

**ANEXO 2** - Genes reprimidos ao longo da germinação em meio nutriente. A tabela não mostra 211 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
BeE60N13A09	O15143 ARP2/3 complex 41 kDa subunit	-0,0369	-0,3860	-1,0400	-0,1890	6
BeE60N08C01	O43242 26S proteasome non-ATPase regulatory subunit 3	0,2240	0,0387	-0,6050	-0,6210	6
BeE120N32H02	O93787 Chs3	0,0065	-0,2520	-0,7880	-1,0200	6
BeG30N02B09	P08004 Chitin synthase 1	0,0231	0,2550	-0,0928	-0,7540	6
BeE30N10C10	P26354 TATA-box binding protein	-0,0635	-0,3170	-0,7320	-0,5440	6
BeE60N03A06	P32561 Histone deacetylase RPD3	-0,1490	-0,5250	-0,8510	-1,0300	6
BeG120N14B08	P38318 Hypothetical 63.0 kDa protein in PYC2-PDB1	0,0315	0,3480	-0,9860	-0,8680	6
BeE30N06D01	P40206 Hypothetical 24.7 kDa protein in POM152-REC	-0,0200	0,1560	-1,0100	-0,6150	6
BeE120N28D07	P40581 Glutathione peroxidase 3	-0,0002	-0,2240	-0,8790	-0,4060	6
BeE60N07E08	P40581 Glutathione peroxidase 3	0,0202	-0,1520	-0,8990	-0,3830	6
BeG30N07A07	P46378 Hypothetical 21.1 kDa protein in fasciation	0,0666	0,0349	-1,0600	-0,9100	6
BeE120N37D08	P49710 Hematopoietic lineage cell specific protein	0,0376	-0,0085	-0,8340	-0,6290	6
BeG30N05E05	P56183 NNP-1 protein	0,0165	0,0670	-0,6420	-0,8800	6
BeE30N11E01	Q07153 Receptor tyrosine kinase	-0,0480	-0,7360	-0,0566	-0,4040	6
BeE60N07G05	Q7QEA3 AgCP7395 (Fragment)	0,0412	-0,4700	-1,0000	-0,6070	6
BeE120N36B05	Q7QK56 AgCP14714	0,0007	-0,1920	-0,9220	-0,6130	6
BeZSPN19E08	Q7RZP8 Hypothetical protein	-0,0750	-0,1890	-0,8770	-0,8930	6
BeG60N01F09	Q7S4C6 Hypothetical protein	0,0270	0,2160	-1,1900	-0,4510	6
BeE30N15D01	Q7SC51 Hypothetical protein	0,1660	-0,6110	-0,6710	-0,8020	6
BeZSPN02C05	Q7SFI0 Hypothetical protein	-0,0216	-0,0754	-1,1500	-0,9560	6
BeG30N04H11	Q7Z8B6 H(+)-ATPase	0,0593	0,1800	-0,8740	-1,0000	6
BeZSPN15E03	Q803R9 Similar to aldehyde dehydrogenase 7 family,	-0,0732	-0,3220	-0,8090	-0,5080	6
BeE60N09D01	Q86A56 Similar to Cucurbita cv. Kurokawa Amakuri.	0,2160	0,1740	-1,0900	-0,6030	6
BeG90N19E11	Q871N5 Probable uracil phosphoribosyltransferase F	0,1100	0,5350	-1,0100	-1,2000	6
BeG30N20F08	Q874F6 Kexin like processing protease	0,0533	-0,3010	-0,9160	-0,4480	6
BeZSPN15E12	Q8BNT3 Hypothetical protein	-0,0032	1,0000	-0,8010	-1,1300	6
BeE30N05B03	Q8D151 Acyl-CoA thioesterase II	-0,1870	-0,2820	-1,2900	-0,8720	6
BeZSPN04B03	Q8G593 Fatty aldehyde dehydrogenase	-0,0002	-0,3080	-0,9010	-0,3670	6
