

ANEXO 1 - Genes induzidos ao longo da germinação em meio nutriente. A tabela não mostra 186 genes, os quais não apresentaram alinhamento significativo com o banco de dados.

Clone	Melhor alinhamento (Swiss-Prot)	t=0	t=30	t=60	t=90	K
BeE30N09G11	O13581 Manganese resistance 1 protein	-0,0267	0,4590	0,7970	0,6700	1
BeG30N12G06	Q9XTG4 PMR1 protein	-0,0500	0,5050	0,9680	1,1200	1
BeE30N13B01	Q8GUQ9 60S ribosomal protein L38	-0,0514	0,4940	0,8260	0,8190	1
BeE30N15E11	P57728 60S ribosomal protein L28-B	0,1190	0,7620	0,7030	0,9990	1
BeE30N22E01	O14339 60S ribosomal protein L17-A	-0,0558	0,9450	0,7840	0,7580	1
BeG120N01H09	Q7SEP1 Hypothetical protein	-0,0497	0,5870	0,6630	0,8730	1
BeG120N06A04	Q9SIP7 40S ribosomal protein, contains C-terminal	-0,0078	0,5840	0,8690	0,7240	1
BeG120N06C12	O75000 60S ribosomal protein L12	-0,0319	0,4710	0,7980	1,0500	1
BeG120N11G04	Q874N9 Ribosomal protein L37A	0,0402	0,5870	0,8570	1,1100	1
BeG120N17C05	O74836 60S ribosomal protein L1-B	0,0065	0,6920	0,8120	0,8520	1
BeG120N22D07	Q05506 Arginyl-tRNA synthetase, cytoplasmic	-0,0429	0,9140	0,8400	0,6600	1
BeG30N07F12	Q889U9 30S ribosomal protein S13	-0,0836	0,6210	0,6940	0,7140	1
BeG30N12B10	Q7QC42 AgCP1729 (Fragment)	-0,0900	0,6730	0,9170	0,8270	1
BeG30N12D10	Q09865 Putative 60S ribosomal protein L6, mitochondrial precursor	-0,0940	0,5700	0,8900	0,9550	1
BeG60N16E09	Q962R4 Ribosomal protein S15	0,0345	0,5080	0,8690	1,2500	1
BeG90N09F06	Q7RVY8 Hypothetical protein	-0,0493	0,6980	0,7930	0,8140	1
BeZSPN12H11	P14249 40S ribosomal protein S24	0,0205	0,5050	0,8450	1,2400	1
BeG60N12E03	O43447 Peptidyl-prolyl cis-trans isomerase H	0,1010	0,4330	0,7140	0,9480	1
BeG120N07A08	Q7SCN0 Hypothetical protein	-0,0421	0,7510	0,9120	0,5190	1
BeE60H30F05	Q96C51 Hypothetical protein (Fragment)	0,2400	0,7040	1,1300	1,2300	1
BeE120N02E05	Q9C9U6 Hypothetical protein	0,0623	0,8490	0,7170	1,1300	1
BeE30N13E04	P28748 GTP-binding nuclear protein spi1	-0,1270	0,4560	1,0500	0,9630	1
BeG90N16G12	Q01475 GTP-binding protein sar1	-0,0842	0,7680	0,8800	1,1700	1
BeZSPN12B03	O13614 40S ribosomal protein S10-B	-0,0157	1,0400	0,7280	0,8550	1
BeE60C19C09	O14095 Hypothetical protein C2F3.12c in chromosome	0,0912	0,8890	0,7820	0,5000	1
BeE60H23E04	O42952 40S ribosomal protein S30	-0,0539	0,6200	0,7860	0,8500	1
BeG90N03H04	O74225 Heat shock protein Hsp88	-0,1350	0,5750	0,8960	0,5230	1
BeE30N07G12	O83041 Probable proline iminopeptidase	0,0217	0,3500	0,6950	0,7150	1
BeE60H29H03	O95320 U5 snRNP-specific 40 kDa protein	-0,0285	0,7320	0,8770	1,0300	1
BeG90N07G03	P10860 Glutamate dehydrogenase, mitochondrial precursor	0,1310	0,6490	0,7670	0,6760	1
BeNSVP11B02	P17735 Tyrosine aminotransferase	0,0339	0,5820	0,9040	0,8340	1
