

Tabela 6: Exemplo do arquivo de saída gerado pelo HTself utilizando todas as réplicas das hibridizações G30 x ZSP.

ID	Best Hit_SwissProt	total	used	x.median	x.mean	x.mad	x.sd	up	down	inside	p.up	p.down	p.inside
BeE120N37C03	O04892 Cytochrome P450 like_TBP GO:0050381 GO:00	6	2	1,46	1,46	0,311	0,297	2	0	0	1	0	0
BeNSVP03B12	No match	6	2	4,41	4,41	0,267	0,255	2	0	0	1	0	0
BeG90N07C02	Q84KQ4 Elongation factor-1alpha (Fragment) GO:0008	12	11	1,12	1,12	0,163	0,21	11	0	0	1	0	0
BeG30N15G10	Q9P7X8 Probable DNA-directed RNA polymerase I poly	12	9	1,46	1,43	0,222	0,228	9	0	0	1	0	0
BeG120N02B04	P32469 Diphthine synthase GO:0016740 GO:0008152 GO	6	6	4,27	3,94	0,497	0,799	6	0	0	1	0	0
BeG90N16C06	P42833 Hexose transporter HXT14 GO:0006810 GO:0016	6	6	1,47	1,77	0,245	0,631	6	0	0	1	0	0
BeG120N13E04	Q9HGT6 Seryl-tRNA synthetase, cytoplasmic GO:00064	6	6	1,93	1,74	0,956	0,863	5	0	1	0,833	0	0,167
BeG120N14H04	O74362 Conserved hypothetical protein GO:0003676	6	6	0,808	1,17	0,354	0,749	5	0	1	0,833	0	0,167
BeE60H26H05	Q09747 Putative ATP-dependent RNA helicase C12C2.0	6	5	0,622	0,911	0,101	0,432	4	0	1	0,8	0	0,2
BeE60N17B06	Q80111 Ribosomal protein L7A (Fragment) GO:0005622	6	5	0,692	0,699	0,246	0,23	4	0	1	0,8	0	0,2
BeZSPN05F10	P20435 DNA-directed RNA polymerases I, II, and III	6	6	0,726	0,399	0,383	0,722	4	1	1	0,667	0,167	0,167
BeG30N17B05	No match	6	6	1,37	0,668	0,0815	1,12	4	2	0	0,667	0,333	0
BeG60N15H06	Q8K268 Similar to hypothetical protein FLJ11198 GO	6	6	0,716	0,161	0,454	1,13	3	2	1	0,5	0,333	0,167
BeE30N10D01	Q9UKU7 Acyl-CoA dehydrogenase family member 8, mit	6	6	-0,0137	-0,00215	0,0132	0,0382	0	0	6	0	0	1
BeE60C04F03	O95461 Glycosyltransferase-like protein LARGE GO:0	6	6	0,0311	-0,0263	0,127	0,16	0	0	6	0	0	1
BeE60N13G10	P40046 Vacuolar transporter chaperone 1 GO:0042144	6	5	-0,118	-0,189	0,546	0,413	0	1	4	0	0,2	0,8
BeE120N35H01	Q7SAQ1 Hypothetical protein GO:0006886 GO:0030125	6	6	-0,4	-0,742	0,34	0,716	0	2	4	0	0,333	0,667
BeG120N04H04	P60468 Protein transport protein SEC61 beta subuni	12	8	0,0115	-0,63	0,238	1,03	0	3	5	0	0,375	0,625
BeZSPN08H10	Q7S4A0 Hypothetical protein GO:0006810 GO:0005415	6	4	-0,552	-0,569	0,338	0,287	0	2	2	0	0,5	0,5
BeZSPN13B01	Q96TW0 Putative arginase (Fragment) GO:0006527 GO:	6	6	-0,57	-0,453	0,281	0,415	0	3	3	0	0,5	0,5
BeE60H05F08	No match	6	5	-0,783	-0,886	0,621	0,641	0	3	2	0	0,6	0,4
BeE60C36G04	Q7VUM3 Putative integral membrane transport protei	6	5	-1,36	-1,37	0,786	0,612	0	4	1	0	0,8	0,2
BeE120N09C08	Q8P9N1 Cationic amino acid transporter GO:0006865	6	6	-0,936	-1,09	0,391	0,496	0	5	1	0	0,833	0,167
BeE30N03A06	Q16550 Transcription initiation protein SPT4 homol	6	6	-0,907	-1,02	0,515	0,475	0	5	1	0	0,833	0,167
BeE120N27B02	P56205 Cytochrome c GO:0006118 GO:0005739 GO:00	12	12	-1,88	-2,08	1,12	1,03	0	12	0	0	1	0
BeE30N02B01	O04974 2-isopropylmalate synthase B GO:0016740 GO:	6	6	-1,15	-1,21	0,203	0,336	0	6	0	0	1	0
BeE60N03D06	O15819 Histone H3 GO:0007001 GO:0003677 GO:00063	6	6	-1,64	-1,47	0,311	0,442	0	6	0	0	1	0

