Supplemental Material to:

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Supplemental Table S1. List of rice genes differentially expressed in the presence of different plant hormones.

Probe Set ID	Locus	Gene description	IAA		BAP		ABA		ACC		SA		JA		Hormone specificity
			Fold change	Regulation	Fold change	Regulation	Fold change	Regulation	Fold change	Regulation	Fold change	Regulation	Fold change	Regulation	
Os.10006.1.S1_at	LOC_Os01g47400	OsMan01 - Endo-Beta-Mannanase, expressed	1.15	up	1.12	up	2.07	down	1.02	up	1.11	down	1.02	up	ABA
Os.10006.2.S1_x_at	LOC_Os01g47400	OsMan01 - Endo-Beta-Mannanase, expressed	1.59	up	1.09	down	2.23	down	1.09	down	1.22	down	1.11	up	ABA
Os.10025.1.S1_a_at	LOC_Os12g43130	phytoene synthase, chloroplast precursor, putative, expressed	1.16	up	1.04	up	3.28	down	1.08	down	1.61	down	1.05	down	ABA
Os.10031.1.S1_at	LOC_Os05g35140	nodulin MtN3 family protein, putative, expressed	1.29	up	1.25	up	7.61	up	1.18	down	1.18	down	1.36	down	ABA
Os.10058.1.S1_at	LOC_Os05g31620	OsCML15 - Calmodulin-related calcium sensor protein, expressed	1.20	down	1.23	down	2.27	up	1.44	down	1.13	up	1.13	down	ABA
Os.10071.1.S1_at	LOC_Os12g44300	CHX28, putative, expressed	1.00	up	1.10	up	1.04	down	1.00	up	1.05	up	6.42	up	JA
Os.10095.1.S1_at	LOC_Os03g60340	leaf senescence related protein, putative, expressed	1.05	up	1.14	up	2.17	down	1.25	down	1.34	down	1.09	down	ABA
Os.10096.1.S1_a_at	LOC_Os01g05830	expressed protein	1.09	up	1.13	down	7.87	up	1.52	down	1.35	up	1.17	down	ABA
Os.10096.1.S1_at	LOC_Os01g05830	expressed protein	1.00	down	1.09	up	6.95	up	1.08	down	1.40	up	1.01	down	ABA
Os.10096.2.S1_x_at	LOC_Os01g05830	expressed protein	1.27	up	1.05	up	7.31	up	1.07	down	1.32	up	1.08	up	ABA
Os.10097.1.S1_at	LOC_Os04g17100	heavy metal-associated domain containing protein, expressed	1.41	up	1.42	down	10.10	up	1.94	down	1.67	up	1.23	down	ABA
Os.10099.1.S1_at	LOC_Os03g13870	expressed protein	1.27	down	1.31	down	5.50	down	1.67	down	2.05	down	1.07	down	2
Os.10099.2.S1_at	LOC_Os03g13870	expressed protein	1.11	down	1.24	up	2.98	down	1.67	down	1.46	down	1.19	down	ABA
Os.10101.1.S1_at	LOC_Os05g36990	ATOFP18/OFP18, putative, expressed	1.11	down	1.04	down	7.95	down	1.05	up	1.40	down	1.31	down	ABA
Os.10117.1.S1_at	LOC_Os04g41460	transporter family protein, putative, expressed	1.06	up	1.12	down	2.05	up	1.12	down	1.12	up	1.11	up	ABA
Os.10120.2.S1_at	LOC_Os11g02424	LTPL9 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.10	down	1.48	up	8.57	down	1.37	down	2.24	down	1.48	down	2
Os.10121.1.S1_at	LOC_Os01g62070	cation efflux family protein, putative, expressed	1.64	up	1.11	up	2.42	up	1.06	up	1.08	up	1.06	up	ABA
Os.10122.1.S1_at	LOC_Os01g32330	heavy metal-associated domain containing protein, expressed	1.41	up	1.01	down	2.58	up	1.09	down	1.08	up	1.15	down	ABA
Os.10123.1.S1_at	LOC_Os01g58114	expressed protein	1.09	up	1.14	down	2.63	up	1.03	down	1.49	up	1.02	up	ABA
Os.10123.2.S1_x_at	LOC_Os01g58114	expressed protein	1.27	up	1.11	down	2.95	up	1.09	up	1.63	up	1.34	up	ABA
Os.10131.1.S1_a_at	LOC_Os05g51670	NAD dependent epimerase/dehydratase family protein, putative, expressed	1.11	down	1.03	up	12.62	up	1.14	up	2.29	up	1.19	up	2
Os.10141.1.S1_at	LOC_Os03g53750	nuclear prelamin A recognition factor, putative, expressed	1.76	up	1.13	down	2.02	up	1.01	up	2.37	up	1.27	up	2
Os.10146.1.S1_at	LOC_Os03g59320	expressed protein	1.31	up	1.46	down	7.42	up	1.11	up	2.16	up	1.27	up	2
Os.10168.1.S1_at	LOC_Os12g25120	core histone H2A/H2B/H3/H4, putative, expressed	1.09	down	1.15	up	2.18	down	1.02	up	1.41	down	1.34	down	ABA
Os.10179.1.S1_at	LOC_Os06g03640	BAG domain containing protein, expressed	1.16	down	1.14	down	3.21	down	1.22	down	1.54	down	1.72	up	ABA
Os.10183.1.S2_at	LOC_Os05g08370	CESA1 - cellulose synthase, expressed	1.04	down	1.05	down	2.21	down	1.29	down	1.57	down	1.17	up	ABA
Os.10186.1.S1_s_at	LOC_Os08g32170	oxidoreductase, 2OG-FeII oxygenase domain containing protein, putative, expressed	1.37	down	1.11	up	2.22	down	1.05	up	1.05	down	1.17	up	ABA
Os.10196.1.S1_at	LOC_Os01g58320	Expressed protein	1.09	down	1.22	up	44.30	up	1.01	down	1.01	up	1.13	down	ABA
Os.10197.1.S1_at	LOC_Os11g24060	permease domain containing protein, putative, expressed	1.95	up	1.13	down	3.91	up	1.07	up	1.14	up	1.81	down	ABA
Os.10204.1.S1_at	LOC_Os01g09590	myb-like DNA-binding domain containing protein, putative, expressed	1.52	down	1.43	up	3.00	down	1.13	up	1.04	down	1.74	up	ABA
Os.10244.1.S1_s_at	LOC_Os02g02340	glycerol-3-phosphate acyltransferase, putative, expressed	1.06	down	1.00	down	2.44	up	1.03	up	1.74	up	3.20	up	2
Os.10245.1.S1_at	LOC_Os04g37700	expressed protein	1.45	down	2.14	up	1.23	down	1.23	down	1.94	up	2.16	down	2
Os.10246.3.S1_at	LOC_Os06g06460	histone H3, putative, expressed	1.26	down	1.25	down	2.84	down	1.31	down	1.96	down	1.79	down	ABA
Os.10246.5.S1_at	LOC_Os06g06490	U-box domain containing heat shock protein, putative, expressed	1.32	down	1.14	down	2.77	down	1.22	down	1.83	down	1.36	down	ABA
Os.10254.1.S1_at	LOC_Os08g38600	copine, putative, expressed	1.46	up	1.19	up	1.38	up	1.52	up	8.13	up	1.12	up	SA
Os.10258.1.S1_at	LOC_Os01g68970	HYS1, putative, expressed	1.01	up	1.19	down	2.05	up	1.03	down	1.29	up	1.10	down	ABA
Os.10262.1.S1_at	LOC_Os08g02140	STIP1 homology and U box-containing protein 1, putative, expressed	1.08	down	1.01	up	2.08	up	1.08	up	1.14	up	1.01	down	ABA
Os.10271.1.S1_x_at	LOC_Os01g15860	pre-mRNA splicing factor-related prp1	1.04	down	1.11	up	2.78	up	1.01	up	1.15	down	1.05	down	ABA
Os.10273.1.S1_at	LOC_Os08g31660	VQ domain containing protein, putative, expressed	1.63	down	2.51	up	3.33	down	1.26	up	1.09	up	1.37	up	2
Os.10280.1.A1_at	LOC_Os02g04510	UOS1, putative, expressed	1.29	up	1.63	down	3.54	down	1.78	up	1.19	up	1.17	up	ABA
Os.10303.1.S2_at	LOC_Os03g01350	expressed protein	1.80	up	1.08	up	2.45	up	1.04	down	1.05	down	1.07	up	ABA
Os.10305.1.S1_at	LOC_Os08g41880	nucleotide pyrophosphatase/phosphodiesterase, putative, expressed	1.68	down	1.14	down	4.21	down	1.52	down	1.54	down	1.64	up	ABA
Os.10306.2.S1_x_at	LOC_Os01g24480	DUF1399 containing protein, putative, expressed	1.05	up	1.35	down	3.48	up	1.04	down	1.26	up	1.27	down	ABA
Os.10310.1.S1_at	LOC_Os01g38359	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed	1.17	up	1.02	down	2.29	down	1.13	up	1.22	down	1.06	up	ABA
Os.10311.1.S1_a_at	LOC_Os06g14324	caleosin related protein, putative, expressed	1.31	up	1.13	up	2.22	down	1.11	down	1.39	down	1.03	down	ABA
Os.10322.1.S1_s_at	LOC_Os07g38170	remorin, putative, expressed	1.75	up	2.18	up	1.66	up	1.04	down	1.07	up	1.28	down	BAP
Os.10339.1.S1_at	LOC_Os03g04770	beta-amylase, putative, expressed	1.35	down	1.14	down	17.09	up	1.10	down	1.31	up	1.10	up	ABA
Os.10348.1.S1_at	LOC_Os01g41430	UDP-glucoronosyl and UDP-glucosyl transferase, putative, expressed	5.24	up	1.25	up	1.48	down	1.75	up	4.43	up	2.31	up	3
Os.10352.1.S1_at	LOC_Os05g01470	methionine S-methyltransferase, putative, expressed	1.14	down	1.28	up	2.24	down	1.04	down	1.33	down	1.33	up	ABA
Os.10356.1.S1_at	LOC_Os03g08320	ZIM domain containing protein, putative, expressed	1.82	up	1.08	down	3.99	up	1.57	down	1.88	up	7.31	up	2

Os.10373.1.S1_at	LOC_Os07g41410	EGG APPARATUS-1, putative, expressed	**1.19**	down	**1.06**	down	**2.16**	down	**1.12**	down	**1.30**	up	**1.16**	down	ABA
Os.10378.2.A1_s_at	LOC_Os01g72570	expressed protein	**1.24**	up	**1.12**	down	**2.47**	up	**1.15**	up	**1.61**	up	**1.41**	up	ABA
Os.10381.1.S1_at	LOC_Os06g06080	serine esterase family protein, putative, expressed	**1.39**	up	**1.05**	up	**3.40**	up	**1.47**	up	**1.31**	up	**1.60**	up	ABA
Os.10382.1.S1_at	LOC_Os07g07974	tesmin/TSO1-like CXC domain containing protein, expressed	**1.28**	up	**1.13**	down	**3.50**	up	**1.04**	down	**1.34**	up	**1.10**	down	ABA
Os.10391.1.S1_a_at	LOC_Os05g51630	early-responsive to dehydration protein-related, putative, expressed	**1.12**	up	**1.11**	down	**2.43**	up	**1.13**	down	**1.08**	down	**1.23**	down	ABA
Os.10399.1.S1_at	LOC_Os05g02310	soluble inorganic pyrophosphatase, putative, expressed	**1.02**	down	**1.07**	down	**2.22**	down	**1.52**	down	**2.41**	down	**1.78**	up	2
Os.1041.1.S1_x_at	LOC_Os01g42850	ThiF family domain containing protein, putative, expressed	**1.35**	up	**1.10**	up	**3.16**	up	**1.07**	up	**1.35**	up	**1.11**	up	ABA
Os.10411.1.S1_at	LOC_Os01g62190	ZOS1-15 - C2H2 zinc finger protein, expressed	**1.64**	up	**1.46**	up	**3.60**	up	**1.05**	down	**3.08**	up	**1.22**	down	2
Os.10416.1.S1_at	CT829780	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN085D03, full insert sequenc	**1.09**	up	**1.29**	up	**2.86**	down	**1.47**	down	**2.16**	down	**3.68**	up	3
Os.10423.1.S1_at	LOC_Os07g48630	ethylene-insensitive 3, putative, expressed	**1.28**	up	**1.16**	up	**3.03**	up	**1.14**	down	**1.08**	up	**2.40**	up	2
Os.10423.1.S1_s_at	LOC_Os07g48630	ethylene-insensitive 3, putative, expressed	**1.11**	up	**1.01**	down	**2.48**	up	**1.07**	down	**1.03**	up	**2.03**	up	2
Os.10424.1.S1_at	LOC_Os08g34220	omega-6 fatty acid desaturase, chloroplast precursor, putative, expressed	**1.15**	up	**1.08**	up	**3.13**	down	**1.05**	down	**1.68**	down	**1.22**	down	ABA
Os.10468.1.S1_at	LOC_Os03g51470	expressed protein	**1.03**	up	**1.08**	down	**1.63**	down	**1.26**	up	**2.36**	up	**1.11**	up	SA
Os.10473.1.S1_at	LOC_Os12g25690	UDP-glucose 6-dehydrogenase, putative, expressed	**1.07**	down	**1.16**	down	**4.84**	down	**1.12**	down	**2.18**	down	**1.14**	up	2
Os.10483.1.S1_at	LOC_Os07g39620	C2 domain containing protein, putative, expressed	**1.19**	up	**1.03**	up	**2.00**	up	**1.24**	up	**1.33**	up	**1.11**	up	ABA
Os.10494.1.S1_at	LOC_Os01g14140	X8 domain containing protein, expressed	**1.06**	down	**1.12**	down	**3.96**	down	**1.14**	down	**2.18**	down	**1.87**	down	2
Os.10497.1.S1_s_at	LOC_Os07g23640	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	**1.16**	down	**1.24**	down	**2.93**	up	**1.30**	down	**1.05**	up	**1.94**	up	ABA
Os.10505.1.S1_a_at	LOC_Os10g39010	TKL_IRAK_CrRLK1L-1.16 - The CrRLK1L-1 subfamily has homology to the CrRLK1L h	**1.03**	up	**1.10**	down	**3.29**	down	**1.18**	up	**1.12**	up	**1.25**	up	ABA
Os.10510.1.S1_at	LOC_Os03g03034	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	**1.10**	up	**2.55**	up	**5.91**	down	**1.26**	up	**2.64**	up	**3.12**	up	4
Os.10512.1.S1_at	LOC_Os04g53740	thioredoxin, putative, expressed	**1.08**	down	**1.01**	up	**2.02**	up	**1.30**	down	**1.06**	up	**1.30**	down	ABA
Os.10524.2.S1_at	LOC_Os12g03070	FHA domain containing protein, putative, expressed	**2.25**	down	**1.03**	up	**2.23**	down	**1.61**	down	**1.51**	down	**1.42**	down	2
Os.10556.1.S1_at	CT837713	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSA011G13, full insert sequenc	**1.01**	down	**2.07**	down	**31.52**	up	**1.15**	down	**1.86**	up	**1.11**	down	2
Os.10570.1.S1_at	LOC_Os06g35960	HSF-type DNA-binding domain containing protein, expressed	**1.35**	up	**1.27**	down	**47.71**	up	**1.97**	down	**1.91**	up	**1.15**	down	ABA
Os.10572.1.S1_at	LOC_Os03g59360	remorin, putative, expressed	**1.10**	up	**1.23**	down	**3.00**	up	**1.17**	down	**1.14**	up	**1.16**	down	ABA
Os.10574.1.S1_at	LOC_Os10g02770	glycosyl hydrolases family 16, putative, expressed	**1.20**	down	**1.17**	up	**3.53**	down	**1.11**	up	**1.32**	down	**1.74**	down	ABA
Os.10576.1.S1_at	LOC_Os02g33550	harpin-induced protein 1 domain containing protein, expressed	**1.07**	up	**1.12**	down	**3.12**	down	**1.07**	down	**1.31**	down	**1.24**	up	ABA
Os.10578.1.A1_at	LOC_Os03g20420	alpha-N-arabinofuranosidase A, putative, expressed	**1.07**	up	**1.17**	down	**1.97**	down	**1.04**	down	**1.91**	down	**2.13**	down	JA
Os.10579.1.S1_at	LOC_Os08g02700	fructose-bisphospate aldolase isozyme, putative, expressed	**1.58**	up	**1.39**	down	**5.28**	up	**1.08**	up	**7.72**	up	**4.53**	up	3
Os.10580.1.S1_at	LOC_Os01g34790	expressed protein	**1.00**	down	**2.01**	up	**1.08**	down	**1.00**	up	**1.04**	down	**1.03**	up	BAP