BeG90N09B01	P25388 Guanine nucleotide-binding protein beta sub	0,0385	1,0000	0,9450	0,9060	1
BeE60H29G12	P32368 Recessive suppressor of secretory defect	0,0892	0,4330	1,0100	0,9470	1
BeG90N13F08	P36088 Hypothetical 19.7 kDa protein in STB6-NUP100 intergenic region	-0,0542	1,2700	0,7590	0,8270	1
BeG30N10H02	P38772 Hypothetical 42.3 kDa protein in VMA10-SRB2 intergenic region	-0,0355	0,6820	0,8320	0,7440	1
BeZSPN17C11	P39958 Secretory pathway GDP dissociation inhibito	-0,2210	0,7980	0,6020	1,2500	1
BeE120N01E11	P58466 Carboxy-terminal domain RNA polymerase II p	0,1850	0,6510	0,9900	0,8700	1
BeE60H30A11	Q00216 Putative disulfide isomerase TIGA precursor	-0,0098	0,8540	0,6660	0,8770	1
BeE60H26H05	Q09747 Putative ATP-dependent RNA helicase C12C2.0	0,0863	0,6220	0,9440	0,7220	1
BeG90N11G02	Q59326 Chitinase precursor	-0,0251	0,4090	1,0800	1,2900	1
BeE30N09B07	Q7RV95 Malate synthase, glyoxysomal	0,1110	0,4800	0,7620	0,7920	1
BeE60N03F03	Q7S0B7 Hypothetical protein	0,0165	0,9030	1,0300	0,7610	1
BeE60N02F01	Q7SEL5 Hypothetical protein	-0,0414	0,9710	0,6890	1,4300	1
BeE60N12A08	Q7SY47 Hypothetical protein	-0,0837	0,2610	0,9280	0,4800	1
BeG120N13B09	Q7WDP3 Isovaleryl-CoA dehydrogenase	-0,0034	0,4090	0,8060	0,7750	1
BeG90N05G10	Q7XPW3 OSJNBa0032F06.18 protein	-0,0546	0,7440	0,9190	0,8770	1
BeE30N05E04	Q7Z940 Succinyl-CoA synthetase, beta subunit	0,0183	0,3920	0,8480	0,9530	1
BeE60N17B06	Q80111 Ribosomal protein L7A (Fragment)	-0,0124	0,6920	1,0400	0,5860	1
BeG60N01B06	Q84P58 Adenosine kinase-like protein (Fragment)	-0,1480	0,9130	0,8690	0,6360	1
BeG90N01E12	Q86AX3 Similar to Mus musculus	-0,0019	0,6440	0,9220	0,8900	1
BeG90N13A04	Q87147 Putative N-acetyltransferase	-0,0880	0,3460	1,0800	0,7260	1

BeG90N10D06	Q8C644 Phenylalanine-tRNA synthetase-like	-0,3500	0,4810	1,0200	0,4660	1
BeE60C08E01	Q8H727 ADP/ATP translocase	-0,0013	0,9360	0,9620	1,0700	1
BeG120N24A07	Q8H727 ADP/ATP translocase	0,0195	0,9640	1,0700	0,6790	1
BeG30N06D06	Q8I7H7 Hypothetical protein C37C3.2c	-0,0897	1,0800	0,9760	0,4860	1
BeG90N05G08	Q8IXM3 Mitochondrial ribosomal protein L41	-0,0037	0,4570	1,0800	0,9230	1
BeG60N15H06	Q8K268 Similar to hypothetical protein FLJ11198	0,0029	0,7160	0,9980	0,8560	1
BeE60H04D06	Q8L9U0 Coclaurine N-methyltransferase	0,0997	0,3010	0,7240	0,6470	1
BeG90N21A12	Q8LFI1 Putative P-protein: chorismate mutase, prephenate dehydratase	-0,1760	0,6280	0,8510	0,8390	1
BeG30N12F08	Q8TZ04 Uncharacterized conserved protein	-0,1090	0,7740	0,8260	0,8550	1
BeG30N10B09	Q98AW1 8-amino-7-oxononanoate synthase, KAPA synthase	-0,0711	0,6540	0,8220	0,8450	1
BeE30N18D06	Q9C474 RNA polymerase II subunit 7	-0,0259	0,5770	0,9310	0,9240	1