Em cores estão destacados os critérios utilizados para classificação dos genes como diferencialmente expressos: vermelho- induzidos; verde- reprimidos; azul- não foram considerados induzidos porque apresentaram menos de 3 réplicas válidas.

Estatísticas calculadas pelo HTself: total- número de réplicas presentes nos micro-arranjos; used- número de réplicas válidas; x.median- mediana dos valores M para todas as rélicas válidas; x.mean- média dos valores M para todas as réplicas válidas; x.mad- desvio absoluto da mediana; x.sd- desvio padrão da média; up, down e inside- número de réplicas acima, abaixo e dentro das curvas homotípicas, respectivamente; p.up, p.down e p.inside- porcentagem das réplicas acima, abaixo e dentro das curvas homotípicas, respectivamente.

Tabela 7: Genes induzidos durante a germinação em meio nutriente cujas categorias funcionais foram destacadas pelo BayGO.

Clone	Melhor alinhamento (Swiss-Prot)	log2 da razão de expressão				K	Descrição GO
		t=0	t=30	t=60	t=90		
BeE30N13B01	Q8GUQ9 60S ribosomal protein L38	-0,0514	0,4940	0,8260	0,8190	1	protein biosynthesis
BeE30N15E11	P57728 60S ribosomal protein L28-B	0,1190	0,7620	0,7030	0,9990	1	protein biosynthesis
BeE30N22E01	O14339 60S ribosomal protein L17-A	-0,0558	0,9450	0,7840	0,7580	1	protein biosynthesis
BeG120N01H09	Q7SEP1 Hypothetical protein	-0,0497	0,5870	0,6630	0,8730	1	protein biosynthesis
BeG120N06A04	Q9SIP7 40S ribosomal protein, contains C-terminal	-0,0078	0,5840	0,8690	0,7240	1	protein biosynthesis
BeG120N06C12	O75000 60S ribosomal protein L12	-0,0319	0,4710	0,7980	1,0500	1	protein biosynthesis
BeG120N11G04	Q874N9 Ribosomal protein L37A	0,0402	0,5870	0,8570	1,1100	1	protein biosynthesis
BeG120N17C05	O74836 60S ribosomal protein L1-B	0,0065	0,6920	0,8120	0,8520	1	protein biosynthesis
BeG120N22D07	Q05506 Arginyl-tRNA synthetase, cytoplasmic	-0,0429	0,9140	0,8400	0,6600	1	protein biosynthesis
BeG30N07F12	Q889U9 30S ribosomal protein S13	-0,0836	0,6210	0,6940	0,7140	1	protein biosynthesis
BeG30N12B10	Q7QC42 AgCP1729 (Fragment)	-0,0900	0,6730	0,9170	0,8270	1	protein biosynthesis
BeG30N12D10	Q09865 Putative 60S ribosomal protein L6, mitochondrial precursor	-0,0940	0,5700	0,8900	0,9550	1	protein biosynthesis
BeG60N16E09	Q962R4 Ribosomal protein S15	0,0345	0,5080	0,8690	1,2500	1	protein biosynthesis
BeG90N09F06	Q7RVY8 Hypothetical protein	-0,0493	0,6980	0,7930	0,8140	1	protein biosynthesis
BeZSPN12H11	P14249 40S ribosomal protein S24	0,0205	0,5050	0,8450	1,2400	1	protein biosynthesis
BeE30N13E04	P28748 GTP-binding nuclear protein spi1	-0,1270	0,4560	1,0500	0,9630	1	small GTPase mediated signal transduction
BeG90N16G12	Q01475 GTP-binding protein sar1	-0,0842	0,7680	0,8800	1,1700	1	small GTPase mediated signal transduction
BeE30N09G11	O13581 Manganese resistance 1 protein	-0,0267	0,4590	0,7970	0,6700	1	calcium ion transport
BeG30N12G06	Q9XTG4 PMR1 protein	-0,0500	0,5050	0,9680	1,1200	1	calcium ion transport
BeG60N12E03	O43447 Peptidyl-prolyl cis-trans isomerase H	0,1010	0,4330	0,7140	0,9480	1	protein folding
BeG120N07A08	Q7SCN0 Hypothetical protein	-0,0421	0,7510	0,9120	0,5190	1	protein folding
BeE60H30F05	Q96C51 Hypothetical protein (Fragment)	0,2400	0,7040	1,1300	1,2300	1	protein folding
BeE120N02E05	Q9C9U6 Hypothetical protein	0,0623	0,8490	0,7170	1,1300	1	protein folding
BeG30N14E06	Q08237 ORF YOL080C	0,1770	1,1200	0,3190	-0,2350	2	rRNA processing
BeG90N22C03	Q9USU2 Dimethyladenosine transferase	-0,2030	1,7100	0,9480	0,2490	2	rRNA processing
BeE30N22H05	O81098 RNA polymerase I, II and III 24.3 kDa subun	-0,0111	0,7000	0,8150	0,2820	2	transcription
BeE120N36F09	O94553 Probable DNA-directed RNA polymerase III 34	-0,1550	0,9370	-0,0728	-0,3890	2	transcription
BeG30N15G10	Q9P7X8 Probable DNA-directed RNA polymerase I poly	0,0241	1,4600	0,6580	0,2760	2	transcription
BeG60N03B08	Q9P6N8 Putative atp-dependent RNA helicase	0,0302	1,1700	0,7730	0,2110	2	transcription