Os.10590.1.S1_at	LOC_Os08g01370	expressed protein similar to seed maturation protein PM28	**1.01**	up	**1.02**	up	**17.92**	up	**1.01**	down	**1.03**	up	**1.09**	up	ABA
Os.10590.1.S1_s_at	LOC_Os08g01370	expressed protein similar to seed maturation protein PM28	**1.01**	down	**1.09**	down	**41.92**	up	**1.02**	up	**1.24**	down	**1.25**	down	ABA
Os.10597.1.S1_at	LOC_Os01g53350	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	**1.04**	up	**1.27**	up	**2.27**	down	**1.08**	up	**1.62**	up	**1.48**	down	ABA
Os.10612.1.S1_at	LOC_Os03g61960	2Fe-2S iron-sulfur cluster binding domain containing protein, expressed	**1.03**	up	**1.00**	down	**1.83**	down	**1.16**	up	**1.29**	up	**2.06**	up	JA
Os.10628.1.S1_at	LOC_Os02g03730	SWIB/MDM2 domain containing protein, expressed	**1.07**	up	**1.06**	up	**2.73**	down	**1.01**	down	**1.55**	down	**1.38**	down	ABA
Os.10652.1.S1_at	LOC_Os03g03810	DEF8 - Defensin and Defensin-like DEFL family, expressed	**1.17**	down	**3.59**	up	**5.59**	up	**1.06**	up	**1.38**	down	**1.86**	up	2
Os.10657.1.S1_at	LOC_Os03g63280	regulatory protein, putative, expressed	**1.45**	down	**1.00**	up	**5.20**	up	**2.10**	down	**1.16**	up	**1.27**	up	2
Os.10662.1.S1_at	LOC_Os01g15320	RALFL9 - Rapid ALkalinization Factor RALF family protein precursor, expressed	**1.12**	down	**1.32**	up	**5.54**	down	**1.14**	down	**2.12**	down	**1.09**	down	2
Os.10665.1.S1_at	LOC_Os12g05550	sialyltransferase family domain containing protein, expressed	**1.35**	down	**1.14**	up	**4.77**	down	**1.07**	up	**1.40**	down	**1.10**	up	ABA
Os.10672.1.S1_at	LOC_Os03g10080	expressed protein	**1.06**	up	**1.07**	down	**3.02**	up	**1.24**	down	**1.01**	up	**1.01**	down	ABA
Os.10679.1.S1_at	LOC_Os02g03740	pyridoxal biosynthesis protein PDX2, putative, expressed	**1.55**	up	**1.14**	up	**1.07**	up	**1.31**	up	**2.01**	up	**2.06**	up	2
Os.10683.1.A1_s_at	LOC_Os02g51300	AP2 domain containing protein, expressed	**1.59**	up	**1.10**	down	**2.68**	up	**1.09**	down	**1.23**	up	**1.25**	down	ABA
Os.10686.1.S1_at	LOC_Os06g41770	bZIP transcription factor domain containing protein, expressed	**1.05**	up	**1.34**	up	**2.03**	down	**1.00**	down	**1.06**	down	**1.00**	up	ABA
Os.10689.1.S1_at	LOC_Os06g02019	cytochrome P450, putative, expressed	**1.51**	up	**1.60**	up	**1.64**	down	**1.26**	up	**3.42**	down	**2.55**	down	2
Os.10733.1.S1_at	LOC_Os07g38130	polygalacturonase inhibitor 1 precursor, putative, expressed	**1.42**	up	**1.25**	up	**7.12**	up	**1.44**	up	**1.32**	up	**1.06**	up	ABA
Os.10735.1.S1_at	LOC_Os09g36860	acyl carrier protein, putative, expressed	**1.07**	down	**1.05**	down	**2.08**	down	**1.05**	down	**1.12**	down	**1.22**	up	ABA
Os.10754.1.S1_at	LOC_Os03g06520	sulfate transporter, putative, expressed	**1.11**	down	**1.25**	up	**13.52**	up	**1.42**	down	**1.02**	up	**1.36**	up	ABA
Os.10760.1.S1_at	LOC_Os01g62110	expressed protein	**1.10**	up	**1.10**	up	**11.64**	down	**2.51**	down	**1.12**	up	**3.79**	down	3
Os.10765.1.S1_at	LOC_Os11g07960	transferase family protein, putative, expressed	**3.50**	up	**1.42**	up	**1.01**	down	**1.94**	up	**2.48**	up	**1.26**	up	2
Os.10779.1.S1_at	LOC_Os03g14690	vacuolar ATP synthase 98 kDa subunit, putative, expressed	**1.02**	up	**1.10**	down	**2.26**	up	**1.01**	down	**1.74**	up	**1.34**	up	ABA
Os.10786.1.S1_at	LOC_Os03g31550	aldehyde oxidase, putative, expressed	**1.04**	up	**1.09**	up	**2.32**	up	**1.05**	up	**1.42**	up	**1.15**	up	ABA
Os.10800.1.S1_at	LOC_Os03g21900	uroporphyrinogen decarboxylase, putative, expressed	**1.14**	up	**1.12**	up	**3.11**	down	**1.21**	down	**1.58**	down	**1.37**	down	ABA
Os.10817.3.S1_x_at	LOC_Os11g32110	auxin response factor, putative, expressed	**2.27**	up	**1.13**	up	**1.22**	up	**1.09**	down	**1.02**	up	**1.08**	up	IAA
Os.10820.1.S1_at	LOC_Os10g39220	tobamovirus multiplication protein, putative, expressed	**1.22**	up	**1.16**	down	**3.53**	up	**1.10**	up	**1.66**	up	**1.20**	up	ABA
Os.10845.1.S1_s_at	LOC_Os03g60370	histidine acid phosphatase, putative, expressed	**1.01**	up	**1.16**	down	**4.64**	up	**1.08**	down	**2.73**	up	**1.27**	up	2
Os.10853.1.S1_at	LOC_Os02g39930	OsTIL-1 Temperature-induced lipocalin-1, expressed	**1.35**	up	**1.03**	up	**3.05**	up	**1.22**	down	**1.21**	up	**1.10**	down	ABA

Os.10855.1.S1_at	LOC_Os03g56060	CSLC9 - cellulose synthase-like family C, expressed	**1.23**	up	**1.20**	up	**4.17**	up	**1.29**	up	**1.39**	up	**1.08**	up	ABA
Os.10859.1.S1_a_at	LOC_Os01g67290	cyclin-related protein, putative, expressed	**1.27**	up	**1.11**	down	**2.31**	up	**1.00**	down	**1.10**	up	**1.12**	up	ABA
Os.10860.2.S1_at	LOC_Os04g44320	transposon protein, putative, unclassified, expressed	**1.12**	down	**1.02**	down	**3.81**	down	**1.03**	up	**1.48**	down	**2.30**	down	2
Os.10870.1.S1_at	LOC_Os02g51890	RNA recognition motif containing protein, putative, expressed	**1.39**	up	**1.23**	down	**4.17**	up	**1.52**	up	**2.15**	up	**1.74**	down	2
Os.10872.1.S1_at	LOC_Os07g09420	ATPase, putative, expressed	**2.08**	up	**1.44**	up	**1.70**	up	**1.12**	up	**2.96**	up	**2.16**	up	3
Os.10884.1.S1_at	LOC_Os03g58790	ATPase, putative, expressed	**1.55**	up	**1.36**	up	**2.32**	down	**1.18**	up	**4.19**	up	**1.07**	up	2
Os.10926.1.S1_at	LOC_Os07g14850	CESA6 - cellulose synthase, expressed	**1.09**	down	**1.07**	down	**2.15**	down	**1.15**	down	**1.58**	down	**1.31**	up	ABA
Os.10930.1.S1_at	LOC_Os02g41670	phenylalanine ammonia-lyase, putative, expressed	**1.01**	down	**1.39**	up	**14.26**	down	**1.31**	up	**1.25**	down	**2.72**	up	2
Os.10933.1.S1_at	LOC_Os01g50910	late embryogenesis abundant protein, group 3, putative, expressed	**1.04**	up	**1.07**	up	**98.33**	up	**1.73**	down	**3.79**	up	**2.90**	up	3
Os.10937.1.S1_at	LOC_Os03g09250	inositol-3-phosphate synthase, putative, expressed	**1.12**	down	**1.14**	down	**3.97**	up	**1.01**	down	**1.45**	up	**1.09**	up	ABA
Os.10956.1.S1_at	LOC_Os01g62370	ENTH domain containing protein, expressed	**1.04**	down	**1.18**	down	**2.25**	up	**1.04**	up	**1.13**	down	**1.41**	down	ABA
Os.10960.1.S1_at	LOC_Os09g39670	oxidoreductase, short chain dehydrogenase/reductase family domain containing family,	**1.08**	down	**1.19**	down	**2.12**	down	**1.07**	down	**1.29**	down	**1.06**	down	ABA
Os.10972.1.S1_at	LOC_Os01g65670	amino acid transporter, putative, expressed	**1.15**	down	**1.35**	down	**2.81**	up	**1.97**	down	**1.38**	up	**1.63**	down	ABA
Os.10972.2.S1_x_at	LOC_Os01g65670	amino acid transporter, putative, expressed	**1.04**	down	**1.29**	down	**4.37**	up	**1.33**	down	**1.36**	up	**1.18**	down	ABA
Os.10982.1.S1_at	LOC_Os02g46170	senescence-associated protein-related	**1.65**	up	**1.92**	up	**5.82**	up	**2.19**	down	**2.19**	down	**3.19**	down	4
Os.10991.1.S1_at	LOC_Os06g13810	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta, putative, exp	**1.03**	down	**1.09**	up	**2.08**	down	**1.04**	up	**1.31**	down	**1.11**	down	ABA
Os.11018.1.S1_at	LOC_Os08g33710	ribonuclease T2 family domain containing protein, expressed	**1.11**	up	**1.24**	down	**6.31**	up	**1.17**	down	**2.67**	up	**1.12**	up	2
Os.11039.1.S1_s_at	LOC_Os04g01740	heat shock protein, putative, expressed	**1.75**	down	**1.07**	down	**1.64**	up	**1.14**	down	**18.55**	up	**6.49**	up	2
Os.11039.3.S1_at	LOC_Os04g01740	heat shock protein, putative, expressed	**1.04**	down	**1.00**	up	**1.33**	up	**1.02**	down	**18.99**	up	**10.08**	up	2
Os.11040.1.S1_x_at	LOC_Os10g31320	retrotransposon protein, putative, unclassified, expressed	**1.15**	down	**1.18**	down	**3.90**	up	**1.06**	down	**1.13**	up	**1.66**	up	ABA
Os.11053.1.S1_at	LOC_Os08g36440	HVA22, putative, expressed	**1.47**	up	**1.08**	up	**110.29**	up	**1.02**	down	**1.16**	down	**1.27**	down	ABA
Os.11053.1.S1_s_at	LOC_Os08g36440	HVA22, putative, expressed	**1.01**	down	**1.21**	up	**44.45**	up	**1.11**	down	**1.07**	down	**1.24**	down	ABA
Os.11061.1.S1_at	LOC_Os10g05210	OsFBX368 - F-box domain containing protein, expressed	**1.38**	up	**1.01**	down	**2.47**	up	**1.10**	up	**1.27**	up	**1.27**	up	ABA
Os.11064.1.S1_a_at	LOC_Os10g25010	OsCML8 - Calmodulin-related calcium sensor protein, expressed	**1.06**	up	**1.30**	down	**3.85**	up	**1.01**	down	**1.53**	up	**1.16**	down	ABA
Os.11076.1.S1_at	LOC_Os12g43550	ras-related protein, putative, expressed	**1.12**	down	**1.18**	down	**2.18**	up	**1.15**	up	**1.41**	up	**1.01**	up	ABA
Os.11092.1.S1_at	LOC_Os04g32950	calreticulin precursor protein, putative, expressed	**1.15**	down	**1.01**	down	**2.31**	down	**1.02**	up	**1.35**	down	**1.10**	up	ABA
Os.11106.1.S1_at	LOC_Os06g46900	phosphosulfolactate synthase-related protein, putative, expressed	**1.07**	down	**1.10**	down	**11.00**	up	**1.02**	up	**1.42**	up	**1.35**	down	ABA
Os.11129.1.S1_at	LOC_Os10g35840	shikimate/quinate 5-dehydrogenase, putative, expressed	**1.71**	up	**1.19**	up	**3.04**	down	**1.24**	down	**1.59**	down	**1.29**	down	ABA
Os.11139.1.S1_at	LOC_Os05g49880	lactate/malate dehydrogenase, putative, expressed	**1.06**	down	**1.06**	up	**2.04**	down	**1.04**	up	**1.11**	down	**1.05**	down	ABA
Os.11143.1.S1_at	LOC_Os03g51980	expressed protein	**1.06**	up	**2.40**	up	**6.95**	up	**1.41**	up	**1.26**	down	**2.02**	down	3
Os.11151.1.S1_a_at	LOC_Os01g61670	ureidoglycolate hydrolase, putative, expressed	**1.06**	down	**1.14**	down	**2.36**	up	**1.09**	down	**1.32**	up	**1.31**	up	ABA
Os.11154.1.S1_a_at	LOC_Os03g06705	3-ketoacyl-CoA synthase, putative, expressed	**1.17**	up	**1.29**	up	**1.42**	down	**4.07**	up	**1.56**	down	**1.00**	up	ACC
Os.11164.1.S1_at	LOC_Os07g03279	SCP-like extracellular protein, expressed	**1.12**	down	**1.21**	up	**2.47**	down	**1.34**	up	**1.16**	down	**1.78**	up	ABA
Os.11166.1.S1_s_at	LOC_Os01g09830	OsGrx_A2 - glutaredoxin subgroup III, expressed	**1.55**	down	**1.07**	down	**2.41**	down	**1.15**	up	**1.30**	down	**1.62**	up	ABA
Os.11183.1.S1_s_at	LOC_Os06g18000	protein kinase domain containing protein, expressed	**1.04**	down	**1.05**	up	**3.01**	down	**1.18**	up	**1.04**	down	**1.12**	down	ABA
Os.11185.1.S1_a_at	LOC_Os02g17500	transporter family protein, putative, expressed	**1.04**	up	**1.14**	down	**2.63**	up	**1.14**	down	**1.18**	up	**1.36**	up	ABA
Os.11193.1.S1_at	LOC_Os03g55240	cytochrome P450, putative, expressed	**1.11**	up	**1.50**	up	**2.65**	up	**1.53**	down	**2.99**	up	**1.16**	down	2
Os.11195.1.S1_at	LOC_Os07g17330	B12D protein, putative, expressed	**1.10**	up	**1.02**	down	**1.39**	up	**1.05**	up	**2.83**	up	**2.60**	up	2
Os.11197.2.S1_x_at	LOC_Os09g30438	expressed protein	**1.22**	up	**1.28**	down	**2.53**	down	**1.01**	up	**4.01**	up	**1.16**	up	2
Os.11198.1.S1_a_at	LOC_Os07g43940	X8 domain containing protein, expressed	**1.12**	down	**1.02**	up	**2.63**	up	**1.07**	down	**1.03**	up	**1.08**	down	ABA
Os.11198.3.S1_x_at	LOC_Os07g43940	X8 domain containing protein, expressed	**1.11**	up	**1.15**	up	**3.25**	up	**1.23**	down	**1.07**	up	**1.46**	down	ABA
Os.11202.1.S1_at	LOC_Os08g06100	O-methyltransferase, putative, expressed	**1.00**	up	**1.00**	up	**2.16**	down	**1.11**	down	**1.30**	down	**1.05**	down	ABA
Os.11212.1.S1_at	LOC_Os07g18750	LTPL42 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.09**	down	**1.08**	up	**3.19**	down	**1.16**	down	**1.70**	down	**1.97**	down	ABA
Os.11219.1.S1_at	LOC_Os03g17084	Core histone H2A	**1.66**	down	**1.22**	down	**2.31**	up	**1.08**	up	**1.22**	up	**1.14**	down	ABA
Os.11222.1.S1_at	LOC_Os01g40630	uncharacterized protein PA4923, putative, expressed	**2.39**	up	**1.31**	up	**2.84**	down	**1.37**	down	**1.57**	down	**1.05**	up	2
Os.11222.2.S1_x_at	LOC_Os01g40630	uncharacterized protein PA4923, putative, expressed	**2.65**	up	**1.41**	up	**2.59**	down	**1.60**	down	**1.57**	down	**1.03**	up	2
Os.11225.1.S1_at	LOC_Os07g40850	retrotransposon protein, putative, unclassified, expressed	**1.14**	up	**1.44**	up	**4.73**	up	**1.23**	down	**1.39**	up	**1.16**	up	ABA
Os.11240.1.S1_at	LOC_Os01g03914	cation efflux family protein, putative, expressed	**1.01**	down	**1.00**	up	**3.50**	up	**1.07**	up	**1.07**	up	**1.04**	down	ABA