BeG90N08B05	Q9P602 ATP synthase oligomycin sensitivity conferr	0,2670	0,3740	0,6570	0,7220	1
BeE30N08D02	Q9P7F8 Putative arsenite-translocating ATPase	0,0271	0,9640	0,9720	0,8300	1
BeE60H29F06	Q9RZ26 GMC oxidoreductase	-0,0832	0,9450	0,9050	0,7070	1
BeG120N10C03	Q9UUU0 NUGM protein precursor	0,0514	0,2710	0,8410	0,3240	1
BeE60H30H07	Q9VR34 CG12194-PA	-0,1580	0,8310	0,6310	0,5160	1
BeG30N10E10	Q9VXY3 CG5599 protein	0,0506	0,4480	0,9060	1,4300	1
BeE60H30E11	Q9WU83 Dolichol-phosphate mannosyltransferase	-0,1680	0,4370	0,7440	0,5670	1
BeG30N07H02	Q13895 Bystin	-0,0100	0,8610	0,7870	0,4140	2
BeG30N19E02	Q8SPM4 SCO-spondin	-0,0856	1,5000	-0,3210	-0,0117	2
BeG30N14E06	Q08237 ORF YOL080C	0,1770	1,1200	0,3190	-0,2350	2
BeG90N22C03	Q9USU2 Dimethyladenosine transferase	-0,2030	1,7100	0,9480	0,2490	2
BeG30N16D09	Q06218 Probable ATP-dependent RNA helicase DBP9	-0,0280	1,0900	0,7050	0,1570	2
BeG30N06D03	P38205 Putative methyltransferase NCL1	-0,0051	1,0500	0,3980	0,3230	2
BeE30N22H05	O81098 RNA polymerase I, II and III 24.3 kDa subun	-0,0111	0,7000	0,8150	0,2820	2
BeE120N36F09	O94553 Probable DNA-directed RNA polymerase III 34	-0,1550	0,9370	-0,0728	-0,3890	2
BeG30N15G10	Q9P7X8 Probable DNA-directed RNA polymerase I poly	0,0241	1,4600	0,6580	0,2760	2
BeG60N03B08	Q9P6N8 Putative atp-dependent RNA helicase	0,0302	1,1700	0,7730	0,2110	2
BeE30N07D04	O13768 Putative dna repair helicase	-0,0888	0,7090	0,0590	-0,0022	2
BeG30N18H02	O14236 Hypothetical gtp-binding protein associated	-0,0499	1,5200	0,8670	0,3120	2
BeZSPN03F10	O14344 Inosine-5'-monophosphate dehydrogenase	0,0333	0,7410	-0,0959	-0,0595	2
BeG30N04E02	P50094 Probable inosine-5'-monophosphate dehydroge	0,0460	1,4900	0,9650	0,4450	2
BeG30N05E04	O60747 Putative G-binding protein (Fragment)	0,0082	1,5400	0,8780	0,2200	2
BeG90N03C01	O74362 Conserved hypothetical protein	-0,1350	1,3000	0,5670	0,1480	2
BeG30N16G09	O80605 Putative sucrose/H+ symporter	0,0189	0,7590	0,3850	-0,0255	2
BeG30N12D07	O93937 PyrABCN	-0,0705	0,8630	0,4190	0,1820	2
BeG90N05B05	O94659 Probable nucleolar GTP-binding protein 1	0,0506	1,0400	0,5180	0,0730	2
BeG30N07A08	P10962 MAK16 protein	-0,0444	1,5900	0,7100	-0,0100	2
BeE60N10A01	P38264 Inorganic phosphate transporter PHO88	0,0195	1,0500	0,9080	0,5370	2
BeG30N17B06	P38861 Nonsense-mediated mRNA decay protein 3	-0,0693	1,1700	0,8620	0,3200	2
BeG30N03D07	P46075 Extracellular elastinolytic metalloproteina	0,0410	0,7770	-0,3910	-0,3200	2
BeZSPN12F04	Q03532 Probable ATP-dependent RNA helicase HAS1	0,2480	1,1400	0,2790	-0,1110	2
BeG30N08H04	Q09719 Putative ATP-dependent RNA helicase C31A2.0	0,0201	0,9630	0,0428	-0,3360	2
BeG30N02D12	Q08601 Chromosome XV reading frame ORF YOR197W	-0,0808	2,0400	0,6800	0,7170	2
