIOLOGICAL_PROCESS	14	-1,78143	0,0615494	L1BKxWTBK
GO:0048046	apoplast	CELLULAR_COMPONENT	14	1,433708	0,24605337	L1BKxWTBK
GO:0030234	enzyme regulator activity	MOLECULAR_FUNCTION	14	-1,99971	0,026153434	L1BKxWTBK
GO:0048046	apoplast	CELLULAR_COMPONENT	13	-2,24025	0,050612528	L6MGxWTMG
GO:0046527	glucosyltransferase activity	MOLECULAR_FUNCTION	13	-1,86436	0,08792622	L6MGxWTMG

GO:0004497	monooxygenase activity	MOLECULAR_FUNCTION	13	1,401232	0,23021637	L6MGxWTMG
GO:0016830	carbon-carbon lyase activity	MOLECULAR_FUNCTION	13	1,395304	0,22919478	L6MGxWTMG
GO:0009856	pollination	BIOLOGICAL_PROCESS	13	1,699911	0,092947945	L6BKxWTBK
GO:0044706	multi-multicellular organism process	BIOLOGICAL_PROCESS	13	1,594337	0,114336975	L6BKxWTBK
GO:0009654	photosystem II oxygen evolving complex	CELLULAR_COMPONENT	13	2,149871	0,015501684	L6BKxWTBK
GO:0009055	electron transfer activity	MOLECULAR_FUNCTION	13	1,759539	0,095491365	L6BKxWTBK
GO:0051186	cofactor metabolic process	BIOLOGICAL_PROCESS	13	-2,40008	0,003571761	L1BKxWTBK
GO:0043933	protein-containing complex subunit organization	BIOLOGICAL_PROCESS	13	-1,75586	0,059985254	L1BKxWTBK
GO:0046394	carboxylic acid biosynthetic process	BIOLOGICAL_PROCESS	13	-1,50805	0,14315812	L1BKxWTBK
GO:0009522	photosystem I	CELLULAR_COMPONENT	12	2,557477	0,001501353	L6MGxWTMG
GO:0098655	cation transmembrane transport	BIOLOGICAL_PROCESS	12	1,924148	0,06489512	L6MGxWTMG
GO:0051082	unfolded protein binding	MOLECULAR_FUNCTION	12	-1,69991	0,14296883	L6MGxWTMG
GO:0009654	photosystem II oxygen evolving complex	CELLULAR_COMPONENT	12	1,463204	0,20512441	L6MGxWTMG
GO:0005216	ion channel activity	MOLECULAR_FUNCTION	12	1,401828	0,23329581	L6MGxWTMG
GO:0022838	substrate-specific channel activity	MOLECULAR_FUNCTION	12	1,391489	0,22925356	L6MGxWTMG
GO:0009856	pollination	BIOLOGICAL_PROCESS	12	1,37026	0,24631335	L6MGxWTMG
GO:0009117	nucleotide metabolic process	BIOLOGICAL_PROCESS	12	1,860011	0,08852043	L6BKxWTBK
GO:0055086	nucleobase-containing small molecule metabolic process	BIOLOGICAL_PROCESS	12	1,844454	0,08562834	L6BKxWTBK
GO:0019693	ribose phosphate metabolic process	BIOLOGICAL_PROCESS	12	1,832575	0,08667314	L6BKxWTBK
GO:0006753	nucleoside phosphate metabolic process	BIOLOGICAL_PROCESS	12	1,786998	0,09580338	L6BKxWTBK
GO:0009875	pollen-pistil interaction	BIOLOGICAL_PROCESS	12	1,607814	0,10911634	L6BKxWTBK
GO:0008037	cell recognition	BIOLOGICAL_PROCESS	12	1,588111	0,11523042	L6BKxWTBK
GO:0048544	recognition of pollen	BIOLOGICAL_PROCESS	12	1,566832	0,11977967	L6BKxWTBK
GO:1901137	carbohydrate derivative biosynthetic process	BIOLOGICAL_PROCESS	12	1,464656	0,17790787	L6BKxWTBK
GO:0006732	coenzyme metabolic process	BIOLOGICAL_PROCESS	12	1,453491	0,18318276	L6BKxWTBK
GO:0009522	photosystem I	CELLULAR_COMPONENT	12	2,798519	1,92E-04	L6BKxWTBK
GO:0042546	cell wall biogenesis	BIOLOGICAL_PROCESS	12	2,055067	0,09837947	L1BKxWTBK

GO:0065003	protein-containing complex assembly	BIOLOGICAL_PROCESS	12	-1,98895	0,026090475	L1BKxWTBK
GO:0032502	developmental process	BIOLOGICAL_PROCESS	12	-1,74267	0,06037467	L1BKxWTBK