Os.11241.1.S1_at	LOC_Os11g03240	MATE efflux family protein, putative, expressed	**2.18**	down	**1.31**	down	**1.50**	down	**1.07**	up	**1.67**	down	**1.06**	up	IAA
Os.11249.1.S1_at	LOC_Os05g15630	membrane associated DUF588 domain containing protein, putative, expressed	**1.19**	up	**1.24**	up	**2.91**	up	**1.56**	down	**1.20**	down	**1.32**	down	ABA
Os.11250.1.S1_at	LOC_Os02g13800	HSF-type DNA-binding domain containing protein, expressed	**1.01**	up	**1.66**	down	**36.43**	up	**1.31**	down	**1.36**	up	**1.08**	down	ABA
Os.11252.1.S1_at	LOC_Os02g37160	heavy metal transport/detoxification protein, putative, expressed	**1.62**	down	**1.31**	up	**2.67**	down	**1.28**	up	**1.07**	up	**1.13**	down	ABA
Os.11260.1.S1_at	LOC_Os05g31670	AWPM-19-like membrane family protein, putative, expressed	**1.04**	down	**1.02**	down	**4.40**	up	**1.02**	down	**1.24**	up	**1.17**	up	ABA
Os.11266.1.S1_at	LOC_Os04g27060	oxidoreductase, aldo/keto reductase family protein, putative, expressed	**3.92**	up	**1.30**	down	**1.14**	down	**1.09**	up	**11.94**	up	**2.07**	up	3
Os.11284.1.S1_at	LOC_Os08g01760	dehydrogenase, putative, expressed	**1.23**	up	**1.26**	down	**1.36**	up	**1.20**	up	**2.14**	up	**1.88**	up	SA

Os.11286.1.A1_at	LOC_Os04g13140	vignain precursor, putative, expressed	**2.13**	down	**4.87**	down	**4.69**	down	**1.83**	down	**2.53**	up	**1.33**	up	4
Os.11287.1.S1_at	LOC_Os06g50920	protein kinase family protein, putative, expressed	**1.02**	up	**1.38**	up	**2.69**	up	**1.38**	up	**2.63**	up	**2.12**	up	3
Os.11296.1.S1_a_at	LOC_Os09g11460	AP2 domain containing protein, expressed	**1.00**	up	**1.45**	up	**2.34**	down	**2.74**	up	**1.15**	up	**1.92**	down	2
Os.11300.2.S1_at	LOC_Os10g38910	expressed protein	**1.32**	up	**1.31**	up	**2.33**	down	**1.14**	down	**1.24**	down	**1.45**	down	ABA
Os.11303.1.S1_at	LOC_Os01g72170	glutathione S-transferase, putative, expressed	**1.35**	up	**1.13**	up	**1.99**	down	**1.01**	up	**2.47**	up	**1.26**	down	SA
Os.11303.1.S1_s_at	LOC_Os01g72170	glutathione S-transferase, putative, expressed	**1.41**	up	**1.07**	up	**1.99**	down	**1.01**	down	**2.54**	up	**1.01**	down	SA
Os.11305.1.S1_at	LOC_Os12g29400	GRAM domain containing protein, expressed	**1.29**	down	**1.31**	down	**55.52**	up	**1.62**	down	**4.70**	up	**1.06**	up	2
Os.11307.1.S1_at	LOC_Os06g40440	expressed protein	**1.02**	up	**1.06**	down	**3.18**	down	**1.01**	up	**1.26**	down	**1.11**	up	ABA
Os.11309.1.S1_x_at	LOC_Os05g04490	peroxidase precursor, putative, expressed	**1.13**	down	**1.52**	up	**4.87**	down	**1.42**	up	**1.24**	down	**1.37**	down	ABA
Os.1131.1.S1_at	LOC_Os06g16350	peroxidase precursor, putative, expressed	**1.01**	up	**1.13**	up	**3.76**	up	**1.20**	down	**1.50**	up	**1.25**	down	ABA
Os.1131.2.S1_x_at	LOC_Os06g16350	peroxidase precursor, putative, expressed	**1.42**	up	**1.25**	up	**4.29**	up	**1.33**	down	**1.40**	up	**1.16**	down	ABA
Os.11323.1.S1_at	LOC_Os03g20120	glycosyl transferase 8 domain containing protein, putative, expressed	**1.08**	down	**1.51**	up	**2.30**	up	**1.26**	down	**1.77**	down	**1.07**	up	ABA
Os.11327.1.S1_at	LOC_Os03g18120	proteins of unknown function domain containing protein, expressed	**1.03**	down	**1.03**	up	**2.39**	up	**1.47**	up	**1.59**	up	**1.49**	up	ABA
Os.11330.1.S2_at	AK105524	Oryza sativa aquaporin (PIP2a) mRNA, complete cds	**1.03**	up	**1.20**	up	**2.21**	down	**1.66**	down	**1.42**	up	**2.65**	up	2
Os.11331.1.S1_at	LOC_Os08g10500	Oryza sativa Japonica Group cDNA clone:001-105-E11, full insert sequence.	**1.04**	up	**1.01**	up	**21.10**	up	**1.66**	down	**2.00**	up	**1.27**	down	ABA
Os.11334.1.S1_x_at	LOC_Os09g25090	CAMK_KIN1/SNF1/Nim1_like.34 - CAMK includes calcium/calmodulin depedent protei	**1.16**	up	**1.17**	up	**12.06**	up	**1.41**	up	**3.35**	up	**1.46**	down	2
Os.11335.1.S1_at	LOC_Os04g33450	expressed protein	**1.32**	up	**1.10**	up	**7.71**	down	**1.34**	down	**1.80**	down	**1.14**	down	ABA
Os.11335.3.S1_x_at	LOC_Os01g52260	serine acetyltransferase protein, putative, expressed	**3.00**	up	**1.14**	down	**6.60**	up	**1.07**	up	**7.17**	up	**2.02**	up	4
Os.11354.1.S1_at	LOC_Os04g51460	glycosyl hydrolases family 16, putative, expressed	**3.00**	up	**1.96**	up	**5.39**	up	**1.83**	up	**2.07**	up	**1.34**	up	3
Os.11356.1.A1_at	LOC_Os02g12670	protein kinase family protein, putative, expressed	**1.06**	up	**1.06**	down	**2.47**	up	**1.29**	down	**1.16**	up	**1.04**	up	ABA
Os.11364.1.S1_at	LOC_Os12g33080	2-oxoglutarate/malate translocator, chloroplast precursor, putative, expressed	**1.00**	down	**1.01**	down	**2.97**	down	**1.04**	down	**1.55**	down	**1.11**	down	ABA
Os.11365.1.S1_at	LOC_Os02g52210	zinc finger, C3HC4 type domain containing protein, expressed	**1.08**	up	**1.36**	down	**9.85**	up	**1.02**	down	**1.32**	up	**3.17**	up	2
Os.11368.1.S1_at	LOC_Os02g37800	lecithin:cholesterol acyltransferase, putative, expressed	**1.10**	up	**1.01**	up	**2.08**	down	**1.27**	down	**1.06**	down	**1.22**	up	ABA
Os.11383.1.S1_a_at	LOC_Os07g22400	POLA3 - Putative DNA polymerase alpha complex subunit, expressed	**1.26**	down	**1.02**	down	**5.05**	down	**1.09**	down	**2.58**	down	**1.79**	down	2
Os.11385.1.S1_a_at	LOC_Os11g34270	ubiquitin carboxyl-terminal hydrolase domain containing protein, expressed	**1.28**	up	**1.01**	up	**3.95**	up	**1.02**	down	**1.25**	up	**1.50**	down	ABA
Os.11392.2.S1_at	LOC_Os02g07820	DUF581 domain containing protein, expressed	**1.14**	down	**1.16**	up	**4.58**	down	**1.34**	down	**1.34**	down	**1.28**	down	ABA
Os.11393.1.S1_at	LOC_Os06g47200	LTPL85 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.25**	up	**1.15**	down	**3.55**	up	**1.01**	up	**3.95**	up	**1.30**	up	2
Os.11393.1.S2_at	LOC_Os06g47200	LTPL85 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.06**	up	**1.09**	down	**2.11**	up	**1.01**	up	**1.85**	up	**1.18**	up	ABA
Os.11407.1.S1_at	LOC_Os04g57550	amine oxidase, flavin-containing, domain containing protein, expressed	**1.43**	up	**1.13**	up	**3.54**	up	**1.22**	up	**3.49**	up	**2.02**	up	3
Os.11408.1.S1_at	LOC_Os09g37100	phospholipase D, putative, expressed	**1.01**	down	**1.12**	up	**5.49**	up	**1.65**	down	**1.13**	down	**1.43**	down	ABA
Os.11408.1.S2_at	LOC_Os09g37100	phospholipase D, putative, expressed	**1.00**	down	**1.05**	up	**8.13**	up	**1.23**	down	**1.37**	up	**1.14**	up	ABA
Os.11419.1.S1_at	LOC_Os03g11910	DnaK family protein, putative, expressed	**1.15**	down	**1.05**	down	**5.01**	up	**1.05**	down	**1.58**	up	**1.17**	down	ABA
Os.11421.1.S1_at	LOC_Os03g58170	stem-specific protein TSJT1, putative, expressed	**1.12**	up	**1.02**	up	**7.32**	up	**1.12**	up	**1.58**	up	**1.04**	down	ABA
Os.11421.2.S1_x_at	LOC_Os03g58170	stem-specific protein TSJT1, putative, expressed	**1.00**	up	**1.04**	down	**7.13**	up	**1.05**	down	**1.54**	up	**1.37**	down	ABA
Os.11423.1.S1_at	LOC_Os11g17610	expressed protein	**1.06**	down	**1.05**	down	**3.97**	up	**1.17**	up	**1.34**	up	**1.23**	up	ABA
Os.11443.1.S1_a_at	LOC_Os01g65630	expressed protein	**1.28**	down	**1.24**	up	**3.91**	down	**1.63**	down	**1.30**	down	**1.80**	down	ABA
Os.11450.1.S1_at	LOC_Os01g52110	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	**1.21**	up	**1.16**	down	**18.58**	up	**1.00**	down	**1.81**	up	**1.39**	down	ABA
Os.11450.1.S2_a_at	LOC_Os01g52110	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	**1.11**	up	**1.04**	down	**17.02**	up	**1.28**	up	**1.76**	up	**1.17**	down	ABA
Os.11450.1.S3_a_at	LOC_Os01g52110	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	**1.10**	up	**1.05**	down	**11.84**	up	**1.31**	up	**1.64**	up	**1.28**	down	ABA
Os.11460.1.S1_at	LOC_Os07g46490	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed	**2.19**	up	**1.00**	down	**2.20**	down	**1.14**	down	**1.20**	down	**1.17**	down	2
Os.11464.1.S1_at	LOC_Os03g41510	oxidoreductase, aldo/keto reductase family protein, putative, expressed	**1.13**	up	**1.03**	up	**2.09**	down	**1.18**	down	**1.35**	down	**1.27**	down	ABA
Os.11471.1.S1_at	LOC_Os04g54610	Conserved hypothetical protein	**1.15**	up	**2.78**	up	**1.00**	up	**3.44**	down	**1.26**	up	**5.26**	up	3
Os.11474.1.S1_at	LOC_Os02g51350	OsFBK10 - F-box domain and kelch repeat containing protein, expressed	**1.06**	up	**1.18**	down	**2.51**	up	**1.20**	up	**2.24**	up	**1.49**	up	2
Os.11491.1.S1_at	LOC_Os03g19290	mitochondrial import inner membrane translocase subunit Tim17, putative, expressed	**1.29**	up	**1.14**	up	**75.29**	up	**1.80**	down	**1.04**	up	**1.08**	up	ABA
Os.11493.1.A1_at	LOC_Os05g35580	amidophosphoribosyltransferase, chloroplast precursor, putative, expressed	**1.28**	up	**1.22**	up	**3.77**	down	**1.17**	up	**1.22**	down	**1.10**	down	ABA
Os.11520.1.S1_at	AK288438	Oryza sativa Japonica Group cDNA, clone: J090034C21, full insert sequence.	**1.10**	down	**1.27**	down	**3.08**	down	**1.49**	down	**1.36**	down	**2.44**	down	2
Os.1153.1.S1_at	LOC_Os01g15830	peroxidase precursor, putative, expressed	**1.18**	up	**1.02**	down	**1.93**	up	**1.20**	down	**1.23**	up	**2.30**	up	JA
Os.11530.1.S1_at	LOC_Os04g31820	hypothetical protein	**1.08**	down	**1.03**	down	**2.09**	down	**1.26**	down	**1.44**	down	**1.23**	down	ABA
Os.11534.1.S1_at	LOC_Os05g10670	zinc finger CCCH type family protein, putative, expressed	**1.17**	up	**1.24**	down	**11.03**	up	**1.10**	up	**1.33**	up	**1.78**	down	ABA
Os.11546.1.S1_at	LOC_Os06g35520	peroxidase precursor, putative, expressed	**2.06**	down	**1.03**	up	**1.66**	down	**2.73**	up	**1.89**	up	**4.87**	up	3
Os.11547.1.S1_s_at	LOC_Os06g48030	peroxidase precursor, putative, expressed	**1.01**	up	**1.60**	up	**4.23**	up	**1.36**	up	**1.21**	up	**1.60**	down	ABA
Os.11548.1.S1_at	LOC_Os03g55420	peroxidase precursor, putative, expressed	**1.44**	down	**1.06**	up	**5.27**	up	**1.98**	up	**1.57**	up	**1.59**	up	ABA
Os.11549.1.S1_at	LOC_Os12g02080	peroxidase precursor, putative, expressed	**1.13**	down	**1.57**	up	**2.51**	up	**1.40**	down	**1.86**	up	**1.18**	down	ABA
Os.11551.1.S1_at	LOC_Os05g04410	peroxidase precursor, putative, expressed	**1.05**	up	**1.19**	down	**2.28**	down	**1.52**	up	**1.01**	up	**2.32**	up	2
Os.11552.1.S1_at	LOC_Os04g59150	peroxidase precursor, putative, expressed	**1.23**	up	**1.11**	up	**3.50**	down	**1.27**	up	**2.35**	down	**1.97**	up	2

Os.11552.1.S2_at	LOC_Os04g59150	peroxidase precursor, putative, expressed	**1.05**	up	**1.23**	up	**2.55**	down	**1.58**	up	**1.91**	down	**2.12**	up	2
Os.11553.1.S1_at	LOC_Os03g02939	peroxidase precursor, putative, expressed	**3.46**	down	**2.63**	down	**15.08**	down	**1.06**	down	**1.45**	down	**1.61**	down	3
Os.11556.1.S1_at	LOC_Os07g48030	peroxidase precursor, putative, expressed	**2.69**	down	**1.24**	down	**22.56**	down	**1.16**	down	**6.52**	down	**1.20**	down	3
Os.11575.1.S1_a_at	LOC_Os03g46440	BTBA4 - Bric-a-Brac,Tramtrack, Broad Complex BTB domain with Ankyrin repeat regior	**1.15**	down	**1.25**	down	**3.84**	down	**1.07**	up	**1.14**	down	**1.32**	up	ABA
Os.11575.3.S1_x_at	LOC_Os08g40480	transposon protein, putative, Pong sub-class, expressed	**1.50**	down	**1.19**	down	**5.48**	down	**1.05**	up	**1.06**	down	**1.53**	up	ABA
Os.11578.1.S1_at	LOC_Os08g40160	thylakoid lumen protein, chloroplast precursor, putative, expressed	**1.13**	up	**1.10**	up	**3.18**	down	**1.07**	down	**1.66**	down	**1.32**	down	ABA
Os.11580.1.S1_at	LOC_Os06g01972	auxin-induced protein 5NG4, putative, expressed	**1.63**	up	**1.65**	up	**10.40**	down	**1.12**	up	**3.09**	down	**2.05**	up	3
Os.11604.1.S1_at	LOC_Os10g42190	leucine rich repeat containing protein, expressed	**1.56**	down	**1.35**	down	**2.29**	up	**1.07**	up	**1.19**	up	**1.12**	down	ABA
Os.11610.1.S1_at	LOC_Os02g42020	expressed protein	**1.17**	up	**1.15**	down	**5.30**	up	**1.13**	down	**1.83**	up	**1.03**	down	ABA
Os.11610.2.S1_at	LOC_Os02g42020	expressed protein	**1.02**	down	**1.61**	down	**2.20**	up	**1.08**	down	**1.48**	up	**1.35**	up	ABA
Os.11622.1.S1_at	LOC_Os06g01360	homogentisate 1,2-dioxygenase, putative, expressed	**1.12**	up	**1.00**	down	**2.79**	up	**1.27**	up	**1.34**	up	**1.24**	up	ABA