BeE120N04F11	Q10248 Putative mitochondrial carrier C4G9.20c	0,1380	0,5650	0,6460	0,4600	2
BeG120N11F05	Q7RYU2 Hypothetical protein	-0,0465	1,0200	0,7790	0,3910	2
BeG120N15F01	Q7RZW8 Hypothetical protein	-0,1240	1,0500	0,3910	0,0953	2
BeG120N20B01	Q7S8R7 Hypothetical protein	-0,0258	0,8140	-0,3110	-0,5410	2
BeE60H32C06	Q7SD62 Hypothetical protein	-0,1040	1,1000	0,5600	0,6670	2
BeZSPN05F06	Q872I6 Probable iron inhibited ABC transporter 2	0,0165	0,6240	0,5240	-0,2950	2
BeE60H28C05	Q8AVD0 Similar to proteasome	0,0088	0,9810	0,7760	0,3400	2
BeE30N02B04	Q8CPE7 Glycerol uptake facilitator	0,0564	0,8140	0,4150	-0,0590	2
BeG60N06F09	Q8H710 Cystathionine beta-synthase	-0,1300	1,2900	1,0300	0,4260	2
BeE60N08G06	Q8N838 Hypothetical protein FLJ40083	-0,0612	0,8420	-0,0480	-0,3740	2

BeG120N16A06	Q8R0B2 Hypothetical protein (Fragment)	0,0372	1,5000	0,9250	0,3330	2
BeG30N08D09	Q92R40 Hypothetical protein R01080	-0,2590	1,4600	0,7300	0,2280	2
BeG30N02C12	Q93HL2 Tyrosinase	0,0450	1,1500	0,4270	-0,0215	2
BeG90N06B05	Q96VN0 Chitin deacetylase	-0,0556	0,9040	0,6440	0,0687	2
BeG60N12C05	Q9BQ67 Glutamate-rich WD-repeat protein 1	-0,0215	1,0900	0,9140	0,3540	2
BeZSPN12A04	Q9BQ67 Glutamate-rich WD-repeat protein 1	-0,0066	1,2100	0,7650	0,5100	2
BeG120N20E02	Q9NPE3 Nop10p	-0,0790	0,7380	1,0300	0,2910	2
BeG30N15C07	Q9NQ55 Suppressor of SWI4 1 homolog	0,4520	0,8320	0,6390	0,4460	2
BeZSPN19H09	Q9P7X8 Probable DNA-directed RNA polymerase I polypeptide 2	0,0711	0,8840	0,8890	0,3700	2
BeE60N19G04	Q9VEA4 CG31241 protein	0,0984	0,4510	0,9710	0,1880	2
BeG60N19A03	Q9W3Y0 CG3224 protein	0,0115	1,5200	1,0300	0,4720	2
BeE120N27D10	Q90YT9 Ribosomal protein L28	-0,0410	0,0113	1,2600	1,1900	3
BeE120N28E09	Q9ATF4 Ribosomal protein L33	0,0197	0,2050	0,6800	0,8980	3
BeE120N28H03	Q7XMJ1 OSJNBb0006N15.8 protein	-0,0371	0,0760	0,9470	0,7760	3
BeE30N02D11	P34091 60S ribosomal protein L6	0,0236	0,2270	0,6390	1,3500	3
BeE30N18E04	Q7RYQ5 Hypothetical protein	-0,0834	0,2870	1,1300	1,2600	3
BeG120N03B09	P04643 40S ribosomal protein S11	-0,0460	0,3120	0,9830	1,1300	3
BeG30N18C11	Q91YK6 Hypothetical protein (Fragment)	0,0229	0,1550	0,7470	0,6940	3
BeG60N14G09	Q9XGL4 60S ribosomal protein L31	0,1540	0,1020	0,7610	1,2400	3
BeG90N05A03	Q86QS0 Ribosomal protein L32	-0,0405	0,2930	0,6840	0,8620	3
BeG90N11F01	Q8ISP7 Ribosomal protein L9	0,0701	0,2290	1,0600	1,2100	3
BeG90N13B05	P23821 40S ribosomal protein S7	-0,2060	0,2570	0,9340	1,4000	3
BeG90N18G12	Q7PJE1 ENSANGP00000023979 (Fragment)	-0,0200	-0,0187	0,6000	0,7420	3
BeG90N19A11	Q9D8Q1 3100001N19Rik protein	-0,0569	0,2210	0,6090	0,9840	3
BeG90N19F06	O42867 60S ribosomal protein L23	0,0840	0,2250	0,8610	0,8940	3