GO:0016209	antioxidant activity	MOLECULAR_FUNCTION	12	-1,97081	0,025234822	L1BKxWTBK
GO:0045229	external encapsulating structure organization	BIOLOGICAL_PROCESS	11	-2,12803	0,045357507	L6MGxWTMG
GO:0071555	cell wall organization	BIOLOGICAL_PROCESS	11	-2,11976	0,038815424	L6MGxWTMG
GO:0030246	carbohydrate binding	MOLECULAR_FUNCTION	11	1,84129	0,08427109	L6MGxWTMG
GO:0005976	polysaccharide metabolic process	BIOLOGICAL_PROCESS	11	-1,74834	0,14955936	L6MGxWTMG
GO:0044264	cellular polysaccharide metabolic process	BIOLOGICAL_PROCESS	11	-1,70887	0,16801819	L6MGxWTMG
GO:0006073	cellular glucan metabolic process	BIOLOGICAL_PROCESS	11	-1,70702	0,15781729	L6MGxWTMG
GO:0044042	glucan metabolic process	BIOLOGICAL_PROCESS	11	-1,69857	0,13543497	L6MGxWTMG
GO:0006778	porphyrin-containing compound metabolic process	BIOLOGICAL_PROCESS	11	-1,45629	0,23452553	L6MGxWTMG
GO:0006779	porphyrin-containing compound biosynthetic process	BIOLOGICAL_PROCESS	11	-1,44907	0,23467039	L6MGxWTMG
GO:0009767	photosynthetic electron transport chain	BIOLOGICAL_PROCESS	11	2,192689	0,012734717	L6BKxWTBK
GO:0009260	ribonucleotide biosynthetic process	BIOLOGICAL_PROCESS	11	1,766082	0,10101095	L6BKxWTBK
GO:0090407	organophosphate biosynthetic process	BIOLOGICAL_PROCESS	11	1,76306	0,09800943	L6BKxWTBK
GO:0009141	nucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	11	1,752489	0,095142215	L6BKxWTBK
GO:0009165	nucleotide biosynthetic process	BIOLOGICAL_PROCESS	11	1,752377	0,09148289	L6BKxWTBK
GO:0009142	nucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	11	1,74277	0,09310371	L6BKxWTBK
GO:0009201	ribonucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	11	1,734448	0,09427622	L6BKxWTBK
GO:1901293	nucleoside phosphate biosynthetic process	BIOLOGICAL_PROCESS	11	1,727002	0,09430026	L6BKxWTBK
GO:0009199	ribonucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	11	1,721789	0,09394008	L6BKxWTBK
GO:0046390	ribose phosphate biosynthetic process	BIOLOGICAL_PROCESS	11	1,720545	0,09165317	L6BKxWTBK
GO:0009259	ribonucleotide metabolic process	BIOLOGICAL_PROCESS	11	1,717324	0,08803318	L6BKxWTBK
GO:0010383	cell wall polysaccharide metabolic process	BIOLOGICAL_PROCESS	11	1,823199	0,11472393	L1BKxWTBK
GO:0071555	cell wall organization	BIOLOGICAL_PROCESS	11	-2,07811	0,018828148	L1BKxWTBK
GO:0045229	external encapsulating structure organization	BIOLOGICAL_PROCESS	11	-2,10587	0,019261288	L1BKxWTBK
GO:0048856	anatomical structure development	BIOLOGICAL_PROCESS	11	-1,54741	0,12565859	L1BKxWTBK

GO:1901135	carbohydrate derivative metabolic process	BIOLOGICAL_PROCESS	11	-1,57315	0,12673466	L1BKxWTBK
GO:0016762	xyloglucan:xyloglucosyl transferase activity	MOLECULAR_FUNCTION	11	1,899814	0,087375544	L1BKxWTBK
GO:0043531	ADP binding	MOLECULAR_FUNCTION	11	1,504908	0,22106002	L1BKxWTBK
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	MOLECULAR_FUNCTION	11	-2,16881	0,014812029	L1BKxWTBK
GO:0004601	peroxidase activity	MOLECULAR_FUNCTION	11	-2,09398	0,018441124	L1BKxWTBK
GO:0004857	enzyme inhibitor activity	MOLECULAR_FUNCTION	11	-2,0628	0,018749831	L1BKxWTBK
