

Table S3. List of commonly up-regulated genes with more than 2.5 fold change between Se/60 and Mo/60 comparisons
Genes not correlated with lesion development (Se/Mo<1) were ruled out and highlighted in red. P, Bonferroni-corrected P value.

probeset_id	PvUIT sequence ID	CDD annotation	Panther annotation	Arabidopsis hit	Rice hit	Ratio(Se/60)	P	Ratio(Mo/60)	P	Ratio(Se/Mo)	P
AP13ITG38511_s_at	AP13ISTG38511	PLN02555/Limonoid glyUDP-GLUCOSYLTRANS/			LOC_Os04g12970.1 13104.m01188 protein/1E-82//	113.02		0	5.31	4.35E-62	0
AP13ITG67309_s_at	AP13ISTG67309	pfam00450/Serine car SERINE CARBOXYPEPT/			LOC_Os10g01134.1 13110.m00014 protein/0//	53.79		0	14.05	0	3.83
KanlowCTG06220_s_at						46.29		0	5.95	9.34E-293	7.78
KanlowCTG09824_s_at	KanlCTG09824	COG0534/Na+-driven rSUBFAMILY NOT NAM/			LOC_Os03g37640.1 13103.m04087 protein/8E-53//	42.52		0	8.59	0	4.95
AP13ITG65101_at	AP13ISTG65101	pfam02956/TT viral or-/	/	/	LOC_Os03g37640.1 13103.m04087 protein/8E-53//	33.56		0	3.92	3.30E-97	8.56
AP13CTG58961_at	AP13CTG58961	PRK12323/DNA polym-/	/	/	LOC_Os01g58140.1 13101.m06174 protein/0.0000000002//	30.22		0	3.66	8.40E-172	8.25
AP13ITG71440_at	AP13ISTG71440	PLN02183/ferulate 5-hSUBFAMILY NOT NAMAT2G30750/LimoneneLOC_Os06g43384.1 13106.m04539 protein/1E-164//			LOC_Os01g58140.1 13101.m06174 protein/0.0000000002//	22.21		0	5.47	0	4.06
AP13CTG09437_at	AP13CTG09437	cd00693/Horseradish y/	AT5G05340/Phenylalanyl	LOC_Os07g48040.1 13107.m05132 protein/2E-108//	21.76		0	4.43	1.73E-47	4.91	2.39E-15
AP13CTG26173_at	AP13CTG26173	pfam00173/CytochroP FAMILY NOT NAMED//			LOC_Os02g43360.1 13102.m04815 protein/1E-41//	19.26		0	11.5	0	1.67
AP13CTG15831_s_at	AP13CTG15831	cd04852/Peptidase S8 SUBTILISIN-LIKE PROT/			LOC_Os01g58280.1 13101.m06185 protein/0//	17.15		0	5.28	0	3.25
AP13ITG42000_at	AP13ISTG42000	pfam00314/Thaumatin/	/	/	LOC_Os12g43430.1 13112.m04577 protein/1E-68//	15.09	3.28E-130	11.13	3.09E-68	1.36	0.329096432
AP13ITG58844_at	AP13ISTG58844	PLN02987/cytochromeSUBFAMILY NOT NAMAT4G19230/CarotenoidLOC_Os07g33440.1 13107.m03397 protein/9E-175//			LOC_Os07g33440.1 13107.m03397 protein/9E-175//	14.2		0	3.46	0	4.11
AP13ITG59977_at	AP13ISTG59977	cd03185/GST_C family GLUTATHIONE S-TRAN/			LOC_Os10g38470.1 13110.m03503 protein/1E-79//	14.09		0	3.77	0	3.74
KanlowCTG07131_s_at	KanlCTG07131	cd05381/SCP_PR-1_lik CHLORIDE CHANNEL C/			LOC_Os12g25200.1 13112.m02555 protein/2E-148//	14.05		0	5.34	0	2.63
KanlowSLT48175_s_at	KanlSLT48175	//	/	/	LOC_Os07g18570.1 13107.m01946 protein/0.00000000000005//	13.92		0	4.77	8.28E-298	2.92
AP13ITG52984_at	AP13ISTG52984	cd01959/nsLTP2: Non-/	/	/	LOC_Os09g23370.2 13109.m02207 protein/4E-64//	13.14		0	4.28	0	3.07
AP13CTG27003_at	AP13CTG27003	PLN02998/hydrolase, IGLYCOSYL HYDROLASI/			LOC_Os09g33680.1 13109.m03354 protein/0/Cyanoamino acid metabolism; Sta	12.73		0	2.57	5.18E-45	4.96
AP13ITG63167_at	AP13CTG63167	PLN02655/ent-kaurenSUBFAMILY NOT NAMAT5G25900/DiterpeneLOC_Os06g37330.1 13106.m03864 protein/0/Diterpenoid biosynthesis; Metab			LOC_Os06g37330.1 13106.m03864 protein/0/Diterpenoid biosynthesis; Metab	12.62		0	6.25	0	2.02
AP13CTG58860_at	AP13CTG58860	cd05381/SCP_PR-1_lik CYSTEINE-RICH SECRE AT2G14610/Plant-pat LOC_Os07g03710.1 13107.m00310 protein/6E-59//			LOC_Os07g03710.1 13107.m00310 protein/6E-59//	12.48		0	7.51	0	1.66
AlamoCTG14398_s_at	AlamCTG14398	//	/	/	LOC_Os09g34160.1 13109.m03430 protein/1E-88//	12.44		0	3.06	3.49E-26	4.07
OTHSWCTG20397_s_at	OthsCTG20397	pfam03060/2-nitroproBLLS091 PROTEIN/0,0/			LOC_Os08g37874.1 13108.m03998 protein/1E-96//	12.39		0	2.55	9.05E-39	4.85
AP13ITG59511_at	AP13ISTG59511	//	/	/	LOC_Os08g37874.1 13108.m03998 protein/1E-96//	12.26		0	3	3.98E-94	4.08
OTHSWCTG15870_at	OthsCTG15870	pfam03106/WRKY DN/	/	/	LOC_Os11g29870.1 13111.m02887 protein/0.000000000000003//	12.21		0	4.88	8.61E-178	2.5
AP13CTG24721_at	AP13CTG24721	PLN02448/UDP-glycos UDP-GLUCOSYLTRANS/AT3G50740/PhenylprLOC_Os04g6990.1 13104.m04753 protein/6E-148/Zearin biosynthesis/3E-147			LOC_Os04g6990.1 13104.m04753 protein/6E-148/Zearin biosynthesis/3E-147	11.77		0	4.78	0	2.46
AP13ITG62483_at	AP13ISTG62483	pfam00967/Barwin far WOUND-INDUCED PR/			LOC_Os11g37950.1 13111.m03723 protein/7E-48//	11.57		0	4.09	0	2.83
KanlowCTG08567_s_at	KanlCTG08567	pfam00230/Major intr SUBFAMILY NOT NAM/			LOC_Os02g44630.2 13102.m04992 protein/4E-135//	11.34		0	4.79	0	2.37
AP13ITG41899_s_at	AP13ISTG41899	//	/	/	LOC_Os05g03750.1 13105.m00366 protein/1E-23//	11.32	1.09E-293	8.69	9.46E-164	1.3	0.268660342
AP13CTG34009_s_at	AP13CTG34009	PLN02849/glycosyl hyl GLYCOSYL HYDROLASI/			LOC_Os05g30350.2 13105.m03099 protein/5E-179/Cyanoamino acid metabolism;	11.24	1.66E-163	3.97	2.77E-15	2.83	2.94E-12
AP13CTG14744_s_at	AP13CTG14744	//	/	/	LOC_Os12g36110.1 13112.m03703 protein/1E-59//	10.15	6.01E-304	6.67	5.58E-118	1.52	0.253560931
KanlowCTG39787RC_s_KanlCTG39787-RC		PHA03247/large tegun FAMILY NOT NAMED//			LOC_Os03g19650.3 13103.m02355 protein/1E-150//	9.77		0	3.89	1.72E-35	2.51
AP13ITG67309_at	AP13ISTG67309	pfam00450/Serine car SERINE CARBOXYPEPT/			LOC_Os10g01134.1 13110.m00014 protein/0//	9.75		0	3.44	0	2.84
AP13CTG27420_at	AP13ISTG27420	smart00774/DNA bind/	/	/	LOC_Os05g25770.1 13105.m02640 protein/4E-43//	9.51		0	3.65	1.10E-136	2.6
AP13ITG70591-RC_at						9.09		0	7.01	1.54E-220	1.3
AP13CTG30873_at	AP13CTG30873	pfam00635/MSP (Majr OS04G0369000 PROTI/			LOC_Os11g1780.1 13111.m01762 protein/1E-39//	8.99		0	16.29	0	0.55
AP13CTG27562_s_at	AP13CTG27562	pfam00083/Sugar (ancSUBFAMILY NOT NAM/			LOC_Os03g11900.1 13103.m01345 protein/0//	8.95		0	4.93	6.47E-291	1.81
AP13CTG48706_at	AP13CTG48706	cd00180/Catalytic don OS11G0212300 PROTI/			LOC_Os11g39450.1 13111.m03897 protein/6E-61//	8.89		0	15.29	0	0.58
AP13CTG14744_at	AP13CTG14744	//	/	/	LOC_Os12g36110.1 13112.m03703 protein/1E-59//	8.75		0	3.22	0	2.72
KanlowCTG47289_s_at	KanlCTG47289	PRK07538/hypothetic MONOXYGENASE/3.6/			LOC_Os03g05900.2 13103.m00642 protein/7E-75//	8.62		0	2.86	8.47E-61	3.01
KanlowCTG12598_s_at	KanlCTG12598	smart00516/Domain irSEC14 CYTOSOLIC FAC/			LOC_Os01g70210.1 13101.m07621 protein/2E-99//	8.61		0	7.86	0	1.09
AP13CTG22556_at	AP13CTG22556	pfam03080/Arabidops/	/	/	LOC_Os07g38590.1 13107.m03991 protein/4E-102//	8.57	2.25E-287	10.76	0	0.8	0.569906754
AP13CTG09569_s_at	AP13CTG09569	PLN00141/Tic62-NAD(SUBFAMILY NOT NAM/			LOC_Os05g01970.5 13105.m00143 protein/5E-123//	8.49		0	3.43	1.71E-58	2.47
AP13CTG02814_s_at	AP13CTG02814	PRK00277/ATP-depenATP-DEPENDENT CLP/			LOC_Os03g19510.1 13103.m02334 protein/4E-119//	8.33		0	2.72	1.11E-203	3.06
AP13CTG27808_at	AP13CTG27808	pfam00450/Serine car SERINE CARBOXYPEPTAT5G09640/PhenylprLOC_Os10g01110.1 13110.m00012 protein/2E-171//			LOC_Os10g01110.1 13110.m00012 protein/2E-171//	8.2	1.03E-105	7.94	2.40E-98	1.03	0.86644618
AP13ITG66548_s_at	AP13ISTG66548	PRK05557/3-ketoacyl-FAMILY NOT NAMED/ AT4G13180/Fatty acidLOC_Os10g31780.1 13110.m02768 protein/6E-109/Fatty acid biosynthesis; Bios			LOC_Os10g31780.1 13110.m02768 protein/6E-109/Fatty acid biosynthesis; Bios	8.17	9.85E-134	7.84	6.45E-122	1.04	0.911779426
KanlowCTG38097_at	KanlCTG38097	PHA02988/hypotheticSUBFAMILY NOT NAM/			LOC_Os11g1780.1 13111.m01762 protein/0.000003//	8.04		0	3.06	8.76E-46	2.63
AP13CTG29478_s_at	AP13CTG29478	PLN02365/2-oxoglutar OXIDOREDUCTASE, 2C/			LOC_Os04g39980.1 13104.m03879 protein/9E-127//	8.02		0	16.24	0	0.49
KanlowCTG26347_at	KanlCTG26347	pfam03492/SAM depe-/	/	/	LOC_Os06g13350.1 13106.m01470 protein/2E-110//	7.65		0	5.73	1.26E-270	1.34
AP13ITG70166_s_at	AP13ISTG70166	pfam00854/POT fami NITRATE TRANSPORTI/			LOC_Os12g44110.2 13112.m04657 protein/6E-150//	7.61		0	4.48	1.19E-191	1.7
OTHSWCTG04721_s_at	OthsCTG04721	//	/	/	LOC_Os12g44110.2 13112.m04657 protein/6E-150//	7.57	2.57E-112	4.47	1.01E-32	1.69	0.113344765
AP13ITG64138_at	AP13ISTG64138	PRK05648/DNA polym-/	/	/	LOC_Os07g38150.1 13107.m03939 protein/1E-38//	7.48	3.72E-144	3.8	2.00E-28	1.97	0.000833787
AP13ITG59134_at	AP13ISTG59134	pfam02201/SWIB/MDIFAMILY NOT NAMED//			LOC_Os12g32280.1 13112.m03293 protein/4E-32//	7.26		0	2.53	8.52E-62	2.87
AP13ITG73548_s_at	AP13ISTG73548	//	/	/	LOC_Os12g32280.1 13112.m03293 protein/8E-32//	7.25		0	2.94	0	2.47
AP13CTG12196_s_at	AP13CTG12196	//	/	/	LOC_Os02g36700.1 13102.m04004 protein/0//	7.19		0	10.4	0	0.68
AP13CTG12078_s_at	AP13CTG12078	PRK00277/ATP-depenATP-DEPENDENT CLP/			LOC_Os03g19510.1 13103.m02334 protein/9E-119//	7.16		0	2.73	1.00E-186	2.63
AP13CTG09699_s_at	AP13CTG09699	PTZ00146/fibrillarin; P UNCHARACTERIZED/5/			LOC_Os04g39010.1 13104.m03765 protein/3E-20//	7.08	5.23E-188	3.09	8.47E-24	2.29	0.000329465
AP13CTG24971_at	AP13CTG24971	pfam05955/Equine heNUCLEOREDOXIN/0.0/			LOC_Os08g31250.1 13108.m03235 protein/2E-57//	6.97		0	4.07	9.78E-113	1.71
AP13CTG22084_s_at	AP13CTG22084	pfam03134/TB2/DP1, I HVA22-LIKE PROTEIN/			LOC_Os11g30500.1 13111.m02953 protein/2E-51//	6.59		0	2.57	0	2.56
AP13ITG56341_s_at	AP13ISTG56341	PRK11325/scaffold prcIRON-SULFUR CLUSTE/			LOC_Os01g47340.1 13101.m04879 protein/1E-63//	6.58		0	3.61	3.24E-89	1.83
AP13ITG73622RC_at	AP13ISTG73622-RC	cd00051/EF-hand, calc CALCIUM-BINDING EF AT3G47480/Plant-pat LOC_Os09g24580.1 13109.m02333 protein/0.00000008/Plant-pathogen interac			LOC_Os09g24580.1 13109.m02333 protein/0.00000008/Plant-pathogen interac	6.56		0	3.42	3.68E-82	1.92
AP13CTG19074_at	AP13CTG19074	smart00219/Tyrosine I SUBFAMILY NOT NAM/			LOC_Os05g40270.7 13105.m04254 protein/0//	6.48	2.37E-287	5.07	6.23E-159	1.28	0.339665239
OTHSWSLT36401_s_at	OthsSLT36401	TIGR00957/multi drub SUBFAMILY NOT NAM/			LOC_Os04g49890.1 13104.m05101 protein/4E-112//	6.4		0	2.96	4.00E-103	2.16
AP13ITG62754_s_at	AP13ISTG62754	COG0412/Dienelacton ENDO-1,3-1,4-BETA-D/			LOC_Os05g33110.1 13105.m03417 protein/1E-113//	6.39		0	3.72	6.50E-102	1.72
AP13ITG67117_at	AP13ISTG67117	//	/	/	LOC_Os06g3060.1 13106.m03620 protein/2E-37//	6.34		0	3.23	6.08E-294	1.96
AP13ITG55801_at	AP13ISTG55801	cd00693/Horseradish y/	AT4G11290/Phenylalanyl	LOC_Os05g06970.1 13105.m00752 protein/6E-133//	6.25	2.12E-232	6.44	2.94E-249	0.97	0.95294716	1.34
KanlowCTG14963_s_at	KanlCTG14963	TIGR00887/phosphate SUBFAMILY NOT NAM/			LOC_Os03g05620.1 13103.m00607 protein/8E-123//	6.21	1.17E-194	4.62	6.53E-95	1.34	0.417802756
AP13ITG56240_at	AP13ISTG56240	//	/	/	LOC_Os03g09020.1 13103.m03166 protein/7E-121/Glycolysis / Gluconeogenesi	6.09		0	3.53	2.04E-172	1.73
KanlowCTG05742_s_at	KanlCTG05742	//	/	/	AT5G57580/PhosphatLOC_Os01g04280.1 13101.m00386 protein/5E-172//	6.06	1.50E-267	3.43	7.34E-63	1.77	0.046787066