BeZSPN09E01	O13989 Putative mannosyltransferase	-0,1360	-0,2800	0,5300	0,8350	3
BeG120N12G05	O14351 Hypothetical oxidoreductase C30D10.05c in chromosome II	-0,0669	0,2560	0,9600	1,5400	3
BeNSVP10B09	O59905 Pyridoxine biosynthesis protein	0,0201	0,1730	0,7070	0,7620	3
BeE60H03F06	O74507 Hypothetical protein	-0,0327	0,2450	1,2700	1,4500	3
BeE30N16B09	O77622 T-complex protein 1, zeta subunit	-0,0494	0,2760	0,4050	1,3800	3
BeNSVP06H10	O94135 Ketol-acid reductoisomerase	0,0498	0,2890	0,3310	0,8040	3
BeE30N22B03	P21976 NADH-ubiquinone oxidoreductase 20.8 kDa sub	0,0159	0,2460	0,7490	0,8200	3
BeE30N03D10	P25007 Peptidyl-prolyl cis-trans isomerase	-0,0083	-0,1400	0,3370	1,1500	3
BeZSPN13D02	P25654 Hypothetical 20.7 kDa protein in FIG2-KIN82	0,0056	-0,2980	0,2460	0,7580	3
BeE60H22D06	Q03554 Hypothetical UPF0198 protein YMR292W	0,0852	0,3830	0,7640	0,6790	3
BeG90N05E08	Q09171 Pyruvate dehydrogenase E1 component beta su	0,1000	0,3530	1,0200	0,8100	3
BeG90N11A02	Q90WD9 Glyceraldehyde 3-phosphate dehydrogenase	0,1180	0,2290	0,9270	2,0900	3
BeE60H29B11	Q7PM28 ENSANGP00000025012	0,0368	0,2460	0,9110	1,0400	3
BeZSPN13B09	Q7QKN6 AgCP10329 (Fragment)	0,0043	-0,1530	0,5790	1,1100	3
BeZSPN13B04	Q7RXP0 Hypothetical protein	-0,0553	-0,0870	0,7510	0,9190	3
BeE60H17F04	Q7RYE5 Hypothetical protein	-0,0667	0,2620	0,9850	0,8480	3
BeE30N02E08	Q7S5S5 Hypothetical protein	-0,0623	0,0050	0,8570	0,7440	3
BeE60H11C04	Q7YXM3 Thioredoxin peroxidase	-0,0753	0,2500	0,4020	1,7700	3
BeE60N07C12	Q7ZWF5 Similar to glutamate oxaloacetate transamin	-0,1600	0,1800	0,0534	1,2000	3
BeE30N22D03	Q86ZV7 Succinyl-CoA synthetase alpha subunit	0,0175	0,3970	0,7300	0,9930	3
BeE120N36H09	Q8EXG1 Conserved hypothetical protein	0,1070	0,1570	1,0400	0,4480	3
BeG120N04D02	Q90YP9 40S ribosomal protein S25	-0,1180	-0,0427	0,8210	1,0100	3
BeG120N23B05	Q99832 T-complex protein 1, eta subunit	0,1310	0,3080	0,8000	1,3600	3
BeE120N25H03	Q9LKK9 14-3-3 protein	-0,1380	0,3040	0,7570	2,1100	3
BeG120N09D05	Q9LKK9 14-3-3 protein	-0,0927	0,2230	0,6320	1,2600	3
BeE120N37H01	Q9MZG9 Polyprotein (Fragment)	0,0079	0,2720	0,6460	0,9220	3
BeE60H29G11	Q9P6I2 Glutamate carboxypeptidase-like protein	0,0776	0,2810	0,9070	0,8840	3
BeE90N06B10	Q9RUE8 Probable ABC transporter binding protein DR	0,0231	0,3080	1,2100	1,1300	3
BeZSPN13G07	Q9RYC2 Aminotransferase, putative	-0,1370	0,0151	1,3900	1,5000	3
BeE60H31D07	Q9USR1 Thioredoxin-like protein	0,0257	0,0092	0,7820	0,9250	3

BeE60N09E09	Q9WUA6 RAC-gamma serine/threonine protein kinase	0,0297	0,2240	1,0500	0,6680	3
BeG30N12H12	Q9Z8P1 Malonyl acyl carrier TRANSCYCLASE	-0,1250	0,2890	0,9950	0,9340	3
BeE30N17H11	Q7RWD9 Hypothetical protein	0,0889	1,0600	1,1800	1,0900	4