BeE90N05B09	Q8GUB3 Putative vacuolar ATPase subunit H	0,0119	-0,5470	-0,8710	-0,7560	6
BeZSPN14H07	Q8GY27 Putative p-nitrophenylphosphatase	-0,0758	-0,0359	-1,1600	-0,9150	6
BeZSPN16F03	Q8J289 YGL104C	0,1020	-0,2740	-0,8910	-1,1100	6
BeZSPN10C05	Q8LPG3 Putative splicing factor	-0,0422	-0,4360	-0,9840	-0,7600	6
BeE120N30B04	Q8MMV2 Hypothetical protein	0,0503	-0,2710	-0,7670	-0,7630	6
BeE120N01D10	Q8S9C7 Flavonoid 3'-hydroxylase	0,0066	-0,3580	-0,8120	-0,8800	6
BeE120N09D11	Q96338 AMP-binding protein	0,0478	-0,4270	-1,1000	-0,3750	6
BeE60H28B12	Q96VZ6 Acetolactate synthase Ilv2	-0,0540	0,3150	-0,9660	0,0326	6
BeG90N09D03	Q99942 Hypothetical protein	0,0267	-0,0157	-0,9350	-0,8830	6
BeG90N18H03	Q9BWD2 Splicing factor 3b, subunit 2, 145kD (Fragment)	-0,0388	0,6510	-0,5020	-0,5140	6
BeE90N04E09	Q9BZE7 Hypothetical protein EVG1	-0,1230	-0,3250	-0,7740	-0,7700	6
BeE60N16D03	Q9C0M0 Acetyl-CoA acetyl transferase	-0,0888	0,0845	-1,1200	-0,7120	6
BeE120N38E10	Q9D5P6 4930403C08Rik protein	0,0303	-0,1660	-0,8280	-0,2920	6
BeG60N14A08	Q9NRD4 Peroxisomal trans 2-enoyl CoA reductase	-0,0232	-0,5550	-0,9800	-0,4150	6
BeE60N15G07	Q9P7G4 Hypothetical peptidase 48 family protein	0,0600	-0,0639	-0,5640	-0,5960	6
BeE120N28E07	Q9HFN1 G protein alpha subunit (Fragment)	0,1210	-0,2120	-0,7720	-0,8200	6
BeE60N16D02	P34046 Guanine nucleotide-binding protein alpha-8	0,0240	-1,0200	-1,1400	-0,9370	7
BeE60N09G02	Q12702 Protein phosphatase PP2A regulatory subunit	-0,1030	-0,8770	-1,4700	-1,1700	7
BeE120N18F01	Q86WN6 Phosphodiesterase PDE9A13	0,0185	-1,2000	-0,8750	-1,0300	7
BeE120N37F12	P39968 Vacuolar protein 8	-0,1300	-0,8080	-1,2800	-1,0400	7
BeE60N10E10	P19984 Profilin II	-0,0528	-1,2700	-1,1800	-0,5110	7
BeE60H15H11	Q7SGN0 Hypothetical protein	0,0070	-1,3600	-1,0300	-0,4110	7
BeE30N02B01	O04974 2-isopropylmalate synthase B	-0,0012	-1,1500	-1,3900	-0,8150	7

BeE60H30F11	O74341 T-complex protein 1, gamma subunit	-0,0138	-1,9400	-1,1800	-1,1400	7
BeE60H30C05	P25349 Hypothetical 26.4 kDa protein in CDC10-CIT2	-0,0403	-0,9280	-1,1700	-0,9570	7
BeE60N04B11	P26587 Aquaporin TIP3.1	0,0776	-0,7000	-1,1300	-0,5180	7
BeZSPN02F03	P33121 Long-chain-fatty-acid--CoA ligase 2	0,0029	-0,9020	-0,8150	-0,3560	7
BeG30N09H07	P52493 Ubiquitin-conjugating enzyme E2-17 kDa	-0,1130	-0,6400	-1,2000	-0,9220	7