Os.11634.1.S1_at	LOC_Os02g05630	protein phosphatase 2C, putative, expressed	**1.24**	up	**1.06**	down	**2.08**	up	**1.04**	down	**1.03**	up	**1.06**	down	ABA
Os.11651.1.S1_at	NM_001060567	Oryza sativa (japonica cultivar-group) Os04g0639200 (Os04g0639200) mRNA, comple	**1.68**	up	**1.42**	down	**2.48**	up	**1.10**	down	**1.35**	up	**1.09**	up	ABA
Os.11657.1.S1_at	LOC_Os01g47760	OsGrx_I1 - glutaredoxin subgroup III, expressed	**1.81**	up	**1.20**	up	**2.23**	up	**1.16**	up	**1.94**	up	**1.51**	up	ABA
Os.11665.1.S1_at	LOC_Os01g58790	GHMP kinases ATP-binding protein, putative, expressed	**1.79**	down	**1.24**	down	**1.44**	down	**1.06**	down	**1.25**	down	**2.18**	up	JA
Os.11666.1.S1_at	LOC_Os09g36200	senescence-inducible chloroplast stay-green protein 1, putative, expressed	**1.26**	down	**1.05**	down	**10.50**	up	**1.01**	up	**1.40**	up	**4.37**	up	2
Os.11666.1.S1_s_at	LOC_Os09g36200	senescence-inducible chloroplast stay-green protein 1, putative, expressed	**1.04**	up	**1.03**	up	**9.95**	up	**1.13**	up	**1.46**	up	**4.18**	up	2
Os.11704.1.S1_at	LOC_Os03g58090	expressed protein	**1.02**	up	**1.00**	up	**2.11**	down	**1.06**	down	**1.25**	down	**1.26**	down	ABA
Os.11711.1.S1_at	LOC_Os12g17880	armadillo/beta-catenin repeat protein-related, putative, expressed	**1.10**	up	**1.09**	down	**3.28**	down	**1.43**	up	**1.19**	up	**1.24**	down	ABA
Os.11717.1.S1_at	LOC_Os01g50450	expressed protein	**1.18**	up	**1.14**	down	**3.09**	up	**1.23**	up	**1.27**	up	**1.13**	up	ABA
Os.11724.2.S1_s_at	LOC_Os06g24730	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.20**	up	**1.25**	down	**7.67**	up	**1.05**	up	**1.16**	up	**1.11**	up	ABA
Os.11724.2.S2_s_at	LOC_Os06g24730	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.25**	down	**1.19**	down	**4.09**	up	**1.13**	up	**1.31**	up	**1.31**	up	ABA
Os.11730.1.S1_at	LOC_Os05g21180	phosphatidic acid phosphatase-related, putative, expressed	**1.33**	up	**1.09**	down	**3.29**	up	**1.21**	up	**1.54**	up	**1.63**	up	ABA
Os.11736.1.S1_at	LOC_Os02g22100	OsRhmbd6 - Putative Rhomboid homologue, expressed	**1.25**	up	**1.18**	down	**3.81**	down	**1.41**	down	**1.58**	down	**1.71**	down	ABA
Os.11752.1.S1_at	LOC_Os04g35570	Regulator of chromosome condensation domain containing protein, expressed	**1.03**	up	**1.11**	down	**2.23**	down	**1.10**	down	**1.14**	down	**1.31**	up	ABA
Os.11757.1.S1_at	LOC_Os03g48660	DUF1336 domain containing protein, expressed	**1.01**	down	**1.12**	down	**2.05**	up	**1.01**	up	**1.16**	up	**1.28**	up	ABA
Os.11766.1.S1_at	LOC_Os07g36170	chitin-inducible gibberellin-responsive protein, putative, expressed	**1.59**	up	**1.01**	up	**2.66**	up	**1.01**	down	**1.57**	up	**1.07**	down	ABA
Os.11771.1.S1_at	LOC_Os06g12320	transmembrane amino acid transporter protein, putative, expressed	**1.46**	up	**1.41**	up	**9.66**	down	**1.74**	down	**6.25**	down	**4.12**	up	3
Os.11781.1.S1_at	LOC_Os02g52780	bZIP transcription factor, putative, expressed	**1.19**	up	**1.51**	down	**7.07**	up	**1.31**	down	**1.52**	up	**1.32**	up	ABA
Os.11789.1.S1_at	LOC_Os03g01880	possible lysine decarboxylase domain containing protein, expressed	**4.75**	up	**1.25**	down	**1.28**	up	**2.13**	down	**1.63**	up	**1.39**	up	2
Os.11798.1.S1_at	LOC_Os07g40290	OsGH3.8 - Probable indole-3-acetic acid-amido synthetase, expressed	**6.94**	up	**2.33**	up	**1.09**	up	**1.29**	up	**1.11**	up	**1.17**	down	2
Os.11803.1.A1_at	AU056598		**1.66**	up	**1.12**	up	**2.83**	up	**1.12**	down	**1.34**	up	**1.08**	up	ABA
Os.11808.1.S1_at	LOC_Os03g06580	MTN26L2 - MtN26 family protein precursor, expressed	**1.31**	up	**1.07**	down	**4.50**	up	**1.16**	up	**1.30**	up	**1.02**	down	ABA
Os.11808.2.S1_at	NM_187768		**2.26**	up	**1.07**	up	**11.88**	up	**1.00**	up	**1.01**	down	**1.07**	down	2
Os.11808.2.S1_x_at	LOC_Os03g06580	MTN26L2 - MtN26 family protein precursor, expressed	**1.14**	up	**1.11**	down	**4.86**	up	**1.05**	up	**1.09**	up	**1.09**	down	ABA
Os.11816.1.S1_at	LOC_Os04g37490	oxidoreductase, aldo/keto reductase family protein, putative, expressed	**9.11**	up	**1.19**	down	**4.26**	up	**1.18**	down	**22.72**	up	**1.18**	up	3
Os.11818.1.S1_at	LOC_Os10g26680	pectinesterase, putative, expressed	**1.02**	down	**1.08**	down	**3.01**	up	**1.50**	up	**1.78**	up	**1.28**	up	ABA
Os.1182.1.S1_x_at	LOC_Os01g03144	white-brown complex homolog protein 7, putative, expressed	**1.19**	up	**1.04**	down	**7.90**	up	**1.20**	up	**2.34**	up	**1.40**	down	2
Os.11826.1.S1_at	LOC_Os06g30130	cysteine-rich receptor-like protein kinase 10 precursor, putative, expressed	**1.14**	up	**1.32**	down	**3.11**	up	**1.18**	up	**1.71**	up	**1.33**	up	ABA
Os.11827.1.S1_a_at	LOC_Os01g34480	NAD dependent epimerase/dehydratase family protein, putative, expressed	**1.74**	up	**1.16**	down	**1.63**	up	**1.16**	up	**2.68**	up	**1.46**	up	SA
Os.11829.1.S2_at	LOC_Os01g25920	expressed protein	**1.42**	down	**1.37**	down	**3.28**	up	**1.59**	down	**5.43**	up	**1.09**	down	2
Os.11833.1.S1_at	LOC_Os07g14610	IAA-amino acid hydrolase ILR1-like 6 precursor, putative, expressed	**1.16**	down	**1.05**	down	**4.31**	up	**1.52**	up	**1.95**	up	**1.07**	up	ABA
Os.11844.1.S1_at	LOC_Os01g37040	retrotransposon protein, putative, Ty1-copia subclass, expressed	**1.23**	up	**1.18**	up	**4.06**	down	**1.17**	down	**1.45**	down	**1.04**	up	ABA
Os.11855.1.S1_at	LOC_Os02g44910	transmembrane protein, putative, expressed	**1.62**	up	**1.07**	down	**4.40**	up	**1.26**	up	**1.42**	up	**1.11**	up	ABA
Os.11875.1.S1_a_at	LOC_Os12g18650	Regulator of chromosome condensation domain containing protein, expressed	**1.09**	up	**1.25**	down	**3.38**	up	**1.09**	up	**1.26**	up	**1.04**	up	ABA
Os.11882.1.S1_at	LOC_Os10g38040	lysM domain containing protein, putative, expressed	**1.11**	up	**1.38**	up	**2.13**	up	**1.21**	up	**2.36**	up	**1.99**	up	2
Os.11885.1.S1_at	LOC_Os08g06010	transporter, major facilitator family, putative, expressed	**1.22**	up	**1.57**	down	**2.77**	up	**1.07**	up	**1.60**	up	**1.41**	down	ABA
Os.1189.1.S1_at	LOC_Os06g16370	CCT/B-box zinc finger protein, putative, expressed	**1.01**	down	**1.00**	up	**3.83**	up	**1.00**	down	**1.00**	up	**1.02**	up	ABA
Os.11897.1.S1_at	LOC_Os03g61150	expressed protein	**1.20**	down	**1.39**	up	**10.68**	up	**1.94**	up	**2.18**	up	**2.72**	down	3
Os.11907.1.S1_at	LOC_Os11g41600	expressed protein	**1.35**	up	**2.06**	down	**5.14**	up	**1.08**	up	**1.78**	up	**2.07**	up	3
Os.11908.1.S1_s_at	LOC_Os11g03230	nucleoside-triphosphatase, putative, expressed	**1.01**	up	**1.27**	down	**2.75**	down	**1.96**	down	**1.31**	up	**2.05**	up	2
Os.11912.1.S1_at	LOC_Os09g25580	monogalactosyldiacylglycerol synthase, putative, expressed	**1.01**	down	**1.05**	up	**2.86**	down	**1.01**	down	**1.27**	down	**1.25**	up	ABA
Os.11914.1.S1_at	LOC_Os06g11240	12-oxophytodienoate reductase, putative, expressed	**5.81**	up	**1.75**	up	**2.00**	down	**1.21**	up	**2.63**	up	**3.71**	up	4
Os.11935.1.S1_at	LOC_Os02g32520	ERD1 protein, chloroplast precursor, putative, expressed	**1.49**	up	**1.12**	down	**6.58**	up	**1.01**	up	**1.25**	up	**1.42**	up	ABA
Os.11939.1.S1_at	LOC_Os10g36000	remorin C-terminal domain containing protein, putative, expressed	**1.39**	up	**1.18**	down	**2.76**	up	**1.79**	down	**1.20**	up	**1.67**	down	ABA

Os.11942.1.S1_at	LOC_Os04g48390	uncharacterized membrane protein, putative, expressed	1.26	up	1.31	down	4.67	up	1.69	down	1.26	up	1.04	up	ABA
Os.11946.1.S1_at	LOC_Os06g21380	OsCttP3 - Putative C-terminal processing peptidase homologue, expressed	1.45	up	1.86	down	6.57	up	1.17	up	1.67	up	1.71	up	ABA
Os.11949.1.S1_at	LOC_Os03g12350	two-component response regulator, putative, expressed	1.18	up	1.20	down	2.52	up	1.05	up	1.32	up	1.03	up	ABA
Os.11960.1.S1_at	LOC_Os07g48160	alpha-galactosidase precursor, putative, expressed	1.11	up	1.09	up	6.28	up	1.11	down	1.21	up	1.51	down	ABA
Os.11963.1.S2_at	LOC_Os04g02910	membrane related protein CP5, putative, expressed	1.08	down	1.02	down	2.04	down	1.19	down	1.27	down	1.14	up	ABA
Os.11967.1.S1_at	LOC_Os03g45170	amino acid permease, putative, expressed	1.11	down	1.38	down	1.51	down	1.30	up	1.21	down	2.01	up	JA
Os.11970.1.S1_at	LOC_Os09g20240	DUF581 domain containing protein, expressed	1.05	up	1.08	down	3.62	down	1.28	up	1.39	down	1.33	down	ABA
Os.11970.2.S1_x_at	LOC_Os09g20240	DUF581 domain containing protein, expressed	1.01	up	1.55	down	3.86	down	1.28	up	1.57	down	1.20	down	ABA
Os.11972.1.S1_at	LOC_Os05g33010	heat shock protein DnaJ, putative, expressed	1.02	up	1.22	up	2.02	up	1.02	up	1.20	up	1.29	down	ABA
Os.11982.1.S1_at	LOC_Os07g07470	transketolase, putative, expressed	1.13	up	1.00	up	3.06	up	1.06	up	1.72	up	1.78	up	ABA
Os.11999.1.S1_at	LOC_Os05g02010	expressed protein	1.18	up	1.07	up	3.15	up	1.19	up	1.41	up	1.15	up	ABA
Os.12012.1.S1_at	LOC_Os10g25290	ZIM domain containing protein, putative, expressed	1.03	up	1.84	up	1.42	up	1.12	up	1.59	up	5.18	up	JA
Os.12021.1.S1_at	LOC_Os12g16290	isoflavone reductase, putative, expressed	1.88	down	1.77	down	4.93	up	1.03	down	1.72	up	1.05	down	ABA
Os.12030.1.S1_at	LOC_Os01g67480	helix-loop-helix DNA-binding domain containing protein, expressed	1.19	up	1.05	down	2.07	up	1.43	up	1.78	up	1.06	down	ABA
Os.12034.2.S1_at	LOC_Os09g39462	nucleic acid binding protein, putative, expressed	2.45	up	1.15	up	1.17	down	1.11	up	1.14	up	1.18	up	IAA
Os.12035.1.S1_at	LOC_Os02g50130	hydrolase, NUDIX family, domain containing protein, expressed	1.21	down	1.11	down	1.78	down	1.25	down	1.42	up	2.03	down	JA
Os.12046.1.S1_at	LOC_Os03g56370	methyltransferase, putative, expressed	1.75	up	1.44	down	3.75	down	1.17	down	1.22	down	1.05	up	ABA
Os.1205.1.S1_at	LOC_Os01g12580	late embryogenesis abundant protein, putative, expressed	1.01	down	2.39	up	904.00	up	1.11	down	1.25	up	1.23	up	2
Os.12058.1.S1_at	LOC_Os02g49870	expressed protein	1.04	up	1.09	up	3.52	down	1.15	down	1.63	down	1.21	down	ABA
Os.12074.1.S1_at	LOC_Os07g09680	ras-related protein, putative, expressed	1.06	up	1.12	down	2.43	up	1.04	up	1.26	up	1.00	down	ABA
Os.12077.1.S1_at	LOC_Os08g44270	vignain precursor, putative, expressed	1.02	up	1.19	up	4.82	up	1.05	down	1.25	down	1.69	down	ABA
Os.12082.1.S1_at	LOC_Os04g39350	heavy metal associated domain containing protein, expressed	1.34	down	1.13	down	2.03	down	1.01	up	1.06	down	1.44	down	ABA
Os.12092.2.S1_a_at	LOC_Os03g05620	inorganic phosphate transporter, putative, expressed	1.07	up	1.16	down	2.31	down	1.09	up	1.04	down	1.18	down	ABA
Os.12094.1.S1_a_at	LOC_Os02g33820	abscisic stress-ripening, putative, expressed	1.05	down	1.01	up	2.45	down	1.00	up	1.11	down	1.48	down	ABA
Os.12134.1.S1_at	LOC_Os04g45810	homeobox associated leucine zipper, putative, expressed	1.13	down	2.45	down	35.35	up	1.49	down	1.46	up	1.12	down	2
Os.12138.1.A1_at	AK062378	Oryza sativa Japonica Group cDNA clone:001-102-B06, full insert sequence.	1.07	down	1.57	up	5.31	up	1.05	up	1.59	up	1.00	up	ABA
Os.12145.1.S1_at	LOC_Os02g47470	cytochrome P450, putative, expressed	1.71	up	1.10	up	6.96	up	1.05	up	1.04	down	1.93	down	ABA
Os.1215.1.S1_at	LOC_Os04g37500	glutamate decarboxylase, putative, expressed	1.18	down	1.04	up	2.55	up	1.08	up	1.16	down	1.54	down	ABA
Os.12163.1.S1_at	LOC_Os03g12510	non-symbiotic hemoglobin 2, putative, expressed	1.76	down	1.17	up	1.85	up	1.80	up	11.44	up	7.25	up	2
Os.12167.1.S1_at	LOC_Os02g44870	dehydrin, putative, expressed	1.04	down	1.13	down	7.54	up	1.15	down	1.34	up	1.75	down	ABA
Os.12186.2.S1_at	BGIOSSFCE010264		1.21	down	1.04	up	2.20	up	1.00	up	1.01	down	1.01	down	ABA
Os.12186.2.S1_x_at	LOC_Os03g21040	stress responsive protein, putative, expressed	1.01	down	1.03	up	3.10	up	1.08	down	1.11	down	1.00	down	ABA
Os.12187.1.S1_at	LOC_Os11g10750	OsSCP48 - Putative Serine Carboxypeptidase homologue, expressed	1.30	down	1.09	down	3.84	down	1.03	up	1.18	down	1.24	down	ABA
Os.12191.1.S1_s_at	LOC_Os03g12510	non-symbiotic hemoglobin 2, putative, expressed	1.55	down	1.20	up	1.15	up	1.37	up	8.56	up	5.18	up	2