BeE30N19G03	Q9UVB8 Ribosomal protein L41	0,0085	0,8580	0,9980	1,3900	4
BeE30N20C09	Q8TDH2 CLL-associated antigen KW-12 (Fragment)	-0,0613	0,5990	1,1700	1,3100	4
BeG120N08B11	Q94JQ7 At1g07830/F24B9_7	0,0809	1,3000	1,5500	0,9350	4
BeG120N08C09	P52810 40S ribosomal protein S9	0,0211	0,7040	1,2300	1,1000	4
BeG120N17E03	P32324 Elongation factor 2	-0,0670	0,9080	1,4300	1,6600	4
BeG120N20B09	P51424 60S ribosomal protein L39	-0,1410	1,1300	1,1800	1,1800	4
BeG30N07D08	P56286 Eukaryotic translation initiation factor 2 alpha subunit	-0,0674	0,9510	1,3100	1,0200	4
BeG30N09B07	O74330 40S ribosomal protein S27	-0,0529	0,4540	1,1600	1,2500	4
BeG60N20C02	O13672 60S ribosomal protein L8	-0,0771	0,8290	1,4400	1,3300	4
BeG90N01C01	O14388 60S ribosomal protein L27-A	0,0176	0,6270	1,1800	1,0400	4
BeG90N02H08	Q9BPV9 Hypothetical protein	-0,0383	1,5600	0,9320	0,9260	4
BeG90N05A04	Q96TJ5 60S acidic ribosomal protein P0	0,0334	1,2500	1,6700	1,2900	4
BeG90N19F12	O14460 Elongation factor 2	-0,0405	0,9570	1,4000	1,2700	4
BeG90N21A07	Q8TFY0 Probable 60S ribosomal protein I5	-0,0286	0,6210	1,2500	1,4800	4
BeZSPN01B08	Q8ISP4 Ribosomal protein S12	0,0678	1,4400	1,5600	1,3200	4
BeE60N03H02	Q9NAR5 Eukaryotic translation initiation factor 2	0,0290	1,2600	2,0500	0,9670	4
BeG30N18E06	Q8S7Q0 Putative eukaryotic initiation factor subun	-0,0735	1,2300	1,0200	0,6030	4
BeG60N09D05	O94083 Eukaryotic translation initiation factor 5A	0,0315	0,9760	1,1200	1,1700	4
BeG30N20H06	Q9VRY0 CG10124 protein	0,1260	1,2800	1,3100	0,4310	4
BeG120N04E02	Q7SF16 Hypothetical protein	-0,0216	1,2800	1,4400	1,4500	4
BeG90N03F03	Q9C5Z2 Eukaryotic translation initiation factor 3	-0,1020	1,3500	1,6500	0,6700	4
BeG30N13C06	O14044 Conserved hypothetical protein	-0,1570	1,8400	1,1700	0,4070	4
BeE30N08D06	O43660 Pleiotropic regulator 1	0,0556	0,6100	1,1600	1,1300	4
BeE60N08F01	O44781 Hypothetical protein	0,1340	0,9750	1,2200	0,6600	4
BeG30N04G05	O60164 Pescadillo homolog	0,0184	2,2500	1,7200	0,4310	4
BeE60H30E02	O60953 Proteasome subunit	0,0269	1,0500	1,5000	1,5700	4
BeE30N06D09	O61219 Hypothetical protein	0,1730	0,8190	1,1900	0,8770	4
BeE60H29B07	O65421 VPS28 protein homolog 2	0,0250	0,8450	1,2900	1,1800	4
BeG90N21E07	O74491 Putative ATP-dependent RNA helicase C285.03	0,0167	1,0700	1,4100	1,2700	4
BeE60N10C01	O82143 OsS5a	0,0153	0,8140	1,3900	1,4300	4
BeG90N15D01	P21588 5'-nucleotidase precursor	-0,0020	0,8910	1,7300	0,9290	4
BeZSPN11E08	P32529 DNA-directed RNA polymerase I 13.7 kDa poly	-0,0432	1,1600	1,7600	0,8620	4
BeE60H22D05	P40513 Mitochondrial acidic protein MAM33, mitocho	0,0457	0,5490	1,2100	1,1100	4
BeE60H14B07	P41887 Heat shock protein 90 homolog	0,0482	0,6780	1,2400	1,7200	4