BeE60H29E07	Q01137 Superoxide dismutase [Cu-Zn]	-0,0128	-0,7190	-1,1300	-0,0616	7
BeG120N13B04	Q02817 Mucin 2 precursor	-0,1710	-1,0400	-0,5410	-0,0484	7
BeG90N09B12	Q27124 Ribonucleotide reductase small subunit	0,0225	-0,7300	-0,9430	-0,5960	7
BeG90N09D02	Q9ZR56 Ribonucleotide reductase	-0,0370	-0,8450	-1,0100	-0,9060	7
BeE30N03A06	Q16550 Transcription initiation protein SPT4 homol	-0,0632	-0,9070	-1,1400	-0,5590	7
BeG90N17G03	Q27532 W05B10.1 protein	0,0645	-1,2500	-1,5100	-1,4700	7
BeZSPN12E10	Q7PRI8 ENSANGP00000016126 (Fragment)	0,0137	-0,9270	-0,5810	-0,3590	7
BeE60H26C05	Q7PY52 AgCP12010 (Fragment)	0,0231	-1,1600	-1,1500	-0,6080	7
BeG90N22B10	Q7Q8R2 AgCP11849 (Fragment)	-0,0412	-1,0500	-0,7010	-0,5460	7
BeE120N08E05	Q7QGP3 AgCP10431	0,0347	-1,0600	-0,8530	-1,0100	7
BeE60C01E02	Q7S2J5 Hypothetical protein	0,0662	-1,5600	-2,1400	-0,5720	7
BeE60N07D05	Q7UHD8 Probable D-alanine-D-alanine ligase	-0,0101	-0,8590	-1,0700	-1,1100	7
BeE60C36G04	Q7VUM3 Putative integral membrane transport protei	-0,1100	-1,3600	-1,4200	-1,0800	7
BeE90N07F09	Q7W512 DNA repair protein	0,0774	-0,7370	-1,1400	-0,7930	7
BeE120N01E04	Q80W96 HesB protein	-0,1170	-1,1700	-1,4100	-0,9300	7
BeE120N01A01	Q87C40 Cationic amino acid transporter	0,0696	-0,8220	-0,6450	-0,7130	7
BeE120N28C07	Q8KU53 EF0108	0,0386	-1,5700	-1,1000	-1,2500	7
BeZSPN14D03	Q8PSH3 Hypothetical protein MM3106	-0,0045	-1,1000	-1,8300	-1,0900	7
BeG90N18F10	Q8SZ87 RE13747p	0,0466	-0,7160	-1,3500	-1,0700	7
BeE60N12C07	Q8T893 Calcineurin-like protein	0,0288	-0,9040	-0,5120	-0,7780	7
BeE60N11H03	Q92356 Probable synaptobrevin homolog C6G9.11	-0,0145	-0,7950	-1,1600	-0,9610	7
BeE60N18D07	Q96W50 Protein kinase Pbs2p	-0,0865	-0,9110	-1,2200	-0,8890	7
BeZSPN02C07	Q9CK00 Hypothetical protein PM1838	-0,0215	-0,8900	-1,2500	-0,8730	7
BeE30N20E04	Q9CPX9 Anaphase promoting complex subunit 11	-0,0060	-1,7200	-0,6480	-1,0300	7
BeZSPN18A12	Q9NUN7 Alkaline phytoceramidase	-0,0296	-1,1700	-1,9100	-0,6600	7
BeZSPN14C12	O43822 Protein C21orf2	-0,1430	-1,1800	-2,2800	-1,4300	8
BeZSPN14D10	O93787 Chs3	-0,0664	-0,9680	-1,9700	-2,3000	8
BeE60H28B01	P10989 Actin	-0,0542	-2,1300	-3,2100	-1,7200	8
BeE120N38D09	P38263 Vacuolar import and degradation protein VID	0,0272	-1,4300	-1,9000	-1,6300	8
BeE60C17C02	P38356 Metal homeostatis protein BSD2	0,2000	-1,2300	-2,3700	-2,4100	8
BeG30N06H02	P48234 Hypothetical WD-repeat protein in MOL1-NAT2 intergenic region	0,0036	-1,4200	-2,2800	-2,0300	8