Os.12199.1.S1_at	LOC_Os01g66120	No apical meristem protein, putative, expressed	1.52	up	1.04	down	4.21	up	1.17	up	1.18	up	1.80	up	ABA
Os.12200.1.S1_s_at	LOC_Os03g57200	glutathione S-transferase, putative, expressed	7.99	up	1.35	up	5.54	up	1.03	down	13.76	up	4.59	up	4
Os.12216.2.S1_a_at	LOC_Os08g04210	cysteine-rich repeat secretory protein 55 precursor, putative, expressed	1.24	down	1.34	down	19.49	up	1.02	down	13.00	up	1.32	up	2
Os.12219.1.S1_at	LOC_Os01g59930	NADH-cytochrome b5 reductase, putative, expressed	1.06	down	1.13	up	2.29	down	1.09	up	1.16	down	1.29	up	ABA
Os.12221.1.S1_at	LOC_Os07g24000	AWPM-19-like membrane family protein, putative, expressed	1.40	down	1.39	down	70.17	up	1.69	down	2.10	up	1.15	up	2
Os.12223.2.S1_at	LOC_Os03g53410	protein kinase domain containing protein, expressed	1.43	down	1.52	up	6.99	up	1.04	down	1.57	up	1.71	down	ABA
Os.12234.1.S1_s_at	LOC_Os10g40730	expansin precursor, putative, expressed	1.10	down	1.15	down	3.10	down	1.14	up	1.29	down	1.02	down	ABA
Os.12251.1.S1_at	LOC_Os03g49190	oleosin, putative, expressed	2.34	down	1.09	down	48.69	up	1.01	down	1.06	down	1.06	down	2
Os.12252.1.S1_at	LOC_Os03g41060	GASR2 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, putative,	1.04	down	1.50	down	5.33	up	1.52	down	1.01	up	1.68	down	ABA
Os.12253.1.S1_at	LOC_Os01g45110	anthocyanin 3-O-beta-glucosyltransferase, putative, expressed	36.63	up	1.53	up	9.07	up	1.28	up	17.26	up	1.63	up	3
Os.12275.1.S1_at	LOC_Os04g57280	expressed protein	1.00	up	1.01	up	16.81	up	1.01	up	1.00	up	1.03	up	ABA
Os.12281.1.S1_at	LOC_Os05g38150	amino acid kinase, putative, expressed	1.12	up	1.06	down	2.67	up	1.22	up	1.24	up	1.04	down	ABA
Os.12282.1.S1_a_at	LOC_Os11g08569	cycloartenol synthase, putative, expressed	1.20	down	1.57	down	2.13	down	1.40	up	1.01	up	1.13	up	ABA
Os.12288.1.S1_at	LOC_Os08g13920	glycosyl hydrolases family 16, putative, expressed	1.10	down	1.38	up	2.39	down	1.06	down	1.58	down	1.28	up	ABA
Os.12305.1.S1_at	LOC_Os05g44050	ras-related protein, putative, expressed	1.09	up	1.00	up	2.01	up	1.01	up	1.15	up	1.16	up	ABA
Os.12309.1.S1_at	LOC_Os03g40550	kinase, pfkB family, putative, expressed	1.73	up	1.58	up	4.89	down	1.21	down	1.94	down	1.31	down	ABA
Os.12312.1.S1_at	LOC_Os01g69920	histidine kinase, putative, expressed	1.06	up	1.51	down	3.03	up	1.01	down	1.26	up	1.23	up	ABA
Os.12314.1.S1_at	LOC_Os05g07650	transmembrane 9 superfamily member, putative, expressed	1.07	up	1.36	down	2.85	down	1.19	down	1.53	down	1.16	up	ABA
Os.12326.1.S1_s_at	LOC_Os07g42160	HD domain containing protein, putative, expressed	1.11	down	1.50	down	5.13	up	1.05	up	1.53	up	1.10	up	ABA
Os.12329.1.S1_at	LOC_Os01g65920	F-box/LRR-repeat protein 2, putative, expressed	1.16	up	1.06	down	3.11	up	1.07	down	1.25	up	1.31	down	ABA
Os.12340.1.S1_at	LOC_Os01g11730	GDSL-like lipase/acylhydrolase, putative, expressed	1.10	up	1.66	up	10.85	down	2.38	up	3.19	down	1.63	down	3

Os.12342.1.S1_at	LOC_Os12g04204	expressed protein	**1.03**	down	**1.22**	up	**2.19**	up	**1.10**	up	**1.37**	up	**1.22**	down	ABA
Os.12342.1.S2_at	LOC_Os12g04204	expressed protein	**1.12**	up	**1.25**	up	**2.06**	up	**1.15**	up	**1.45**	up	**1.08**	down	ABA
Os.12347.1.S1_x_at	LOC_Os11g04390	RNA recognition motif containing protein, expressed	**1.36**	up	**1.11**	up	**4.83**	up	**1.18**	down	**1.14**	up	**1.18**	down	ABA
Os.12363.1.S1_at	LOC_Os04g58200	protochlorophyllide reductase A, chloroplast precursor, putative, expressed	**1.09**	up	**1.01**	down	**13.27**	down	**1.65**	down	**2.80**	down	**1.46**	down	2
Os.12372.1.S1_s_at	LOC_Os08g06280	LSD1 zinc finger domain containing protein, expressed	**1.16**	down	**1.02**	down	**3.58**	down	**1.05**	down	**1.23**	down	**1.27**	down	ABA
Os.12372.2.S1_x_at	LOC_Os08g06280	LSD1 zinc finger domain containing protein, expressed	**1.15**	down	**1.10**	up	**3.68**	down	**1.03**	down	**1.28**	down	**1.24**	down	ABA
Os.12374.1.S1_at	LOC_Os12g42876	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative, expr	**1.01**	up	**1.06**	up	**2.13**	down	**1.02**	up	**1.19**	down	**1.25**	up	ABA
Os.12393.1.S2_a_at	LOC_Os06g50300	heat shock protein, putative, expressed	**1.19**	down	**1.09**	up	**2.25**	down	**1.11**	up	**1.20**	down	**1.23**	up	ABA
Os.12393.2.S1_at	LOC_Os08g01380	2Fe-2S iron-sulfur cluster binding domain containing protein, expressed	**1.73**	up	**1.00**	down	**3.94**	down	**1.83**	down	**2.42**	down	**1.54**	down	2
Os.12400.2.S1_x_at	LOC_Os08g30020	membrane protein, putative, expressed	**1.28**	down	**1.09**	down	**3.95**	up	**1.13**	down	**1.03**	up	**4.32**	up	2
Os.12400.4.S1_at	LOC_Os08g30020	membrane protein, putative, expressed	**1.22**	down	**1.15**	down	**2.96**	up	**1.14**	down	**1.06**	down	**4.28**	up	2
Os.12402.2.S1_x_at	LOC_Os05g44320	WD domain, G-beta repeat domain containing protein, expressed	**1.06**	up	**1.20**	up	**2.33**	down	**1.19**	up	**1.16**	down	**1.24**	down	ABA
Os.12403.1.S1_a_at	LOC_Os06g40360	OsFBL30 - F-box domain and LRR containing protein, expressed	**1.05**	down	**1.12**	down	**1.15**	up	**2.03**	up	**1.03**	up	**1.24**	down	ACC
Os.12412.1.S1_at	LOC_Os02g16500	arabinogalactan-protein (AGP16)	**1.13**	down	**1.25**	down	**2.79**	down	**1.19**	down	**1.69**	down	**1.52**	down	ABA
Os.12415.1.S1_at	CT829836	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN080M19, full insert sequenc	**2.54**	up	**1.50**	up	**383.95**	up	**1.39**	up	**2.29**	up	**1.40**	down	3
Os.12419.1.S1_at	AK062306	expressed protein	**2.69**	up	**1.07**	up	**4.90**	down	**1.26**	down	**1.67**	down	**1.23**	down	2
Os.12420.1.S1_at	LOC_Os08g27720	pirin, putative, expressed	**1.00**	up	**1.88**	down	**1.98**	down	**1.03**	down	**2.23**	up	**1.37**	up	SA
Os.12421.1.S1_at	LOC_Os11g42960	integral membrane protein TIGR01569 containing protein, expressed	**2.11**	down	**1.80**	down	**4.52**	down	**1.27**	up	**1.47**	up	**2.00**	up	3
Os.12429.1.S1_at	LOC_Os07g07040	erythrocyte binding protein 3, putative, expressed	**1.18**	down	**1.08**	down	**10.27**	up	**1.02**	down	**1.08**	up	**1.06**	down	ABA
Os.12440.1.S1_at	AK243174	expressed protein	**1.22**	up	**1.08**	down	**2.34**	up	**1.38**	down	**1.05**	down	**1.13**	down	ABA
Os.12457.1.S1_at	LOC_Os03g31679	annexin A7, putative, expressed	**1.05**	down	**1.17**	up	**4.80**	down	**1.13**	up	**1.66**	down	**1.11**	down	ABA
Os.12475.1.S1_s_at	LOC_Os05g37470	transmembrane amino acid transporter protein, putative, expressed	**1.19**	down	**1.14**	up	**5.86**	down	**1.15**	down	**1.57**	down	**1.41**	down	ABA
Os.12501.1.S1_at	LOC_Os01g55940	OsGH3.2 - Probable indole-3-acetic acid-amido synthetase, expressed	**9.64**	up	**1.47**	down	**1.18**	up	**1.23**	up	**5.74**	up	**1.56**	up	2
Os.12528.1.S1_x_at	LOC_Os03g31750	pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed	**1.67**	down	**1.22**	down	**2.74**	up	**2.21**	up	**3.41**	up	**1.32**	down	3
Os.12568.1.S1_at	LOC_Os05g03820	glutamate--cysteine ligase, chloroplast precursor, putative, expressed	**1.51**	up	**1.04**	up	**1.71**	up	**1.26**	up	**2.24**	up	**1.49**	up	SA
Os.12583.1.S1_at	LOC_Os03g16440	outer membrane protein, OMP85 family, putative, expressed	**1.08**	up	**1.04**	up	**2.24**	down	**1.00**	down	**1.44**	down	**1.19**	down	ABA
Os.12591.2.S1_x_at	LOC_Os11g10480	dehydrogenase, putative, expressed	**1.15**	down	**1.00**	down	**2.54**	up	**1.52**	up	**1.75**	up	**1.30**	up	ABA
Os.12614.1.A1_at	LOC_Os11g12320	disease resistance protein RPM1, putative	**1.39**	down	**1.46**	up	**6.41**	down	**1.34**	up	**1.48**	down	**1.49**	down	ABA
Os.12628.1.S1_at	LOC_Os06g02380	T-complex protein, putative, expressed	**1.02**	down	**1.03**	down	**2.12**	down	**1.05**	down	**1.29**	down	**1.11**	down	ABA
Os.12633.1.S1_s_at	LOC_Os11g26790	dehydrin, putative, expressed	**1.63**	up	**3.65**	up	**9.11**	up	**1.11**	down	**1.21**	down	**1.01**	up	2
Os.12644.1.S1_at	LOC_Os07g41140	receptor-like protein kinase precursor, putative, expressed	**1.10**	up	**1.08**	down	**2.62**	up	**1.33**	up	**1.44**	up	**1.23**	up	ABA
Os.12645.1.S1_at	LOC_Os03g27280	CAMK_CAMK_like.19 - CAMK includes calcium/calmodulin depedent protein kinases, e	**1.18**	up	**1.13**	down	**6.59**	up	**1.03**	up	**1.93**	up	**1.37**	up	ABA
Os.12646.1.S1_at	LOC_Os01g64970	CAMK_CAMK_like.11 - CAMK includes calcium/calmodulin depedent protein kinases, e	**1.13**	up	**1.02**	up	**2.00**	up	**1.01**	up	**1.11**	up	**1.28**	down	ABA
Os.12654.1.S1_at	LOC_Os09g39930	tyrosine protein kinase domain containing protein, putative, expressed	**1.01**	down	**1.01**	up	**2.52**	up	**1.01**	down	**1.13**	up	**1.16**	up	ABA
Os.12660.1.S1_at	LOC_Os07g38800	lectin-like receptor kinase, putative, expressed	**1.23**	up	**1.05**	down	**2.42**	down	**1.22**	down	**1.19**	down	**1.16**	down	ABA
Os.12664.1.S1_at	LOC_Os07g35810	TKL_IRAK_DUF26-ld.6 - DUF26 kinases have homology to DUF26 containing loci, exp	**1.41**	down	**1.33**	up	**8.51**	down	**1.90**	up	**1.22**	down	**1.64**	down	ABA
Os.12669.1.S1_at	LOC_Os09g03620	wall-associated receptor kinase-like 20 precursor, putative, expressed	**1.11**	up	**1.08**	down	**2.68**	up	**1.00**	down	**1.10**	up	**1.06**	down	ABA
Os.12686.1.S1_at	LOC_Os05g16824	SHR5-receptor-like kinase, putative, expressed	**1.17**	up	**1.04**	down	**1.43**	up	**1.18**	up	**1.60**	up	**6.72**	up	JA
Os.12693.3.S1_at	LOC_Os07g49400	OsAPx2 - Cytosolic Ascorbate Peroxidase encoding gene 4,5,6,8, expressed	**2.09**	down	**1.82**	down	**1.52**	up	**1.24**	up	**1.35**	up	**1.33**	up	IAA
Os.12701.1.S1_at	LOC_Os04g55650	oryzain alpha chain precursor, putative, expressed	**1.09**	up	**1.54**	down	**2.13**	up	**1.01**	down	**1.14**	up	**1.45**	up	ABA
Os.12703.1.S1_at	LOC_Os03g10090	transporter family protein, putative, expressed	**1.38**	up	**1.24**	down	**2.70**	up	**1.74**	down	**1.08**	down	**1.22**	up	ABA
Os.12710.1.S1_at	LOC_Os07g42370	zinc-finger protein, putative, expressed	**1.13**	up	**1.11**	up	**2.09**	down	**1.12**	up	**1.43**	down	**2.29**	up	2
Os.12714.1.S1_at	AK058850	Oryza sativa Japonica Group cDNA clone:001-004-H10, full insert sequence.	**1.35**	up	**1.22**	down	**3.33**	up	**1.51**	up	**2.50**	up	**1.45**	up	2
Os.12715.1.S1_at	LOC_Os01g12650	reticulon domain containing protein, putative, expressed	**1.05**	down	**1.03**	up	**2.51**	down	**1.07**	down	**1.72**	down	**1.19**	down	ABA
Os.12724.1.S1_a_at	LOC_Os08g36320	decarboxylase, putative, expressed	**1.22**	up	**1.31**	down	**12.11**	up	**1.64**	down	**1.23**	up	**1.68**	down	ABA
Os.12725.1.S1_at	LOC_Os06g06560	starch synthase, putative, expressed	**1.39**	up	**1.21**	up	**11.13**	up	**1.04**	up	**1.04**	down	**1.19**	down	ABA
Os.12732.1.S1_a_at	LOC_Os10g42320	nonsense-mediated mRNA decay protein 3, putative, expressed	**1.50**	up	**1.26**	up	**1.13**	down	**1.24**	up	**2.50**	up	**1.18**	up	SA
Os.12737.1.S1_at	LOC_Os06g43800	methyltransferase domain containing protein, putative, expressed	**1.32**	up	**1.15**	up	**2.35**	down	**1.05**	up	**1.19**	down	**1.09**	down	ABA
Os.12738.1.S2_a_at	LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed	**1.13**	up	**1.44**	down	**2.64**	up	**1.03**	down	**5.71**	up	**1.74**	up	2
Os.12751.1.S1_at	LOC_Os02g48470	expressed protein	**1.02**	up	**1.19**	down	**2.50**	down	**1.31**	down	**1.59**	down	**1.09**	up	ABA
Os.12758.1.S1_at	LOC_Os08g42040	LTPL80 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.28**	up	**1.01**	down	**2.22**	down	**1.01**	down	**1.08**	down	**1.08**	up	ABA
Os.12761.1.S1_at	LOC_Os03g46060	thaumatin family domain containing protein, expressed	**1.20**	down	**4.22**	up	**4.07**	up	**1.31**	down	**1.12**	up	**1.29**	down	2
Os.12766.1.S1_at	LOC_Os03g14570	expressed protein	**1.19**	up	**1.36**	down	**3.52**	up	**1.34**	down	**1.13**	up	**1.24**	down	ABA
Os.12769.1.S1_at	AK119705	Oryza sativa Japonica Group cDNA clone:J023119K19, full insert sequence.	**1.07**	down	**1.00**	up	**2.62**	down	**1.08**	down	**1.30**	down	**1.23**	up	ABA
Os.12780.1.S1_at	LOC_Os08g02120	kinase, pfkB family, putative, expressed	**1.08**	up	**1.02**	down	**3.35**	down	**1.11**	down	**1.50**	down	**1.09**	up	ABA