GO:0016853	isomerase activity	MOLECULAR_FUNCTION	11	-1,50082	0,14321142	L1BKxWTBK
GO:0015291	secondary active transmembrane transporter activity	MOLECULAR_FUNCTION	11	-1,41722	0,19575903	L1BKxWTBK
GO:0008104	protein localization	BIOLOGICAL_PROCESS	10	-1,90919	0,07503562	L6MGxWTMG
GO:0016051	carbohydrate biosynthetic process	BIOLOGICAL_PROCESS	10	1,7732	0,10501183	L6MGxWTMG
GO:0098662	inorganic cation transmembrane transport	BIOLOGICAL_PROCESS	10	1,768113	0,1035716	L6MGxWTMG
GO:0048522	positive regulation of cellular process	BIOLOGICAL_PROCESS	10	-1,68781	0,12820067	L6MGxWTMG
GO:0031325	positive regulation of cellular metabolic process	BIOLOGICAL_PROCESS	10	-1,68539	0,123194836	L6MGxWTMG
GO:0009893	positive regulation of metabolic process	BIOLOGICAL_PROCESS	10	-1,68094	0,11457945	L6MGxWTMG
GO:0048544	recognition of pollen	BIOLOGICAL_PROCESS	10	1,594619	0,19253677	L6MGxWTMG
GO:0009875	pollen-pistil interaction	BIOLOGICAL_PROCESS	10	1,56491	0,18641014	L6MGxWTMG
GO:0008037	cell recognition	BIOLOGICAL_PROCESS	10	1,561476	0,18001008	L6MGxWTMG
GO:0009145	purine nucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	10	1,719143	0,08987489	L6BKxWTBK
GO:0009150	purine ribonucleotide metabolic process	BIOLOGICAL_PROCESS	10	1,684646	0,094603986	L6BKxWTBK
GO:0072522	purine-containing compound biosynthetic process	BIOLOGICAL_PROCESS	10	1,684133	0,09229341	L6BKxWTBK
GO:0006164	purine nucleotide biosynthetic process	BIOLOGICAL_PROCESS	10	1,683448	0,089864634	L6BKxWTBK
GO:0009205	purine ribonucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	10	1,676503	0,09056087	L6BKxWTBK
GO:0009152	purine ribonucleotide biosynthetic process	BIOLOGICAL_PROCESS	10	1,673488	0,0894989	L6BKxWTBK
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	BIOLOGICAL_PROCESS	10	1,66355	0,0918733	L6BKxWTBK
GO:0006163	purine nucleotide metabolic process	BIOLOGICAL_PROCESS	10	1,661494	0,09060511	L6BKxWTBK
GO:0009144	purine nucleoside triphosphate metabolic process	BIOLOGICAL_PROCESS	10	1,639625	0,0983313	L6BKxWTBK

GO:0072521	purine-containing compound metabolic process	BIOLOGICAL_PROCESS	10	1,634272	0,098706305	L6BKxWTBK
GO:0016051	carbohydrate biosynthetic process	BIOLOGICAL_PROCESS	10	1,397484	0,20935503	L6BKxWTBK
GO:0016746	transferase activity, transferring acyl groups	MOLECULAR_FUNCTION	10	-2,09216	0,10583338	L6BKxWTBK
GO:0043492	ATPase activity, coupled to movement of substances	MOLECULAR_FUNCTION	10	1,417629	0,2038006	L6BKxWTBK
GO:0042623	ATPase activity, coupled	MOLECULAR_FUNCTION	10	1,405436	0,2068813	L6BKxWTBK
GO:0010410	hemicellulose metabolic process	BIOLOGICAL_PROCESS	10	1,990902	0,061336596	L1BKxWTBK
GO:0010411	xyloglucan metabolic process	BIOLOGICAL_PROCESS	10	2,004207	0,07110318	L1BKxWTBK
GO:0009765	photosynthesis, light harvesting	BIOLOGICAL_PROCESS	10	2,010371	0,09087982	L1BKxWTBK
GO:0006979	response to oxidative stress	BIOLOGICAL_PROCESS	10	-2,31263	0,006103362	L1BKxWTBK
GO:0006952	defense response	BIOLOGICAL_PROCESS	10	-1,77957	0,058615148	L1BKxWTBK
GO:0046982	protein heterodimerization activity	MOLECULAR_FUNCTION	10	-2,94804	0	L1BKxWTBK