AP13ITG60086_at	AP13ISTG60086	smart00774/DNA bind /	/	LOC_Os07g48260.1 13107.m05157 protein/2E-43//	6.05	0	3.15	0	1.92	0.034281629
AP13CTG06246-2_s_at					6.04	7.81E-72	9.07	7.41E-181	0.67	0.073194301
KanlowCTG47117_s_at	KanlCTG47117	PLN02183/ferulate 5-hSUBFAMILY NOT NAM	AT5G25140/LimoneneLOC_Os04g10160.1 13104.m00909 protein/1E-88//	6.01	0	4.08	1.56E-197	1.47	0.275708038	
KanlowCTG47529_s_at	KanlCTG47529	PLN02183/ferulate 5-hOS07G0291800 PROTI	AT3G26300/LimoneneLOC_Os04g10160.1 13104.m00909 protein/5E-43//	5.94	8.85E-101	4.04	3.37E-39	1.47	0.309248821	
KanlowCTG01327_s_at	KanlCTG01327	PLN02609/catalase/0 FAMILY NOT NAMED/	AT1G20630/TryptophiLOC_Os02g02400.1 13102.m00175 protein/0/Tryptophan metabolism; Metabol	5.91	2.75E-261	8.35	0	0.71	0.404073106	
OTHSWCTG19595_at	OthsCTG19595	PLN00113/leucine-rich OS10G0120300 PROTI/	LOC_Os01g41770.1 13101.m04285 protein/1E-60//	5.89	0	5.67	0	1.04	0.870435331	
KanlowSLT53174_s_at	KanlSGLT53174	//	/	5.8	5.03E-149	4.26	7.23E-70	1.36	0.22376577	
AP13CTG03745_at	AP13CTG03745	PLN02790/transketola TRANSKETOLASE/0	AT2G45290/Pentose fLOC_Os04g19740.1 13104.m01814 protein/0/Pentose phosphate pathway; Carl	5.78	0	5.64	0	1.02	0.933245522	
KanlowCTG38102_s_at	KanlCTG38102	cd03250/Domain 1 of :SUBFAMILY NOT NAM/	LOC_Os04g49890.1 13104.m05101 protein/4E-115//	5.71	7.50E-183	2.73	3.15E-26	2.09	5.27E-06	
KanlowCTG14163_at	KanlCTG14163	PLN02448/UDP-glycos UDP-GLUCOSYLTRAN	AT3G50740/PhenylprLOC_Os04g46990.1 13104.m04753 protein/2E-133/Zeatn biosynthesis/9E-133	5.7	0	3.34	1.91E-197	1.71	0.119004511	
AP13ITG71141_at	AP13ISTG71141	cd00180/Catalytic donSUBFAMILY NOT NAM/	LOC_Os12g26940.1 13112.m02739 protein/8E-58//	5.69	0	8.08	0	0.7	0.194517513	
AP13ITG52579_x_at	AP13ISTG52579	pfam00182/Chitinase iGB DEF: CHITINASE (F	AT3G12500/Amino suLOC_Os03g04060.1 13103.m00413 protein/2E-46/Amino sugar and nucleotide :	5.67	2.13E-86	9.78	1.73E-299	0.58	0.05340598	
AP13CTG27594_at	AP13CTG27594	TIGR01377/sarcosine cPEROXISOMAL SARCO/	LOC_Os09g32290.2 13109.m07548 protein/9E-173//	5.66	4.46E-112	7.04	5.96E-187	0.8	0.399642533	
VS16ITG16394_at	VS16ISTG16394	//	/	5.65	0	3.15	2.00E-141	1.79	0.003861523	
AP13ITG64260_s_at	AP13ISTG64260	//	/	5.6	2.14E-191	4.76	5.50E-129	1.17	0.544613796	
KanlowCTG01918_at	KanlCTG01918	//	MALIC ENZYME/0	AT5G25880/Pyruvate LOC_Os05g09440.1 13105.m01052 protein/0/Pyruvate metabolism; Carbon fixa	5.58	2.23E-258	2.93	2.66E-47	1.91	4.20E-05
AP13ITG46253_s_at				5.57	0	4.35	0	1.28	0.639445479	
AP13ITG62309_at	AP13ISTG62309	cd06660/Aldo-cto keto ALDO/KETO REDUCTA/	LOC_Os04g26910.1 13104.m02546 protein/9E-162//	5.55	1.84E-114	5.21	2.32E-98	1.06	0.849910929	
AP13ITG62725_at	AP13ISTG62725	pfam00407/Pathogene/	LOC_Os03g18850.1 13103.m02258 protein/2E-74//	5.49	0	4.31	0	1.27	0.534964941	
KanlowCTG121384_x_at	KanlCTG121384	PLN02183/ferulate 5-hSUBFAMILY NOT NAM	AT3G26160/LimoneneLOC_Os04g10160.1 13104.m00909 protein/1E-59//	5.48	2.87E-78	5.86	7.69E-92	0.93	0.843253222	
AP13ITG44916-RC_s_at				5.47	1.72E-129	4.33	1.08E-72	1.26	0.526193977	
AP13ITG44757_s_at	AP13ISTG44757	cd04666/Members of :FAMILY NOT NAMED//	LOC_Os11g32750.1 13111.m03193 protein/1E-97//	5.43	0	3.67	5.43E-182	1.48	0.078980232	
AP13CTG10204_at	AP13CTG10204	//	/	5.34	7.59E-76	3.52	1.13E-26	1.52	0.022680236	
AP13CTG24955_x_at	AP13CTG24955	//	/	5.29	1.04E-123	3.54	2.15E-44	1.5	0.087931132	
AP13ITG65600-RC_at				5.26	0	5.41	0	0.97	0.841632496	
OTHSWCTG12073_s_at	OthsCTG12073	pfam00407/Pathogene/	LOC_Os12g36830.1 13112.m03777 protein/9E-26//	5.18	5.47E-24	6.6	1.15E-41	0.79	0.324586126	
OTHSWCTG13770_s_at	OthsCTG13770	//	/	5.17	0	2.55	2.84E-79	2.02	5.52E-06	
AP13ITG44735_s_at	AP13ISTG44735	smart00219/Tyrosine iSUBFAMILY NOT NAM/	LOC_Os03g24930.1 13103.m02938 protein/0//	5.16	1.85E-112	5.46	1.21E-128	0.95	0.846019739	
AP13ITG54363_at	AP13ISTG54363	pfam04788/Protein of /	LOC_Os03g07120.1 13103.m00787 protein/2E-129//	5.08	6.42E-84	2.6	3.01E-14	1.96	1.31E-09	
AP13ITG76492_at	AP13ISTG76492	//	ALPHA-AMYLASE/5.6E	AT4G25000/Starch anLOC_Os06g49970.2 13106.m05364 protein/0/Starch and sucrose metabolism; A	5.07	0	6.48	1.00E-105	0.78	3.68E-102
OTHSWSLT35464_at	OthsSGLT35464	PRK00013/chaperonin RUBISCO SUBUNIT Bii/	LOC_Os06g02380.2 13106.m00160 protein/3E-27/RNA degradation/3E-27	5.05	4.72E-108	5.85	7.40E-154	0.86	0.370507918	
OTHSWCTG09951_s_at	OthsCTG09951	PLN02592/ent-copalyl /	AT4G02780/DiterpenLOC_Os04g09900.1 13104.m00881 protein/4E-57/Diterpenoid biosynthesis; Bio	5.04	2.89E-228	6.86	0	0.73	0.251475711	
AP13ITG66210_at	AP13ISTG66210	pfam02365/No apical /	LOC_Os06g51070.1 13106.m05496 protein/7E-97//	4.95	1.53E-46	3.83	1.07E-24	1.29	0.283129979	
KanlowCTG40626_s_at	KanlCTG40626	pfam01657/Domain ofSUBFAMILY NOT NAM/	LOC_Os10g04730.1 13110.m00390 protein/5E-57//	4.93	0	2.67	2.38E-113	1.84	2.50E-06	
AP13ITG50188_s_at	AP13ISTG50188	cd00180/Catalytic donSUBFAMILY NOT NAM/	LOC_Os10g04730.1 13110.m00390 protein/1E-91//	4.91	7.20E-242	2.57	1.64E-40	1.91	2.49E-06	
OTHSWCTG17675_s_at	OthsCTG17675	OTHSW0112/Papain farCYSTEINE PROTEASE/	LOC_Os09g27030.2 13109.m02621 protein/7E-67//	4.86	0	2.64	7.67E-125	1.84	0.000728674	
KanlowCTG23219_s_at	KanlCTG23219	//	SUBFAMILY NOT NAM/	LOC_Os04g49890.1 13104.m05101 protein/2E-144//	4.85	0	2.69	8.12E-122	1.8	2.42E-07
OTHSWCTG14105_s_at	OthsCTG14105	//	/	4.84	0	2.6	1.02E-72	1.86	5.27E-05	
AP13CTG07636_at	AP13CTG07636	pfam01490/Transmemr FAMILY NOT NAMED//	LOC_Os08g03350.1 13108.m00291 protein/0//	4.84	1.70E-41	4.01	4.19E-26	1.21	0.389634556	
AP13ITG72235_s_at				4.84	1.22E-200	10.52	0	0.46	0.000232423	
OTHSWCTG11457_at	OthsCTG11457	cd00684/Plant Terpen/	LOC_Os08g07080.1 13108.m00725 protein/9E-106//	4.65	2.28E-84	5.27	9.28E-115	0.88	0.622590513	
AP13ITG66423_s_at	AP13ISTG66423	//	/	4.57	0	3.03	3.45E-26	1.51	1.02E-14	
KanlowCTG17154_s_at	KanlCTG17154	pfam00069/Protein kirSUBFAMILY NOT NAM/	LOC_Os01g02840.1 13101.m00223 protein/2E-87//	4.54	5.63E-141	6.82	0	0.67	0.142911571	
AP13CTG00637_at	AP13CTG00637	pfam00083/Sugar (ancSUBFAMILY NOT NAM/	LOC_Os10g41190.1 13110.m03832 protein/0//	4.48	0	5.39	0	0.83	0.198236745	
KanlowSLT55446_s_at	KanlSGLT55446	PRK12270/alpha-ketog /	LOC_Os06g46740.1 13106.m04941 protein/0.0007//	4.48	0	2.57	5.81E-115	1.74	1.40E-06	
AP13ITG63384_s_at	AP13ISTG663384	pfam02956/TT viral or/	LOC_Os03g17680.1 13103.m02113 protein/0.0001//	4.43	6.85E-55	4.53	8.02E-58	0.98	0.892665852	
AP13ITG63673-RC_at				4.43	4.30E-155	4.18	1.54E-133	1.06	0.86501752	
KanlowCTG35516_at	KanlCTG35516	//	SUBFAMILY NOT NAM/	LOC_Os01g15580.1 13101.m01725 protein/0.000000000001//	4.33	0	3.8	0	1.14	0.714009859
AP13ITG41562_s_at	AP13ISTG41562	pfam00635/MSP (MajvVESICLE-ASSOCIATED /	LOC_Os11g17380.1 13111.m01762 protein/8E-56//	4.31	0	3.29	0	1.31	0.171063098	
KanlowCTG11533_s_at	KanlCTG11533	pfam02956/TT viral or/	LOC_Os03g17680.1 13103.m02113 protein/0.00008//	4.25	2.89E-59	4.45	1.76E-66	0.96	0.768834389	
AP13CTG30443_at	AP13CTG30443	//	SUBFAMILY NOT NAM/	LOC_Os11g45600.1 13111.m04557 protein/2E-23//	4.25	0	4.02	0	1.06	0.81106624
AP13ITG44875_at	AP13ISTG44875	PRK12323/DNA polym/	LOC_Os11g45600.1 13111.m04557 protein/2E-23//	4.25	4.97E-69	2.79	3.27E-22	1.52	0.002532083	
AP13CTG00450_at	AP13CTG00450	PLN03059/beta-galact:SUBFAMILY NOT NAM	AT3G52840/GalactoseLOC_Os12g24170.1 13112.m02458 protein/0//	4.22	0	3.77	0	1.12	0.519624854	
KanlowCTG13191_s_at	KanlCTG13191	PHA03247/large tegun/	LOC_Os09g26999.1 13109.m02618 protein/0.006//	4.11	4.60E-129	4.07	1.29E-125	1.01	0.968770642	
AlamoCTG04547_s_at	AlamCTG04547	pfam02713/Domain of/	LOC_Os09g15835.1 13109.m07521 protein/1E-113//	4.08	2.13E-198	2.77	1.75E-66	1.48	0.056240134	
AP13CTG17193_at	AP13CTG17193	//	/	4.01	0	3.09	3.86E-89	1.3	2.26E-10	
AP13CTG04635_at	AP13CTG04635	pfam00069/Protein kirSUBFAMILY NOT NAM/	LOC_Os06g38340.1 13106.m03968 protein/3E-132//	3.99	1.34E-80	3.03	5.44E-38	1.32	0.202219363	
OTHSWCTG27954_at	OthsCTG27954	COG0515/Serine/threcSUBFAMILY NOT NAM/	LOC_Os02g40180.1 13102.m04472 protein/4E-51//	3.98	5.60E-162	5.14	0	0.77	0.347275716	
AP13CTG65129_s_at	AP13CTG65129	smart00219/Tyrosine iPROTEIN KINASE ATM/	LOC_Os12g06670.1 13112.m00686 protein/1E-155//	3.97	9.12E-67	5.32	0	0.75	0.000808527	
AP13ITG38393_at	AP13ISTG38393	TIGR03389/laccase, pliLACCASE/0	LOC_Os03g16610.1 13103.m01973 protein/0//	3.97	9.73E-44	7.61	9.81E-210	0.52	7.40E-17	
AlamoCTG06651_s_at	AlamCTG06651	//	/	3.92	3.86E-135	2.76	1.48E-50	1.42	0.000117451	
AP13ITG62258-RC_at				3.87	3.62E-64	3.73	1.74E-58	1.04	0.899606165	
AP13ITG39900_s_at	AP13ISTG39900	pfam00069/Protein kirOS12G0249900 PROTI/	LOC_Os12g14610.1 13112.m01551 protein/2E-64//	3.85	2.22E-28	5.75	1.29E-75	0.67	0.004148966	
AP13ITG49381_at	AP13ISTG49381	//	/	3.84	0	4.06	1.20E-88	0.95	0.482493166	
OTHSWCTG14285_at	OthsCTG14285	//	/	3.83	0	2.97	1.73E-191	1.29	0.243914326	
OTHSWCTG08671_s_at	OthsCTG08671	TIGR00957/multi drug SUBFAMILY NOT NAM/	LOC_Os04g13220.1 13104.m01213 protein/0//	3.81	1.39E-82	4.33	2.56E-115	0.88	0.615770674	
AP13ITG54952_at	AP13ISTG54952	//	UNKNOWN PROTEIN/	LOC_Os02g36940.1 13102.m04038 protein/7E-59//	3.77	5.79E-71	4.05	7.77E-86	0.93	0.771345593
AP13ITG67384-RC_at				3.76	1.33E-51	4.13	5.53E-66	0.91	0.828890036	
OTHSWCTG13588_s_at	OthsCTG13588	PLN02526/acyl-CoA oxSUBFAMILY NOT NAM	AT3G51840/Fatty acidLOC_Os05g07090.3 13105.m00774 protein/5E-56/Fatty acid metabolism; alpha	3.74	1.24E-69	3.47	1.12E-56	1.08	0.734875676	
AP13ITG41643_s_at	AP13ISTG41643	cd03244/Domain 2 of :SUBFAMILY NOT NAM/	LOC_Os04g13220.1 13104.m01213 protein/4E-126//	3.72	6.30E-93	4.04	2.64E-115	0.92	0.766502702	
KanlowCTG23219_at	KanlCTG23219	//	SUBFAMILY NOT NAM/	LOC_Os04g49890.1 13104.m05101 protein/2E-144//	3.69	7.06E-105	2.99	4.55E-58	1.24	0.086396878

AP13CTG19859_at	AP13CTG19859	cd00180/Catalytic don	SUBFAMILY NOT NAM/	LOC_Os04g43730.1 13104.m04348 protein/3E-138//	3.68	2.82E-225	3.08	1.83E-136	1.19	0.597594836	
AP13ITG65301_at	AP13ISTG65301	PHA03249/DNA packa/	/	LOC_Os01g02130.1 13101.m00151 protein/9E-20//	3.64	2.21E-68	3.9	4.99E-82	0.93	0.758536014	
AlamoCTG04793_at	AlamCTG04793	cd01459/VWA Copine: COPINE: 0.000000000/	/	LOC_Os06g40650.2 13106.m04232 protein/3E-68//	3.61	0	2.51	6.83E-117	1.44	0.014171803	
AP13ITG59978_at	AP13ISTG59978	cd03185/GST_C family GLUTATHIONE S-TRAN/	/	LOC_Os10g38470.1 13110.m03503 protein/9E-80//	3.61	1.70E-52	5.04	3.29E-123	0.72	0.180214218	
AP13CTG24727_at	AP13CTG24727	cd05476/Chroloplast A CHLOROPLAST NUCLE/	/	LOC_Os07g34940.1 13107.m03570 protein/8E-137//	3.59	3.60E-151	3.85	6.48E-182	0.93	0.824433241	
AP13ITG42171RC_at	AP13ISTG42171-RC	pfam02469/Fasciclin d PERIOSTIN-RELATED/4/	/	LOC_Os01g06580.1 13101.m00650 protein/5E-67//	3.59	4.43E-65	3.08	8.72E-43	1.16	0.444585704	
AP13ITG63170_at	AP13ISTG63170	pfam03018/Dirigent-III FAMILY NOT NAMED//	/	LOC_Os10g18760.1 13110.m01548 protein/0.000000000000002//	3.57	1.14E-24	3.54	0	1.01	0.801121659	
AP13CTG14747_s_at	AP13CTG14747	PLN02290/cytokinin tr SUBFAMILY NOT NAM/	/	LOC_Os03g25480.1 13103.m03006 protein/0//	3.53	2.13E-80	3.34	9.19E-69	1.06	0.797210625	
KanlowCTG42496_s_at	KanlCTG42496	PLN02640/glucose-6-p FAMILY NOT NAMED/	ATSG35790/Pentose p	LOC_Os03g29950.1 13103.m03430 protein/3E-114/Pentose phosphate pathwa/	3.52	4.47E-117	3.75	2.47E-139	0.94	0.716288558	
AlamoCTG02492_x_at	AlamCTG02492	smart00813/Alpha-L-a/	/	LOC_Os11g03730.3 13111.m00315 protein/1E-133//	3.48	2.40E-178	2.58	4.17E-74	1.35	0.116298925	
AP13CTG21882_s_at	AP13CTG21882	PLN02420/hydrolase, I FAMILY NOT NAMED//	/	LOC_Os02g50490.1 13102.m05730 protein/0//	3.47	8.23E-162	2.53	3.40E-63	1.37	0.033327474	
AP13ITG76663RC_at	AP13ISTG76663-RC	PHA03247/large tegun/	/	LOC_Os05g51780.1 13105.m05599 protein/7E-33//	3.43	9.92E-248	2.89	6.28E-151	1.19	0.374597487	
OTHSWCTG10420_at	OthsCTG10420	//	/	LOC_Os12g25170.1 13112.m02552 protein/8E-40//	3.4	4.10E-80	3.07	5.86E-60	1.11	0.597229179	
AP13ITG64790RC_at	AP13ISTG64790-RC	PHA03247/large tegun/	/	LOC_Os01g60930.1 13101.m06486 protein/7E-101//	3.37	1.60E-33	3.06	8.49E-26	1.1	0.667687412	
KanlowCTG22618_s_at	KanlCTG22618	PHA03245/large tegun/	/	///	3.37	9.69E-08	3.33	1.54E-07	1.01	0.978736632	
OTHSWCTG07191_at	OthsCTG07191	//	/	///	3.36	3.81E-13	3.32	8.38E-13	1.01	0.967344262	
OTHSWSLT35408_at	OthsSGLT35408	//	/	LOC_Os01g24340.1 13101.m02574 protein/0.0000000000000002//	3.24	1.50E-85	3.62	7.67E-117	0.89	0.381885648	
OTHSWCTG35380_s_at	OthsCTG35380	//	SUBFAMILY NOT NAM/	LOC_Os01g02290.1 13101.m00169 protein/1E-20//	3.23	8.66E-107	6.35	0	0.51	0.026978284	
AP13CTG04921_s_at	AP13CTG04921	pfam01535/PPR repea	FAMILY NOT NAMED//	LOC_Os10g28600.1 13110.m02438 protein/0//	3.2	0	3.05	1.25E-150	1.05	0.32875217	
AP13CTG23391_at	AP13CTG23391	//	SUBFAMILY NOT NAM/	LOC_Os03g62430.1 13103.m06892 protein/3E-50//	3.16	3.59E-38	3.66	2.38E-57	0.86	0.312236418	
AP13ITG45589_s_at	AP13ISTG45589	//	/	///	3.16	0	3.23	1.51E-66	0.98	0.781788464	
KanlowCTG42196_s_at	KanlCTG42196	cd00180/Catalytic don	OS04G0109100 PROTI/	LOC_Os04g01874.1 13104.m00100 protein/3E-84//	3.15	7.70E-43	2.74	1.06E-28	1.15	0.552279355	
AP13CTG29146_at	AP13CTG29146	pfam03018/Dirigent-III	OS10G0335000 PROTI/	LOC_Os10g18760.1 13110.m01548 protein/4E-21//	3.14	3.42E-62	3.07	0	1.02	0.45687962	
AP13ITG45888_s_at	AP13ISTG45888	//	SUBFAMILY NOT NAM/	LOC_Os07g43810.1 13107.m04605 protein/6E-58//	3.07	9.09E-137	3.11	4.27E-142	0.99	0.940878264	
AP13ITG55233_at	AP13ISTG55233	PLN02640/glucose-6-p FAMILY NOT NAMED/	ATSG35790/Pentose p	LOC_Os03g29950.1 13103.m03430 protein/0/Pentose phosphate pathway; Glu/	3.07	2.86E-94	3.09	7.14E-96	0.99	0.964090129	
KanlowCTG22694_at	KanlCTG22694	//	UNKNOWN PROTEIN/	LOC_Os02g36940.1 13102.m04038 protein/6E-59//	3.07	5.45E-48	3.16	3.40E-52	0.97	0.893850744	
KanlowCTG42715_at	KanlCTG42715	PLN00113/leucine-rich	SUBFAMILY NOT NAM/	LOC_Os02g40240.2 13102.m04480 protein/2E-81//	3.05	8.79E-53	4.09	2.62E-117	0.75	0.120951283	
AP13CTG004050_s_at	AP13CTG004050	PLN03059/beta-galact	SUBFAMILY NOT NAM	AT3G52840/Galactose	LOC_Os12g24170.1 13112.m02458 protein/0//	3.04	3.01E-202	2.79	3.91E-156	1.09	0.578334949
AP13CTG11976_s_at	AP13CTG11976	PLN02687/flavonoid 3'	SUBFAMILY NOT NAM/	LOC_Os08g01450.1 13108.m00065 protein/8E-172//	3.03	2.59E-104	2.96	1.37E-97	1.02	0.897735784	
KanlowCTG23500_s_at	KanlCTG23500	//	UDP-GLUCOSYLTRANS/	LOC_Os07g32010.1 13107.m03237 protein/2E-88//	2.99	7.12E-66	2.65	4.48E-46	1.13	0.601092244	
AP13ITG71998-RC_at					2.98	5.19E-29	2.78	7.41E-24	1.07	0.648224917	
AP13CTG09743_at	AP13CTG09743	pfam02536/mTERF. Th	SUBFAMILY NOT NAM/	LOC_Os07g39430.1 13107.m04084 protein/0//	2.95	4.89E-40	3.31	3.77E-55	0.89	0.460711786	
AP13CTG00528_at	AP13CTG00528	pfam04884/Protein of	SUBFAMILY NOT NAM/	LOC_Os03g11500.1 13103.m01297 protein/9E-156//	2.94	3.39E-81	2.63	6.14E-58	1.12	0.420762581	
AlamoCTG03711_s_at	AlamCTG03711	//	/	LOC_Os09g36290.1 13109.m03573 protein/1E-77//	2.88	1.18E-61	2.69	3.14E-50	1.07	0.72842844	
AP13ITG65392_at	AP13ISTG65392	PLN02152/UDP-glucos	PUTATIVE GLUCOSYL	AT4G14090/Anthocya	LOC_Os05g08750.1 13105.m00970 protein/5E-150//	2.87	2.62E-22	3.73	1.77E-45	0.77	0.042591239
AP13CTG05682_s_at	AP13CTG05682	cd03407/A subgroup c	BAND 7 FAMILY PROT/	LOC_Os05g51420.2 13105.m05539 protein/2E-149//	2.86	6.31E-41	3.87	7.21E-95	0.74	0.093134852	
AP13ITG50374_s_at	AP13ISTG50374	pfam03069/Acetamide/	AT4G37560/Glyoxylat	LOC_Os01g55950.1 13101.m05909 protein/5E-122/Glyoxylate and dicarboxylat/	2.85	1.55E-12	3.04	5.91E-15	0.94	0.766762	
OTHSWCTG14772_at	OthsCTG14772	pfam03018/Dirigent-III	OS10G0335000 PROTI/	LOC_Os10g18870.1 13110.m01559 protein/0.0000000000006//	2.82	1.97E-43	3.03	0	0.93	0.344843681	
AP13CTG24597_at	AP13CTG24597	PHA03247/large tegun	OS03G0335300 PROTI/	LOC_Os04g52190.1 13104.m05345 protein/0//	2.82	2.42E-51	2.59	1.62E-39	1.09	0.69609287	
AP13CTG22276_s_at	AP13CTG22276	cd03419/Glutaredoxin	GLUTAREDOXIN/1.6E-/	LOC_Os02g40500.1 13102.m04514 protein/5E-47//	2.8	8.10E-37	2.89	9.78E-41	0.97	0.883091726	
AP13CTG14697_s_at	AP13CTG14697	pfam00069/Protein kir	SUBFAMILY NOT NAM/	LOC_Os04g03830.1 13104.m00305 protein/4E-75//	2.79	8.87E-14	3.34	1.58E-22	0.83	0.153062513	
AP13CTG15597_at	AP13CTG15597	pfam12049/Protein of	/	LOC_Os02g58120.1 13102.m06728 protein/3E-120//	2.78	0	2.6	1.02E-58	1.07	0.221478802	
KanlowSLT52258_at	KanlSGLT52258	//	/	LOC_Os05g39130.1 13105.m04119 protein/0.00000000004//	2.78	1.39E-78	2.72	3.90E-73	1.02	0.906445296	
AP13ITG47602_s_at	AP13ISTG47602	cd03407/A subgroup c	BAND 7 FAMILY PROT/	LOC_Os05g51420.7 13105.m05540 protein/3E-85//	2.77	1.38E-30	4.29	1.09E-101	0.64	0.001517568	
AP13ITG41137_at	AP13ISTG41137	cd01989/The N-termin/	/	LOC_Os09g39650.3 13109.m03981 protein/4E-86//	2.73	3.85E-101	4.1	0	0.67	0.000440838	
KanlowCTG41582_s_at	KanlCTG41582	TIGR03389/laccase, pl	LACCASE/3E-228	LOC_Os03g16610.1 13103.m01973 protein/0//	2.73	1.76E-27	4.52	1.79E-108	0.6	1.52E-05	
AP13CTG21472_s_at	AP13CTG21472	pfam05140/ResB-like	t/	LOC_Os03g55970.1 13103.m06098 protein/0//	2.67	0	2.57	1.83E-28	1.04	0.549155944	
OTHSWCTG17938_at	OthsCTG17938	PLN00113/leucine-rich	SUBFAMILY NOT NAM/	LOC_Os02g40180.1 13102.m04472 protein/4E-62//	2.67	5.38E-15	3.09	1.53E-22	0.86	0.483485158	
OTHSWSLT26755_at	OthsSGLT26755	//	/	///	2.66	1.12E-71	3.96	5.08E-224	0.67	1.82E-07	
AP13CTG06087_s_at	AP13CTG06087	COG2802/Uncharacter	FAMILY NOT NAMED//	LOC_Os03g29540.3 13103.m12878 protein/1E-68//	2.65	2.71E-22	3.19	3.19E-38	0.83	0.133185301	
AP13ITG76471_s_at	AP13ISTG76471	//	SUBFAMILY NOT NAM/	LOC_Os03g10100.1 13103.m01126 protein/0//	2.65	7.86E-22	2.85	6.78E-27	0.93	0.519980024	
AP13CTG006369_at	AP13CTG006369	cd01876/The Yiha [En]	FAMILY NOT NAMED//	LOC_Os01g53150.2 13101.m05568 protein/1E-132//	2.65	2.11E-152	2.76	3.27E-172	0.96	0.781095061	
AP13CTG32494_s_at	AP13CTG32494	//	OS04G0192800 PROTI/	LOC_Os11g14340.1 13111.m01470 protein/3E-54//	2.63	0	4.49	3.63E-280	0.59	8.30E-37	
KanlowCTG43401_s_at	KanlCTG43401	pfam04884/Protein of	SUBFAMILY NOT NAM/	LOC_Os03g11500.1 13103.m01297 protein/5E-37//	2.63	3.50E-104	2.51	1.06E-90	1.04	0.743877262	
AP13CTG11164_s_at	AP13CTG11164	PLN02189/cellulose sy	SUBFAMILY NOT NAM/	LOC_Os09g25490.1 13109.m02439 protein/7E-139//	2.61	2.80E-07	6.42	1.15E-66	0.41	1.14E-10	
AP13CTG13909_s_at	AP13CTG13909	//	/	///	2.6	5.80E-65	2.94	5.99E-95	0.88	0.248814027	
AP13ITG42951-RC_at					2.57	6.08E-23	7.53	0	0.34	0	
OTHSWCTG26966_s_at	OthsCTG26966	//	OS12G0477100 PROTI/	LOC_Os06g16790.1 13106.m01851 protein/0.000000005//	2.56	2.51E-42	2.52	1.59E-40	1.01	0.940058441	
AP13CTG00613_at	AP13CTG00613	cd00180/Catalytic don	FAMILY NOT NAMED//	LOC_Os12g14610.1 13112.m01551 protein/5E-60//	2.56	1.61E-57	2.7	1.37E-67	0.95	0.563172712	
AP13CTG20027_at	AP13CTG20027	//	/	///	2.55	1.45E-10	2.54	1.29E-09	1	0.966882108	
KanlowCTG36954_at	KanlCTG36954	PRK05653/3-ketoacyl- <i>t</i>	SUBFAMILY NOT NAM	AT2G29150/Tropane,	LOC_Os11g43200.1 13111.m04296 protein/2E-90//	2.55	4.10E-32	2.99	5.14E-52	0.85	0.145765565
KanlowCTG15086_s_at	KanlCTG15086	//	/	LOC_Os01g03110.1 13101.m00262 protein/2E-87//	2.52	3.78E-45	2.82	2.12E-64	0.89	0.484160365	
AP13CTG52756_s_at	AP13CTG52756	cd06899/legume lectin	SUBFAMILY NOT NAM/	LOC_Os07g03900.1 13107.m00328 protein/5E-116//	2.51	2.38E-13	2.86	1.75E-19	0.88	0.547546191	