Os.12812.1.S1_at	LOC_Os05g28210	small hydrophilic plant seed protein, putative, expressed	**2.17**	up	**1.48**	up	**5.54**	up	**1.39**	down	**1.28**	up	**1.01**	up	2
Os.12829.1.S1_at	LOC_Os02g44320	LTPL113 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.11**	up	**1.05**	down	**3.54**	down	**1.02**	up	**1.41**	down	**1.25**	down	ABA
Os.12830.1.S1_at	LOC_Os04g55920	zinc-finger protein, putative, expressed	**1.22**	down	**1.13**	down	**1.12**	down	**1.08**	up	**1.10**	down	**2.34**	up	JA
Os.12843.1.S1_at	LOC_Os03g22020	peroxidase precursor, putative, expressed	**5.68**	up	**4.01**	up	**6.06**	up	**1.78**	up	**9.62**	up	**3.29**	up	5
Os.12851.1.S1_at	LOC_Os01g14670	Cupin domain containing protein, expressed	**1.44**	down	**1.16**	up	**2.70**	down	**1.03**	down	**1.44**	down	**1.06**	down	ABA
Os.12866.1.S1_at	LOC_Os02g48360	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha, putative, ex	**1.16**	down	**1.13**	down	**3.53**	down	**1.03**	down	**1.86**	down	**1.32**	down	ABA
Os.12918.2.S1_x_at	LOC_Os04g58320	zinc finger, RING-type, putative, expressed	**1.09**	down	**1.39**	down	**2.03**	up	**1.05**	down	**1.15**	up	**1.12**	down	ABA
Os.12934.1.S1_at	LOC_Os01g24030	AMP-binding enzyme, putative, expressed	**3.63**	up	**1.53**	up	**1.51**	up	**1.20**	up	**13.20**	up	**1.69**	up	2
Os.12950.1.S1_at	LOC_Os03g29180	ubiquinone biosynthesis protein COQ9, mitochondrial precursor, putative, expressed	**1.24**	up	**1.01**	down	**2.98**	up	**1.15**	up	**1.65**	up	**1.21**	up	ABA
Os.12952.1.S1_at	LOC_Os01g71860	glycosyl hydrolases family 17, putative, expressed	**1.60**	down	**1.05**	down	**1.26**	up	**1.84**	up	**1.30**	up	**5.70**	up	JA
Os.12965.1.S1_at	LOC_Os09g25290	methyladenine glycosylase, putative, expressed	**1.84**	down	**1.26**	down	**3.13**	down	**1.30**	down	**1.53**	down	**1.33**	down	ABA
Os.12974.1.S1_at	LOC_Os11g29380	MCM2 - Putative minichromosome maintenance MCM complex subunit 2, expressed	**1.35**	down	**1.05**	down	**4.89**	down	**1.11**	down	**2.01**	down	**1.82**	down	2
Os.12979.3.S1_x_at	LOC_Os01g61720	IQ calmodulin-binding motif domain containing protein, expressed	**1.01**	down	**1.17**	down	**2.37**	down	**1.04**	down	**1.07**	down	**1.21**	down	ABA
Os.12990.1.S1_x_at	LOC_Os03g50970	retrotransposon protein, putative, Ty1-copia subclass, expressed	**1.70**	down	**1.73**	down	**1.79**	down	**1.35**	up	**1.09**	up	**2.91**	up	JA
Os.12993.1.S1_at	LOC_Os05g07090	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed	**1.11**	up	**1.02**	down	**4.48**	up	**1.28**	up	**2.11**	up	**2.58**	up	3
Os.12995.1.S1_at	LOC_Os04g59420	expressed protein	**1.64**	up	**1.22**	down	**5.70**	up	**1.66**	up	**1.63**	up	**1.30**	down	ABA
Os.12999.1.S1_at	NM_001060566	Oryza sativa (japonica cultivar-group) Os04g0639100 (Os04g0639100) mRNA, comple	**1.22**	down	**1.12**	up	**1.72**	down	**2.95**	down	**1.22**	down	**1.83**	up	ACC
Os.13014.1.S1_a_at	LOC_Os10g38140	glutathione S-transferase, putative, expressed	**1.07**	up	**1.00**	down	**2.37**	down	**1.07**	down	**1.08**	up	**1.02**	down	ABA
Os.13016.1.S1_a_at	LOC_Os07g07320	glutathione S-transferase, putative, expressed	**1.04**	up	**1.21**	up	**3.55**	down	**1.37**	down	**1.18**	up	**1.69**	up	ABA
Os.1307.1.S1_a_at	LOC_Os11g05190	phytosulfokines precursor, putative, expressed	**1.40**	down	**5.96**	up	**2.79**	down	**1.47**	up	**1.02**	up	**4.83**	up	3
Os.13102.1.S1_at	LOC_Os01g55650	phospholipase, patatin family, putative, expressed	**1.03**	up	**1.15**	down	**2.47**	up	**1.40**	up	**1.83**	up	**1.47**	up	ABA
Os.1311.1.S1_at	LOC_Os02g02410	DnaK family protein, putative, expressed	**1.54**	down	**1.08**	up	**3.05**	down	**1.13**	up	**1.40**	down	**1.13**	up	ABA
Os.1316.1.S2_at	LOC_Os02g04780	expressed protein	**1.00**	down	**1.07**	down	**328.27**	up	**1.13**	down	**2.35**	up	**1.01**	down	2
Os.13246.1.S1_at	LOC_Os01g59870	LTPL65 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.23**	up	**1.06**	up	**5.32**	down	**1.03**	up	**1.05**	down	**1.03**	up	ABA
Os.1344.1.S1_at	LOC_Os02g43700	triacylglycerol lipase like protein, putative, expressed	**1.39**	up	**1.17**	up	**1.35**	down	**1.10**	down	**1.07**	down	**4.02**	up	JA
Os.13466.1.S1_at	LOC_Os02g43300	expressed protein	**1.18**	down	**1.11**	down	**2.89**	up	**1.05**	up	**1.08**	up	**1.01**	up	ABA
Os.13497.1.S2_at	LOC_Os03g13820	protein kinase family protein, putative, expressed	**1.22**	up	**1.19**	down	**2.11**	up	**1.08**	down	**1.05**	down	**1.10**	down	ABA
Os.13500.1.S1_at	LOC_Os01g20940	PHS1, putative, expressed	**1.03**	down	**1.04**	up	**2.10**	up	**1.14**	down	**1.11**	down	**1.22**	down	ABA
Os.13500.2.S1_x_at	LOC_Os01g20940	PHS1, putative, expressed	**1.56**	up	**1.00**	up	**2.98**	up	**1.11**	down	**1.06**	down	**1.11**	up	ABA
Os.13516.1.S1_at	LOC_Os12g05540	Ser/Thr protein phosphatase family protein, putative, expressed	**1.16**	down	**1.00**	up	**49.30**	up	**1.02**	up	**4.47**	up	**1.07**	up	2
Os.13543.1.S1_at	LOC_Os12g23280	heavy metal-associated domain containing protein, expressed	**1.44**	down	**1.11**	down	**2.37**	down	**1.04**	down	**1.03**	down	**1.43**	up	ABA
Os.13544.1.S1_x_at	LOC_Os01g37832	thioredoxin, putative, expressed	**1.01**	up	**1.06**	up	**2.48**	up	**1.18**	down	**1.09**	up	**1.21**	down	ABA
Os.13595.1.S1_at	LOC_Os01g70310	inducer of CBF expression 2, putative, expressed	**1.01**	up	**1.38**	down	**5.96**	up	**1.06**	up	**1.05**	down	**1.05**	up	ABA
Os.13595.2.S1_x_at	LOC_Os01g70310	inducer of CBF expression 2, putative, expressed	**1.59**	up	**1.42**	down	**7.31**	up	**1.01**	down	**1.03**	down	**1.04**	up	ABA
Os.13596.1.S1_at	LOC_Os03g10320	expressed protein	**1.07**	down	**1.57**	up	**3.96**	up	**1.14**	down	**1.31**	up	**1.00**	up	ABA
Os.13604.1.S1_at	LOC_Os02g30100	cytochrome P450, putative, expressed	**1.35**	up	**1.20**	down	**4.33**	up	**1.17**	up	**2.61**	up	**5.06**	up	3
Os.13615.1.S1_at	LOC_Os01g47262	AMSH-like protease, putative, expressed	**1.06**	up	**1.24**	down	**2.57**	up	**1.12**	down	**1.06**	up	**1.48**	down	ABA
Os.13615.4.S1_x_at	LOC_Os01g47262	AMSH-like protease, putative, expressed	**1.25**	up	**1.15**	down	**3.18**	up	**1.04**	down	**1.05**	up	**1.31**	down	ABA
Os.13624.1.S1_at	LOC_Os01g38510	Oryza sativa Japonica Group cDNA clone:J013042A04, full insert sequence.	**1.24**	down	**1.13**	up	**3.37**	down	**1.05**	up	**1.25**	down	**1.18**	up	ABA
Os.13690.1.S1_at	LOC_Os02g42000	expressed protein	**1.94**	up	**1.01**	down	**5.11**	up	**1.04**	up	**1.63**	up	**1.02**	down	ABA
Os.13704.1.S1_x_at	AK288399	Oryza sativa Japonica Group cDNA, clone: J090029F22, full insert sequence.	**1.01**	up	**1.02**	up	**2.57**	up	**1.41**	up	**64.53**	up	**1.13**	up	2
Os.13708.2.A1_at	LOC_Os03g22790	beta-amylase, putative, expressed	**1.36**	down	**1.01**	down	**10.87**	up	**1.23**	up	**1.60**	up	**1.25**	up	ABA
Os.13735.1.S1_at	LOC_Os02g58150	expressed protein	**1.37**	down	**1.32**	down	**2.61**	up	**1.08**	up	**1.30**	up	**1.28**	up	ABA
Os.1376.1.S1_at	LOC_Os03g11540	RPA1B - Putative single-stranded DNA binding complex subunit 1, expressed	**1.40**	down	**1.09**	down	**11.42**	down	**1.24**	down	**2.54**	down	**1.96**	down	2
Os.13781.1.S2_at	LOC_Os02g54254	saccharopine dehydrogenase, putative, expressed	**1.38**	down	**1.19**	down	**4.68**	up	**1.26**	up	**1.46**	up	**1.58**	up	ABA
Os.13800.1.S1_at	LOC_Os05g04870	oxidoreductase, short chain dehydrogenase/reductase family protein, putative, express	**1.00**	down	**1.00**	up	**291.57**	up	**1.01**	up	**1.04**	up	**1.02**	up	ABA
Os.13812.1.S1_a_at	LOC_Os03g61600	phosphoribosylformylglycinamidine synthase, putative, expressed	**1.06**	down	**1.02**	up	**2.14**	down	**1.16**	up	**1.30**	down	**1.05**	down	ABA
Os.13917.1.S1_at	LOC_Os05g49170	cold acclimation protein WCOR413, putative, expressed	**1.12**	up	**1.14**	down	**3.26**	up	**1.31**	down	**1.13**	down	**1.04**	up	ABA
Os.13954.1.S1_x_at	LOC_Os08g31950	hypothetical protein	**1.33**	up	**1.09**	up	**17.73**	up	**1.37**	up	**1.46**	up	**1.37**	up	ABA
Os.13968.1.S1_a_at	AF503583	Oryza sativa (indica cultivar-group) early drought induced protein (R1G1B) mRNA, com	**1.05**	up	**1.03**	up	**2.75**	up	**1.01**	up	**1.38**	up	**1.01**	down	ABA
Os.13968.2.S1_a_at	LOC_Os05g04700	Hydrophobic protein LTI6b, putative	**1.13**	down	**1.03**	up	**6.70**	up	**1.02**	down	**1.33**	up	**1.07**	up	ABA
Os.13972.1.S1_at	LOC_Os07g44430	peroxiredoxin, putative	**1.20**	up	**1.16**	up	**381.99**	up	**1.47**	up	**6.91**	up	**1.95**	up	2
Os.13996.1.S1_at	LOC_Os07g40860	retrotransposon protein, putative, unclassified, expressed	**1.22**	up	**1.26**	up	**2.60**	up	**1.43**	down	**1.05**	down	**1.23**	down	ABA
Os.13999.1.S1_at	LOC_Os02g08150	CCT/B-box zinc finger protein, putative, expressed	**1.07**	up	**1.18**	up	**3.08**	down	**1.01**	up	**1.73**	down	**1.07**	up	ABA
Os.14042.1.S1_at	CT833862	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA031G18, full insert sequence	**1.12**	up	**1.02**	down	**3.53**	up	**1.11**	down	**1.59**	down	**1.24**	down	ABA

Os.14052.1.S1_at	LOC_Os03g45210	2-aminoethanethiol dioxygenase, putative, expressed	**1.47**	down	**1.26**	down	**41.03**	up	**1.01**	up	**1.01**	down	**1.02**	up	ABA
Os.14071.1.S1_at	LOC_Os09g29940	auxin-independent growth promoter protein, putative, expressed	**1.04**	down	**1.57**	up	**6.13**	up	**1.13**	up	**1.40**	up	**1.59**	up	ABA
Os.14080.1.S1_s_at	LOC_Os03g47120	CBS domain containing protein, expressed	**1.01**	up	**1.04**	down	**5.91**	up	**1.07**	up	**1.06**	up	**1.33**	up	ABA
Os.14084.1.S1_at	LOC_Os03g61920	electron transfer flavoprotein subunit alpha, mitochondrial precursor, putative, expresse	**1.08**	up	**1.10**	up	**3.25**	up	**1.12**	up	**1.74**	up	**1.25**	up	ABA
Os.14088.1.S1_at	LOC_Os08g04830	expressed protein	**1.09**	up	**1.19**	down	**3.97**	up	**1.03**	down	**1.23**	up	**1.00**	up	ABA
Os.14092.1.S1_at	LOC_Os02g44710	expressed protein	**1.02**	down	**1.15**	down	**2.10**	down	**1.11**	down	**1.15**	down	**1.79**	down	ABA
Os.14101.3.S1_at	LOC_Os01g61200	GDSL-like lipase	**3.25**	up	**1.78**	up	**2.07**	up	**1.52**	up	**1.01**	up	**1.38**	down	2
Os.14105.1.S1_at	LOC_Os11g05380	cytochrome P450, putative, expressed	**2.14**	up	**1.30**	up	**1.53**	down	**1.11**	up	**4.76**	up	**11.32**	up	3
Os.1411.1.S1_at	LOC_Os01g10890	CAMK_KIN1/SNF1/Nim1_like.8 - CAMK includes calcium/calmodulin depedent protein	**1.29**	up	**1.23**	down	**9.07**	up	**2.04**	down	**1.39**	up	**1.32**	down	2
Os.14119.2.S1_x_at	LOC_Os10g41040	ternary complex factor MIP1, putative, expressed	**1.07**	up	**1.08**	up	**2.02**	down	**1.04**	down	**1.39**	up	**1.05**	up	ABA
Os.14121.1.S1_at	LOC_Os11g06900	amidase family protein, putative, expressed	**1.08**	up	**1.04**	up	**10.50**	down	**1.08**	down	**2.22**	down	**1.09**	down	2
Os.14122.1.S1_at	LOC_Os01g13210	salt stress root protein RS1, putative, expressed	**1.42**	up	**1.28**	down	**2.57**	up	**1.09**	down	**1.09**	up	**1.15**	down	ABA
Os.14139.1.S1_at	LOC_Os04g31340	CBS domain containing membrane protein, putative, expressed	**1.04**	up	**1.13**	up	**2.18**	up	**1.02**	up	**1.28**	up	**1.04**	down	ABA
Os.14152.1.S1_at	LOC_Os09g19790	puromycin-sensitive aminopeptidase, putative, expressed	**1.01**	up	**1.09**	down	**1.07**	up	**1.02**	down	**1.02**	up	**2.89**	up	JA
Os.14184.1.S1_at	LOC_Os06g11410	cyclin, putative, expressed	**1.30**	down	**1.23**	up	**3.36**	down	**1.01**	down	**1.36**	down	**1.76**	down	ABA
Os.14191.1.S1_at	LOC_Os08g04310	plastocyanin-like domain containing protein, putative, expressed	**1.04**	up	**1.06**	up	**2.40**	down	**1.02**	down	**1.06**	down	**1.11**	down	ABA
Os.14200.1.S1_at	LOC_Os10g24070	expressed protein	**1.06**	up	**1.05**	down	**2.50**	up	**1.04**	down	**1.17**	up	**1.07**	down	ABA
Os.14200.2.S1_x_at	LOC_Os10g24070	expressed protein	**1.10**	up	**1.14**	down	**2.66**	up	**1.03**	up	**1.23**	up	**1.29**	up	ABA
Os.14205.1.S1_at	LOC_Os05g41620	expressed protein	**1.17**	up	**1.03**	up	**8.00**	up	**1.15**	down	**1.61**	up	**1.18**	down	ABA