BeG30N16D09	Q06218 Probable ATP-dependent RNA helicase DBP9	-0,0280	1,0900	0,7050	0,1570	2	ribosome biogenesis/rRNA processing
BeG30N06D03	P38205 Putative methyltransferase NCL1	-0,0051	1,0500	0,3980	0,3230	2	ribosome biogenesis
BeZSPN03F10	O14344 Inosine-5'-monophosphate dehydrogenase	0,0333	0,7410	-0,0959	-0,0595	2	purine nucleotide biosynthesis
BeG30N04E02	P50094 Probable inosine-5'-monophosphate dehydroge	0,0460	1,4900	0,9650	0,4450	2	purine nucleotide biosynthesis
BeG30N07H02	Q13895 Bystin	-0,0100	0,8610	0,7870	0,4140	2	cell adesion
BeG30N19E02	Q8SPM4 SCO-spondin	-0,0856	1,5000	-0,3210	-0,0117	2	cell adesion
BeG30N12D07	O93937 PyrABCN	-0,0705	0,8630	0,4190	0,1820	2	amino acid metabolism
BeG60N06F09	Q8H710 Cystathionine beta-synthase	-0,1300	1,2900	1,0300	0,4260	2	amino acid metabolism
BeE120N27D10	Q90YT9 Ribosomal protein L28	-0,0410	0,0113	1,2600	1,1900	3	protein biosynthesis
BeE120N28E09	Q9ATF4 Ribosomal protein L33	0,0197	0,2050	0,6800	0,8980	3	protein biosynthesis
BeE120N28H03	Q7XMJ1 OSJNBb0006N15.8 protein	-0,0371	0,0760	0,9470	0,7760	3	protein biosynthesis
BeE30N02D11	P34091 60S ribosomal protein L6	0,0236	0,2270	0,6390	1,3500	3	protein biosynthesis
BeE30N18E04	Q7RYQ5 Hypothetical protein	-0,0834	0,2870	1,1300	1,2600	3	protein biosynthesis
BeG120N03B09	P04643 40S ribosomal protein S11	-0,0460	0,3120	0,9830	1,1300	3	protein biosynthesis
BeG30N18C11	Q91YK6 Hypothetical protein (Fragment)	0,0229	0,1550	0,7470	0,6940	3	protein biosynthesis
BeG60N14G09	Q9XGL4 60S ribosomal protein L31	0,1540	0,1020	0,7610	1,2400	3	protein biosynthesis
BeG90N05A03	Q86QS0 Ribosomal protein L32	-0,0405	0,2930	0,6840	0,8620	3	protein biosynthesis
BeG90N11F01	Q8ISP7 Ribosomal protein L9	0,0701	0,2290	1,0600	1,2100	3	protein biosynthesis
BeG90N13B05	P23821 40S ribosomal protein S7	-0,2060	0,2570	0,9340	1,4000	3	protein biosynthesis
BeG90N18G12	Q7PJE1 ENSANGP0000023979 (Fragment)	-0,0200	-0,0187	0,6000	0,7420	3	protein biosynthesis
BeG90N19A11	Q9D8Q1 3100001N19Rik protein	-0,0569	0,2210	0,6090	0,9840	3	protein biosynthesis
BeG90N19F06	O42867 60S ribosomal protein L23	0,0840	0,2250	0,8610	0,8940	3	protein biosynthesis
BeG90N05E08	Q09171 Pyruvate dehydrogenase E1 component beta su	0,1000	0,3530	1,0200	0,8100	3	glycolysis
BeG90N11A02	Q90WD9 Glyceraldehyde 3-phosphate dehydrogenase	0,1180	0,2290	0,9270	2,0900	3	glycolysis
BeE30N17H11	Q7RWD9 Hypothetical protein	0,0889	1,0600	1,1800	1,0900	4	protein biosynthesis
BeE30N19G03	Q9UVB8 Ribosomal protein L41	0,0085	0,8580	0,9980	1,3900	4	protein biosynthesis
BeE30N20C09	Q8TDH2 CLL-associated antigen KW-12 (Fragment)	-0,0613	0,5990	1,1700	1,3100	4	protein biosynthesis
BeG120N08B11	Q94JQ7 At1g07830/F24B9_7	0,0809	1,3000	1,5500	0,9350	4	protein biosynthesis
BeG120N08C09	P52810 40S ribosomal protein S9	0,0211	0,7040	1,2300	1,1000	4	protein biosynthesis
BeG120N17E03	P32324 Elongation factor 2	-0,0670	0,9080	1,4300	1,6600	4	protein biosynthesis