BeE120N27B02	P56205 Cytochrome c	0,0530	-1,8800	-2,1400	-1,0500	8
BeE60N12B03	P56812 Programmed cell death protein 5	-0,0163	-0,9770	-2,1500	-1,9700	8
BeZSPN16F12	Q12317 Chromosome XV reading frame ORF YOL112W	0,0079	-1,1900	-2,1300	-1,4100	8
BeZSPN16G12	Q7NYB4 Large conductance mechanosensitive channel	-0,0245	-0,9460	-2,2100	-1,9700	8
BeE60N18D05	Q7RVR4 Hypothetical protein	0,0546	-1,1000	-2,1200	-1,4100	8
BeZSPN03D06	Q9HDN1 Histone H3	-0,1230	-1,1100	-2,4600	-2,2000	8
BeZSPN04C10	Q9P7L5 Probable ornithine aminotransferase	-0,0355	-1,0600	-2,0500	-1,1500	8
BeZSPN10F08	O01497 Hypothetical protein	0,0187	-0,2150	-0,9970	-1,1800	9
BeG30N19A07	Q9XUS8 K08E3.1 protein	-0,0852	0,6800	-1,0900	-1,3000	9
BeE60H08G12	Q869M8 Similar to Magnaporthe grisea	0,0026	-0,6910	-1,4800	-0,9630	9
BeG30N07G09	Q7NI34 Gll2350 protein	0,0860	-0,1250	-1,3700	-0,8480	9
BeE120N09C08	Q8P9N1 Cationic amino acid transporter	0,0699	-0,9360	-1,5800	-1,5900	9
BeE60H21G09	Q8RBT1 Amino acid transporters	0,0161	-0,6540	-1,3100	-0,9980	9
BeE30N06E01	Q9A910 Amino acid permease family protein	-0,0638	-0,6410	-1,8400	-1,3100	9
BeZSPN05A11	Q9QXA6 B(0,+)-type amino acid transporter 1	0,0964	-0,3790	-1,7100	-1,0700	9
BeE120N36E01	Q88LQ4 Sensor histidine kinase/response regulator	0,0475	-0,3040	-1,2100	-1,1800	9
BeE60N03C06	Q9HDE1 Calcineurin B regulatory subunit	0,1060	-0,9230	-1,7600	-1,0200	9
BeE120N04B04	Q95WR8 PXF isoform C	0,0031	-0,2230	-1,2400	-1,1600	9

BeG60N08H03	Q8J0B8 G protein alpha subunit	0,0336	-0,5020	-1,2900	-1,4200	9
BeE60N11G06	Q05116 Dual specificity mitogen-activated protein	-0,1950	-0,2990	-1,2700	-1,0400	9
BeZSPN16D09	Q12741 cAMP-dependent protein kinase catalytic sub	0,0615	-0,7520	-1,5200	-0,8600	9
BeZSPN18G07	Q9HEW4 Ste20 a kinase	0,0562	-0,5940	-1,4300	-1,1900	9
BeE120N28F02	Q9Y7W8 MAP kinase kinase	0,0476	-0,4270	-1,1100	-0,8470	9
BeE60N18F10	O74846 Exocyst complex component sec6	0,0713	-0,2120	-1,4300	-1,2000	9
BeZSPN10C02	Q62896 BET1 homolog	-0,0143	-0,6740	-1,7600	-1,1000	9
BeE120N35H01	Q7SAQ1 Hypothetical protein	0,1390	-0,4000	-2,1100	-1,6600	9
BeG30N03G06	Q9C0R0 (AF343071) TIM23	-0,0395	-0,3170	-1,1900	-0,9210	9
BeG30N06C03	Q9P7N2 Putative clathrin-associated protein	0,2440	-0,2310	-1,6300	-1,1300	9
BeG30N11C03	Q942T3 Putative receptor protein kinase	-0,0206	-0,4130	-1,2200	-1,1400	9