Table S4. List of commonly down-regulated genes with more than 2.5 fold change between Se/60 and Mo/60 comparisons
 Genes not correlated with lesion development (Se/Mo>1) were ruled out and highlighted in blue. P, Bonferroni-corrected P value.

probeset_id	PvIUT sequence ID	CDD annotation	Panther annotation	Arabidopsis hit	Rice hit	Ratio(Se/60)	P	Ratio(Mo/60)	P	Ratio(Se/Mo)	P
KanlowCTG15097_at	KanlCTG15097	pfam02902/Ulp1 protease	/	/	LOC_Os08g27759.1 13108.m02864 protein/7E-23//	0.06	0	0.08	0	0.68	5.06E-18
AP13ITG56127_x_at	AP13ISTG56127	pfam00235/Profilin,1E-1	FAMILY NOT NAMED/1.1E-	/	LOC_Os10g17680.1 13110.m01449 protein/2E-72//	0.1	0	0.12	0	0.79	0.227125134
AP13CTG25577_at	AP13CTG25577	//	/	/	///	0.11	2.12E-96	0.06	0	1.7	5.08E-06
AP13CTG40946_s_at	AP13CTG40946	pfam09713/Plant protein	/	/	LOC_Os05g36860.1 13105.m04062 protein/8E-33//	0.13	1.12E-32	0.36	8.18E-12	0.38	0.002086835
AP13ITG64729_at	AP13ISTG64729	TIGR02189/Glutaredoxin	GLUTAREDOXIN/6.4E-43	/	LOC_Os12g5330.1 13112.m03614 protein/3E-45//	0.13	3.84E-156	0.19	6.84E-15	0.7	0.085064035
AP13ITG70427_at	AP13ISTG70427	pfam03242/Late embryon	/	/	LOC_Os01g21250.1 13101.m02261 protein/0.0000002//	0.13	7.50E-106	0.22	7.63E-09	0.59	0.021712227
AP13ITG37591_at	AP13ISTG37591	//	/	/	///	0.14	4.90E-37	0.19	9.90E-44	0.77	0.45993667
AlamoSLT15807_at	AlamSGLT15807	//	/	/	LOC_Os04g51090.1 13104.m05196 protein/0.00001//	0.15	5.69E-150	0.19	1.14E-31	0.82	0.292689791
AP13ITG63308-RC_at						0.15	2.15E-125	0.18	3.04E-148	0.83	0.341115395
AlamoCTG06663_at	AlamCTG06663	//	/	/	///	0.16	0	0.12	0	1.31	0.001114078
AP13CTG37783_s_at	AP13CTG37783	pfam02956/TT viral orf	/	/	LOC_Os06g43810.1 13106.m04592 protein/0.00000000006//	0.16	0	0.17	7.74E-168	0.98	0.873664064
AP13ITG51564_s_at	AP13ISTG51564	pfam01073/3-beta hydrox	3 BETA-HYDROXYSTEROID	/	LOC_Os03g29150.1 13103.m03345 protein/5E-51//	0.16	9.40E-12	0.31	2.47E-25	0.53	0.028458665
AP13ITG60650_at	AP13ISTG60650	pfam06376/Protein of u	/	/	LOC_Os05g12580.1 13105.m01366 protein/0.0000000000002//	0.16	1.09E-93	0.11	0	1.4	0.025136064
AP13CTG02927_at	AP13CTG02927	pfam01073/3-beta hydrox	3 BETA-HYDROXYSTEROID	AT4G33360/Flavonol	LOC_Os03g29170.2 13103.m03348 protein/2E-119/Amino sugar a	0.17	2.40E-10	0.32	3.97E-23	0.51	0.021452177
KanlowCTG25668_at	KanlCTG25668	TIGR02882/cytochrome	/	/	LOC_Os04g51090.1 13104.m05196 protein/5E-21//	0.17	0	0.29	4.92E-24	0.59	0.011423108
KanlowCTG26782_s_a	KanlCTG26782	cd00693/Horseradish pe	/	AT5G05340/Phenylalanine	LOC_Os03g32050.1 13103.m03658 protein/6E-78/Phenylalanine r	0.17	8.80E-96	0.29	4.39E-24	0.58	0.002209208
VS16ITG03134_s_at	VS16ISTG03134	cd01837/SGNH_plant_li	LATERAL SIGNALING TARGE	/	LOC_Os06g06250.2 13106.m10511 protein/3E-179//	0.17	0	0.11	0	1.48	0.007109794
KanlowCTG42704_at	KanlCTG42704	pfam09507/DNA polymer	/	/	LOC_Os04g51090.1 13104.m05196 protein/1E-53//	0.18	3.40E-127	0.21	2.04E-58	0.85	0.331619905
VS16ITG11260_at	VS16ISTG11260	//	/	/	///	0.18	4.42E-97	0.26	8.84E-11	0.69	0.038220887
AP13CTG14980_at	AP13CTG14980	//	/	AT4G13710/Pentose	LOC_Os04g05050.1 13104.m00426 protein/0/Pentose and glucuro	0.19	0	0.21	3.57E-18	0.91	0.714292151
AP13CTG16698_s_at	AP13CTG16698	cd00693/Horseradish pe	/	AT5G14130/Phenylalanine	LOC_Os08g42030.1 13108.m04518 protein/3E-125/Phenylalanine	0.19	8.33E-61	0.15	2.11E-132	1.26	0.243719571
AP13ITG74644_x_at	AP13ISTG74644	PLN03023/expansin-rela	/	/	LOC_Os10g40700.1 13110.m03773 protein/1E-104//	0.19	1.85E-121	0.24	6.48E-21	0.79	0.140259782
AP13CTG09520_at	AP13CTG09520	COG2198/FOG: HPT dom	/	/	LOC_Os05g09410.1 13105.m01049 protein/1E-70//	0.2	9.92E-28	0.37	3.21E-12	0.54	0.020605124
OTHSWSLT24122_s_a	OthsSGLT24122	PHA03247/large tegume	/	/	///	0.2	0	0.08	0	2.49	4.74E-15
AP13ITG72073_at	AP13ISTG72073	//	UNCHARACTERIZED/4.8E-2	/	LOC_Os04g39360.1 13104.m03811 protein/0.00000000000002//	0.21	1.51E-27	0.23	0	0.9	0.086649303
KanlowCTG00319_at	KanlCTG00319	PLN00166/aquaporins of	TONOPLAST INTRINSIC PRC	/	LOC_Os06g22960.1 13106.m02470 protein/4E-136//	0.21	1.14E-105	0.28	6.64E-56	0.73	0.041362562
KanlowCTG06768_at	KanlCTG06768	pfam01679/Uncharacter	FAMILY NOT NAMED/1.9E-	/	LOC_Os07g44180.1 13107.m04647 protein/0.0000000000000000C	0.21	9.03E-209	0.12	9.69E-118	1.67	0.001143448
AP13CTG28955_at	AP13CTG28955	cd00693/Horseradish pe	/	AT1G05260/Phenylalanine	LOC_Os10g39170.1 13110.m03584 protein/1E-74//	0.22	0	0.19	8.29E-62	1.19	7.66E-08
AP13ITG54183_at	AP13ISTG54183	//	/	/	///	0.22	0	0.28	0	0.77	0.326201408
VS16ITG11260_s_at	VS16ISTG11260	//	/	/	///	0.22	1.36E-35	0.35	1.20E-11	0.63	0.04213291
AP13CTG30547_s_at	AP13CTG30547	//	/	/	///	0.23	0	0.27	2.02E-81	0.85	0.013168887
AP13ITG76439_at	AP13ISTG76439	//	POTENTIAL UNCHARACTERIZ	/	LOC_Os01g20830.1 13101.m02207 protein/0.00000000000003//	0.23	3.39E-37	0.37	4.20E-20	0.63	0.02425193
AlamoCTG14387_s_at	AlamCTG14387	//	FAMILY NOT NAMED/0.00C	AT2G06510/DNA rege	LOC_Os03g08400.1 13103.m00965 protein/2E-57//	0.24	0	0.34	0	0.7	0.161096627
AP13CTG23694_at	AP13CTG23694	pfam04770/ZF-HD prote	/	/	LOC_Os11g03420.1 13111.m00281 protein/2E-28//	0.24	8.33E-30	0.25	5.94E-84	0.96	0.804271346
AP13CTG26572_s_at	AP13CTG26572	pfam06728/GPI transmem	FAMILY NOT NAMED/8.8E-	AT1G63110/Glycosyl	LOC_Os02g46350.1 13102.m05202 protein/3E-37/Glycosylphosph	0.24	8.46E-18	0.33	1.76E-16	0.72	0.254891148
KanlowCTG25136_s_a	KanlCTG25136	PLN02336/phosphoetha	SUBFAMILY NOT NAMED/5	AT3G18000/Glycerol	LOC_Os05g47540.1 13105.m05037 protein/9E-83//	0.24	3.29E-229	0.36	6.52E-08	0.66	2.55E-07
KanlowCTG37283_s_a	KanlCTG37283	cd01837/SGNH_plant_li	LATERAL SIGNALING TARGE	/	LOC_Os06g05630.1 13106.m00551 protein/2E-136//	0.24	0	0.23	0	1.02	0.833197369
OTHSWCTG25697_at	OthsCTG25697	//	/	/	///	0.25	1.11E-69	0.28	9.17E-10	0.9	0.506168018
AP13ITG41402_s_at	AP13ISTG41402	PHA03247/large tegume	/	/	LOC_Os01g07240.1 13101.m00724 protein/8E-20//	0.25	0	0.24	0	1.05	0.706627797
AP13ITG63962-RC_at						0.25	3.01E-39	0.28	1.28E-78	0.89	0.422833378
KanlowCTG47101_at	KanlCTG47101	PLN02270/phospholipase	OS09G0421300 PROTEIN/8	AT4G11840/Glycerol	LOC_Os09g25390.1 13109.m02428 protein/2E-39/Glycerophosph	0.25	1.96E-71	0.34	3.84E-118	0.74	0.001791649
OTHSWCTG07240_at	OthsCTG07240	PLN00191/enolase/2E-1	FAMILY NOT NAMED/0.00C	AT2G36530/Glycolys	LOC_Os10g08550.5 13110.m00739 protein/0.0000000000001 glycc	0.25	0	0.24	0	1.04	0.883510469
OTHSWCTG07571_s_a	OthsCTG07571	cd02947/TRX family; con	SUBFAMILY NOT NAMED/5	/	LOC_Os09g38670.2 13109.m03857 protein/0.00000000000000002	0.25	3.28E-23	0.11	0	2.38	4.54E-10
AP13CTG11853_at	AP13CTG11853	smart00102/Actin depol	FAMILY NOT NAMED/5.8E-	/	LOC_Os05g02250.2 13105.m00186 protein/5E-58//	0.26	0	0.36	0	0.72	0.241783372
AP13ITG41762-RC_at						0.26	7.86E-13	0.27	3.29E-227	0.96	0.598875941
KanlowCTG43989_s_a	KanlCTG43989	PLN00113/leucine-rich r	FAMILY NOT NAMED/2.5E-	/	LOC_Os07g31840.1 13107.m03222 protein/2E-73//	0.26	0	0.26	0	1.02	0.903812123
AP13CTG22648_at	AP13CTG22648	//	SUBFAMILY NOT NAMED/9	/	LOC_Os05g49240.1 13105.m05266 protein/4E-36//	0.27	2.50E-31	0.39	5.76E-08	0.71	0.069229322
AP13CTG28423_s_at	AP13CTG28423	PHA03307/transcription	SUBFAMILY NOT NAMED/7	/	LOC_Os11g01330.1 13111.m00041 protein/0//	0.27	5.78E-17	0.4	1.20E-21	0.69	0.048578624
AP13ITG40815_s_at	AP13ISTG40815	cd01837/SGNH_plant_li	LATERAL SIGNALING TARGE	/	LOC_Os01g42730.1 13101.m04398 protein/3E-81//	0.28	0	0.2	0	1.42	0.255161812
KanlowCTG20903_s_a	KanlCTG20903	cd00403/Ribosomal prot	PBK1-RELATED/4.9E-20	/	LOC_Os05g48422.1 13105.m00515 protein/4E-54//	0.28	1.57E-36	0.24	2.88E-28	1.16	0.497490022
KanlowCTG37283_at	KanlCTG37283	cd01837/SGNH_plant_li	LATERAL SIGNALING TARGE	/	LOC_Os06g05630.1 13106.m00551 protein/2E-136//	0.28	1.23E-66	0.28	1.82E-215	0.98	0.819121686
AP13CTG14141_s_at	AP13CTG14141	TIGR00393/KpsF/GutG	fCAPSULE EXPRESSION PRO	/	LOC_Os02g06360.1 13102.m00699 protein/4E-101//	0.29	0	0.35	0	0.84	0.602108082
AP13CTG16272_s_at	AP13CTG16272	pfam04483/Protein of u	/	/	LOC_Os09g11520.1 13109.m01034 protein/3E-59//	0.29	1.91E-14	0.35	1.64E-38	0.84	0.252762848
AP13CTG23886_s_at	AP13CTG23886	COG2072/Predicted flav	MONOOXYGENASE/2.5E-2	AT5G43890/Tryptop	LOC_Os04g03980.1 13104.m00320 protein/0/Tryptophan metabol	0.29	4.94E-12	0.33	0	0.9	0.00027368
AP13CTG27072_s_at	AP13CTG27072	PLN00113/leucine-rich r	OS05G0180300 PROTEIN/3	/	LOC_Os05g08770.2 13105.m10346 protein/1E-159//	0.29	1.70E-45	0.23	9.38E-36	1.27	0.203384759
AP13ITG58736_s_at	AP13ISTG58736	pfam02519/Auxin respon	/	/	LOC_Os09g37394.1 13109.m03709 protein/3E-49//	0.29	1.33E-20	0.27	0	1.07	0.284197316
AP13ITG66747_at	AP13ISTG66747	PRK12678/transcription	/	/	LOC_Os04g31350.1 13104.m02996 protein/1E-46//	0.29	1.64E-260	0.2	0	1.43	4.18E-10
KanlowCTG26938_s_a	KanlCTG26938	pfam08161/NUC173 dor	UNCHARACTERIZED NODUI	/	LOC_Os01g72780.1 13101.m07932 protein/2E-21//	0.29	4.98E-50	0.28	0	1.05	0.44736041
KanlowCTG42674_s_a	KanlCTG42674	//	/	/	///	0.29	2.95E-17	0.17	6.24E-141	1.69	0.000253248
AP13CTG31634_at	AP13CTG31634	//	/	/	///	0.3	0	0.33	0	0.9	0.608941651
AP13ITG37441_at	AP13ISTG37441	PLN02236/choline kinase	SUBFAMILY NOT NAMED/7	/	LOC_Os05g45880.1 13105.m04881 protein/1E-159/Glycerophosph	0.3	0	0.25	0	1.19	0.684178316
AP13ITG38712_s_at	AP13ISTG38712	cd02176/Xyloglucan end	/	/	LOC_Os10g39840.1 13110.m03671 protein/3E-119//	0.3	7.50E-79	0.34	1.07E-13	0.89	0.310751326
AP13ITG72601_s_at	AP13ISTG72601	PRK06664/flagellar hook	EUKARYOTIC INITIATION	FA AT5G57870/RNA tra	LOC_Os10g11240.1 13110.m01019 protein/2E-32//	0.3	1.26E-199	0.34	1.72E-67	0.91	0.18031122
KanlowCTG30657_s_a	KanlCTG30657	cd00083/Helix-loop-heli	UPSTREAM TRANSCRIPTION	/	LOC_Os03g07540.1 13103.m00847 protein/3E-24//	0.3	5.32E-84	0.28	0	1.07	0.262353252