BeG120N20B09	P51424 60S ribosomal protein L39	-0,1410	1,1300	1,1800	1,1800	4	protein biosynthesis
BeG30N07D08	P56286 Eukaryotic translation initiation factor 2 alpha subunit	-0,0674	0,9510	1,3100	1,0200	4	protein biosynthesis
BeG30N09B07	O74330 40S ribosomal protein S27	-0,0529	0,4540	1,1600	1,2500	4	protein biosynthesis
BeG60N20C02	O13672 60S ribosomal protein L8	-0,0771	0,8290	1,4400	1,3300	4	protein biosynthesis
BeG90N01C01	O14388 60S ribosomal protein L27-A	0,0176	0,6270	1,1800	1,0400	4	protein biosynthesis
BeG90N02H08	Q9BPV9 Hypothetical protein	-0,0383	1,5600	0,9320	0,9260	4	protein biosynthesis
BeG90N05A04	Q96TJ5 60S acidic ribosomal protein P0	0,0334	1,2500	1,6700	1,2900	4	protein biosynthesis
BeG90N19F12	O14460 Elongation factor 2	-0,0405	0,9570	1,4000	1,2700	4	protein biosynthesis
BeG60N09D05	O94083 Eukaryotic translation initiation factor 5A	0,0315	0,9760	1,1200	1,1700	4	protein biosynthesis
BeG30N20H06	Q9VRY0 CG10124 protein	0,1260	1,2800	1,3100	0,4310	4	protein biosynthesis
BeG90N21A07	Q8TFY0 Probable 60S ribosomal protein I5	-0,0286	0,6210	1,2500	1,4800	4	protein biosynthesis/translation initiation factor activity
BeZSPN01B08	Q8ISP4 Ribosomal protein S12	0,0678	1,4400	1,5600	1,3200	4	protein biosynthesis/translation initiation factor activity
BeE60N03H02	Q9NAR5 Eukaryotic translation initiation factor 2	0,0290	1,2600	2,0500	0,9670	4	protein biosynthesis/translation initiation factor activity
BeG30N18E06	Q8S7Q0 Putative eukaryotic initiation factor subun	-0,0735	1,2300	1,0200	0,6030	4	protein biosynthesis/translation initiation factor activity
BeG60N09D05	O94083 Eukaryotic translation initiation factor 5A	0,0315	0,9760	1,1200	1,1700	4	protein biosynthesis/translation initiation factor activity
BeG120N04E02	Q7SF16 Hypothetical protein	-0,0216	1,2800	1,4400	1,4500	4	protein biosynthesis/translation initiation factor activity
BeG90N03F03	Q9C5Z2 Eukaryotic translation initiation factor 3	-0,1020	1,3500	1,6500	0,6700	4	protein biosynthesis/translation initiation factor activity
BeG90N21A07	Q8TFY0 Probable 60S ribosomal protein I5	-0,0286	0,6210	1,2500	1,4800	4	protein biosynthesis/translation initiation factor activity
BeZSPN01B08	Q8ISP4 Ribosomal protein S12	0,0678	1,4400	1,5600	1,3200	4	protein biosynthesis/translation initiation factor activity
BeE60N03H02	Q9NAR5 Eukaryotic translation initiation factor 2	0,0290	1,2600	2,0500	0,9670	4	protein biosynthesis/translation initiation factor activity
BeG30N18E06	Q8S7Q0 Putative eukaryotic initiation factor subun	-0,0735	1,2300	1,0200	0,6030	4	protein biosynthesis/translation initiation factor activity
BeG90N16C06	P42833 Hexose transporter HXT14	0,1010	1,4700	1,1900	0,8430	4	carbohydrate transport
BeG120N22G10	Q7S5F0 Hypothetical protein	0,0346	1,7400	1,5400	1,2300	4	carbohydrate transport
BeE30N10D02	Q06593 Similar to S. CEREVISIAE hypothetical prote	-0,0137	2,2400	3,3800	1,9700	4	oligopeptide transport
BeE30N06H12	Q86AU7 Similar to Gallus gallus	0,0746	1,5000	1,4500	1,3000	4	oligopeptide transport
BeG30N12D04	Q25330 Cyclin-dependent kinases regulatory subunit	-0,1440	0,7110	1,0100	0,5700	4	cell cycle
BeE120N28B12	Q9C1M3 Septin	0,0529	1,0700	1,0100	0,6020	4	cell cycle
BeG120N23E01	O13302 Isocitrate dehydrogenase [NAD] subunit 1, m	-0,0217	1,8300	3,2600	1,2700	5	tricarboxylic acid cycle
BeG60N06H10	Q7ZVY5 Similar to citrate synthase	-0,0623	1,0800	2,0000	1,6500	5	tricarboxylic acid cycle
BeG90N18E08	Q8X097 Probable ATP-citrate synthase subunit 1	-0,1050	0,2160	1,6000	2,4000	5	tricarboxylic acid cycle
BeE60N11F06	Q8X1D0 Isocitrate dehydrogenase (Fragment)	-0,0448	0,8400	1,8500	1,5700	5	tricarboxylic acid cycle
BeG30N17H01	O94122 Pyruvate kinase	-0,1210	1,5800	2,6300	2,0000	5	glycolysis