BeG30N12D04	Q25330 Cyclin-dependent kinases regulatory subunit	-0,1440	0,7110	1,0100	0,5700	4
BeE120N28B12	Q9C1M3 Septin	0,0529	1,0700	1,0100	0,6020	4
BeG90N16C06	P42833 Hexose transporter HXT14	0,1010	1,4700	1,1900	0,8430	4
BeG120N22G10	Q7S5F0 Hypothetical protein	0,0346	1,7400	1,5400	1,2300	4
BeE30N10D02	Q06593 Similar to S. CEREVISIAE hypothetical prote	-0,0137	2,2400	3,3800	1,9700	4
BeE30N06H12	Q86AU7 Similar to Gallus gallus	0,0746	1,5000	1,4500	1,3000	4
BeG120N16D10	P87216 Protein vip1	0,0239	0,7040	1,2200	0,7980	4
BeE30N02B11	Q03529 Inositolphosphorylceramide-B C-26 hydroxyla	0,0537	0,7720	1,2000	0,9450	4
BeE60H21G01	Q7PMI7 ENSANGP00000021048 (Fragment)	-0,0928	0,7460	1,6600	1,4600	4
BeE60N04C06	Q7PRC0 ENSANGP00000022132 (Fragment)	-0,1650	0,6400	1,3100	0,4930	4
BeG60N05A06	Q7PSD1 ENSANGP00000016179	-0,0340	0,9780	1,4000	0,9810	4
BeG90N07B07	Q7Q192 AgCP8591 (Fragment)	0,1540	0,7640	1,4200	1,1900	4
BeE60H31G05	Q7Q1H1 AgCP8372	0,0940	0,8760	1,1500	1,1900	4
BeG30N01A06	Q7RZW8 Hypothetical protein	0,2480	1,1000	1,3100	0,3290	4
BeG90N22A10	Q7SGH1 Hypothetical protein	0,0238	1,0700	0,9620	1,1400	4
BeE60C06H06	Q7WWT9 Putative NagM-like protein	0,0827	0,4630	1,2100	1,1900	4
BeG120N08A09	Q810V0 Similar to U3 small nucleolar ribonucleopro	0,0523	1,2200	1,1100	0,4440	4
BeE90N17C02-1	Q83PF0 Putative aldolase yihT	-0,0485	1,1100	1,1700	1,2800	4

BeG90N02H02	Q871M5 Probable nucleosome assembly protein I	-0,0443	2,5100	2,3000	1,6400	4
BeG30N08H02	Q87FJ3 Hypothetical protein	-0,1480	2,0800	1,9200	0,9900	4
BeG30N16G07	Q8AVK7 Similar to hypothetical protein FLJ40452	-0,1830	1,3500	1,2700	0,1470	4
BeG30N15D01	Q8K1A0 Similar to HSPC133 protein	0,2200	1,5400	1,1200	0,8770	4
BeG90N21H11	Q8NDH3 Probable aminopeptidase NPEPL1	-0,0412	0,7340	1,3300	1,2500	4
BeG30N06H12	Q8NEY6 Gastric cancer antigen Zg14 (Fragment)	0,0461	2,0100	1,4200	0,4470	4
BeG120N09C02	Q8NIH8 Nuclease Le3	0,0612	0,7260	1,4900	0,8290	4
BeG90N06E01	Q8VZZ5 Eukaryotic release factor 1	0,1810	1,5900	1,3000	0,5690	4
BeG90N01D10	Q8WZW8 Probable YHM1	0,3020	1,0900	1,4700	1,0800	4
BeG30N14D03	Q93WB0 Putative GTPase	0,1350	1,8400	1,5900	0,4040	4
BeE60N10G05	Q96MM6 Heat shock 70 kDa protein 12B	0,0362	1,6400	2,3700	0,3600	4
BeE60N03E07	Q99JZ6 Hypothetical protein	-0,1250	0,8440	1,5700	1,5900	4
BeG120N23E11	Q99L23 Similar to NADH dehydrogenase (Fragment)	-0,1230	1,1200	1,5500	1,2500	4
BeE60H31F10	Q9HCT3 RP42 protein	-0,0153	1,2300	1,1100	0,9150	4
BeE30N07B02	Q9HFY6 Calmodulin	0,0202	0,9780	0,9880	0,9820	4
BeE30N09G01	Q9M4C4 Probable prefoldin subunit 4	0,0792	0,6290	1,2300	1,0900	4
BeG30N03H11	Q9P7X8 Probable DNA-directed RNA polymerase I polypeptide 2	-0,0364	1,0300	0,8430	0,5060	4
BeG90N18F12	Q9SA73 T5I8.3 protein	0,0473	2,6800	2,5300	2,2100	4