OTHSWCTG17826_s_a	OthsCTG17826	//	LYSOSOMAL ALPHA-MANN AT5G66150/Other gl	LOC_Os10g05069.1	[13110.m00422]	protein/8E-68/Other glycan de	0.3	0	0.38	0	0.8	0.552822806	
KanlowCTG08571_s_a	KanlCTG08571	pfam00827/Ribosomal L FAMILY NOT NAMED/6.3E-	AT4G16720/Ribosom	LOC_Os05g19370.1	[13105.m02044]	protein/1E-100/Ribosome/4E-1	0.31	1.30E-25	0.27	1.04E-21	1.13	0.585412442	
AP13ITG61328_at	AP13ISTG61328	pfam05498/Rapid Alkali /	/	LOC_Os02g44940.1	[13102.m05036]	protein/0.009//	0.31	2.62E-62	0.4	2.18E-19	0.78	0.034968274	
AP13ITG64329_at	AP13ISTG64329	//	/	///			0.31	8.46E-216	0.25	1.03E-62	1.26	0.004083766	
AP13ITG74038_at	AP13ISTG74038	PLN02294/cytochrome c CYTOCHROME C OXIDASE S	AT3G15640/Oxidativ	LOC_Os01g42650.1	[13101.m04385]	protein/1E-30/Oxidative phosph	0.31	3.17E-27	0.26	1.66E-40	1.18	0.393664079	
KanlowCTG30345_s_a	KanlCTG30345	cd00693/Horseradish pe /	AT2G18980/Phenyla	LOC_Os06g48030.1	[13106.m05104]	protein/3E-49/Phenylalanine rr	0.31	1.05E-51	0.34	1.13E-32	0.92	0.535169912	
KanlowCTG39226_s_a	KanlCTG39226	pfam01074/Glycosyl hyd	LYSOSOMAL ALPHA-MANN AT5G66150/Other gl	LOC_Os10g05069.1	[13110.m00422]	protein/1E-101/Other glycan d	0.31	0	0.4	0	0.79	0.507938665	
AP13CTG12778_at	AP13ISTG12778	smart00579/domain in F /	/	LOC_Os07g36530.1	[13107.m03751]	protein/0.000000000000001//	0.32	1.81E-13	0.33	2.39E-25	0.95	0.811964344	
AP13ITG40821_s_at	AP13ISTG40821	cd01837/SGNH_plant_lil	LATERAL SIGNALING TARGE	LOC_Os01g42730.1	[13101.m04398]	protein/2E-77//	0.32	0	0.23	0	1.41	0.07868336	
AP13ITG54974_at	AP13ISTG54974	pfam04770/ZF-HD prote /	/	LOC_Os11g03420.1	[13111.m00281]	protein/9E-30//	0.32	1.42E-41	0.33	6.67E-144	0.97	0.74224083	
AP13ITG72069-RC_at							0.32	3.80E-69	0.18	4.98E-88	1.71	0.00075455	
KanlowCTG00595-3_s_at							0.32	0	0.34	0	0.95	0.829507648	
KanlowCTG17757_at	KanlCTG17757	//	/	///			0.32	3.75E-20	0.24	3.59E-34	1.34	0.194075687	
OTHSWCTG15634_s_a	OthsCTG15634	smart00547/Zinc finger c FAMILY NOT NAMED/0.00C /	/	LOC_Os01g37460.1	[13101.m03808]	protein/0.0000000000000004/	0.32	4.18E-10	0.28	6.09E-13	1.15	0.686234986	
AP13ITG54401_at	AP13ISTG54401	PTZ00009/heat shock 70 FAMILY NOT NAMED/0	AT3G12580/Spliceos	LOC_Os03g16920.1	[13103.m02017]	protein/0/Spliceosome; Protein	0.33	1.42E-08	0.21	1.84E-11	1.59	0.375514401	
AP13ITG63880RC_at	AP13ISTG63880-RC	smart00380/DNA-bindin PREDICTED PROTEIN/0.000 /	/	LOC_Os02g42585.1	[13102.m12308]	protein/2E-103//	0.33	7.76E-21	0.36	9.47E-14	0.93	0.708730872	
AP13ITG64473_at	AP13ISTG64473	pfam02956/TT viral orf 10S10G0116300 PROTEIN/9 /	/	LOC_Os09g30490.1	[13109.m03059]	protein/1E-27//	0.33	0	0.39	0	0.83	0.584081397	
OTHSWCTG17935_s_a	OthsCTG17935	pfam10184/Uncharacter /	/	LOC_Os07g10495.1	[13107.m01067]	protein/3E-60//	0.33	0	0.39	0	0.83	0.419418977	
OTHSWCTG18646_at	OthsCTG18646	//	/	///			0.33	1.08E-200	0.34	8.82E-22	0.95	0.487895557	
AP13CTG11801_at	AP13CTG11801	smart00220/Serine/Thre SUBFAMILY NOT NAMED/6 /	/	LOC_Os01g10890.1	[13101.m01175]	protein/2E-178//	0.34	2.77E-09	0.33	4.53E-17	1.03	0.888903341	
AP13ITG43189_s_at	AP13ISTG43189	pfam02469/Fascinlin dor FLA (FASCICLIN-LIKE ARABII /	/	LOC_Os09g30486.1	[13109.m03058]	protein/4E-70//	0.34	4.42E-14	0.29	3.37E-45	1.19	0.283385213	
KanlowCTG19494_s_a	KanlCTG19494	//	/	///			0.34	1.31E-16	0.3	9.90E-21	1.16	0.537310286	
KanlowCTG28988_at	KanlCTG28988	pfam00856/SET domain.SET DOMAIN PROTEIN/0.0C /	/	LOC_Os02g03030.1	[13102.m00269]	protein/3E-63//	0.34	1.67E-220	0.36	0	0.94	0.003909875	
KanlowCTG44452_s_a	KanlCTG44452	pfam05667/Protein of ui /	/	LOC_Os02g14500.1	[13102.m01613]	protein/1E-21//	0.34	8.17E-12	0.33	1.24E-15	1.02	0.94051114	
VS16ITG20386_s_at	VS16ISTG20386	//	/	/	LOC_Os07g47450.1	[13107.m05050]	protein/0.0000000000000002//	0.34	9.29E-32	0.34	1.10E-66	0.99	0.915774362
AP13CTG10505_at	AP13CTG10505	TIGR00393/KpsF/GutQ f;CAPSULE EXPRESSION PRO /	/	LOC_Os02g06360.1	[13102.m00699]	protein/5E-171//	0.35	7.57E-37	0.33	6.88E-21	1.07	0.661488353	
AP13ITG56710_s_at	AP13ISTG56710	PLN02580/trehalose-phT TREHALOSE-6-PHOSPHATE /	/	LOC_Os02g44230.3	[13102.m04935]	protein/1E-144//	0.35	1.62E-08	0.34	9.75E-181	1.03	0.673991551	
AP13ITG60355_at	AP13ISTG60355	PLN02555/limonoid gluc UDP-GLUCOSYLTRANSFERA AT1G22400/Zeatin b	LOC_Os04g37820.1	[13104.m03621]	protein/0//	0.35	1.08E-15	0.26	0	1.31	0.195168916		
AP13ITG67617_s_at	AP13ISTG67617	PRK04537/ATP-depende /	/	LOC_Os11g27540.2	[13111.m02640]	protein/8E-40//	0.35	1.33E-14	0.4	1.13E-23	0.88	0.446771462	
KanlowCTG17315_s_a	KanlCTG17315	pfam01843/DIL domain. SUBFAMILY NOT NAMED/1 /	/	LOC_Os03g53660.1	[13103.m05865]	protein/1E-38//	0.35	5.30E-261	0.37	1.44E-27	0.95	0.320669323	
KanlowCTG41891_s_a	KanlCTG41891	pfam01357/Pollen allerg FAMILY NOT NAMED/0.00C /	/	LOC_Os10g40720.1	[13110.m03775]	protein/2E-39//	0.35	1.73E-16	0.39	9.99E-16	0.91	0.651081736	
AlamoCTG12892_s_at	AlamCTG12892	smart00219/Tyrosine kir SUBFAMILY NOT NAMED/6 /	/	LOC_Os01g21970.1	[13101.m02335]	protein/6E-75//	0.36	7.33E-09	0.39	2.63E-08	0.94	0.844390777	
AP13CTG01671_at	AP13CTG01671	PLN00221/tubulin, alpha FAMILY NOT NAMED/0	AT4G14960/Phagosc	LOC_Os07g38730.1	[13107.m04008]	protein/0/Phagosome/0	0.36	2.15E-32	0.39	3.21E-22	0.91	0.516770789	
AP13ITG38936_s_at	AP13ISTG38936	PHA03247/large tegume SUBFAMILY NOT NAMED/4 /	/	LOC_Os03g04710.1	[13103.m00491]	protein/7E-108//	0.36	1.27E-25	0.27	3.30E-36	1.36	0.099282184	
AP13ITG65721_at	AP13ISTG65721	//	/	///			0.36	1.78E-11	0.33	6.49E-15	1.08	0.754919161	
AP13ITG70020_at	AP13ISTG70020	COG0484/DnaJ-class mo OS05G0427900 PROTEIN/3 /	/	LOC_Os01g65480.1	[13101.m07075]	protein/4E-106//	0.36	3.14E-58	0.36	3.58E-246	0.99	0.916709498	
KanlowCTG09985_s_a	KanlCTG09985	PRK10811/ribonuclease /	/	///			0.36	5.42E-13	0.39	2.16E-20	0.92	0.650705217	
KanlowCTG16242_s_a	KanlCTG16242	TIGR01833/3-hydroxy-3- SUBFAMILY NOT NAMED/2	AT4G11820/Synthes	LOC_Os03g02710.1	[13103.m00242]	protein/1E-112/Synthesis and c	0.36	5.73E-13	0.4	5.02E-21	0.9	0.533177522	
KanlowCTG19450_s_a	KanlCTG19450	PLN00191/enolase/0 FAMILY NOT NAMED/1.6E-	AT2G36530/Glycolys	LOC_Os06g04510.1	[13106.m00409]	protein/0/Glycolysis / Gluconec	0.36	0	0.4	0	0.89	0.341308102	
KanlowCTG20720_s_a	KanlCTG20720	cd05032/Catalytic doma ANKYRIN-KINASE/2.4E-34 /	/	LOC_Os01g66860.3	[13101.m07243]	protein/3E-50//	0.36	0	0.37	0	0.98	0.484279147	
OTHSWCTG11406_s_a	OthsCTG11406	//	/	///			0.36	0	0.3	0	1.2	0.160579056	
AP13CTG11412_at	AP13CTG11412	pfam06027/Eukaryotic p DUF914/ANTHOCYANIN MI /	/	LOC_Os08g42720.1	[13108.m04615]	protein/1E-147//	0.37	0	0.29	0	1.26	0.153398673	
AP13CTG15858_at	AP13CTG15858	PLN02766/coniferyl-alde ALDEHYDE DEHYDROGENA: AT3G24503/Phenylp	LOC_Os01g40860.1	[13101.m04187]	protein/0/Phenylpropanoid bic	0.37	0	0.37	0	1	0.996484564		
AP13CTG24367_at	AP13CTG24367	pfam07522/DNA repair r FAMILY NOT NAMED/9.7E- /	/	LOC_Os01g57440.1	[13101.m06094]	protein/1E-164//	0.37	0	0.36	0	1.05	0.815039518	
AP13CTG24945_at	AP13CTG24945	pfam01466/Skp1 family, SKP1/5.9E-60	AT4G34210/Ubiquiti	LOC_Os07g43180.1	[13107.m04538]	protein/9E-26/Ubiquitin media	0.37	0	0.39	1.30E-42	0.95	0.036886728	
AP13ITG65828_s_at	AP13ISTG65828	pfam06376/Protein of ui /	/	LOC_Os02g16500.1	[13102.m01845]	protein/0.000000000000009//	0.37	0	0.28	0	1.33	0.319070164	
KanlowCTG21445_s_a	KanlCTG21445	pfam00249/Myb-like DN MYB DNA BINDING / TRAN: /	/	LOC_Os05g04820.1	[13105.m00495]	protein/6E-135//	0.37	5.44E-08	0.22	8.42E-83	1.66	0.000223093	
KanlowCTG44049_at	KanlCTG44049	//	/	/	LOC_Os04g51090.1	[13104.m05196]	protein/7E-99//	0.37	2.20E-26	0.34	2.07E-67	1.08	0.474559549
AlamoCTG07438_at	AlamCTG07438	PHA03245/large tegume /	/	LOC_Os01g62970.2	[13101.m06755]	protein/1E-29//	0.38	4.44E-16	0.4	2.44E-15	0.96	0.865124985	
AlamoCTG12062_s_at	AlamCTG12062	//	/	/	LOC_Os01g62970.2	[13101.m06755]	protein/0.003//	0.38	0	0.37	0	1.02	0.884124667
AP13CTG11451_s_at	AP13CTG11451	PLN02870/polygalacturo SUBFAMILY NOT NAMED/7	AT5G15470/Starch a	LOC_Os03g11330.1	[13103.m01277]	protein/0/Starch and sucrose n	0.38	0	0.31	3.50E-31	1.24	0	
AP13CTG22184RC_at	AP13CTG22184-RC	pfam01843/DIL domain. MYOSIN XI/1.8E-88 /	/	LOC_Os03g53660.1	[13103.m05865]	protein/3E-112//	0.38	4.28E-74	0.35	4.83E-97	1.08	0.380261259	
AP13CTG02233_s_at	AP13CTG02233	//	/	/	LOC_Os01g47050.1	[13101.m04843]	protein/0//	0.39	1.80E-77	0.29	0	1.33	2.12E-08
AP13CTG02287_s_at	AP13CTG02287	TIGR01833/3-hydroxy-3- SUBFAMILY NOT NAMED/1	AT4G11820/Synthes	LOC_Os03g02710.1	[13103.m00242]	protein/0/Synthesis and degrad	0.39	9.82E-29	0.38	1.49E-54	1.02	0.817694261	
AP13CTG30517_at	AP13CTG30517	//	/	///			0.39	1.60E-12	0.35	1.76E-67	1.1	0.328181502	
AP13ITG41401_at	AP13ISTG41401	PHA03247/large tegume /	/	LOC_Os01g07240.1	[13101.m00724]	protein/8E-20//	0.39	2.92E-36	0.35	7.26E-31	1.11	0.426551698	
AP13ITG77659_at	AP13ISTG77659	pfam04043/Plant invertz /	/	LOC_Os10g36500.2	[13110.m07835]	protein/6E-23//	0.39	0	0.16	0	2.47	0.0001787	
KanlowCTG03398_at	KanlCTG03398	//	/	/	LOC_Os01g02900.2	[13101.m00231]	protein/1E-173//	0.39	9.42E-11	0.32	6.21E-16	1.24	0.374596673
AP13CTG13387_at	AP13CTG13387	PLN02203/aldehyde deh ALDEHYDE DEHYDROGENA: AT4G36250/Glycolys	LOC_Os02g43194.1	[13102.m04795]	protein/0/Glycolysis / Gluconec	0.4	4.86E-09	0.36	5.45E-28	1.1	0.537334558		
KanlowCTG13385_s_a	KanlCTG13385	cd01812/Ubiquitin-like c OS09G0524800 PROTEIN/4 /	/	LOC_Os06g03640.1	[13106.m00300]	protein/8E-81//	0.4	0	0.35	0	1.13	0.437739097	
KanlowCTG31345_at	KanlCTG31345	PRK12323/DNA polymer FAMILY NOT NAMED/5.3E- /	/	LOC_Os01g37460.1	[13101.m03808]	protein/2E-61//	0.4	6.55E-38	0.4	2.63E-225	1	0.96664998	
KanlowCTG47138_s_a	KanlCTG47138	pfam01419/Jacalin-like I;JASMONATE INDUCIBLE PR /	/	LOC_Os05g43240.3	[13105.m04549]	protein/8E-108//	0.4	1.03E-09	0.35	2.18E-11	1.12	0.650503419	

The transcript ratios of targeted MTHFR and COMT genes were listed below.

AP13CTG11172_s_at	AP13CTG11172	//	METHYLENETHETRAHYDROF AT3G59970/One car LOC_Os03g60090.1	[13103.m06595]	protein/7E-101/One carbon po	0.44	1.28116E-22	0.64	1.13934E-09	0.69	0.000604736
KanlowCTG20791_s_a	KanlCTG20791	pfam00891/O-methyltra FAMILY NOT NAMED/8.9E-	AT5G54160/Flavone LOC_Os08g06100.1	[13108.m00605]	protein/1E-75/Flavone and flav	0.18	1.4477E-290	0.76	0.029673022	0.23	3.42E-146

Table S5. List of significantly DEGs in different pathways in four comparisons

List of significantly DEGs involved in hormone metabolism and development pathway in Exp/Ctrl comparison

Hormone		id	type	description	Exp/Ctrl (log2)
BinCode	BinName				
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos	ap13itg09951_s_at	Transcript	very weakly similar to (87.8) AT4G02780 Symbols: GA1, ABC33, ATPC51 GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase/ magnesium ion binding ch	2.283089
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos	ap13itg72235_s_at	Transcript	weakly similar to (197) loc_os04g09900 12004.m35118 protein ent-kaurene synthase A, chloroplast precursor, putative, expressed no original description	2.5106273
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (241) loc_os06g11210 12006.m	4.7242365
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDweakly similar to (167) loc_os06g11210 12006.m058:	3.2742903
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARDweakly similar to (1:	2.168549
Development		id	type	description	Exp/Ctrl (log2)
BinCode	BinName				
33.99	development.unspecified	ap13itg63590_at	Transcript	weakly similar to (198) loc_os01g51870 12001.m11363 protein S-adenosylmethionine-dependent methyltransferase, putative, expressed no original description	2.8097055
33.99	development.unspecified	ap13itg57467-rc_s_at	Transcript	very weakly similar to (88.6) AT5G48850 Symbols: ATSD11 ATSD11 (SULPHUR DEFICIENCY-INDUCED 1); binding chr5:19805576-19807699 REVERSEweakly simil	1.9713516
33.99	development.unspecified	ap13itg76686_at	Transcript	weakly similar to (151) AT5G48850 Symbols: ATSD11 ATSD11 (SULPHUR DEFICIENCY-INDUCED 1); binding chr5:19805576-19807699 REVERSEmoderately simil	1.8074428

List of significantly DEGs involved in signalling, hormone, cell and transport pathway in Mo/60 comparison

Signalling		id	type	description	Mo/60 (log2)
BinCode	BinName				
30.1	signalling.in sugar and nutrient physiology	ap13itg74992_at	Transcript	weakly similar to (117) loc_os02g54640 12002.m10493 protein glutamate receptor 2.9 precursor, putative, expressed no original description	1.119977
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	ap13itg61870_at	Transcript	weakly similar to (116) loc_os11g07240 12011.m04920 protein receptor protein kinase CLAVATA1 precursor, putative, expressed no original description	1.1316558
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg12119_at	Transcript	very weakly similar to (80.1) AT3G47580 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17532687-17535810 FORWARDweakly sir	1.0568756
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg27954_s_at	Transcript	weakly similar to (132) loc_os02g40180 12002.m09104 protein receptor-like protein kinase precursor, putative, expressed no original description	2.0184202
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	ap13ctg04179_at	Transcript	weakly similar to (105) loc_os01g65650 12001.m12674 protein receptor-like protein kinase 5 precursor, putative, expressed no original description	-1.9957428
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	kanlowctg42715_at	Transcript	weakly similar to (107) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARDmoderately sin	2.03235
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg19246_at	Transcript	very weakly similar to (84.0) AT3G47110 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17347103-17350296 REVERSEweakly simi	1.51942
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	ap13ctg16678_s_at	Transcript	very weakly similar to (81.3) AT5G48380 Symbols: leucine-rich repeat family protein / protein kinase family protein chr5:19604584-19606532 REVERSEweakly	1.0412167
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg17938_at	Transcript	weakly similar to (115) AT2G15080 Symbols: AtRLP19 AtRLP19 (Receptor Like Protein 19); kinase/ protein binding chr2:6533764-6536715 FORWARDweakly si	1.6272969
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg17630_at	Transcript	weakly similar to (174) loc_os02g40240 12002.m33414 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed no original descripti	1.6988038
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	ap13ctg50688_s_at	Transcript	weakly similar to (105) loc_os04g15630 12004.m06749 protein leucine-rich repeat receptor protein kinase EXS precursor, putative no original description	1.5420277
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	kanlowctg19800_s_at	Transcript	very weakly similar to (90.9) loc_os02g40180 12002.m09104 protein receptor-like protein kinase precursor, putative, expressed no original description	1.3183337
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswslt25490_at	Transcript	weakly similar to (114) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARDmoderately sin	1.2138089
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	ap13ctg03762_at	Transcript	weakly similar to (181) loc_os02g40240 12002.m33414 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed no original descripti	1.5610776
30.2.1.1	signalling.receptor kinases.leucine rich repeat XI	othswctg18100_at	Transcript	weakly similar to (131) loc_os11g36190 12011.m080025 protein receptor-like protein kinase 5 precursor, putative, expressed no original description	1.3126502
30.2.1.6	signalling.receptor kinases.Catharanthus roseus-like RLK1	ap13ctg04617_at	Transcript	weakly similar to (143) loc_os06g22810 12006.m06934 protein protein kinase, putative, expressed no original description	-1.1393493
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m060077 protein ATP binding protein, putative, expressed no original description	2.0351868
30.2.1.7	signalling.receptor kinases.DUF 26	othswctg18108_at	Transcript	very weakly similar to (97.8) AT1G11330 Symbols: S-locus lectin protein kinase family protein chr1:3810372-3813416 FORWARDweakly similar to (148) loc_os	1.9088267
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg69009_at	Transcript	very weakly similar to (90.1) AT4G23160 Symbols: protein kinase family protein chr4:12129485-12134086 FORWARDweakly similar to (166) loc_os05g39130	1.1350458
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg77404_s_at	Transcript	very weakly similar to (94.7) AT4G03230 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	1.5196985
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg39900_s_at	Transcript	very weakly similar to (91.3) loc_os12g14480 12012.m05416 protein ATP binding protein, putative no original description	2.5227633
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg76323_at	Transcript	weakly similar to (116) loc_os01g02390 12001.m42838 protein TAK14, putative, expressed no original description	2.8866818
30.2.1.7	signalling.receptor kinases.DUF 26	ap13itg47888_s_at	Transcript	very weakly similar to (86.7) loc_os11g11780 12011.m05370 protein serine/threonine protein kinase, putative, expressed no original description	-1.1535704
30.2.1.7	signalling.receptor kinases.DUF 26	ap13ctg07687_at	Transcript	weakly similar to (159) loc_os01g02800 12001.m06920 protein receptor-like kinase ARK1AS, putative, expressed no original description	1.2190235
30.2.1.7	signalling.receptor kinases.DUF 26	ap13ctg48706_at	Transcript	very weakly similar to (98.6) AT4G23130 Symbols: CRK5, RLK6 CRK5 (CYSTEINE-RICH RLK5); kinase chr4:12117688-12120134 REVERSEvery weakly similar to (8	3.9346542
30.2.1.7	signalling.receptor kinases.DUF 26	ap13ctg11071_s_at	Transcript	weakly similar to (102) loc_os07g35290 12007.m07785 protein receptor-like serine-threonine protein kinase, putative, expressed no original description	1.346304
30.2.1.7	signalling.receptor kinases.DUF 26	ap13ctg22926_at	Transcript	very weakly similar to (90.5) AT4G23180 Symbols: CRK10, RLK4 CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine ki	-1.065511
30.2.2.5	signalling.receptor kinases.wall associated kinase	ap13ctg19859_at	Transcript	weakly similar to (142) loc_os04g43730 12004.m09332 protein OsWAK51 - OsWAK receptor-like protein kinase, expressed no original description	1.6219307
30.2.2.5	signalling.receptor kinases.wall associated kinase	ap13ctg14697_s_at	Transcript	weakly similar to (162) loc_os04g03830 12004.m05691 protein OsWAK29 - OsWAK receptor-like protein kinase, expressed no original description	1.7394327
30.2.2.5	signalling.receptor kinases.wall associated kinase	othswctg14972_at	Transcript	weakly similar to (130) loc_os02g42150 12002.m09252 protein OsWAK14 - OsWAK receptor-like protein kinase, expressed no original description	3.268809
30.2.2.5	signalling.receptor kinases.wall associated kinase	alamoqtg14172_at	Transcript	very weakly similar to (88.6) loc_os02g42150 12002.m09252 protein OsWAK14 - OsWAK receptor-like protein kinase, expressed no original description	1.109805
30.2.2.5	signalling.receptor kinases.wall associated kinase	ap13ctg23391_at	Transcript	weakly similar to (116) loc_os03g62430 12003.m11119 protein OsWAK28 - OsWAK receptor-like protein kinase, expressed no original description	1.8729477
30.2.2.5	signalling.receptor kinases.wall associated kinase	ap13itg48098_at	Transcript	very weakly similar to (94.4) AT1G21230 Symbols: WAK5 WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase chr1:7429980-743234	-1.1851537
30.2.9.9	signalling.receptor kinases.misc	ap13itg77449-rc_rc	Transcript	weakly similar to (138) loc_os05g44970 12005.m08622 protein senescence-induced receptor-like serine/threonine-protein kinase precursor, putative no original c	1.7617186
30.2.9.9	signalling.receptor kinases.misc	ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m060077 protein ATP binding protein, putative, expressed no original description	2.0351868
30.2.9.9	signalling.receptor kinases.misc	kanlowctg38494_at	Transcript	very weakly similar to (95.9) AT2G28970 Symbols: leucine-rich repeat protein kinase, putative chr2:12443919-12448163 FORWARDweakly similar to (165) loc	1.0940689
30.2.9.9	signalling.receptor kinases.misc	ap13itg58665_at	Transcript	weakly similar to (132) AT2G28970 Symbols: leucine-rich repeat protein kinase, putative chr2:12443919-12448163 FORWARDweakly similar to (105) NOR	1.2050234
30.2.9.9	signalling.receptor kinases.misc	ap13itg48098_at	Transcript	very weakly similar to (94.4) AT1G21230 Symbols: WAK5 WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase chr1:7429980-743234	-1.1851537
30.3	signalling.calcium	ap13itg66751_s_at	Transcript	weakly similar to (117) AT2G18750 Symbols: calmodulin-binding protein chr2:8125827-8128363 FORWARDmoderately similar to (220) loc_os12g36920 1201	1.5560796
30.3	signalling.calcium	kanlowctg04099_s_at	Transcript	weakly similar to (104) AT1G27770 Symbols: ACA1, PEAT ACA1 (AUTO-INHIBITED CA2+-ATPASE 1); calcium channel/ calcium-transporting ATPase/ calmodulin t	1.0539427
30.3	signalling.calcium	ap13ctg14744_s_at	Transcript	weakly similar to (128) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed no original description	2.738117
30.3	signalling.calcium	ap13ctg08973_s_at	Transcript	very weakly similar to (81.6) AT4G37640 Symbols: ACA2 ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ cal	1.1298444
30.5	signalling.G-proteins	kanlowctg44370_s_at	Transcript	very weakly similar to (91.3) loc_os06g02130 12006.m31954 protein guanyl nucleotide binding protein, putative, expressed no original description	1.6158048
30.1	signalling.phosphorelay	ap13ctg09520_at	Transcript	very weakly similar to (100) AT3G16360 Symbols: AHP4 AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring pho:	-1.4311115
30.11.1	signalling.light.COP9 signalosome	ap13ctg07211_at	Transcript	very weakly similar to (96.7) loc_os07g26440 12007.m079669 protein CIP7, putative, expressed no original description	-1.7148267

Hormone					
BinCode	BinName	id	type	description	Mo/60 (log2)
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg71573-rc_at	Transcript	no original description	1.2041686
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg62309_at	Transcript	weakly similar to (172) AT1G60730 Symbols: aldo/keto reductase family protein chr1:22358613-22360082 REVERSEweakly similar to (115) A115_TOBAC Aux	2.3817716
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg58736_s_at	Transcript	very weakly similar to (85.5) loc_os09g37430 12009.m06690 protein OsSAUR48 - Auxin-responsive SAUR gene family member no original description	-1.8851447
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg42880-rc_at	Transcript	weakly similar to (114) loc_os01g67010 12001.m12806 protein expressed protein no original description	-1.200312
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg70591-rc_at	Transcript	weakly similar to (111) loc_os04g51890 12004.m10084 protein OsSAUR20 - Auxin-responsive SAUR gene family member, expressed no original description	2.8087711
17.5.1	hormone metabolism.ethylene.synthesis-degradation	ap13ctg10284_at	Transcript	very weakly similar to (85.1) loc_os08g32170 12008.m07211 protein oxidoreductase, putative, expressed no original description	-1.4918615
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphosphatase	ap13itg09951_s_at	Transcript	very weakly similar to (87.8) AT4G02780 Symbols: GA1, ABC33, ATPC51 GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase/ magnesium ion binding chr	2.7778554
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphosphatase	ap13itg72235_s_at	Transcript	weakly similar to (197) loc_os04g09900 12004.m35118 protein ent-kaurene synthase A, chloroplast precursor, putative, expressed no original description	3.394579
17.7.1.2	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	kanlowctg41234_at	Transcript	very weakly similar to (100) LOCXC_ORYSA Probable lipoxygenase 8, chloroplast precursor (EC 1.13.11.12) - Oryza sativa (Rice)very weakly similar to (100) loc_os0	2.234458
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation	kanlowctg26347_at	Transcript	very weakly similar to (89.7) AT3G11480 Symbols: BSMT1, ATBSMT1 BSMT1; S-adenosylmethionine-dependent methyltransferase chr3:3614544-3617137 FOI	2.5175083