BeG90N13C04	Q874Q4 Phosphoglucose isomerase	-0,0552	1,1000	1,3600	1,8400	5	glycolysis
BeG120N16E05	P43098 Fatty acid synthase subunit alpha	-0,1550	0,4170	1,6100	1,9600	5	fatty acid biosynthesis
BeG60N06G05	P79078 Delta-9 fatty acid desaturase	0,0282	1,7700	3,9200	4,2200	5	fatty acid biosynthesis
BeE60N13C09	P07144 Outer mitochondrial membrane protein porin	0,1310	1,0000	1,4600	2,6300	5	anion transport
BeG120N12G04	Q8TFN0 Nucleoside diphosphate kinase	-0,1990	2,4700	3,2600	3,2000	5	GTP/UTP biosynthesis
BeG120N07E03	Q9P8H0 Rph1	0,1830	0,5430	1,5200	2,0600	5	protein-nucleus import

**Tabela 10: Genes reprimidos durante a germinação em meio nutriente cujas categorias funcionais foram destacadas pelo BayGO.**

Clone	Melhor alinhamento (Swiss-Prot)	log2 da razão de expressão				K	Descrição GO
		t=0	t=30	t=60	t=90		
BeE120N32H02	O93787 Chs3	0,0065	-0,2520	-0,7880	-1,0200	6	chitin synthase activity
BeG30N02B09	P08004 Chitin synthase 1	0,0231	0,2550	-0,0928	-0,7540	6	chitin synthase activity
BeE90N05B09	Q8GUB3 Putative vacuolar ATPase subunit H	0,0119	-0,5470	-0,8710	-0,7560	6	proton transport
BeG30N04H11	Q7Z8B6 H(+)-ATPase	0,0593	0,1800	-0,8740	-1,0000	6	proton transport
BeE60N16D02	P34046 Guanine nucleotide-binding protein alpha-8	0,0240	-1,0200	-1,1400	-0,9370	7	signal transduction
BeE60N09G02	Q12702 Protein phosphatase PP2A regulatory subunit	-0,1030	-0,8770	-1,4700	-1,1700	7	signal transduction
BeE120N18F01	Q86WN6 Phosphodiesterase PDE9A13	0,0185	-1,2000	-0,8750	-1,0300	7	signal transduction
BeE60N10E10	P19984 Profilin II	-0,0528	-1,2700	-1,1800	-0,5110	7	actin binding activity
BeE60H15H11	Q7SGN0 Hypothetical protein	0,0070	-1,3600	-1,0300	-0,4110	7	actin binding activity
BeZSPN16G12	Q7NYB4 Large conductance mechanosensitive channel	-0,0245	-0,9460	-2,2100	-1,9700	8	ion channel activity
BeG30N07G09	Q7NI34 Gli2350 protein	0,0860	-0,1250	-1,3700	-0,8480	9	amino acid transport
BeE120N09C08	Q8P9N1 Cationic amino acid transporter	0,0699	-0,9360	-1,5800	-1,5900	9	amino acid transport
BeE60H21G09	Q8RBT1 Amino acid transporters	0,0161	-0,6540	-1,3100	-0,9980	9	amino acid transport