BeE30N02F10	Q9VDV2 CG6195 protein	0,1040	1,6700	1,8000	1,1200	4
BeG30N08D01	Q9Y3D8 Protein CGI-137	-0,0241	2,2500	1,8300	0,2840	4
BeG120N26D12	Q9Y8G5 NAD-specific glutamate dehydrogenase	-0,0873	0,5250	2,3700	2,4200	4
BeG120N16E05	P43098 Fatty acid synthase subunit alpha	-0,1550	0,4170	1,6100	1,9600	5
BeG60N06G05	P79078 Delta-9 fatty acid desaturase	0,0282	1,7700	3,9200	4,2200	5
BeG30N17H01	O94122 Pyruvate kinase	-0,1210	1,5800	2,6300	2,0000	5
BeG90N13C04	Q874Q4 Phosphoglucose isomerase	-0,0552	1,1000	1,3600	1,8400	5
BeG120N23E01	O13302 Isocitrate dehydrogenase [NAD] subunit 1, m	-0,0217	1,8300	3,2600	1,2700	5
BeG60N06H10	Q7ZVY5 Similar to citrate synthase	-0,0623	1,0800	2,0000	1,6500	5
BeG90N18E08	Q8X097 Probable ATP-citrate synthase subunit 1	-0,1050	0,2160	1,6000	2,4000	5
BeE60N11F06	Q8X1D0 Isocitrate dehydrogenase (Fragment)	-0,0448	0,8400	1,8500	1,5700	5
BeG90N10C12	O42156 Heterochromatin protein 1 gamma (Fragment)	-0,0596	1,5200	1,6200	1,8400	5
BeG60N08E04	O42468 PP2A inhibitor	-0,1580	2,3400	2,8900	1,6300	5
BeE60H32E04	O42993 FK506-binding protein	0,0619	1,2000	2,0100	2,1000	5
BeG90N10B10	P02992 Elongation factor Tu, mitochondrial precurs	-0,0754	0,9970	1,5500	1,6000	5
BeE60N13C09	P07144 Outer mitochondrial membrane protein porin	0,1310	1,0000	1,4600	2,6300	5
BeG120N02B04	P32469 Diphthine synthase	-0,0535	4,2700	3,9800	2,6000	5
BeE30N17A03	P40897 Oligopeptide transporter 1	0,1970	2,0000	3,2900	2,6700	5
BeE30N15A04	P79083 Eukaryotic translation initiation factor 3	0,0092	1,8400	2,3100	1,3800	5
BeE60H15C05	P87144 Threonyl-tRNA synthetase, cytoplasmic	0,1220	2,3400	2,2900	1,0300	5
BeE60H30F10	Q10481 Mitochondrial import inner membrane translo	0,0295	1,3400	1,7600	1,6900	5
BeE60N10H11	Q7PVB7 ENSANGP00000021149 (Fragment)	-0,2010	0,7190	1,4000	1,8900	5
BeG90N10E12	Q7SEL5 Hypothetical protein	-0,3110	1,2500	1,4400	1,6900	5
BeE60C24C07	Q7ZA53 FK506-binding protein FKBP12	-0,0452	1,0200	1,5300	2,2200	5
BeE60N10F07	Q7ZWR6 Similar to ATP synthase, H+ transporting mi	-0,0463	0,9930	2,0100	2,0100	5
BeG90N07C02	Q84KQ4 Elongation factor-1alpha (Fragment)	0,1770	1,1200	1,7700	1,9400	5
BeNSVP07H09	Q84KQ4 Elongation factor-1alpha (Fragment)	-0,0119	1,1000	1,6400	1,9200	5
BeG30N20G08	Q8NIH8 Nuclease Le3	-0,0628	2,5800	3,1500	2,2300	5
BeG120N12G04	Q8TFN0 Nucleoside diphosphate kinase	-0,1990	2,4700	3,2600	3,2000	5
BeG30N15D05	Q8Y2Q8 Probable carbonic anhydrase protein	0,0098	2,7200	2,1500	2,2100	5
BeG120N13E04	Q9HGT6 Seryl-tRNA synthetase, cytoplasmic	0,3040	1,9300	2,0000	1,4000	5
BeG120N07E03	Q9P8H0 Rph1	0,1830	0,5430	1,5200	2,0600	5
BeG30N20D08	Q9UUG1 Brix domain containing protein 1 homolog	-0,0591	4,5200	3,6300	1,5100	5