BeE30N06H07	O14224 Rho gdp dissociation inhibitor	-0,0639	-0,8600	-1,9800	-0,5320	9
BeE120N29D03	O14270 Putative forkhead-related transcription fac	-0,1170	-0,2120	-1,5000	-1,1000	9
BeZSPN06B03	O74477 Hypothetical protein	0,0074	-0,0754	-1,4000	-0,9110	9
BeG60N05H09	O75207 Hypothetical protein	0,0762	-0,5910	-1,8600	-1,4200	9
BeE60H27E01	O93787 Chs3	0,1900	-0,2530	-1,3100	-1,6000	9
BeZSPN16H02	P10869 Aspartokinase	-0,0253	-0,5000	-1,8600	-1,8300	9
BeE30N07B04	P53326 Hypothetical 81.2 kDa protein in MES1-FOL2	0,0818	-0,0907	-1,2000	-0,9720	9
BeZSPN17F02	Q12284 ERV2 protein, mitochondrial precursor	0,0519	-0,6330	-1,6100	-1,1700	9
BeE120N30H05	Q7RV08 Hypothetical protein	0,0319	-0,6050	-1,4300	-0,5740	9
BeZSPN10H02	Q7RW00 Hypothetical protein	0,0115	-0,6750	-1,5000	-0,9890	9
BeG120N03B03	Q7S4N5 Hypothetical protein	0,0645	-0,3970	-1,6700	-1,5100	9
BeE120N32B08	Q7SF59 Predicted protein	0,0696	-1,5700	-0,7060	-0,6930	9
BeE90N18A07	Q7X9R8 Chitinase	0,1630	-0,3880	-0,9240	-1,0600	9
BeE120N24G04	Q7Z8T1 Ubiquitin-conjugating enzyme9	0,0016	-0,5810	-1,6900	-1,7600	9
BeG90N18H02	Q7Z8T1 Ubiquitin-conjugating enzyme9	-0,0209	-0,3020	-1,7300	-2,0900	9
BeE60N07G09	Q872U9 Probable chaperonin of the TCP1 ring comple	-0,1410	-0,3970	-1,2100	-0,9180	9
BeG60N10A05	Q8MRC3 RE14858p	0,0501	-0,3320	-1,3400	-0,8900	9
BeE60N19B01	Q95R88 SD01152p	0,0789	-0,3510	-1,3000	-1,0200	9
BeE60N04A02	Q962V4 RNA helicase p47	-0,0436	-0,7300	-1,4700	-1,4700	9
BeG30N08E03	Q96VN6 Phosphate transporter (Fragment)	0,1200	-0,3570	-1,2900	-2,3800	9
BeE120N37B07	Q9C005 Dpy-30-like protein	0,0754	-0,1420	-1,3000	-1,0800	9
BeE60N12E11	Q9NY68 CTL2 protein	-0,0450	-0,8020	-1,2500	-1,5200	9
BeZSPN18H03	Q9SQF7 Chitinase	-0,0775	-0,7290	-1,5600	-1,1000	9
BeE60H31B10	Q9Y8H1 Pol	0,0653	-0,6020	-1,0600	-1,0500	9
BeE60H06B09	Q07135 Histone H2A, orphon	-0,0148	-1,2900	-2,9000	-3,5900	10
BeE30N02C10	Q9HDN1 Histone H3	-0,0298	-1,6500	-3,4900	-3,5100	10
BeE60N03D06	O15819 Histone H3	0,0684	-1,6400	-3,0500	-2,5600	10
BeZSPN11B02	Q8NIQ8 Histone H4	-0,0490	-1,9900	-3,4000	-3,4200	10
BeE30N14D03	Q7ZUY3 Hypothetical protein	0,0996	-1,3200	-2,9700	-2,8400	10
BeZSPN17H06	O06479 YFNA protein	0,0035	-1,8900	-3,7200	-2,8700	10
BeZSPN17B12	Q7XPC6 OSJNBa0042N22.14 protein	0,0081	-0,9940	-3,0400	-2,9200	10
BeZSPN16H11	Q8W0U2 Hypothetical protein	-0,0055	-1,2500	-3,1900	-3,3100	10