Cell					
BinCode	BinName	id	type	description	Mo/60 (log2)
31.1	cell.organisation	kanlowctg17315_s_at	Transcript	very weakly similar to (91.7) AT1G17580 Symbols: MYA1, ATMYA1, XI-1 MYA1 (MYOSIN 1); motor/ protein binding chr1:6039453-6049309 FORWARDweakly s	-1.4481871
31.1	cell.organisation	ap13itg43667_s_at	Transcript	moderately similar to (204) loc_os09g27990 12009.m05950 protein fiber annexin, putative, expressed no original description	-1.2644771
31.1	cell.organisation	alamoctg04112_s_at	Transcript	very weakly similar to (87.0) loc_os02g56840 12002.m10706 protein phloem-specific lectin, putative, expressed no original description	-1.3655809
31.1	cell.organisation	ap13ctg07009-3_s_at	Transcript	weakly similar to (129) AT5G59370 Symbols: ACT4 ACT4 (ACTIN 4); structural constituent of cytoskeleton chr5:23950109-23951586 FORWARDweakly similar	-1.1168817
31.1	cell.organisation	ap13itg58453_s_at	Transcript	very weakly similar to (97.4) AT1G42550 Symbols: PM11 PM11 (PLASTID MOVEMENT IMPAIRED1) chr1:15977131-15979734 FORWARDweakly similar to (173)	1.1272439
31.1	cell.organisation	othswctg18861_at	Transcript	very weakly similar to (83.2) AT1G01750 Symbols: ADP11 ADP11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding chr1:275528-276126 FORWARDVery wei	-1.0301489
31.1	cell.organisation	ap13ctg09579_s_at	Transcript	very weakly similar to (83.2) loc_os02g56840 12002.m10706 protein phloem-specific lectin, putative, expressed no original description	-1.3673071
31.1	cell.organisation	kanlowctg39465_s_at	Transcript	weakly similar to (116) AT5G20490 Symbols: XIK, ATXIK, XI-17 XIK; motor/ protein binding chr5:6927064-6936079 REVERSEweakly similar to (173) loc_os03g!	-1.4964712
31.3	cell.cycle	ap13ctg04056_s_at	Transcript	very weakly similar to (92.4) loc_os05g33040 12005.m083714 protein PREG-like protein, putative, expressed no original description	1.1040965
31.3	cell.cycle	ap13ctg01864_s_at	Transcript	very weakly similar to (93.6) loc_os05g33040 12005.m083714 protein PREG-like protein, putative, expressed no original description	1.1424375
31.3.1	cell.cycle.peptidylprolyl isomerase	ap13ctg59022_at	Transcript	weakly similar to (153) AT4G38740 Symbols: ROC1 ROC1 (ROTAMASE CYP 1); peptidyl-prolyl cis-trans isomerase chr4:18083620-18084138 REVERSEweakly si	-1.8485379
31.4	cell.vesicle transport	ap13ctg01136_s_at	Transcript	very weakly similar to (100) AT5G50380 Symbols: ATEXO70F1 ATEXO70F1 (exocyst subunit EXO70 family protein F1); protein binding chr5:20516382-205184:	1.2529333

Transport					
BinCode	BinName	id	type	description	Mo/60 (log2)
34.2	transport.sugars	ap13ctg00637_at	Transcript	very weakly similar to (83.2) HEX6_RICCO Hexose carrier protein HEX6 - Ricinus communis (Castor bean)weakly similar to (112) loc_os10g41190 12010.m21970 pr	2.4313943
34.2	transport.sugars	ap13itg70211_at	Transcript	weakly similar to (158) AT3G20660 Symbols: AtOCT4 AtOCT4 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER4); carbohydrate transmembra	1.0388335
34.2	transport.sugars	ap13itg70443_s_at	Transcript	weakly similar to (143) AT4G02050 Symbols: sugar transporter, putative chr4:898387-900095 REVERSEweakly similar to (148) STA_RICCO Sugar carrier prote	-1.158267
34.2	transport.sugars	ap13ctg11906_s_at	Transcript	very weakly similar to (87.8) loc_os03g10510 12003.m35080 protein outer mitochondrial membrane protein porin, putative, expressed no original description	1.4663844
34.2	transport.sugars	ap13ctg20106_s_at	Transcript	weakly similar to (149) AT4G00370 Symbols: ANTR2, PHT4;4 ANTR2; inorganic phosphate transmembrane transporter/ organic anion transmembrane transpor	-1.4338477
34.3	transport.amino acids	kanlowctg08378_s_at	Transcript	weakly similar to (154) AT1G77380 Symbols: AAP3, ATAAP3 AAP3; amino acid transmembrane transporter chr1:29075201-29077252 REVERSEweakly similar	-1.2104665
34.3	transport.amino acids	ap13ctg18715_at	Transcript	weakly similar to (113) AT1G77380 Symbols: AAP3, ATAAP3 AAP3; amino acid transmembrane transporter chr1:29075201-29077252 REVERSEweakly similar	-1.1444991
34.3	transport.amino acids	ap13ctg10274_at	Transcript	weakly similar to (103) AT1G48640 Symbols: lysine and histidine specific transporter, putative chr1:17986358-17988991 FORWARDweakly similar to (118) lo	1.6404837
34.6	transport.sulphate	ap13itg48925_at	Transcript	very weakly similar to (80.5) AT1G78000 Symbols: SULTR1;2, SEL1 SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter chr1:29329889	-1.2702786
34.6	transport.sulphate	kanlowctg39328_s_at	Transcript	weakly similar to (123) loc_os03g09940 12003.m06448 protein low affinity sulphate transporter 3, putative, expressed no original description	-1.0337564
34.12	transport.metal	ap13ctg59129_at	Transcript	weakly similar to (105) loc_os01g61070 12001.m12234 protein heavy metal-associated domain containing protein, expressed no original description	-1.109565
34.12	transport.metal	ap13ctg02699rc_at	Transcript	very weakly similar to (98.2) loc_os05g10940 12005.m05564 protein zinc transporter 4, chloroplast precursor, putative, expressed no original description	-1.1010977
34.13	transport.peptides and oligopeptides	ap13ctg10045_s_at	Transcript	very weakly similar to (100) AT5G64410 Symbols: ATOPT4, OPT4 OPT4 (OLIGOPEPTIDE TRANSPORTER 4); oligopeptide transporter chr5:25750921-25754974	1.0626531
34.13	transport.peptides and oligopeptides	kanlowctg20886_s_at	Transcript	weakly similar to (134) AT1G65730 Symbols: YSL7 YSL7 (YELLOW STRIPE LIKE 7); oligopeptide transporter chr1:24442639-24446122 FORWARDweakly similar	1.3935986
34.14	transport.unspecified cations	ap13itg65313_s_at	Transcript	very weakly similar to (99.0) AT3G19640 Symbols: magnesium transporter CorA-like family protein (MRS2-3) chr3:6820969-6823104 FORWARDweakly similar	1.0777143
34.15	transport.potassium	othswslt24805_at	Transcript	weakly similar to (122) AT4G13420 Symbols: HAK5, ATHAK5 HAK5 (HIGH AFFINITY K+ TRANSPORTER 5); potassium ion transmembrane transporter/ potassium	1.1228445
34.16	transport.ABC transporters and multidrug resistance systems	othswslt36401_s_at	Transcript	very weakly similar to (95.5) AT3G60160 Symbols: ATMRP9 ATMRP9; ATPase, coupled to transmembrane movement of substances chr3:22223829-22229195	1.5637729
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg14418_at	Transcript	weakly similar to (113) AT1G15520 Symbols: PDR12, ATPDR12 PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of :	1.2239101
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg23219_s_at	Transcript	weakly similar to (129) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-22561575 FC	1.429423
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg38102_s_at	Transcript	weakly similar to (124) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-22561575 FC	1.4499054
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg47473rc_s_at	Transcript	weakly similar to (120) AT3G60160 Symbols: ATMRP9 ATMRP9; ATPase, coupled to transmembrane movement of substances chr3:22223829-22229195 REVE	1.1958963
34.16	transport.ABC transporters and multidrug resistance systems	othswctg17884rc_s_at	Transcript	weakly similar to (132) AT1G02520 Symbols: PGP11 PGP11 (P-GLYCOPROTEIN 11); ATPase, coupled to transmembrane movement of substances chr1:524134	1.0409052
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg12305_s_at	Transcript	very weakly similar to (95.9) AT3G43790 Symbols: ZIFL2 ZIFL2 (ZINC INDUCED FACILITATOR-like 2); carbohydrate transmembrane transporter/ sugar/hydrogen s	2.0609794
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg11369-1_s_at	Transcript	very weakly similar to (84.0) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-225615	1.2177197
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg15102_s_at	Transcript	weakly similar to (133) AT1G66950 Symbols: PDR11, ATPDR11 PDR11 (PLEIOTROPIC DRUG RESISTANCE 11); ATPase, coupled to transmembrane movement of :	3.3915749
34.99	transport.misc	othswctg19026_s_at	Transcript	weakly similar to (135) AT1G20925 Symbols: auxin efflux carrier family protein chr1:7290612-7292507 FORWARDweakly similar to (165) loc_os09g31478 120	1.2368882
34.99	transport.misc	kanlowctg12598_s_at	Transcript	weakly similar to (133) AT1G01630 Symbols: SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative chr1:229206-230675 FORWARDw	2.9746048

List of significantly DEGs involved in hormone, transport, misc and major CHO pathway in Se/60 comparison

Hormone					
BinCode	BinName	id	type	description	Se/60 (log2)
17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	ap13itg64998_at	Transcript	very weakly similar to (95.1) loc_os04g46470 12004.m09596 protein dioxigenase RAMOSU55, putative, expressed no original description	1.784
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg71573-rc_at	Transcript	no original description	2.353
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg62309_at	Transcript	weakly similar to (172) AT1G60730 Symbols: aldo/keto reductase family protein chr1:22358613-22360082 REVERSEweakly similar to (115) A115_TOBAC Aux	2.472
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg58736_s_at	Transcript	very weakly similar to (85.5) loc_os09g37430 12009.m06690 protein OsSAUR48 - Auxin-responsive SAUR gene family member no original description	-1.785
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg42880-rc_at	Transcript	very weakly similar to (93.6) GH312_ORYSA Probable indole-3-acetic acid-amido synthetase GH3.12 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 12) (OsGH3-12)	-1.134
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	kanlowctg33522_at	Transcript	weakly similar to (138) AT1G60730 Symbols: aldo/keto reductase family protein chr1:22358613-22360082 REVERSEweakly similar to (106) A115_TOBAC Aux	2.143
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13itg70591-rc_at	Transcript	weakly similar to (111) loc_os04g51890 12004.m10084 protein OsSAUR20 - Auxin-responsive SAUR gene family member, expressed no original description	3.184
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13ctg17086_at	Transcript	weakly similar to (103) IAA6_ORYSA Auxin-responsive protein IAA6 (Indoleacetic acid-induced protein 6) - Oryza sativa (Rice)weakly similar to (103) loc_os01g538:	2.052

17.3.1.2.8	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.D\ap13ctg15125_s_at	Transcript	weakly similar to (195) AT3G19820 Symbols: DWF1, DIM, EVE1, DIM1, CBB1 DWF1 (DWARF 1); calmodulin binding / catalytic chr3:6879835-6881616 REVERSI	1.596
17.5.1	hormone metabolism.ethylene.synthesis-degradation.ap13itg74891-rc_at	Transcript	weakly similar to (196) AT1G06620 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:2025618-2027094 FORWARDweakly similar to (187) DV4	1.023
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos\otshwctg09951_s_at	Transcript	very weakly similar to (87.8) AT4G02780 Symbols: GA1, ABC33, ATPC51 GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase/ magnesium ion binding ch	2.333
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos\otshwctg07572_at	Transcript	weakly similar to (105) loc_os02g17780 12002.m07022 protein ent-kaurene synthase A, chloroplast precursor, putative, expressed no original description	2.139
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos\ap13itg72235_s_at	Transcript	weakly similar to (197) loc_os04g09900 12004.m35118 protein ent-kaurene synthase A, chloroplast precursor, putative, expressed no original description	2.274
17.6.1.3	hormone metabolism.gibberelin.synthesis-degradation.ent-kaurene ox kanlowctg40278_s_at	Transcript	weakly similar to (136) AT5G25900 Symbols: GA3, CYP701A3, ATK01 GA3 (GA REQUIRING 3); ent-kaurene oxidase/ oxygen binding chr3:9036073-9038278 FC	2.266
17.7.1.2	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase.ap13itg70317_at	Transcript	weakly similar to (143) AT3G45140 Symbols: LOX2, ATLOX2 LOX2 (LIPOXYGENASE 2); lipoxygenase chr3:16525437-16529233 FORWARDweakly similar to (19	2.746
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r\kanlowctg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (241) loc_os06g11210 12006.m	5.946
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r\ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDweakly similar to (167) loc_os06g11210 12006.m058:	4.576
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r\ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARDweakly similar to (1;	3.127
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r\ap13itg69033_at	Transcript	weakly similar to (162) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (220) loc_os06g11290 12006.m	2.318
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation.kanlowctg26347_at	Transcript	very weakly similar to (89.7) AT3G11480 Symbols: BSMT1, ATBSMT1 BSMT1; S-adenosylmethionine-dependent methyltransferase chr3:3614544-3617137 FOI	2.935
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation.ap03ctg19731_s_at	Transcript	weakly similar to (119) AT3G11480 Symbols: BSMT1, ATBSMT1 BSMT1; S-adenosylmethionine-dependent methyltransferase chr3:3614544-3617137 FORWA	1.674

Transport

BinCode	BinName	id	type	description	Se/60 (log2)
34.2	transport.sugars	ap13itg70443_s_at	Transcript	weakly similar to (143) AT4G02050 Symbols: sugar transporter, putative chr4:898387-900095 REVERSEweakly similar to (148) STA_RICCO Sugar carrier prote	-1.4809461
34.3	transport.amino acids	ap13ctg25184_s_at	Transcript	weakly similar to (134) loc_os04g38680 12004.m08857 protein amino acid/polyamine transporter II, putative, expressed no original description	2.2175243
34.6	transport.sulphate	ap13ctg19867_at	Transcript	weakly similar to (107) AT1G22150 Symbols: SULTR1.3 SULTR1.3; sulfate transmembrane transporter chr1:7818361-7821344 FORWARDweakly similar to (11	1.7543813
34.6	transport.sulphate	kanlowctg46743_s_at	Transcript	very weakly similar to (96.3) loc_os01g52130 12001.m11387 protein sulfate transporter 3.5, putative, expressed no original description	2.3649237
34.12	transport.metal	ap13ctg25265_s_at	Transcript	very weakly similar to (95.5) AT1G63440 Symbols: HMA5 HMA5 (HEAVY METAL ATPASE 5); ATPase, coupled to transmembrane movement of ions, phosphoryla	-1.46212
34.12	transport.metal	ap13itg53636_s_at	Transcript	very weakly similar to (100) AT1G80830 Symbols: NRAMP1, PMIT1, ATNRAMP1 NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inor	-1.0665691
34.13	transport.peptides and oligopeptides	ap13ctg13702_s_at	Transcript	very weakly similar to (82.4) AT4G10770 Symbols: ATOPT7, OPT7 OPT7 (OLIGOPEPTIDE TRANSPORTER 7); oligopeptide transporter chr4:6628646-6632517 RE	2.3295274
34.15	transport.potassium	kanlowctg10065_at	Transcript	very weakly similar to (98.2) loc_os01g70490 12001.m13096 protein potassium transporter 5, putative, expressed no original description	3.421157
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg24230_at	Transcript	very weakly similar to (93.6) AT3G62150 Symbols: PGP21 PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances chr3:23	3.3023396
34.16	transport.ABC transporters and multidrug resistance systems	otshwslt36401_s_at	Transcript	very weakly similar to (95.5) AT3G60160 Symbols: ATMRP9 ATMRP9; ATPase, coupled to transmembrane movement of substances chr3:22223829-22229195	2.6775858
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg27505_s_at	Transcript	very weakly similar to (81.3) AT5G52050 Symbols: MATTE efflux protein-related chr5:21138933-21140450 FORWARDweakly similar to (119) loc_os04g48290 1	-1.0269383
34.16	transport.ABC transporters and multidrug resistance systems	otshwctg05668_s_at	Transcript	very weakly similar to (81.3) loc_os12g22284 12012.m06072 protein ATP-binding cassette sub-family G member 2, putative, expressed no original description	-1.1764
34.16	transport.ABC transporters and multidrug resistance systems	ap13itg73678_at	Transcript	weakly similar to (125) loc_os08g43120 12008.m08288 protein ABC transporter, putative, expressed no original description	-1.6854094
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg45231_s_at	Transcript	weakly similar to (138) AT5G61700 Symbols: ATATH16, ATH16 ATATH16; ATPase, coupled to transmembrane movement of substances / transporter chr5:24;	2.4373958
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg20944_at	Transcript	moderately similar to (271) AT4G18050 Symbols: PGP9 PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to transmembrane movement of substances chr4:10022	3.7330322
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg07825_at	Transcript	weakly similar to (146) AT2G28070 Symbols: ABC transporter family protein chr2:11956432-11959782 FORWARDweakly similar to (188) loc_os03g64200 12c	1.0885959
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg30924_x_at	Transcript	weakly similar to (106) PDR2_ORYSA Probable pleiotropic drug resistance protein 2 - Oryza sativa (Rice)weakly similar to (106) loc_os01g42370 12001.m10503 pr	1.8209134
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg24230_s_at	Transcript	moderately similar to (213) AT4G18050 Symbols: PGP9 PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to transmembrane movement of substances chr4:10022	3.2684987
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg23219_s_at	Transcript	weakly similar to (129) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-22561575 FC	2.278649
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg38102_s_at	Transcript	weakly similar to (124) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-22561575 FC	2.5144386
34.16	transport.ABC transporters and multidrug resistance systems	ap13itg73678rc_s_at	Transcript	very weakly similar to (95.5) loc_os08g43120 12008.m08288 protein ABC transporter, putative, expressed no original description	-1.2439208
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg47473rc_s_a	Transcript	weakly similar to (120) AT3G60160 Symbols: ATMRP9 ATMRP9; ATPase, coupled to transmembrane movement of substances chr3:22223829-22229195 REVE	1.8580594
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg11369-1_s_at	Transcript	very weakly similar to (84.0) AT3G60970 Symbols: ATMRP15 ATMRP15; ATPase, coupled to transmembrane movement of substances chr3:22557535-225615	1.9506253
34.16	transport.ABC transporters and multidrug resistance systems	ap13ctg12939-2_at	Transcript	very weakly similar to (87.8) loc_os01g52550 12001.m11428 protein multidrug resistance protein 22, putative, expressed no original description	1.6844735
34.16	transport.ABC transporters and multidrug resistance systems	kanlowctg38775_s_at	Transcript	weakly similar to (155) AT3G47760 Symbols: ATATH4, ATH4 ATATH4; ATPase, coupled to transmembrane movement of substances / transporter chr3:176117	1.8283375
34.16	transport.ABC transporters and multidrug resistance systems	ap13itg61011_at	Transcript	weakly similar to (156) AT4G01830 Symbols: PGPS PGPS (P-GLYCOPROTEIN 5); ATPase, coupled to transmembrane movement of substances chr4:785683-79	1.834321
34.16	transport.ABC transporters and multidrug resistance systems	kanlowslt56395_at	Transcript	weakly similar to (109) AT4G18050 Symbols: PGP9 PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to transmembrane movement of substances chr4:10022205:	3.5532231
34.99	transport.misc	kanlowctg46528_s_at	Transcript	weakly similar to (114) AT5G52450 Symbols: MATTE efflux protein-related chr5:21289042-21291749 REVERSEweakly similar to (156) loc_os10g11354 12010.r	2.378194
34.99	transport.misc	ap13ctg27505_s_at	Transcript	very weakly similar to (81.3) AT5G52050 Symbols: MATTE efflux protein-related chr5:21138933-21140450 FORWARDweakly similar to (119) loc_os04g48290 12	-1.0269383
34.99	transport.misc	otshwctg19026_s_at	Transcript	weakly similar to (135) AT1G20925 Symbols: auxin efflux carrier family protein chr1:7290612-7292507 FORWARDweakly similar to (165) loc_os09g31478 12c	2.0320575
34.99	transport.misc	ap13itg52747_s_at	Transcript	very weakly similar to (96.3) AT5G65980 Symbols: G auxin efflux carrier family protein chr5:26392444-26394232 FORWARDweakly similar to (120) loc_os09g38	1.7859634
34.99	transport.misc	kanlowctg12598_s_at	Transcript	weakly similar to (133) AT1G01630 Symbols: SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative chr1:229206-230675 FORWARDw	3.1054966

Misc

BinCode	BinName	id	type	description	Se/60 (log2)
26.1	misc.misc2	ap13ctg15239_at	Transcript	weakly similar to (116) loc_os10g35500 12010.m06374 protein epoxide hydrolase, putative, expressed no original description	1.9422607
26.1	misc.misc2	ap13itg58554_at	Transcript	very weakly similar to (85.9) loc_os05g33110 12005.m083715 protein endo-1,3,1,4-beta-D-glucanase precursor, putative, expressed no original description	3.5439093
26.1	misc.misc2	ap13ctg11976_s_at	Transcript	very weakly similar to (87.8) C71C2_MAIZE Cytochrome P450 71C2 (EC 1.14.-.) (Benzoxazinellness 3) - Zea mays (Maize)weakly similar to (104) loc_os06g22020 120	1.6060661
26.1	misc.misc2	ap13itg73544_at	Transcript	weakly similar to (140) loc_os10g35500 12010.m06374 protein epoxide hydrolase, putative, expressed no original description	2.6115177
26.1	misc.misc2	ap13itg62754_s_at	Transcript	very weakly similar to (81.3) AT3G23600 Symbols: dienelactone hydrolase family protein chr3:8473833-8475655 FORWARDweakly similar to (105) loc_os05g:	2.6760173
26.1	misc.misc2	ap13ctg56716_at	Transcript	weakly similar to (144) loc_os10g35500 12010.m06374 protein epoxide hydrolase, putative, expressed no original description	1.0979897
26.1	misc.misc2	ap13ctg12203_at	Transcript	weakly similar to (112) AT4G19185 Symbols: integral membrane family protein chr4:10489201-10491488 REVERSEweakly similar to (157) loc_os06g49500 1:	2.7201333
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg60355_at	Transcript	weakly similar to (151) AT1G22370 Symbols: ATUGT85A5 ATUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glyco	-1.5335133
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg65392_at	Transcript	very weakly similar to (100) loc_os05g08750 12005.m05389 protein cold-induced glucosyl transferase, putative, expressed no original description	1.521799
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg67351_at	Transcript	very weakly similar to (93.2) CZOG2_MAIZE Cis-zeatin O-glucosyltransferase 2 (EC 2.4.1.215) (cisZOG2) - Zea mays (Maize)very weakly similar to (87.8) loc_os04g46	1.0609822
26.2	misc.UDP glucosyl and glucuronyl transferases	kanlowctg46878_s_at	Transcript	weakly similar to (145) AT4G02500 Symbols: ATXT2, XXT2, XT2 XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase, transferri	-1.075472
26.2	misc.UDP glucosyl and glucuronyl transferases	kanlowctg42845_s_at	Transcript	very weakly similar to (92.8) AT2G38650 Symbols: GAUT7, LG77 GAUT7 (GALACTURONOSYLTRANSFERASE 7); polygalacturonate 4-alpha-galacturonosyltransfer	-1.0060872
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg67222_at	Transcript	weakly similar to (146) loc_os10g07970 12010.m0410 protein anthocyanidin 5,3-O-glucosyltransferase, putative, expressed no original description	1.2526202
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg62195_at	Transcript	weakly similar to (117) AT3G02100 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr3:368840-370484 REVERSEvery weakly similar to (	1.2497023
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg68735_at	Transcript	weakly similar to (107) AT4G01070 Symbols: GT72B1, UGT72B1 GT72B1; UDP-glucosyltransferase/ UDP-glucosyltransferase/ transferase, transferring glucosyl g	1.0957323
26.2	misc.UDP glucosyl and glucuronyl transferases	kanlowctg41220_s_at	Transcript	very weakly similar to (95.5) loc_os06g13760 12006.m06091 protein transferase, transferring glycosyl groups, putative, expressed no original description	-1.2659137
26.2	misc.UDP glucosyl and glucuronyl transferases	kanlowctg23500_s_at	Transcript	weakly similar to (125) AT1G07240 Symbols: UGT71C5 UGT71C5 (UDP-GLUCOSYL TRANSFERASE 71C5); UDP-glucosyltransferase/ quercetin 3-O-glucosyltransfe	1.5789853
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg75785rc_at	Transcript	moderately similar to (202) AT1G05680 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:1703196-1704639 REVERSEweakly similar t	2.163164
26.2	misc.UDP glucosyl and glucuronyl transferases	ap13itg74837_at	Transcript	very weakly similar to (95.1) AT1G01390 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:148319-149761 REVERSEweakly similar to (	3.7462993
26.2	misc.UDP glucosyl and glucuronyl transferases	kanlowctg14906_s_at	Transcript	weakly similar to (119) loc_os01g45110 12001.m10717 protein cytokinin-O-glucosyltransferase 1, putative, expressed no original description	2.3178332