Os.14208.1.S1_at	LOC_Os06g28000	carboxyl-terminal peptidase, putative, expressed	**1.52**	down	**1.74**	down	**2.06**	down	**1.08**	down	**1.07**	down	**1.19**	down	ABA
Os.14210.1.S1_at	LOC_Os10g36360	expressed protein	**4.72**	up	**1.17**	up	**5.64**	up	**1.13**	up	**1.00**	up	**2.01**	down	3
Os.14232.1.S1_at	LOC_Os01g46120	GDSL-like lipase/acylhydrolase, putative, expressed	**1.06**	up	**1.32**	up	**1.72**	down	**2.07**	down	**1.13**	up	**1.19**	up	ACC
Os.14251.1.S1_a_at	LOC_Os03g14380	autophagy protein 9, putative, expressed	**1.00**	up	**1.25**	down	**3.36**	up	**1.20**	up	**1.41**	up	**1.36**	up	ABA
Os.14251.1.S1_at	LOC_Os03g14380	autophagy protein 9, putative, expressed	**1.30**	up	**1.07**	down	**2.91**	up	**1.01**	up	**1.33**	up	**1.20**	up	ABA
Os.14251.1.S2_at	LOC_Os03g14380	autophagy protein 9, putative, expressed	**1.20**	up	**1.11**	down	**3.11**	up	**1.13**	up	**1.42**	up	**1.25**	up	ABA
Os.14251.2.S1_x_at	LOC_Os03g14380	autophagy protein 9, putative, expressed	**1.10**	up	**1.27**	down	**3.48**	up	**1.13**	up	**1.38**	up	**1.38**	up	ABA
Os.14289.1.S1_at	LOC_Os04g45750	expressed protein	**1.02**	down	**1.43**	down	**2.73**	up	**1.07**	up	**1.38**	up	**1.25**	up	ABA
Os.14332.1.S1_at	LOC_Os02g28340	transferase family protein, putative, expressed	**1.83**	up	**1.08**	up	**3.09**	up	**1.18**	up	**8.89**	up	**2.00**	up	3
Os.14358.1.S1_at	LOC_Os02g12730	beta-galactosidase precursor, putative, expressed	**1.71**	down	**1.06**	down	**3.84**	down	**1.45**	down	**1.48**	down	**1.50**	down	ABA
Os.14358.4.S1_x_at	LOC_Os02g12730	beta-galactosidase precursor, putative, expressed	**1.21**	down	**1.16**	down	**4.92**	down	**1.67**	down	**1.69**	down	**1.39**	down	ABA
Os.14366.1.S1_s_at	LOC_Os08g37840	phosphate-induced protein 1 conserved region domain containing protein, expressed	**1.01**	up	**1.31**	down	**2.48**	up	**1.13**	down	**2.32**	up	**2.61**	up	3
Os.14381.1.S1_at	LOC_Os03g28300	protein kinase domain containing protein, expressed	**1.03**	up	**1.28**	down	**2.39**	up	**1.69**	down	**1.20**	up	**1.31**	down	ABA
Os.14390.1.S1_at	LOC_Os06g11380	geminivirus Rep-interacting motor protein, putative, expressed	**1.23**	up	**1.19**	up	**2.21**	down	**1.29**	down	**1.30**	down	**1.32**	down	ABA
Os.14395.1.S1_at	LOC_Os01g07700	expressed protein	**1.05**	up	**1.07**	down	**4.04**	up	**1.04**	down	**1.08**	up	**1.12**	up	ABA
Os.14407.1.S1_at	LOC_Os08g01890	DNA binding protein, putative, expressed	**1.08**	up	**1.05**	down	**3.06**	up	**1.11**	down	**1.19**	down	**1.30**	down	ABA
Os.14427.1.S1_at	LOC_Os01g57420	diacylglycerol kinase, putative, expressed	**1.08**	up	**1.02**	down	**8.82**	up	**1.23**	down	**1.06**	up	**1.13**	up	ABA
Os.1443.1.S1_a_at	LOC_Os01g06640	basic helix-loop-helix, putative, expressed	**1.09**	down	**1.24**	down	**8.45**	up	**1.01**	down	**2.15**	up	**1.29**	up	2
Os.14430.1.S1_at	LOC_Os02g20540	fasciclin domain containing protein, expressed	**1.14**	down	**1.30**	down	**5.00**	down	**1.24**	down	**1.69**	down	**1.17**	down	ABA
Os.1445.1.S1_at	LOC_Os01g06660	thiamine pyrophosphate enzyme, C-terminal TPP binding domain containing protein, ex	**1.16**	up	**1.00**	up	**5.76**	up	**1.19**	up	**3.18**	up	**1.58**	up	2
Os.14476.1.S1_a_at	LOC_Os02g07230	porphobilinogen deaminase, chloroplast precursor, putative, expressed	**1.18**	up	**1.02**	down	**2.70**	down	**1.06**	down	**1.51**	down	**1.05**	down	ABA
Os.14546.1.S1_at	LOC_Os02g26650	delta14-sterol reductase, putative, expressed	**1.02**	down	**1.13**	down	**2.13**	down	**1.08**	down	**1.26**	down	**1.20**	down	ABA
Os.14563.1.S1_at	LOC_Os07g49460	response regulator receiver domain containing protein, expressed	**1.23**	up	**1.10**	up	**2.28**	up	**1.11**	up	**9.36**	up	**4.28**	up	3
Os.14565.1.S1_at	LOC_Os07g12250	ribosomal protein L24, putative, expressed	**1.02**	down	**1.06**	up	**2.25**	down	**1.01**	down	**1.39**	down	**1.21**	down	ABA
Os.14574.1.S1_at	LOC_Os04g51970	synaptic vesicle 2-related protein, putative, expressed	**1.36**	up	**1.07**	down	**2.44**	up	**1.04**	down	**1.66**	up	**1.25**	up	ABA
Os.14592.1.S1_at	LOC_Os06g39260	solute carrier family 35 member B1, putative, expressed	**1.60**	down	**1.20**	up	**3.69**	down	**1.14**	up	**1.68**	down	**1.32**	up	ABA
Os.14616.1.S1_at	LOC_Os07g34260	chalcone and stilbene synthases, putative, expressed	**1.02**	down	**1.27**	down	**4.75**	down	**1.02**	down	**1.08**	up	**2.21**	up	2
Os.14645.1.S1_s_at	LOC_Os05g11840	expressed protein	**1.18**	down	**1.06**	down	**2.78**	up	**1.17**	down	**1.24**	up	**1.05**	down	ABA
Os.14645.3.S1_at	LOC_Os05g11840	expressed protein	**1.04**	up	**1.17**	down	**7.57**	up	**1.01**	up	**1.25**	up	**1.25**	up	ABA
Os.14762.3.S1_at	LOC_Os11g47930	alpha-hemolysin, putative	**1.75**	down	**1.14**	down	**3.57**	up	**1.61**	up	**1.76**	up	**1.26**	up	ABA
Os.14775.1.S1_at	LOC_Os01g67420	lipase, putative, expressed	**1.25**	up	**1.04**	down	**2.07**	up	**1.04**	up	**1.69**	up	**1.21**	up	ABA
Os.14791.1.S1_at	LOC_Os11g32500	rubredoxin family protein, putative, expressed	**1.28**	up	**1.06**	down	**3.75**	down	**1.17**	down	**1.90**	down	**1.36**	down	ABA
Os.14809.1.S1_at	LOC_Os03g56430	expressed protein	**1.12**	down	**1.11**	down	**2.36**	down	**1.43**	down	**1.66**	down	**1.55**	up	ABA
Os.14823.1.S1_s_at	LOC_Os03g20090	MYB family transcription factor, putative, expressed	**1.09**	up	**1.19**	down	**1.33**	up	**1.03**	up	**1.06**	down	**2.25**	up	JA
Os.14844.1.A1_at	NM_001055743	Oryza sativa (japonica cultivar-group) Os03g0187300 (Os03g0187300) mRNA, partial	**1.03**	down	**1.06**	up	**2.53**	up	**1.05**	down	**1.16**	up	**1.21**	down	ABA
Os.14848.1.S1_at	LOC_Os06g48040	zinc finger, C3HC4 type domain containing protein, expressed	**1.01**	down	**1.10**	down	**3.35**	up	**1.15**	up	**1.00**	down	**1.06**	down	ABA

Os.14852.1.A1_at	LOC_Os06g40060	glycosyltransferase family protein, putative, expressed	1.02	up	1.01	down	2.98	up	1.00	up	1.14	up	1.18	up	ABA
Os.14854.1.S1_at	LOC_Os05g36360	U-box domain containing protein, expressed	1.13	down	1.07	down	3.84	down	1.31	up	1.32	down	1.26	down	ABA
Os.14862.1.S1_s_at	LOC_Os08g10320	SHR5-receptor-like kinase, putative, expressed	1.21	down	1.73	up	5.95	down	1.95	up	2.42	down	1.42	down	2
Os.14869.1.S1_at	LOC_Os01g49110	prenyltransferase, putative, expressed	1.20	down	1.01	down	3.32	down	1.16	down	1.29	down	1.25	up	ABA
Os.14885.1.S1_at	LOC_Os05g43460	DUF567 domain containing protein, putative, expressed	1.01	down	1.55	down	2.41	up	1.35	down	1.01	down	1.11	down	ABA
Os.14901.1.A1_a_at	LOC_Os09g33820	lecithine cholesterol acyltransferase, putative, expressed	1.05	up	1.04	up	6.24	up	1.34	up	1.68	up	1.50	up	ABA
Os.14911.1.S1_at	LOC_Os08g16480	ATPase, AFG1 family domain containing protein, expressed	1.04	up	1.07	down	2.35	up	1.31	up	1.49	up	1.17	up	ABA
Os.14917.1.S1_x_at	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	1.02	up	1.11	up	2.01	down	1.18	up	1.37	down	1.08	down	ABA
Os.14934.1.S1_at	LOC_Os04g08740	ethylene receptor, putative, expressed	1.14	up	1.45	up	1.43	down	2.67	up	1.08	down	1.31	down	ACC
Os.14934.2.S1_at	LOC_Os04g08740	ethylene receptor, putative, expressed	1.12	down	1.88	up	1.03	down	10.48	up	1.25	up	1.08	up	ACC
Os.14946.1.S1_at	LOC_Os03g04920	multidrug resistance-associated protein, putative, expressed	1.10	down	1.06	down	3.36	up	1.06	down	1.81	up	1.13	up	ABA
Os.14951.1.S1_at	LOC_Os08g39730	cytochrome P450, putative, expressed	1.40	down	1.51	up	8.98	up	1.53	down	4.25	up	2.63	up	3
Os.14963.1.S1_at	LOC_Os04g52140	protein kinase domain containing protein, expressed	1.24	up	1.31	down	2.23	up	1.15	down	3.00	up	1.61	down	2
Os.14978.1.S1_a_at	LOC_Os07g35510	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	1.06	down	1.15	up	2.64	up	1.22	down	1.75	up	1.38	up	ABA
Os.1503.1.S1_at	LOC_Os06g45140	bZIP transcription factor domain containing protein, expressed	1.04	up	1.05	down	3.24	down	1.13	down	1.47	up	1.87	up	ABA
Os.15045.1.S1_at	LOC_Os04g56790	TLD family protein, putative, expressed	1.54	up	1.04	up	6.26	up	1.04	down	1.31	up	1.01	down	ABA
Os.15046.1.S1_at	LOC_Os02g33230	nucleoside-diphosphate-sugar epimerase, putative, expressed	1.15	down	1.03	down	2.21	up	1.09	up	1.36	up	1.11	up	ABA
Os.15077.1.S1_a_at	LOC_Os01g32080	thiamine pyrophosphate enzyme, C-terminal TPP binding domain containing protein, ex	1.25	up	1.03	up	1.33	up	1.06	up	2.11	up	1.22	up	SA
Os.15087.1.S1_at	LOC_Os03g12150	serine/threonine-protein kinase receptor precursor, putative, expressed	1.14	up	1.26	down	5.69	down	1.27	down	1.33	down	1.61	down	ABA
Os.15092.1.S1_at	LOC_Os09g31130	citrate transporter, putative, expressed	2.87	up	1.22	up	26.19	up	1.31	down	3.93	up	1.39	up	3
Os.15125.1.S1_x_at	LOC_Os04g07110	expressed protein	1.00	down	1.18	down	2.24	down	1.29	up	1.43	down	4.25	up	2
Os.152.1.S1_at	LOC_Os11g01340	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed	1.10	down	1.16	down	4.62	down	1.10	down	1.48	down	1.03	up	ABA
Os.15206.1.S1_at	LOC_Os01g21630	pectinacetylesterase domain containing protein, expressed	1.29	down	1.47	down	5.43	up	1.17	up	1.08	up	1.02	down	ABA
Os.15216.1.S1_at	LOC_Os05g36190	OsFBT7 - F-box and tubby domain containing protein, expressed	1.06	up	1.39	down	2.29	up	1.00	down	1.11	up	1.30	up	ABA
Os.15219.1.S1_at	LOC_Os06g11320	peptidyl-prolyl cis-trans isomerase CYP40, putative, expressed	1.14	down	1.00	down	2.61	down	1.16	up	1.50	down	1.29	down	ABA
Os.15220.1.S2_at	LOC_Os07g07230	protein kinase, putative, expressed	1.08	down	1.11	down	2.15	up	1.01	down	1.12	up	1.02	up	ABA
Os.15259.1.S2_at	LOC_Os09g24990	CAF1 family ribonuclease containing protein, putative, expressed	1.04	down	1.10	down	2.04	up	1.00	up	1.01	down	1.00	down	ABA
Os.15260.1.S1_s_at	LOC_Os01g70550	heparan-alpha-glucosaminide N-acetyltransferase, putative, expressed	1.12	down	1.08	up	4.45	up	1.03	down	1.01	up	1.30	down	ABA
Os.15281.1.S1_x_at	LOC_Os07g46920	sex determination protein tasselseed-2, putative, expressed	2.12	down	1.66	down	2.30	down	4.63	down	1.07	up	5.05	up	4
Os.15298.1.S1_at	LOC_Os03g19990	WD40-like Beta Propeller Repeat family protein, expressed	1.53	down	1.14	down	10.38	down	1.72	up	1.98	down	1.06	up	ABA
Os.153.1.S1_at	LOC_Os05g41990	peroxidase precursor, putative, expressed	1.98	down	1.87	down	6.78	down	1.01	down	2.00	down	1.36	down	3
Os.15304.1.A1_at	LOC_Os02g10780	SPX domain containing protein, putative, expressed	1.02	down	1.73	down	4.66	up	1.21	up	1.37	up	1.98	down	ABA
Os.15398.1.S1_at	LOC_Os07g17970	AMP-binding domain containing protein, expressed	1.57	down	1.21	down	5.70	down	1.05	up	1.86	down	1.10	up	ABA
Os.15426.1.S1_at	LOC_Os07g35370	TKL_IRAK_DUF26-lc.15 - DUF26 kinases have homology to DUF26 containing loci, ex	1.23	down	1.11	down	7.09	down	1.57	up	1.10	down	1.02	down	ABA
Os.15428.1.S1_at	LOC_Os01g50622	DNA-binding protein DSP1, putative, expressed	2.03	up	1.62	up	3.49	down	1.00	up	1.22	down	1.39	down	2
Os.15430.1.A1_at	LOC_Os02g48170	class E vacuolar protein-sorting machinery protein HSE1, putative, expressed	1.17	up	1.54	down	3.94	up	1.01	down	1.12	up	1.10	down	ABA
Os.15454.2.S1_at	LOC_Os06g06760	protein kinase, putative, expressed	1.10	down	1.39	down	3.67	up	1.17	up	1.37	up	1.30	up	ABA
Os.15471.1.S1_at	LOC_Os07g44410	WD40-like Beta Propeller Repeat family protein, expressed	1.13	up	1.19	up	6.95	up	1.55	up	6.58	up	1.73	up	2
Os.15490.1.S1_at	LOC_Os01g16170	PQ loop repeat domain containing protein, expressed	1.43	up	1.04	up	6.01	up	1.28	down	3.42	up	1.03	up	2
Os.15557.1.S1_at	CT829996	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN033J11, full insert sequence	1.37	up	1.25	down	56.84	up	1.05	up	5.98	up	1.28	up	2
Os.15573.1.A1_s_at	LOC_Os04g58734	expressed protein	7.44	up	1.50	down	1.66	up	1.22	down	1.06	up	1.46	down	IAA
Os.15574.1.S1_at	LOC_Os03g08390	expressed protein	1.15	up	1.06	up	3.99	up	1.06	down	1.24	down	1.18	down	ABA
Os.15580.1.S1_at	LOC_Os03g42600	expressed protein	1.05	up	1.82	down	5.68	up	1.79	down	1.27	up	1.28	down	ABA