BeE30N06E01	Q9A910 Amino acid permease family protein	-0,0638	-0,6410	-1,8400	-1,3100	9	amino acid transport
BeZSPN05A11	Q9QXA6 B(0,+)-type amino acid transporter 1	0,0964	-0,3790	-1,7100	-1,0700	9	amino acid transport
BeE60N18F10	O74846 Exocyst complex component sec6	0,0713	-0,2120	-1,4300	-1,2000	9	intracellular protein transport
BeZSPN10C02	Q62896 BET1 homolog	-0,0143	-0,6740	-1,7600	-1,1000	9	intracellular protein transport
BeE120N35H01	Q7SAQ1 Hypothetical protein	0,1390	-0,4000	-2,1100	-1,6600	9	intracellular protein transport
BeG30N03G06	Q9C0R0 (AF343071) TIM23	-0,0395	-0,3170	-1,1900	-0,9210	9	intracellular protein transport
BeG30N06C03	Q9P7N2 Putative clathrin-associated protein	0,2440	-0,2310	-1,6300	-1,1300	9	intracellular protein transport
BeE60N11G06	Q05116 Dual specificity mitogen-activated protein	-0,1950	-0,2990	-1,2700	-1,0400	9	protein serine/threonine kinase activity
BeZSPN16D09	Q12741 cAMP-dependent protein kinase catalytic sub	0,0615	-0,7520	-1,5200	-0,8600	9	protein serine/threonine kinase activity
BeZSPN18G07	Q9HEW4 Ste20 a kinase	0,0562	-0,5940	-1,4300	-1,1900	9	protein serine/threonine kinase activity
BeE120N28F02	Q9Y7W8 MAP kinase kinase	0,0476	-0,4270	-1,1100	-0,8470	9	protein serine/threonine kinase activity
BeE60N03C06	Q9HDE1 Calcineurin B regulatory subunit	0,1060	-0,9230	-1,7600	-1,0200	9	calcium ion binding activity

BeE120N04B04	Q95WR8 PXF isoform C	0,0031	-0,2230	-1,2400	-1,1600	9	calcium ion binding activity/signal transducer activity
BeG60N08H03	Q8J0B8 G protein alpha subunit	0,0336	-0,5020	-1,2900	-1,4200	9	signal transducer activity
BeE60H06B09	Q07135 Histone H2A, orphon	-0,0148	-1,2900	-2,9000	-3,5900	10	chromosome organization and biogenesis
BeE30N02C10	Q9HDN1 Histone H3	-0,0298	-1,6500	-3,4900	-3,5100	10	chromosome organization and biogenesis
BeE60N03D06	O15819 Histone H3	0,0684	-1,6400	-3,0500	-2,5600	10	chromosome organization and biogenesis
BeZSPN11B02	Q8NIQ8 Histone H4	-0,0490	-1,9900	-3,4000	-3,4200	10	chromosome organization and biogenesis
BeE30N14D03	Q7ZUY3 Hypothetical protein	0,0996	-1,3200	-2,9700	-2,8400	10	chromosome organization and biogenesis