26.2	misc.UDP glucosyl and glucoronyl transferases	ap13itg47952_s_at	Transcript	weakly similar to (117) loc_os03g55050 12003.m10421 protein cytokinin-O-glucosyltransferase 2, putative, expressed no original description	2.4126816
26.2	misc.UDP glucosyl and glucoronyl transferases	ap13ctg09529_at	Transcript	weakly similar to (162) AT1G05680 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:1703196-1704639 REVERSEweakly similar to (14	3.837729
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg22294_at	Transcript	weakly similar to (137) loc_os01g16310 12001.m08227 protein glycosyl hydrolases family 31 protein, expressed no original description	3.1825423
26.3	misc.gluco-, galacto- and mannosidases	alamoctg05610_at	Transcript	very weakly similar to (89.7) loc_os10g05069 12010.m20212 protein lysosomal alpha-mannosidase precursor, putative, expressed no original description	-2.55163
26.3	misc.gluco-, galacto- and mannosidases	othswctg11061_at	Transcript	weakly similar to (150) AT1G61820 Symbols: BGLU46 BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compound:	-1.4892396
26.3	misc.gluco-, galacto- and mannosidases	ap13ctg34009_s_at	Transcript	weakly similar to (111) AT4G27820 Symbols: BGLU9 BGLU9 (BETA GLUCOSIDASE 9); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds c	3.4901724
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg08905_s_at	Transcript	weakly similar to (108) loc_os05g30350 12005.m27797 protein non-cyanogenic beta-glucosidase precursor, putative, expressed no original description	3.3038359
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg19994_s_at	Transcript	very weakly similar to (100) AT4G21760 Symbols: BGLU47 BGLU47 (beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compoun	2.0472379
26.3	misc.gluco-, galacto- and mannosidases	ap13itg52053_s_at	Transcript	very weakly similar to (82.0) AT1G61810 Symbols: BGLU45 BGLU45 (BETA-GLUCOSIDASE 45); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl comp	3.2846618
26.3.2	misc.gluco-, galacto- and mannosidases.beta-galactosidase	ap13ctg00450_s_at	Transcript	weakly similar to (106) AT2G32810 Symbols: BGAL9 BGAL9 (Beta galactosidase 9); beta-galactosidase/ catalytic/ cation binding / sugar binding chr2:1391941f	1.6042432
26.3.4	misc.gluco-, galacto- and mannosidases.endoglucanase	kanlowctg19895_x_at	Transcript	weakly similar to (152) AT5G49720 Symbols: ATGH9A1, DEC, KOR, RSW2, IRX2, KOR1 ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase	1.6259547
26.4	misc.beta 1,3 glucan hydrolases	ap13itg58279_s_at	Transcript	weakly similar to (122) AT3G07320 Symbols: glycosyl hydrolase family 17 protein chr3:2332324-2333925 REVERSEweakly similar to (177) loc_os09g32550 12	1.6846392
26.4.1	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase	ap13itg70254_at	Transcript	weakly similar to (113) AT4G16260 Symbols: catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds chr4:9200180-9201441 REVERSEweakly	2.7916436
26.4.1	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase	ap13itg5652_at	Transcript	weakly similar to (122) AT3G57260 Symbols: BGL2, PR2, BG2, PR-2 BGL2 (BETA-1,3-GLUCANASE 2); cellulase/ glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzi	1.9357486
26.7	misc.oxidases - copper, flavone etc	kanlowctg47289_s_at	Transcript	weakly similar to (107) loc_os03g05900 12003.m101192 protein monooxygenase, putative, expressed no original description	3.107287
26.7	misc.oxidases - copper, flavone etc	kanlowctg44665_s_at	Transcript	weakly similar to (108) loc_os03g05900 12003.m101192 protein monooxygenase, putative, expressed no original description	2.4343748
26.7	misc.oxidases - copper, flavone etc	ap13ctg04320_at	Transcript	weakly similar to (155) loc_os04g14690 12004.m06706 protein monooxygenase/ oxidoreductase, putative, expressed no original description	1.1771873
26.7	misc.oxidases - copper, flavone etc	ap13ctg02095_at	Transcript	weakly similar to (103) loc_os09g37620 12009.m06709 protein monooxygenase/ oxidoreductase, putative, expressed no original description	2.7133992
26.8	misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline oxi	kanlowctg36954_at	Transcript	very weakly similar to (91.3) AT2G29330 Symbols: TRI TRI (tropinone reductase); binding / catalytic/ oxidoreductase chr2:12594604-12596196 FORWARDwea	1.3482957
26.9	misc.glutathione S transferases	ap13ctg18609_at	Transcript	very weakly similar to (91.3) AT3G55040 Symbols: GSTL2 GSTL2 chr3:20398718-20400305 REVERSEvery weakly similar to (97.4) IN21_MAIZE IN2-1 protein - Ze	3.4394202
26.9	misc.glutathione S transferases	ap13itg59978_at	Transcript	very weakly similar to (82.0) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)weakly simil	1.8530868
26.9	misc.glutathione S transferases	ap13itg52395_s_at	Transcript	very weakly similar to (89.7) AT1G10370 Symbols: GST30, ATGSTU17, GST30B, ERD9 ERD9 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase c	2.6250345
26.9	misc.glutathione S transferases	ap13ctg04320_at	Transcript	weakly similar to (116) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)weakly similar to i	2.3023114
26.9	misc.glutathione S transferases	ap13itg64056_at	Transcript	weakly similar to (107) loc_os10g38340 12010.m06607 protein glutathione S-transferase GSTU6, putative, expressed no original description	2.9521643
26.9	misc.glutathione S transferases	ap13ctg24964_at	Transcript	very weakly similar to (93.6) AT3G62760 Symbols: ATGSTF13 ATGSTF13; glutathione transferase chr3:23217425-23218246 REVERSEweakly similar to (135) G	1.6238625
26.9	misc.glutathione S transferases	ap13ctg16606_s_at	Transcript	very weakly similar to (90.5) AT3G55040 Symbols: GSTL2 GSTL2 chr3:20398718-20400305 REVERSEweakly similar to (149) IN21_MAIZE IN2-1 protein - Zea m	1.6981143
26.9	misc.glutathione S transferases	ap13itg54282_at	Transcript	very weakly similar to (92.4) AT3G62760 Symbols: ATGSTF13 ATGSTF13; glutathione transferase chr3:23217425-23218246 REVERSEweakly similar to (164) G	1.7701411
26.1	misc.cytochrome P450	ap13itg42917_at	Transcript	weakly similar to (142) AT2G45560 Symbols: CYP76C1 CYP76C1; electron carrier/ heme binding / iron ion binding / monooxygenase chr2:18777240-1877835	1.3938608
26.1	misc.cytochrome P450	ap13ctg16768_at	Transcript	weakly similar to (149) AT2G46950 Symbols: CYP709B2 CYP709B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr2:3	-1.2707354
26.1	misc.cytochrome P450	ap13itg72766_at	Transcript	weakly similar to (125) AT5G36130 Symbols: cytochrome P450 family chr5:14209293-14209811 REVERSEvery weakly similar to (87.8) Q9002_ORYSA Cytochr	1.8341962
26.1	misc.cytochrome P450	ap13ctg15593_s_at	Transcript	very weakly similar to (89.7) AT3G14620 Symbols: CYP72A8 CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr	4.025958
26.1	misc.cytochrome P450	kanlowctg40278_at	Transcript	weakly similar to (136) AT5G25900 Symbols: GA3, CYP701A3, ATK01 GA3 (GA REQUIREING 3); ent-kaurene oxidase/ oxygen binding chr5:9036073-9038278 FC	2.2658863
26.1	misc.cytochrome P450	kanlowctg47117_s_at	Transcript	weakly similar to (130) AT3G26300 Symbols: CYP71B34 CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr3:5	2.586461
26.1	misc.cytochrome P450	kanlowctg47529_s_at	Transcript	very weakly similar to (85.5) loc_os04g10160 12004.m06268 protein cytochrome P450 CYP99A1, putative, expressed no original description	2.5708113
26.1	misc.cytochrome P450	ap13ctg11976_s_at	Transcript	very weakly similar to (87.8) C71C2_MAIZE Cytochrome P450 71C2 (EC 1.14.-.) (Benzoxazinediol 3) - Zea mays (Maize)weakly similar to (104) loc_os06g22020 120	1.6006612
26.1	misc.cytochrome P450	ap13itg70557_s_at	Transcript	weakly similar to (124) AT1G01190 Symbols: CYP78A8 CYP78A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:83f	-1.4512961
26.1	misc.cytochrome P450	kanlowctg21384_x_at	Transcript	weakly similar to (123) AT3G26160 Symbols: CYP71B17 CYP71B17; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:83c	2.4542496
26.1	misc.cytochrome P450	ap13itg67659_at	Transcript	weakly similar to (122) AT1G11610 Symbols: CYP71A18 CYP71A18; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:3	1.6206986
26.1	misc.cytochrome P450	ap13ctg18744_at	Transcript	weakly similar to (157) AT2G46950 Symbols: CYP709B2 CYP709B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr2:3	-1.2985505
26.11	misc.alcohol dehydrogenases	ap13itg56240_at	Transcript	weakly similar to (156) AT4G22110 Symbols: alcohol dehydrogenase, putative chr4:11711422-11713946 REVERSEweakly similar to (101) ADHX_ORYSA Alcoh	2.606027
26.12	misc.peroxidases	ap13ctg09437_at	Transcript	very weakly similar to (89.0) PER2_ORYSA Peroxidase 2 precursor (EC 1.11.1.7) - Oryza sativa (Rice)very weakly similar to (91.3) loc_os07g48040 12007.m09019 pr	4.4435215
26.12	misc.peroxidases	ap13ctg01107_at	Transcript	weakly similar to (139) AT1G68850 Symbols: peroxidase, putative chr1:25883806-25885177 REVERSEvery weakly similar to (80.9) PER2_ORYSA Peroxidase 2	1.0435702
26.12	misc.peroxidases	kanlowctg26782_s_at	Transcript	weakly similar to (155) AT5G05340 Symbols: peroxidase, putative chr5:1579142-1580819 REVERSEweakly similar to (164) PER2_ORYSA Peroxidase 2 precurs	-2.5861895
26.13	misc.acid and other phosphatases	kanlowctg21816_s_at	Transcript	weakly similar to (113) AT4G29260 Symbols: acid phosphatase class B family protein chr4:14422310-14423409 REVERSEweakly similar to (122) VSPA_SOYBN	2.1954758
26.13	misc.acid and other phosphatases	ap13itg70120_at	Transcript	weakly similar to (128) AT4G29260 Symbols: acid phosphatase class B family protein chr4:14422310-14423409 REVERSEweakly similar to (144) VSPA_SOYBN	1.8381319
26.13	misc.acid and other phosphatases	ap13ctg24864_s_at	Transcript	weakly similar to (132) AT3G18220 Symbols: phosphatidic acid phosphatase family protein / PAP2 family protein chr3:6248355-6249799 FORWARDweakly sir	1.2430536
26.16	misc.myrosinases-lectin-jacalin	ap13ctg22520_at	Transcript	weakly similar to (105) AT2G37710 Symbols: RLK RLK (receptor lectin kinase); kinase chr2:15814934-15816961 REVERSEweakly similar to (191) loc_os09g095	2.909293
26.16	misc.myrosinases-lectin-jacalin	ap13itg61865_s_at	Transcript	weakly similar to (133) AT1G19715 Symbols: jacalin lectin family protein chr1:6816934-6819244 REVERSEmoderately similar to (226) loc_os05g43240 12005.	-1.1359279
26.16	misc.myrosinases-lectin-jacalin	kanlowctg44153_s_at	Transcript	weakly similar to (152) AT1G19715 Symbols: jacalin lectin family protein chr1:6816934-6819244 REVERSEmoderately similar to (208) loc_os05g43240 12005.	-1.0720758
26.16	misc.myrosinases-lectin-jacalin	ap13itg71141_at	Transcript	weakly similar to (105) AT4G02420 Symbols: lectin protein kinase, putative chr4:1064363-1066372 REVERSEweakly similar to (150) loc_os12g26940 12012.r	2.509205
26.16	misc.myrosinases-lectin-jacalin	ap13ctg52756_s_at	Transcript	weakly similar to (144) AT3G53810 Symbols: lectin protein kinase, putative chr3:19933153-19935186 REVERSEmoderately similar to (221) loc_os07g03900 1	1.3268741
26.16	misc.myrosinases-lectin-jacalin	othswctg17780_at	Transcript	weakly similar to (113) AT1G19715 Symbols: jacalin lectin family protein chr1:6816934-6819244 REVERSEweakly similar to (162) loc_os05g43240 12005.m08	-1.0945748
26.16	misc.myrosinases-lectin-jacalin	ap13ctg08614_s_at	Transcript	weakly similar to (135) loc_os07g03900 12007.m04860 protein lectin-like receptor kinase 7, putative no original description	1.2371218
26.16	misc.myrosinases-lectin-jacalin	ap13itg69554_at	Transcript	weakly similar to (123) AT4G19840 Symbols: ATPP2-A1, ATPP2A-1, PP2-A1 ATPP2-A1; carbohydrate binding chr4:10774336-10775701 FORWARDweakly simil	-1.1787097
26.17	misc.dynamnin	alamoctg05018_s_at	Transcript	weakly similar to (162) AT3G60190 Symbols: ADL4, ADLP2, ED3, DRP1E, ADL1E ADL1E (ARABIDOPSIS DYNAMIN-LIKE 1E); GTP binding / GTPase chr3:222443f	1.7328136
26.19	misc.plastocyanin-like	ap13itg68926_at	Transcript	very weakly similar to (94.0) AT2G32300 Symbols: UCC1 UCC1 (UCLACYANIN 1); copper ion binding / electron carrier chr2:13722510-13723464 FORWARDwea	2.5588279
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family	kanlowctg30642_s_at	Transcript	very weakly similar to (84.7) AT3G22142 Symbols: structural constituent of cell wall chr3:7803604-7808046 REVERSEweakly similar to (120) loc_os04g52260 :	-1.1937379
26.22	misc.short chain dehydrogenase/reductase (SDR)	ap13ctg04703_at	Transcript	weakly similar to (142) AT5G04900 Symbols: short-chain dehydrogenase/reductase (SDR) family protein chr5:1434826-1437194 FORWARDweakly similar to (	1.2028159
26.22	misc.short chain dehydrogenase/reductase (SDR)	ap13itg39602_s_at	Transcript	weakly similar to (121) loc_os04g45000 12004.m35391 protein short-chain dehydrogenase/reductase SDR, putative, expressed no original description	1.6323588
26.22	misc.short chain dehydrogenase/reductase (SDR)	ap13itg69277_at	Transcript	weakly similar to (112) loc_os04g44924 12004.m101862 protein short-chain dehydrogenase/reductase SDR, putative, expressed no original description	3.1048453
26.24	misc.GCN5-related N-acetyltransferase	ap13itg61578_at	Transcript	weakly similar to (128) AT2G32030 Symbols: GCN5-related N-acetyltransferase (GNAT) family protein chr2:13632675-13633241 REVERSEweakly similar to (1	4.6877933
26.28	misc.GDSL-motif lipase	ap13ctg04366_s_at	Transcript	weakly similar to (172) AT1G54790 Symbols: GDSL-motif lipase/hydrolase family protein chr1:20441124-20443997 REVERSEvery weakly similar to (94.4) EST_	-1.082419
26.28	misc.GDSL-motif lipase	kanlowctg08094_s_at	Transcript	very weakly similar to (97.8) AT5G45910 Symbols: GDSL-motif lipase/hydrolase family protein chr5:18620420-18622264 REVERSEweakly similar to (172) loc_	-1.2245063
26.28	misc.GDSL-motif lipase	ap13itg43227_s_at	Transcript	weakly similar to (102) AT5G22810 Symbols: GDSL-motif lipase, putative chr5:7621568-7623367 FORWARDweakly similar to (150) loc_os06g05630 12006.m	-1.0792964
26.28	misc.GDSL-motif lipase	ap13itg64098-rc_at	Transcript	weakly similar to (134) loc_os06g06230 12006.m05349 protein carboxylic ester hydrolase/ hydrolase, acting on ester bonds, putative no original description	2.2048423
26.28	misc.GDSL-motif lipase	kanlowctg37283_s_at	Transcript	weakly similar to (128) AT3G16370 Symbols: GDSL-motif lipase/hydrolase family protein chr3:5556928-5558351 FORWARDweakly similar to (188) loc_os06g	-2.0885303

Major CHO

BinCode	BinName	id	type	description	Se/60 (log2)
2.1.2.1	major CHO metabolism.synthesis.starch.AGPase	ap13ctg08222_s_at	Transcript	weakly similar to (115) AT5G19220 Symbols: ADG2, APL1 APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenyltyltransfe	2.8284266
2.1.2.2	major CHO metabolism.synthesis.starch.starch synthase	kanlowctg41507_at	Transcript	very weakly similar to (80.5) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Pi	-1.247854

2.1.2.3	major CHO metabolism.synthesis.starch.starch branching	othswslt23495_s_at	Transcript	weakly similar to (115) GLGB_ORYSA 1,4-alpha-glucan branching enzyme, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme) - Oryza sativa	2.107312
2.1.2.3	major CHO metabolism.synthesis.starch.starch branching	ap13.12703.m00018_s_	Transcript	weakly similar to (117) AT5G03650 Symbols: SBE2.2 SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme chr5:931924-937470 FORWAF	2.4501665
2.1.2.5	major CHO metabolism.synthesis.starch.transporter	ap13ctg04140_at	Transcript	weakly similar to (114) AT3G08580 Symbols: AAC1 AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding chr3:2605706-2607030 REVERSEweakly similar t	1.9033846
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	ap13ctg03321_s_at	Transcript	weakly similar to (119) AT3G29320 Symbols: glucan phosphorylase, putative chr3:11252871-11257587 FORWARDweakly similar to (120) PHSL_IPOBA Alpha-	2.940816
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	ap13ctg01611-1_s_at	Transcript	moderately similar to (304) AT3G29320 Symbols: glucan phosphorylase, putative chr3:11252871-11257587 FORWARDmoderately similar to (306) PHSL1_SO	2.7809234
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	othswctg11635_s_at	Transcript	weakly similar to (151) AT3G46970 Symbols: ATPHS2, PHS2 PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl group	2.6235723

List of significantly DEGs involved in hormone, misc and major CHO pathway in Se/Mo comparison

Hormone					
BinCode	BinName	id	type	description	Se/Mo (log2)
17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	ap13ctg31837_s_at	Transcript	weakly similar to (155) AT5G20960 Symbols: AAO1, AO1, ATAO, ATA01 AAO1 (ARABIDOPSIS ALDEHYDE OXIDASE 1); aldehyde oxidase/ indole-3-acetaldehyde o	2.250
17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	kanlowctg13272_s_at	Transcript	weakly similar to (152) AT5G20960 Symbols: AAO1, AO1, ATAO, ATA01 AAO1 (ARABIDOPSIS ALDEHYDE OXIDASE 1); aldehyde oxidase/ indole-3-acetaldehyde o	-1.074
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	kanlowctg33522_at	Transcript	weakly similar to (138) AT1G60730 Symbols: aldo/keto reductase family protein chr1:22358613-22360082 REVERSEweakly similar to (106) A115_TOBAC Aux	1.928
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	ap13ctg17086_at	Transcript	weakly similar to (103) IAA6_ORYSA Auxin-responsive protein IAA6 (Indoleacetic acid-induced protein 6) - Oryza sativa (Rice)weakly similar to (103) loc_os01g538	1.630
17.5.1.2	hormone metabolism.ethylene.synthesis-degradation.1-aminocycloprc	ap13itg55664_at	Transcript	very weakly similar to (86.3) AT1G62380 Symbols: ACO2, ATACO2 ACO2 (ACC OXIDASE 2); 1-aminocyclopropane-1-carboxylate oxidase chr1:23082340-23084	2.119
17.6.1.1	hormone metabolism.gibberelin.synthesis-degradation.copalyl diphos	othswctg07572_at	Transcript	weakly similar to (105) loc_os02g17780 12002.m07022 protein ent-kaurene synthase A, chloroplast precursor, putative, expressed no original description	1.957
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (241) loc_os06g11210 12006.m	5.748
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDweakly similar to (167) loc_os06g11210 12006.m058:	4.396
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARDweakly similar to (1;	3.112
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-r	ap13itg69033_at	Transcript	weakly similar to (162) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (220) loc_os06g11290 12006.m	2.429
Misc					
BinCode	BinName	id	type	description	Se/Mo (log2)
26.1	misc.misc2	ap13itg58554_at	Transcript	very weakly similar to (85.9) loc_os05g33110 12005.m083715 protein endo-1,3;-1,4-beta-D-glucanase precursor, putative, expressed no original description	3.1168656
26.1	misc.misc2	ap13itg73544_at	Transcript	weakly similar to (140) loc_os10g35500 12010.m06374 protein epoxide hydrolase, putative, expressed no original description	2.049936
26.1	misc.misc2	ap13ctg12203_at	Transcript	weakly similar to (112) AT4G19185 Symbols: integral membrane family protein chr4:10489201-10491488 REVERSEweakly similar to (157) loc_os06g49500 1;	1.7140203
26.2	misc.UDP glucosyl and glucoronyl transferases	ap13itg75785rc_at	Transcript	moderately similar to (202) AT1G05680 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:1703196-1704639 REVERSEweakly similar t	2.1618404
26.2	misc.UDP glucosyl and glucoronyl transferases	ap13itg74837_at	Transcript	very weakly similar to (95.1) AT1G01390 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:148319-149761 REVERSEweakly similar to (	2.4085305
26.2	misc.UDP glucosyl and glucoronyl transferases	kanlowctg14906_s_at	Transcript	weakly similar to (119) loc_os01g45110 12001.m10717 protein cytokinin-O-glucosyltransferase 1, putative, expressed no original description	2.1462197
26.2	misc.UDP glucosyl and glucoronyl transferases	ap13itg47952_s_at	Transcript	weakly similar to (117) loc_os03g55050 12003.m10421 protein cytokinin-O-glucosyltransferase 2, putative, expressed no original description	2.362382
26.2	misc.UDP glucosyl and glucoronyl transferases	ap13ctg09529_at	Transcript	weakly similar to (162) AT1G05680 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:1703196-1704639 REVERSEweakly similar to (1;	3.4648933
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg22294_at	Transcript	weakly similar to (137) loc_os01g16310 12001.m08227 protein glycosyl hydrolases family 31 protein, expressed no original description	3.0952632
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg08905_s_at	Transcript	weakly similar to (108) loc_os05g30350 12005.m27797 protein non-cyanogenic beta-glucosidase precursor, putative, expressed no original description	2.0905576
26.3	misc.gluco-, galacto- and mannosidases	kanlowctg19994_s_at	Transcript	very weakly similar to (100) AT4G21760 Symbols: BGLU47 BGLU47 (Beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glucosyl compoun	3.0748846
26.3	misc.gluco-, galacto- and mannosidases	ap13itg52053_s_at	Transcript	very weakly similar to (82.0) AT1G61810 Symbols: BGLU45 BGLU45 (BETA-GLUCOSIDASE 45); catalytic/ cation binding / hydrolase, hydrolyzing O-glucosyl compi	2.22551
26.3.4	misc.gluco-, galacto- and mannosidases.endoglucanase	kanlowctg19895_x_at	Transcript	weakly similar to (152) AT5G49720 Symbols: ATGH9A1, DEC, KOR, RSW2, IRX2, KOR1 ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase	2.2666078
26.4	misc.beta 1,3 glucan hydrolases	ap13itg58279_s_at	Transcript	weakly similar to (122) AT3G07320 Symbols: glycosyl hydrolase family 17 protein chr3:2332324-2333925 REVERSEweakly similar to (177) loc_os09g32550 12	1.7381021
26.4.1	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase	kanlowctg10503rc_s_a	Transcript	weakly similar to (102) GUB2_HORVU Lichenase-2 precursor (EC 3.2.1.73) (Lichenase II) (Endo-beta-1,3-1,4 glucanase II) ((1->3,1->4)-beta-glucanase isoenzyme EI	-1.907923
26.4.1	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase	ap13itg70254_at	Transcript	weakly similar to (113) AT4G16260 Symbols: catalytic/ cation binding / hydrolase, hydrolyzing O-glucosyl compounds chr4:9200180-9201441 REVERSEweakly t	1.7229776
26.6	misc.O-methyl transferases	ap13ctg23081_s_at	Transcript	very weakly similar to (98.2) AT3G12270 Symbols: ATPRMT3, PRMT3 PRMT3 (PROTEIN ARGININE METHYLTRANSFERASE 3); methyltransferase/ zinc ion binding	1.9541873
26.7	misc.oxidases - copper, flavone etc	kanlowctg47289_s_at	Transcript	weakly similar to (107) loc_os03g05900 12003.m101192 protein monooxygenase, putative, expressed no original description	1.5915792
26.7	misc.oxidases - copper, flavone etc	ap13ctg02095_at	Transcript	weakly similar to (103) loc_os09g37620 12009.m06709 protein monooxygenase/ oxidoreductase, putative, expressed no original description	1.8820726
26.9	misc.glutathione S transferases	ap13itg52395_s_at	Transcript	very weakly similar to (89.7) AT1G10370 Symbols: GST30, ATGSTU17, GST30B, ERD9 ERD9 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase c	2.0166132
26.9	misc.glutathione S transferases	ap13ctg23895_at	Transcript	weakly similar to (116) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)weakly similar to (	1.9411697
26.1	misc.cytochrome P450	ap13ctg15166_s_at	Transcript	moderately similar to (233) AT2G32440 Symbols: KAO2, CYP88A4 KAO2 (ENT-KAURENOIC ACID HYDROXYLASE 2); ent-kaurenoate oxidase/ oxygen binding ch	-1.3691137
26.1	misc.cytochrome P450	ap13ctg31838_s_at	Transcript	weakly similar to (102) loc_os02g30100 12002.m08153 protein cytochrome P450 81E1, putative, expressed no original description	2.0546823
26.1	misc.cytochrome P450	ap13ctg15593_s_at	Transcript	very weakly similar to (89.7) AT3G14620 Symbols: CYP72A8 CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr	3.6020677
26.1	misc.cytochrome P450	kanlowctg12693-1_s_a	Transcript	weakly similar to (108) AT1G12740 Symbols: CYP87A2 CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:43;	1.1912225
26.12	misc.peroxidases	ap13ctg09437_at	Transcript	very weakly similar to (89.0) PER2_ORYSA Peroxidase 2 precursor (EC 1.11.1.7) - Oryza sativa (Rice)very weakly similar to (91.3) loc_os07g48040 12007.m09019 pr	2.2950435
26.13	misc.acid and other phosphatases	kanlowctg21816_s_at	Transcript	weakly similar to (113) AT4G29260 Symbols: acid phosphatase class B family protein chr4:14422310-14423409 REVERSEweakly similar to (122) VSPA_SOYBN	1.9629114
26.13	misc.acid and other phosphatases	ap13itg70120_at	Transcript	weakly similar to (128) AT4G29260 Symbols: acid phosphatase class B family protein chr4:14422310-14423409 REVERSEweakly similar to (144) VSPA_SOYBN	2.079594
26.16	misc.myrosinases-lectin-jacalin	ap13ctg22520_at	Transcript	weakly similar to (105) AT2G37710 Symbols: RLK RLK (receptor lectin kinase); kinase chr2:15814934-15816961 REVERSEweakly similar to (191) loc_os09g095	1.9184065
26.19	misc.plastocyanin-like	ap13itg68926_at	Transcript	very weakly similar to (94.0) AT2G32300 Symbols: UCC1 UCC1 (UCLACYANIN 1); copper ion binding / electron carrier chr2:13722510-13723464 FORWARDwe	1.6645914
26.22	misc.short chain dehydrogenase/reductase (SDR)	ap13itg69277_at	Transcript	weakly similar to (112) loc_os04g44924 12004.m101862 protein short-chain dehydrogenase/reductase SDR, putative, expressed no original description	2.5772862
Major CHO					
BinCode	BinName	id	type	description	Se/Mo (log2)
2.1.2.1	major CHO metabolism.synthesis.starch.AGPase	ap13ctg08222_s_at	Transcript	weakly similar to (115) AT5G19220 Symbols: ADG2, APL1 APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenylyltransfe	1.7421138
2.1.2.3	major CHO metabolism.synthesis.starch.starch branching	othswslt23495_s_at	Transcript	weakly similar to (115) GLGB_ORYSA 1,4-alpha-glucan branching enzyme, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme) - Oryza sativa	2.1660018
2.1.2.3	major CHO metabolism.synthesis.starch.starch branching	ap13.12703.m00018_s_	Transcript	weakly similar to (117) AT5G03650 Symbols: SBE2.2 SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme chr5:931924-937470 FORWAF	2.2696276
2.1.2.5	major CHO metabolism.synthesis.starch.transporter	ap13ctg04140_at	Transcript	weakly similar to (114) AT3G08580 Symbols: AAC1 AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding chr3:2605706-2607030 REVERSEweakly similar t	1.5862548
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	ap13ctg03321_s_at	Transcript	weakly similar to (119) AT3G29320 Symbols: glucan phosphorylase, putative chr3:11252871-11257587 FORWARDweakly similar to (120) PHSL_IPOBA Alpha-	2.5334692
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	ap13ctg01611-1_s_at	Transcript	moderately similar to (304) AT3G29320 Symbols: glucan phosphorylase, putative chr3:11252871-11257587 FORWARDmoderately similar to (306) PHSL1_SO	2.3238447
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	othswctg11635_s_at	Transcript	weakly similar to (151) AT3G46970 Symbols: ATPHS2, PHS2 PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl group	2.72060457

Table S6. List of significantly DEGs related to biotic and abiotic stress pathways in four comparisons

List of significantly DEGs involved in hormone metabolism, regulation of transcription factor and abiotic stress pathway in Exp/Ctrl comparison

Hormone					
BinCode	BinName	id	type	description	Exp/Ctrl (log2)
17.7.1.2	hormone metabolism.jasmonat	ap13itg70317_at	Transcript	weakly similar to (143) AT3G45140 Symbols: LOX2, ATLOX2 LOX2 (LPOXYGENASE 2); lipoxygenase chr3:16525437-16529233 FORWARDweakly similar to (199) LOX2	2.5209846
17.7.1.5	hormone metabolism.jasmonat	kanlowctg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (241) loc_os06g11210 12006.m05838	4.7242365
17.7.1.5	hormone metabolism.jasmonat	ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDweakly similar to (167) loc_os06g11210 12006.m05838 prot	3.2742903
17.7.1.5	hormone metabolism.jasmonat	ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARDweakly similar to (128) loc_	2.168549

Transcription factor

BinCode	BinName	id	type	description	Exp/Ctrl (log2)
27.3.26	RNA.regulation of transcription	ap13ctg22648_at	Transcript	very weakly similar to (81.6) AT4G39250 Symbols: ATRL1 ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor chr4:18271457-18271857 REVERSEwe	-1.7655948
27.3.26	RNA.regulation of transcription	ap13itg63308-rc_at	Transcript	very weakly similar to (88.6) AT1G75250 Symbols: ATRL6 ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor chr1:28244463-28245453 REVERSEweakly similar to (	-2.389372
27.3.35	RNA.regulation of transcription	ap13itg72122_at	Transcript	very weakly similar to (89.7) AT1G08320 Symbols: bZIP family transcription factor chr1:26221123-2627451 REVERSEvery weakly similar to (80.5) TGA21_TOBAC TGAC	-2.9408507

Abiotic stress

BinCode	BinName	id	type	description	Exp/Ctrl (log2)
20.2.1	stress.abiotic.heat	ap13itg66986_at	Transcript	weakly similar to (164) AT3G12580 Symbols: HSP70 HSP70 (heat shock protein 70); ATP binding chr3:3991487-3993689 REVERSEweakly similar to (163) HSP7C_PETI	1.7140276
20.2.1	stress.abiotic.heat	ap13itg70020_at	Transcript	weakly similar to (102) loc_os01g65480 12001.m12659 protein dnaJ protein homolog 1, putative, expressed no original description	-1.2925655
20.2.2	stress.abiotic.cold	kanlowctg06768_at	Transcript	very weakly similar to (89.0) LT16A_ORYSA Hydrophobic protein LT16A (Low temperature-induced protein 6A) - Oryza sativa (Rice)very weakly similar to (89.0) loc_os07g4	-2.341828
20.2.3	stress.abiotic.drought/salt	ap13ctg19249_at	Transcript	very weakly similar to (92.4) loc_os01g73960 12001.m43394 protein fb2, putative, expressed no original description	-1.1559153

List of significantly DEGs involved in abiotic stress, signalling, regulation of trancription factor and cell wall pathway in Mo/60 comparison

Abiotic stress					
BinCode	BinName	id	type	description	Mo/60 (log2)
20.2.1	stress.abiotic.heat	ap13ctg12560_s_at	Transcript	weakly similar to (149) loc_os02g32590 12002.m33703 protein heat shock factor protein 2, putative, expressed no original description	-1.1621747
20.2.1	stress.abiotic.heat	ap13itg70020_at	Transcript	weakly similar to (102) loc_os01g65480 12001.m12659 protein dnaJ protein homolog 1, putative, expressed no original description	-1.47846
20.2.2	stress.abiotic.cold	kanlowctg06768_at	Transcript	very weakly similar to (89.0) LT16A_ORYSA Hydrophobic protein LT16A (Low temperature-induced protein 6A) - Oryza sativa (Rice)very weakly similar to (89.0) loc_os07g4	-3.0117598
20.2.3	stress.abiotic.drought/salt	ap13ctg19249_at	Transcript	very weakly similar to (92.4) loc_os01g73960 12001.m43394 protein fb2, putative, expressed no original description	-1.3544257
20.2.3	stress.abiotic.drought/salt	ap13ctg30618_at	Transcript	weakly similar to (129) AT2G18250 Symbols: ATCOAD ATCOAD (4-phosphopantetheine adenlyl(transferase); nucleotidyltransferase/ pantetheine-phosphate adenlyl	-1.3595558
20.2.4	stress.abiotic.touch/wounding	kanlowctg10783_s_at	Transcript	very weakly similar to (85.9) loc_os04g54280 12004.m10320 protein retrotransposon protein, putative, unclassified no original description	-1.1250397
20.2.4	stress.abiotic.touch/wounding	ap13itg73873_s_at	Transcript	moderately similar to (201) loc_os05g27580 12005.m07046 protein wound-induced protein W112 containing protein no original description	-1.0588257
20.2.4	stress.abiotic.touch/wounding	kanlowctg09577_s_at	Transcript	weakly similar to (164) loc_os05g27580 12005.m07046 protein wound-induced protein W112 containing protein no original description	-1.2653005
20.2.4	stress.abiotic.touch/wounding	kanlowctg16979_s_at	Transcript	very weakly similar to (92.0) loc_os04g54300 12004.m78995 protein wound induced protein, putative, expressed no original description	-1.3814937
20.2.4	stress.abiotic.touch/wounding	ap13ctg24346_at	Transcript	very weakly similar to (86.3) AT4G10270 Symbols: wound-responsive family protein chr4:6374805-6375077 FORWARDweakly similar to (115) loc_os04g54280 1200	-1.7902399
20.2.4	stress.abiotic.touch/wounding	ap13itg39065_s_at	Transcript	very weakly similar to (80.5) AT4G10265 Symbols: wound-responsive protein, putative chr4:6373226-6373477 REVERSEweakly similar to (113) loc_os04g54280 1200	-1.7631652
20.2.4	stress.abiotic.touch/wounding	ap13itg60359_s_at	Transcript	weakly similar to (106) loc_os04g54280 12004.m10320 protein retrotransposon protein, putative, unclassified no original description	-1.0302726
20.2.4	stress.abiotic.touch/wounding	ap13ctg59032_at	Transcript	very weakly similar to (88.6) loc_os04g54280 12004.m10320 protein retrotransposon protein, putative, unclassified no original description	-1.8604492

Signalling

BinCode	BinName	id	type	description	Mo/60 (log2)
30.1	signalling.in sugar and nutrient	ap13itg74992_at	Transcript	weakly similar to (117) loc_os02g54640 12002.m10493 protein glutamate receptor 2.9 precursor, putative, expressed no original description	1.119977
30.2.11	signalling.receptor kinases.leuc	ap13itg61870_at	Transcript	weakly similar to (116) loc_os11g07240 12011.m04920 protein receptor protein kinase CLAVATA1 precursor, putative, expressed no original description	1.1316558
30.2.11	signalling.receptor kinases.leuc	othswctg12119_at	Transcript	very weakly similar to (80.1) AT3G47580 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17532687-17535810 FORWARDweakly similar to	1.0568756
30.2.11	signalling.receptor kinases.leuc	othswctg27954_s_at	Transcript	weakly similar to (132) loc_os02g40180 12002.m09104 protein receptor-like protein kinase precursor, putative, expressed no original description	2.0184202
30.2.11	signalling.receptor kinases.leuc	ap13ctg04179_at	Transcript	weakly similar to (105) loc_os01g65650 12001.m12674 protein receptor-like protein kinase 5 precursor, putative, expressed no original description	-1.9957428
30.2.11	signalling.receptor kinases.leuc	kanlowctg42715_at	Transcript	weakly similar to (107) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARDmoderately similar to	2.03235
30.2.11	signalling.receptor kinases.leuc	othswctg19246_at	Transcript	very weakly similar to (84.0) AT3G47110 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17347103-17350296 REVERSEweakly similar to (	1.51942
30.2.11	signalling.receptor kinases.leuc	ap13ctg16678_s_at	Transcript	very weakly similar to (81.3) AT5G48380 Symbols: leucine-rich repeat family protein / protein kinase family protein chr5:19604584-19606532 REVERSEweakly similar	1.0412167
30.2.11	signalling.receptor kinases.leuc	othswctg17938_at	Transcript	weakly similar to (115) AT2G15080 Symbols: ATRLP19 ATRLP19 (Receptor Like Protein 19); kinase/ protein binding chr2:6533764-6536715 FORWARDweakly similar t	1.6272969
30.2.11	signalling.receptor kinases.leuc	othswctg17630_at	Transcript	weakly similar to (174) loc_os02g40240 12002.m33414 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed no original description	1.6988038
30.2.11	signalling.receptor kinases.leuc	ap13ctg50688_s_at	Transcript	weakly similar to (105) loc_os04g15630 12004.m06749 protein leucine-rich repeat receptor protein kinase EXS precursor, putative no original description	1.5420277
30.2.11	signalling.receptor kinases.leuc	kanlowctg19800_s_at	Transcript	very weakly similar to (90.9) loc_os02g40180 12002.m09104 protein receptor-like protein kinase precursor, putative, expressed no original description	1.3183337
30.2.11	signalling.receptor kinases.leuc	othswslt25490_at	Transcript	weakly similar to (114) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARDmoderately similar to	1.2138089
30.2.11	signalling.receptor kinases.leuc	ap13itg03762_at	Transcript	weakly similar to (181) loc_os02g40240 12002.m33414 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed no original description	1.5610776
30.2.11	signalling.receptor kinases.leuc	othswctg18100_at	Transcript	weakly similar to (131) loc_os11g36190 12011.m080025 protein receptor-like protein kinase 5 precursor, putative, expressed no original description	1.3126502
30.2.16	signalling.receptor kinases.Catf	ap13ctg04617_at	Transcript	weakly similar to (143) loc_os06g22810 12006.m06934 protein protein kinase, putative, expressed no original description	-1.1393493
30.2.17	signalling.receptor kinases.DUF	ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m060077 protein ATP binding protein, putative, expressed no original description	2.0351868
30.2.17	signalling.receptor kinases.DUF	othswctg18108_at	Transcript	very weakly similar to (97.8) AT1G11330 Symbols: S-locus lectin protein kinase family protein chr1:3810372-3813416 FORWARDweakly similar to (148) loc_os04g54	1.9088267
30.2.17	signalling.receptor kinases.DUF	ap13itg69009_at	Transcript	very weakly similar to (90.1) AT4G23160 Symbols: protein kinase family protein chr4:12129485-12134086 FORWARDweakly similar to (166) loc_os05g39130 12005.i	1.1350458
30.2.17	signalling.receptor kinases.DUF	ap13itg77404_s_at	Transcript	very weakly similar to (94.7) AT4G03230 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding chr4:	1.5196985
30.2.17	signalling.receptor kinases.DUF	ap13itg39900_s_at	Transcript	very weakly similar to (91.3) loc_os12g14480 12012.m05416 protein ATP binding protein, putative no original description	2.5227633
30.2.17	signalling.receptor kinases.DUF	ap13itg76323_at	Transcript	weakly similar to (116) loc_os01g02390 12001.m42838 protein TAK14, putative, expressed no original description	2.8866818
30.2.17	signalling.receptor kinases.DUF	ap13itg47888_s_at	Transcript	very weakly similar to (86.7) loc_os11g11780 12011.m05370 protein serine/threonine protein kinase, putative, expressed no original description	-1.1535704
30.2.17	signalling.receptor kinases.DUF	ap13ctg07687_at	Transcript	weakly similar to (159) loc_os01g02800 12001.m06920 protein receptor-like kinase ARK1AS, putative, expressed no original description	1.2190235
30.2.17	signalling.receptor kinases.DUF	ap13ctg48706_at	Transcript	very weakly similar to (98.6) AT4G23130 Symbols: CRK5, RLK6 CRK5 (CYSTEINE-RICH RLK5); kinase chr4:12117688-12120134 REVERSEvery weakly similar to (82.8) NC	3.9346542
30.2.17	signalling.receptor kinases.DUF	ap13ctg11071_s_at	Transcript	weakly similar to (102) loc_os07g35290 12007.m07785 protein receptor-like serine-threonine protein kinase, putative, expressed no original description	1.346304

30.2.17	signalling.receptor.kinases.DUF.ap13ctg22926_at	Transcript	very weakly similar to (90.5) AT4G23180 Symbols: CRK10, RLK4 CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/	-1.065511
30.2.25	signalling.receptor.kinases.wall.ap13ctg19859_at	Transcript	weakly similar to (142) loc_os04g43730 12004.m09332 protein OsWAK51 - OsWAK receptor-like protein kinase, expressed no original description	1.6219307
30.2.25	signalling.receptor.kinases.wall.ap13ctg14697_s_at	Transcript	weakly similar to (162) loc_os04g03830 12004.m05691 protein OsWAK29 - OsWAK receptor-like protein kinase, expressed no original description	1.7394327
30.2.25	signalling.receptor.kinases.wall.othswctg14972_at	Transcript	weakly similar to (130) loc_os02g42150 12002.m09252 protein OsWAK14 - OsWAK receptor-like protein kinase, expressed no original description	3.268809
30.2.25	signalling.receptor.kinases.wall.alamoctg14172_at	Transcript	very weakly similar to (88.6) loc_os02g42150 12002.m09252 protein OsWAK14 - OsWAK receptor-like protein kinase, expressed no original description	1.109805
30.2.25	signalling.receptor.kinases.wall.ap13ctg23391_at	Transcript	weakly similar to (116) loc_os03g62430 12003.m11119 protein OsWAK28 - OsWAK receptor-like protein kinase, expressed no original description	1.8729477
30.2.25	signalling.receptor.kinases.wall.ap13itg48098_at	Transcript	very weakly similar to (94.4) AT1G21230 Symbols: WAK5 WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase chr1:7429980-7432346 FORN	-1.1851537
30.2.99	signalling.receptor.kinases.misc.ap13itg77449-rc_at	Transcript	weakly similar to (138) loc_os05g44970 12005.m08622 protein senescence-induced receptor-like protein kinase precursor, putative no original descript	1.7617186
30.2.99	signalling.receptor.kinases.misc.ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m060077 protein ATP binding protein, putative, expressed no original description	2.0351868
30.2.99	signalling.receptor.kinases.misc.kanlowctg38494_at	Transcript	very weakly similar to (95.9) AT2G28970 Symbols: leucine-rich repeat protein kinase, putative chr2:12443919-12448163 FORWARD	1.0940689
30.2.99	signalling.receptor.kinases.misc.ap13itg58665_at	Transcript	weakly similar to (132) AT2G28970 Symbols: leucine-rich repeat protein kinase, putative chr2:12443919-12448163 FORWARD	1.2050234
30.2.99	signalling.receptor.kinases.misc.ap13itg48098_at	Transcript	very weakly similar to (94.4) AT1G21230 Symbols: WAK5 WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase chr1:7429980-7432346 FORN	-1.1851537
30.3	signalling.calcium.ap13itg66751_s_at	Transcript	weakly similar to (117) AT2G18750 Symbols: calmodulin-binding protein chr2:8125827-8128363 FORWARD	1.5560796
30.3	signalling.calcium.kanlowctg04099_s_at	Transcript	weakly similar to (104) AT1G27770 Symbols: ACA1, PEA1 ACA1 (AUTO-INHIBITED CA2+-ATPASE 1); calcium channel/ calcium-transporting ATPase/ calmodulin binding	1.0539427
30.3	signalling.calcium.ap13ctg14744_s_at	Transcript	weakly similar to (128) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed no original description	2.738117
30.3	signalling.calcium.ap13ctg08973_s_at	Transcript	very weakly similar to (81.6) AT4G37640 Symbols: ACA2 ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmoduli	1.1298444
30.5	signalling.G-proteins.kanlowctg44370_s_at	Transcript	very weakly similar to (91.3) loc_os06g02130 12006.m31954 protein guanyl nucleotide binding protein, putative, expressed no original description	1.6158048

Transcription factor

BinCode	BinName	id	type	description	Mo/60 (log2)
27.3.26	RNA.regulation of transcription.ap13ctg22648_at	Transcript	very weakly similar to (81.6) AT4G39250 Symbols: ATRL1 ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor chr4:18271457-18271857 REVERSE	-1.3755075	
27.3.26	RNA.regulation of transcription.ap13itg3308-rc_at	Transcript	very weakly similar to (88.6) AT1G75250 Symbols: ATRL6 ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor chr1:28244463-28245453 REVERSE	-2.4642951	
27.3.26	RNA.regulation of transcription.ap13itg71040_at	Transcript	weakly similar to (106) loc_os01g09280 12001.m07553 protein myb-related transcription activator, putative, expressed no original description	-1.0700543	

Cell wall

BinCode	BinName	id	type	description	Mo/60 (log2)
26.4.1	misc.beta 1,3 glucan hydrolase: kanlowctg10503rc_s_ε	Transcript	weakly similar to (102) GUB2_HORVU Lichenase-2 precursor (EC 3.2.1.73) (Lichenase II) (Endo-beta-1,3-1,4 glucanase II) ((1->3,1->4)-beta-glucanase isoenzyme EII) (Fragr	1.4965644	
26.4.1	misc.beta 1,3 glucan hydrolase: kanlowctg24512_s_at	Transcript	weakly similar to (106) AT3G57260 Symbols: BGL2, PR2, BG2, PR-2 BGL2 (BETA-1,3-GLUCANASE 2); cellulase/ glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-gl	2.3199854	

List of significantly DEGs involved in hormone, regulation of transcription factor and glutathione S transferases, and signalling pathway in Se/60 comparison

Hormone

BinCode	BinName	id	type	description	Se/60 (log2)
17.7.1.2	hormone metabolism.jasmonat.ap13itg70317_at	Transcript	weakly similar to (143) AT3G45140 Symbols: LOX2, ATLOX2 LOX2 (LIPOXYGENASE 2); lipoxygenase chr3:16525437-16529233 FORWARD	weakly similar to (199) LOX2	2.7463124
17.7.1.5	hormone metabolism.jasmonat.kanlowctg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARD	moderately similar to (241) loc_os06g11210 12006.m05838	5.94585
17.7.1.5	hormone metabolism.jasmonat.ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARD	weakly similar to (167) loc_os06g11210 12006.m05838 prot	4.575795
17.7.1.5	hormone metabolism.jasmonat.ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARD	weakly similar to (128) loc	3.1269832
17.7.1.5	hormone metabolism.jasmonat.ap13itg69033_at	Transcript	weakly similar to (162) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARD	moderately similar to (220) loc_os06g11290 12006.m05846	2.3178062

Transcription factor

BinCode	BinName	id	type	description	Se/60 (log2)
27.3.26	RNA.regulation of transcription.ap13ctg22648_at	Transcript	very weakly similar to (81.6) AT4G39250 Symbols: ATRL1 ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor chr4:18271457-18271857 REVERSE	-1.8795223	
27.3.26	RNA.regulation of transcription.ap13itg63308-rc_at	Transcript	very weakly similar to (88.6) AT1G75250 Symbols: ATRL6 ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor chr1:28244463-28245453 REVERSE	-2.725983	

Glutathione S transferases

BinCode	BinName	id	type	description	Se/60 (log2)	
26.9	misc.glutathione S transferases	ap13ctg18609_at	Transcript	very weakly similar to (91.3) AT3G55040 Symbols: GSTL2 GSTL2 chr3:20398718-20400305 REVERSE	very weakly similar to (97.4) IN21_MAIZE IN2-1 protein - Zea mays (Ma)	3.4394202
26.9	misc.glutathione S transferases	ap13itg59978_at	Transcript	very weakly similar to (82.0) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)	very weakly similar to (1)	1.8530868
26.9	misc.glutathione S transferases	ap13itg52395_s_at	Transcript	very weakly similar to (89.7) AT1G10370 Symbols: GST30, ATGSTU17, GST30B, ERD9 ERD9 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase chr1:33	very weakly similar to (133)	2.6520345
26.9	misc.glutathione S transferases	ap13ctg23895_at	Transcript	weakly similar to (116) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)	weakly similar to (116) k	2.3023114
26.9	misc.glutathione S transferases	ap13itg64056_at	Transcript	weakly similar to (107) loc_os10g38340 12010.m06607 protein glutathione S-transferase GSTU6, putative, expressed no original description		2.9526143
26.9	misc.glutathione S transferases	ap13ctg24964_at	Transcript	very weakly similar to (93.6) AT3G62760 Symbols: ATGSTF13 ATGSTF13; glutathione transferase chr3:23217425-23218246 REVERSE	very weakly similar to (135) GSTF4_M	1.6238625
26.9	misc.glutathione S transferases	ap13ctg16606_s_at	Transcript	very weakly similar to (90.5) AT3G55040 Symbols: GSTL2 GSTL2 chr3:20398718-20400305 REVERSE	very weakly similar to (149) IN21_MAIZE IN2-1 protein - Zea mays (Ma)	1.6981143
26.9	misc.glutathione S transferases	ap13itg54282_at	Transcript	very weakly similar to (92.4) AT3G62760 Symbols: ATGSTF13 ATGSTF13; glutathione transferase chr3:23217425-23218246 REVERSE	very weakly similar to (164) GSTF4_M	1.7701411

Signalling

BinCode	BinName	id	type	description	Se/60 (log2)
30.1	signalling.in.sugar.and.nutrient.ap13itg51186_at	Transcript	weakly similar to (111) AT5G11180 Symbols: ATGLR2.6, GLR2.6 ATGLR2.6; intracellular ligand-gated ion channel chr5:3557261-3561575 REVERSE	Every weakly similar	2.129366
30.1	signalling.in.sugar.and.nutrient.othswctg22609_at	Transcript	very weakly similar to (85.1) AT5G27100 Symbols: ATGLR2.1, GLR2.1 ATGLR2.1; intracellular ligand-gated ion channel chr5:9535160-9538311 REVERSE	Emoderately sir	2.047804
30.2.3	signalling.receptor.kinases.leuc.kanlowctg45110_s_at	Transcript	weakly similar to (133) AT5G58300 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:23572821-23574871 FORWARD	Weakly similar to (175)	2.0986495
30.2.11	signalling.receptor.kinases.leuc.ap13itg61870_at	Transcript	weakly similar to (116) loc_os11g07240 12011.m04920 protein receptor protein kinase CLAVATA1 precursor, putative, expressed no original description		1.5433446
30.2.11	signalling.receptor.kinases.leuc.kanlowctg40038_at	Transcript	very weakly similar to (88.2) loc_os02g13510 12002.m06597 protein receptor-like protein kinase 5 precursor, putative, expressed no original description		1.063403
30.2.11	signalling.receptor.kinases.leuc.kanlowctg42715_at	Transcript	weakly similar to (107) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARD	moderately similar to	1.6100112
30.2.11	signalling.receptor.kinases.leuc.othswctg17938_at	Transcript	weakly similar to (115) AT2G15080 Symbols: ATRLP19 ATRLP19 (Receptor Like Protein 19); kinase/ protein binding chr2:6533764-6536715 FORWARD	Weakly similar to	1.4178946
30.2.11	signalling.receptor.kinases.leuc.ap13ctg31498_at	Transcript	very weakly similar to (85.1) loc_os06g36270 12006.m091721 protein receptor-like protein kinase 5 precursor, putative, expressed no original description		1.7436931
30.2.11	signalling.receptor.kinases.leuc.ap13itg69687_at	Transcript	very weakly similar to (96.3) loc_os06g18000 12006.m06512 protein protein kinase domain containing protein, expressed no original description		1.9588789
30.2.11	signalling.receptor.kinases.leuc.kanlowctg19800_s_at	Transcript	very weakly similar to (90.9) loc_os02g40180 12002.m09104 protein receptor-like protein kinase precursor, putative, expressed no original description		1.3234391
30.2.11	signalling.receptor.kinases.leuc.ap13itg46221_s_at	Transcript	very weakly similar to (91.7) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARD	Weakly similar to	1.4062259
30.2.11	signalling.receptor.kinases.leuc.ap13itg38195_s_at	Transcript	very weakly similar to (86.7) AT3G47570 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17527611-17530748 FORWARD	Weakly similar to	-1.5182016
30.2.11	signalling.receptor.kinases.leuc.ap13ctg03762_at	Transcript	weakly similar to (181) loc_os02g40240 12002.m33414 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed no original description		1.2937868
30.2.11	signalling.receptor.kinases.leuc.othswt52539_at	Transcript	weakly similar to (101) loc_os02g40200 12002.m33773 protein receptor-like protein kinase precursor, putative, expressed no original description		1.0442657

30.2.11	signalling.receptor.kinases.leuc.othswctg18100_at	Transcript	weakly similar to (131) loc_os11g36190 12011.m080025 protein receptor-like protein kinase 5 precursor, putative, expressed no original description	2.5745566
30.2.16	signalling.receptor.kinases.Cath.ap13ctg04617_at	Transcript	weakly similar to (143) loc_os06g22810 12006.m06934 protein protein kinase, putative, expressed no original description	-1.5115253
30.2.17	signalling.receptor.kinases.DUF.ap13itg49945_at	Transcript	very weakly similar to (85.5) AT4G03230 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding chr4:	1.9965222
30.2.17	signalling.receptor.kinases.DUF.ap13ctg32578_s_at	Transcript	weakly similar to (101) AT4G23260 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase chr4:12167528-12170055 REVER	1.8421704
30.2.17	signalling.receptor.kinases.DUF.ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m06077 protein ATP binding protein, putative, expressed no original description	1.4479766
30.2.17	signalling.receptor.kinases.DUF.kanlowctg22148_s_at	Transcript	weakly similar to (142) AT4G21390 Symbols: B120 B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding chr4:11394458-11397474 REV	1.0061057
30.2.17	signalling.receptor.kinases.DUF.ap13itg75057-rc_at	Transcript	weakly similar to (101) loc_os11g45540 12011.m08386 protein protein kinase domain containing protein, expressed no original description	1.0871619
30.2.17	signalling.receptor.kinases.DUF.ap13.13172.m00006_s_at	Transcript	weakly similar to (188) AT4G32300 Symbols: SD2-5 SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase chr4:15599970-15602435 FORWARDweakl	1.8033427
30.2.17	signalling.receptor.kinases.DUF.ap13ctg22601_at	Transcript	very weakly similar to (84.3) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)weakly similar to (123) loc_os03g30890 1200	2.7661867
30.2.17	signalling.receptor.kinases.DUF.othswctg03176_s_at	Transcript	very weakly similar to (89.4) AT1G16670 Symbols: protein kinase family protein chr1:5697846-5699492 FORWARDweakly similar to (181) loc_os12g41710 12012.m5	1.7296312
30.2.17	signalling.receptor.kinases.DUF.kanlowctg26345_at	Transcript	weakly similar to (117) loc_os10g04730 12010.m03883 protein protein kinase, putative, expressed no original description	3.9657865
30.2.17	signalling.receptor.kinases.DUF.ap13itg69009_at	Transcript	very weakly similar to (90.1) AT4G23160 Symbols: protein kinase family protein chr4:12129485-12134086 FORWARDweakly similar to (166) loc_os05g39130 12005.1	1.0446063
30.2.17	signalling.receptor.kinases.DUF.ap13itg39900_s_at	Transcript	very weakly similar to (91.3) loc_os12g14480 12012.m05416 protein ATP binding protein, putative no original description	1.944933
30.2.17	signalling.receptor.kinases.DUF.ap13itg44603_s_at	Transcript	weakly similar to (189) AT1G66920 Symbols: serine/threonine protein kinase, putative chr1:24965410-24967432 REVERSEweakly similar to (111) KPRO_MAIZE Puta	1.4607781
30.2.17	signalling.receptor.kinases.DUF.ap13ctg11652_at	Transcript	weakly similar to (148) loc_os05g03920 12005.m04926 protein protein kinase, putative, expressed no original description	2.3945124
30.2.17	signalling.receptor.kinases.DUF.ap13itg62115-rc_at	Transcript	very weakly similar to (87.8) AT4G03230 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding chr4:	3.419504
30.2.17	signalling.receptor.kinases.DUF.ap13itg69687_at	Transcript	very weakly similar to (96.3) loc_os06g18000 12006.m06512 protein protein kinase domain containing protein, expressed no original description	1.9588789
30.2.17	signalling.receptor.kinases.DUF.ap13.13172.m00009_s_at	Transcript	weakly similar to (132) AT5G38240 Symbols: serine/threonine protein kinase, putative chr5:15277239-15279317 REVERSEvery weakly similar to (91.7) KPRO_MAIZE	1.9894791
30.2.17	signalling.receptor.kinases.DUF.kanlowctg36906_at	Transcript	weakly similar to (106) AT4G32300 Symbols: SD2-5 SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase chr4:15599970-15602435 FORWARDmode	1.2610515
30.2.17	signalling.receptor.kinases.DUF.ap13ctg10220_s_at	Transcript	very weakly similar to (96.3) loc_os04g52840 12004.m35461 protein serine/threonine-protein kinase receptor precursor, putative, expressed no original description	1.7833976
30.2.17	signalling.receptor.kinases.DUF.ap13itg53823_at	Transcript	weakly similar to (149) loc_os05g03920 12005.m04926 protein protein kinase, putative, expressed no original description	2.1282532
30.2.17	signalling.receptor.kinases.DUF.alamoctg01412_at	Transcript	very weakly similar to (83.6) AT4G05200 Symbols: protein kinase family protein chr4:2677933-2682309 REVERSEweakly similar to (122) loc_os11g11780 12011.m05	3.216593
30.2.17	signalling.receptor.kinases.DUF.ap13ctg21940_s_at	Transcript	weakly similar to (117) AT4G23260 Symbols: ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase chr4:12167528-12170055 REVER	1.703489
30.2.17	signalling.receptor.kinases.DUF.alamoctg05899_at	Transcript	weakly similar to (101) loc_os11g39490 12011.m07796 protein jacalin-like lectin domain containing protein no original description	2.349271
30.2.17	signalling.receptor.kinases.DUF.ap13ctg05226_at	Transcript	very weakly similar to (87.0) POLX_TOBAC Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.4	2.6510656
30.2.17	signalling.receptor.kinases.DUF.ap13itg73202_at	Transcript	weakly similar to (145) AT4G21390 Symbols: B120 B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding chr4:11394458-11397474 REV	3.079479
30.2.17	signalling.receptor.kinases.DUF.ap13ctg48706_at	Transcript	very weakly similar to (98.6) AT4G23130 Symbols: CRK5, RLK6 CRK5 (CYSTEINE-RICH RLK5); kinase chr4:12117688-12120134 REVERSEvery weakly similar to (82.8) NC	3.1529233
30.2.17	signalling.receptor.kinases.DUF.ap13ctg25718_at	Transcript	weakly similar to (133) loc_os01g02770 12001.m06917 protein YRK1, putative, expressed no original description	1.6382468
30.2.17	signalling.receptor.kinases.DUF.ap13ctg09428_at	Transcript	weakly similar to (114) AT4G38240 Symbols: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding chr4:1419	1.7944332
30.2.17	signalling.receptor.kinases.DUF.ap13ctg22926_at	Transcript	very weakly similar to (90.5) AT4G23180 Symbols: CRK10, RLK4 CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ r	-1.2402747
30.2.17	signalling.receptor.kinases.DUF.kanlowctg43024_s_at	Transcript	very weakly similar to (88.6) AT4G11480 Symbols: protein kinase family protein chr4:6971408-6973799 FORWARDweakly similar to (167) loc_os11g11890 12011.m0	-1.3382376
30.2.17	signalling.receptor.kinases.DUF.kanlowctg38437_at	Transcript	very weakly similar to (96.3) AT3G45860 Symbols: receptor-like protein kinase, putative chr3:16863401-16866041 REVERSEvery weakly similar to (91.3) loc_os08g25	1.8606993
30.2.20	signalling.receptor.kinases.whe.ap13ctg12364_s_at	Transcript	weakly similar to (142) AT5G39030 Symbols: protein kinase family protein chr5:15620066-15622486 FORWARDmoderately similar to (212) loc_os01g49614 12001.r	1.8368353
30.2.20	signalling.receptor.kinases.whe.ap13itg40018_s_at	Transcript	weakly similar to (134) AT5G38260 Symbols: serine/threonine protein kinase, putative chr5:15283692-15285837 REVERSEweakly similar to (186) loc_os01g04480 1:	1.79677
30.2.24	signalling.receptor.kinases.S-lol.kanlowctg40669_s_at	Transcript	weakly similar to (121) AT4G00340 Symbols: RLK4 RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding chr4:148958-151496 FORWARDweakly si	1.614365
30.2.25	signalling.receptor.kinases.wall.ap13ctg19859_at	Transcript	weakly similar to (142) loc_os04g43730 12004.m09332 protein OsWAK51 - OsWAK receptor-like protein kinase, expressed no original description	1.8788317
30.2.25	signalling.receptor.kinases.wall.ap13ctg14697_s_at	Transcript	weakly similar to (162) loc_os04g03830 12004.m05691 protein OsWAK29 - OsWAK receptor-like protein kinase, expressed no original description	1.4781888
30.2.25	signalling.receptor.kinases.wall.ap13ctg31202_at	Transcript	very weakly similar to (99.4) AT1G79670 Symbols: RFO1, WAKL22 RFO1 (RESISTANCE TO FUSARIUM OXYSPORIUM 1); kinase chr1:29976887-29979337 REVERSEweakl	1.1971111
30.2.25	signalling.receptor.kinases.wall.ap13ctg03484_at	Transcript	weakly similar to (139) loc_os09g29584 12009.m06109 protein OsWAK84 - OsWAK receptor-like protein (OsWAK-RLP), expressed no original description	2.2482157
30.2.25	signalling.receptor.kinases.wall.ap13ctg09468_at	Transcript	very weakly similar to (90.1) AT1G12140 Symbols: WAK3 WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase chr1:7434303-7436702 FORWARD	3.0043032
30.2.25	signalling.receptor.kinases.wall.ap13ctg23391_at	Transcript	weakly similar to (116) loc_os03g62430 12003.m11119 protein OsWAK28 - OsWAK receptor-like protein kinase, expressed no original description	1.6576523
30.2.99	signalling.receptor.kinases.misc.ap13itg41137_at	Transcript	weakly similar to (142) loc_os09g39650 12009.m060077 protein ATP binding protein, putative, expressed no original description	1.4479766
30.2.99	signalling.receptor.kinases.misc.ap13ctg30066_s_at	Transcript	weakly similar to (101) loc_os03g05470 12003.m06070 protein nodulation receptor kinase precursor, putative, expressed no original description	1.4151226
30.3	signalling.calcium.ap13itg60345_at	Transcript	weakly similar to (108) AT2G18750 Symbols: calmodulin-binding protein chr2:8125827-8128363 FORWARDweakly similar to (181) loc_os12g36110 12012.m07401 p	2.19195
30.3	signalling.calcium.ap13ctg23761_at	Transcript	weakly similar to (105) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed no original description	2.2064536
30.3	signalling.calcium.ap13ctg14744_s_at	Transcript	weakly similar to (128) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed no original description	3.343881
30.3	signalling.calcium.othswstl36625_s_at	Transcript	weakly similar to (114) AT4G23650 Symbols: CDPK6, CPK3 CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-depende	1.9494499
30.3	signalling.calcium.ap13ctg13690_s_at	Transcript	moderately similar to (202) AT1G76040 Symbols: CPK29 CPK29; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase chr	-1.1846402
30.3	signalling.calcium.ap13ctg15995_at	Transcript	very weakly similar to (100) AT4G35310 Symbols: CPK5, ATPCK5 CPK5 (calmodulin-domain protein kinase 5); ATP binding / calcium ion binding / calmodulin-depende	-1.2281529
30.3	signalling.calcium.ap13ctg08973_s_at	Transcript	very weakly similar to (81.6) AT4G37640 Symbols: ACA2 ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmoduli	1.11844
30.3	signalling.calcium.ap13ctg15995rc_at	Transcript	very weakly similar to (100) AT4G35310 Symbols: CPK5, ATPCK5 CPK5 (calmodulin-domain protein kinase 5); ATP binding / calcium ion binding / calmodulin-depende	-1.1966637
30.3	signalling.calcium.ap13itg72133-rc_at	Transcript	weakly similar to (135) loc_os05g05460 12005.m05073 protein calcium ion binding protein, putative, expressed no original description	-1.5819521
30.5	signalling.G-proteins.ap13ctg29685_at	Transcript	very weakly similar to (89.4) AT4G21130 Symbols: EMB2271 EMB2271 (EMBRYO DEFECTIVE 2271); nucleotide binding chr4:11274308-11276286 FORWARDweakly si	1.7296008
30.5	signalling.G-proteins.kanlowctg21689_s_at	Transcript	weakly similar to (200) AT1G56050 Symbols: GTP-binding protein-related chr1:20963793-20966181 FORWARDmoderately similar to (231) loc_os03g56840 12003.r	1.4021398
30.5	signalling.G-proteins.ap13ctg56018_at	Transcript	r.very weakly similar to (91.7) loc_os03g58540 12003.m35462 protein small GTP-binding protein domain, putative, expressed no original description	1.0517408
30.5	signalling.G-proteins.ap13ctg29685_s_at	Transcript	weakly similar to (118) AT4G21130 Symbols: EMB2271 EMB2271 (EMBRYO DEFECTIVE 2271); nucleotide binding chr4:11274308-11276286 FORWARDweakly similar	2.074366
30.5	signalling.G-proteins.ap13ctg06899_at	Transcript	weakly similar to (136) AT1G48630 Symbols: RACKB1_AT RACKB1_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding chr1:17981977-17983268 REVEF	1.5308554
30.7	signalling.14-3-3.proteins.kanlowctg01295-2_s_at	Transcript	weakly similar to (107) AT1G64790 Symbols: binding chr1:24065232-24081908 REVERSEweakly similar to (163) loc_os03g51140 12003.m10094 protein GCN1-like p	1.5249975
30.1	signalling.phosphorelay.ap13ctg09520_at	Transcript	very weakly similar to (100) AT3G16360 Symbols: AHP4 AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphoru	-2.3115356

List of significantly DEGs involved in hormone metabolism pathway in Se/Mo comparison

Hormone						Se/Mo (log2)
BinCode	BinName	id	type	description		
17.7.1.5	hormone metabolism.jasmonat	kanlowctg23007_at	Transcript	weakly similar to (176) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (241) loc_os06g11210 12006.m05838	5.7484293	
17.7.1.5	hormone metabolism.jasmonat	ap13itg71073_s_at	Transcript	weakly similar to (110) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDweakly similar to (167) loc_os06g11210 12006.m05838 prot	4.396457	
17.7.1.5	hormone metabolism.jasmonat	ap13itg67010_s_at	Transcript	weakly similar to (115) AT1G76680 Symbols: OPR1, ATOPR1 OPR1; 12-oxophytodienoate reductase chr1:28776982-28778271 FORWARDweakly similar to (128) loc_	3.1115298	
17.7.1.5	hormone metabolism.jasmonat	ap13itg69033_at	Transcript	weakly similar to (162) AT1G76690 Symbols: OPR2, ATOPR2 OPR2 chr1:28778976-28780355 FORWARDmoderately similar to (220) loc_os06g11290 12006.m05846	2.4289663	