Os.15587.1.S1_x_at	LOC_Os04g41100	cyclin-dependent kinase G-2, putative, expressed	1.06	up	1.02	down	2.16	up	1.08	down	1.19	up	1.09	down	ABA
Os.15637.1.S1_s_at	LOC_Os03g14420	cytochrome P450, putative, expressed	1.61	up	1.26	down	2.28	up	1.20	down	1.09	down	1.02	up	ABA
Os.15671.1.A2_at	LOC_Os11g42510	tyrosine aminotransferase, putative, expressed	1.22	down	1.05	up	2.02	up	1.04	up	1.55	up	1.20	up	ABA
Os.15679.1.S1_s_at	LOC_Os08g35210	ferric reductase, putative, expressed	1.52	down	1.02	up	3.00	down	1.11	down	1.72	down	1.52	up	ABA
Os.15696.1.S1_a_at	LOC_Os02g43010	vacuolar-processing enzyme precursor, putative, expressed	1.02	up	1.01	up	5.60	up	1.10	up	1.32	up	1.15	up	ABA
Os.15700.1.S1_at	LOC_Os05g07130	6PF-2-K/Fru-2,6-P2ASE liver isozyme, putative, expressed	1.20	up	1.01	up	2.78	down	1.05	down	1.41	down	1.12	down	ABA
Os.15708.1.S1_a_at	LOC_Os04g38720	no apical meristem protein, putative, expressed	1.06	up	1.26	up	12.17	up	1.36	down	1.31	down	1.47	down	ABA
Os.15711.1.S1_at	LOC_Os09g28310	bZIP transcription factor, putative, expressed	1.04	up	1.02	down	2.49	up	1.33	down	1.15	up	1.08	down	ABA
Os.15713.1.S1_a_at	LOC_Os04g42620	uncharacterized protein At4g06744 precursor, putative, expressed	1.11	down	1.33	down	3.22	down	1.06	down	1.37	down	1.06	up	ABA
Os.15729.2.S1_x_at	LOC_Os04g49570	glutamate receptor, putative, expressed	1.39	up	1.06	down	2.77	down	1.45	down	1.28	down	1.10	up	ABA
Os.15732.1.S1_s_at	LOC_Os03g29850	metal cation transporter, putative, expressed	1.22	down	1.36	down	2.04	down	1.20	up	1.04	up	1.02	down	ABA
Os.15738.1.S1_at	LOC_Os12g44020	Ser/Thr protein phosphatase family protein, putative, expressed	1.38	down	1.35	up	3.42	down	1.25	up	1.37	down	2.10	down	2

Os.15747.1.A1_at	LOC_Os09g39910	ABC transporter, ATP-binding protein, putative, expressed	**1.02**	up	**1.23**	down	**21.15**	up	**1.12**	up	**3.51**	up	**1.71**	up	2
Os.15757.1.S1_at	LOC_Os02g39710	CCT/B-box zinc finger protein, putative, expressed	**1.38**	down	**1.01**	down	**2.08**	down	**1.07**	up	**1.49**	down	**1.48**	down	ABA
Os.15767.2.S1_x_at	LOC_Os10g37210	FAD dependent oxidoreductase domain containing protein, expressed	**1.15**	up	**1.02**	up	**2.55**	up	**1.14**	up	**1.78**	up	**1.42**	up	ABA
Os.15780.1.S1_at	LOC_Os02g08220	expressed protein	**1.25**	up	**1.00**	down	**5.00**	down	**1.10**	down	**1.16**	down	**1.19**	down	ABA
Os.15789.1.S1_at	LOC_Os12g08920	peroxidase precursor, putative, expressed	**1.25**	up	**1.85**	up	**8.82**	down	**2.19**	up	**1.54**	down	**1.24**	down	2
Os.15789.1.S1_x_at	LOC_Os12g08920	peroxidase precursor, putative, expressed	**1.15**	up	**1.60**	up	**7.39**	down	**1.72**	up	**1.48**	down	**1.25**	down	ABA
Os.15797.1.S1_at	LOC_Os05g06990	TKL_IRAK_CrRLK1L-1.10 - The CrRLK1L-1 subfamily has homology to the CrRLK1L h	**1.32**	up	**1.07**	down	**3.33**	up	**1.22**	up	**1.23**	up	**1.11**	down	ABA
Os.15798.1.S1_at	LOC_Os06g07040	OsIAA20 - Auxin-responsive Aux/IAA gene family member, expressed	**21.52**	up	**1.00**	up	**5.69**	up	**1.27**	up	**2.22**	up	**1.31**	up	3
Os.15799.1.S1_at	LOC_Os03g11420	Os3bglu6 - beta-glucosidase/beta-fucosidase/beta-galactosidase, expressed	**1.06**	down	**1.09**	up	**4.96**	up	**1.17**	up	**1.01**	down	**1.79**	down	ABA
Os.158.1.S1_at	LOC_Os10g02070	peroxidase precursor, putative, expressed	**1.69**	down	**1.56**	down	**10.61**	down	**1.36**	up	**1.37**	down	**2.22**	up	2
Os.15807.1.S1_s_at	LOC_Os12g32260	expressed protein	**1.62**	down	**1.24**	up	**2.16**	down	**1.11**	down	**1.17**	down	**1.12**	up	ABA
Os.15809.1.S1_at	AK108095	Oryza sativa Japonica Group cDNA clone:002-139-A07, full insert sequence.	**1.14**	down	**1.03**	down	**7.98**	up	**1.09**	down	**1.08**	up	**1.05**	down	ABA
Os.15813.1.S1_at	LOC_Os03g56610	expressed protein	**1.18**	up	**1.05**	up	**2.18**	down	**1.10**	down	**1.11**	down	**1.28**	up	ABA
Os.15815.1.S1_at	LOC_Os08g01490	cytochrome P450, putative, expressed	**1.05**	down	**1.27**	up	**2.60**	up	**1.66**	down	**1.68**	up	**1.82**	up	ABA
Os.15815.2.S1_x_at	LOC_Os08g01490	cytochrome P450, putative, expressed	**1.05**	down	**1.08**	up	**3.30**	up	**2.35**	down	**1.45**	up	**2.36**	up	3
Os.15821.3.A1_at	LOC_Os05g01240	AML1, putative, expressed	**1.25**	up	**1.13**	up	**3.38**	up	**1.20**	down	**1.11**	down	**1.91**	down	ABA
Os.15822.1.S1_s_at	LOC_Os08g32980	expressed protein	**1.24**	up	**1.04**	up	**6.53**	up	**1.49**	down	**1.19**	up	**1.01**	up	ABA
Os.15825.1.S2_at	LOC_Os04g53720	SNF2 family N-terminal domain containing protein, expressed	**1.08**	down	**1.37**	down	**2.59**	up	**1.20**	up	**1.56**	up	**1.12**	down	ABA
Os.15830.1.S1_at	LOC_Os05g39760	VHS and GAT domain containing protein, expressed	**1.60**	down	**1.10**	up	**9.17**	up	**1.68**	up	**1.56**	up	**3.53**	up	2
Os.15841.1.S1_a_at	LOC_Os11g05290	stress responsive A/B Barrel domain containing protein, expressed	**1.17**	up	**1.53**	up	**2.93**	down	**1.29**	down	**1.81**	down	**1.48**	down	ABA
Os.15852.1.S1_at	LOC_Os10g03320	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.06**	up	**1.25**	up	**2.32**	up	**1.25**	up	**1.19**	up	**1.22**	up	ABA
Os.15853.1.S1_at	LOC_Os02g37610	expressed protein	**1.19**	down	**1.67**	up	**2.64**	up	**1.68**	down	**1.24**	down	**3.02**	down	2
Os.15867.1.A1_at	LOC_Os02g45690	uncharacterized mscS family protein, putative, expressed	**1.01**	down	**1.02**	up	**18.63**	up	**1.00**	down	**1.00**	up	**1.01**	up	ABA
Os.15874.1.A1_at	LOC_Os03g60570	ZOS3-22 - C2H2 zinc finger protein, expressed	**1.70**	up	**1.64**	up	**3.41**	up	**1.64**	down	**2.87**	up	**1.32**	down	2
Os.15908.1.S1_s_at	LOC_Os01g72330	OsRR4 type-A response regulator, expressed	**2.13**	down	**7.82**	up	**1.90**	down	**1.19**	up	**4.50**	down	**3.33**	down	4
Os.15913.1.S1_a_at	LOC_Os02g37880	cyclin G-associated kinase, putative, expressed	**1.11**	up	**1.05**	down	**2.07**	up	**1.09**	down	**1.05**	down	**1.26**	down	ABA
Os.15914.1.S1_at	LOC_Os09g23350	trehalose synthase, putative, expressed	**1.72**	up	**1.19**	down	**3.03**	up	**1.01**	down	**1.25**	up	**1.10**	up	ABA
Os.15918.1.S1_x_at	LOC_Os03g63060	P21-Rho-binding domain containing protein, putative, expressed	**1.21**	down	**1.03**	up	**2.24**	up	**1.30**	down	**1.32**	down	**1.22**	down	ABA
Os.1592.1.S1_at	LOC_Os01g51380	ATP synthase, putative, expressed	**1.22**	up	**1.04**	up	**2.86**	up	**1.61**	down	**1.21**	up	**1.05**	down	ABA
Os.15938.1.S1_at	LOC_Os03g17790	OsRCI2-5 - Putative low temperature and salt responsive protein, expressed	**1.21**	up	**1.29**	up	**52.85**	up	**1.18**	down	**1.22**	up	**1.18**	up	ABA
Os.15939.1.S2_at	LOC_Os01g53670	ENTH domain containing protein, expressed	**1.02**	up	**1.14**	down	**2.90**	up	**1.17**	up	**1.36**	up	**1.02**	down	ABA
Os.15941.2.S1_x_at	LOC_Os01g65510	OsFBX31 - F-box domain containing protein, expressed	**1.35**	up	**1.17**	up	**11.20**	up	**1.27**	down	**1.58**	down	**1.99**	down	ABA
Os.15951.1.S1_at	LOC_Os03g48150	Oryza sativa Japonica Group cDNA clone:J013022N15, full insert sequence.	**1.26**	down	**1.06**	up	**2.16**	down	**1.11**	down	**1.39**	down	**1.33**	down	ABA
Os.15985.1.S1_at	LOC_Os11g24570	PPR repeat domain containing protein, putative, expressed	**1.14**	up	**1.21**	up	**2.27**	down	**1.02**	up	**1.27**	down	**1.35**	down	ABA
Os.15988.1.S1_at	LOC_Os06g27770	isoflavone reductase homolog IRL, putative, expressed	**1.79**	up	**1.01**	up	**5.43**	up	**1.44**	up	**3.11**	up	**1.28**	up	2
Os.16010.1.S1_at	LOC_Os05g42150	OsGH3.4 - Probable indole-3-acetic acid-amido synthetase, expressed	**20.34**	up	**1.90**	up	**1.20**	up	**1.34**	up	**1.05**	up	**1.81**	up	IAA
Os.16018.1.S1_at	LOC_Os01g63010	universal stress protein domain containing protein, putative, expressed	**1.01**	down	**1.00**	down	**4.94**	up	**1.01**	down	**1.00**	up	**1.01**	up	ABA
Os.16030.1.S1_at	AK107816	Oryza sativa (japonica cultivar-group) Os03g0371400 (Os03g0371400) mRNA, partial	**3.06**	up	**1.15**	up	**1.78**	down	**3.09**	down	**1.81**	down	**3.34**	down	3
Os.16037.1.S1_at	AK242368	Oryza sativa Japonica Group cDNA, clone: J080035A07, full insert sequence.	**1.08**	up	**1.03**	down	**4.42**	down	**1.57**	down	**1.02**	up	**1.04**	down	ABA
Os.16039.1.S1_s_at	LOC_Os02g28720	spotted leaf 11, putative, expressed	**1.27**	up	**1.13**	down	**3.57**	up	**1.24**	down	**1.25**	up	**1.13**	down	ABA
Os.16041.1.S1_at	LOC_Os03g16940	glyoxalase family protein, putative, expressed	**1.00**	up	**1.00**	up	**90.68**	up	**1.18**	down	**1.16**	down	**1.15**	down	ABA
Os.16043.1.S1_at	LOC_Os11g45290	retrotransposon protein, putative, unclassified, expressed	**1.10**	up	**1.09**	down	**2.14**	down	**1.21**	down	**1.91**	down	**1.36**	down	ABA
Os.16044.1.S1_at	LOC_Os02g30910	nodulin MtN3 family protein, putative, expressed	**7.27**	up	**1.37**	up	**705.84**	up	**1.89**	up	**1.17**	up	**1.43**	up	2
Os.16049.1.S1_at	LOC_Os09g36360	protein of unknown function containing protein, expressed	**1.02**	up	**1.00**	up	**2.92**	up	**1.00**	up	**1.13**	up	**1.02**	down	ABA
Os.16068.1.S1_at	AK064638	Oryza sativa Japonica Group cDNA clone:002-114-A10, full insert sequence.	**1.25**	up	**1.19**	up	**11.57**	up	**1.02**	up	**2.17**	up	**1.02**	up	2
Os.16068.3.S1_at	LOC_Os02g47840	universal stress protein domain containing protein, putative, expressed	**1.10**	up	**1.15**	up	**7.60**	up	**1.18**	down	**3.59**	up	**1.15**	up	2
Os.16089.1.A1_at	LOC_Os05g32320	integral membrane transporter family protein, putative, expressed	**1.24**	up	**1.18**	down	**9.02**	up	**1.11**	down	**1.04**	up	**1.03**	down	ABA
Os.16105.1.S1_at	LOC_Os10g07450	expressed protein	**1.16**	down	**1.07**	down	**2.28**	down	**1.14**	up	**1.05**	up	**1.12**	up	ABA
Os.16119.1.S1_at	LOC_Os03g05310	pheophorbide a oxygenase, chloroplast precursor, putative, expressed	**1.38**	down	**1.41**	down	**2.91**	up	**1.31**	up	**1.26**	up	**1.61**	up	ABA
Os.16133.1.S1_at	LOC_Os01g11960	histone-lysine N-methyltransferase ATX5, putative, expressed	**1.09**	down	**1.13**	down	**2.84**	up	**1.15**	down	**1.05**	down	**1.36**	down	ABA
Os.16142.1.S1_at	LOC_Os03g31510	cysteine proteinase inhibitor 8 precursor, putative, expressed	**1.01**	up	**1.04**	down	**2.98**	up	**1.27**	up	**1.25**	up	**1.06**	up	ABA
Os.16151.1.S1_at	LOC_Os03g12160	leucine-rich repeat family protein, putative, expressed	**1.17**	down	**1.37**	down	**5.52**	up	**1.17**	up	**1.31**	up	**1.04**	up	ABA
Os.16163.1.S1_at	LOC_Os02g15740	expressed protein	**1.01**	up	**1.01**	up	**261.96**	up	**1.08**	up	**1.01**	down	**1.02**	up	ABA
Os.16164.1.S1_at	LOC_Os06g10530	expressed protein	**1.21**	up	**1.61**	up	**49.91**	up	**1.35**	up	**1.34**	up	**1.10**	down	ABA
Os.1617.1.S1_at	LOC_Os01g04910	TP53RK-binding protein, putative, expressed	**1.06**	down	**1.13**	up	**2.04**	down	**1.13**	down	**1.41**	down	**1.11**	down	ABA

Os.16187.1.S1_at	LOC_Os02g10630	GRAM and C2 domains containing protein, putative, expressed	**1.12**	up	**1.13**	up	**4.62**	up	**1.01**	up	**1.16**	up	**1.64**	down	ABA
Os.16214.1.S1_at	LOC_Os11g05490	expressed protein	**1.64**	down	**2.04**	up	**8.04**	down	**1.19**	down	**1.02**	up	**1.58**	down	2
Os.16218.1.S1_at	LOC_Os06g30370	osMFT1 MFT-Like1 homologous to Mother of FT and TFL1 gene; contains Pfam profil	**1.49**	up	**1.26**	up	**88.45**	up	**1.10**	down	**1.44**	up	**1.16**	down	ABA
Os.16231.1.S1_s_at	LOC_Os04g36890	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed	**1.04**	down	**1.03**	up	**2.29**	down	**1.04**	down	**1.01**	down	**1.10**	up	ABA
Os.1625.1.S1_at	LOC_Os01g05010	mitochondrial glycoprotein, putative, expressed	**1.11**	up	**1.12**	up	**2.54**	down	**1.27**	up	**1.34**	down	**1.02**	down	ABA
Os.16282.1.A1_at	LOC_Os06g37080	L-ascorbate oxidase precursor, putative, expressed	**1.12**	down	**1.05**	up	**2.23**	down	**1.13**	up	**1.40**	down	**1.18**	up	ABA
Os.16320.1.S1_at	LOC_Os07g39520	STE_PAK_Ste20_Slob_Wnk.5 - STE kinases include homologs to sterile 7, sterile 11 a	**1.89**	up	**1.16**	up	**6.22**	up	**1.29**	up	**3.47**	up	**1.24**	up	2
Os.16326.1.S1_at	LOC_Os02g17780	ent-kaurene synthase, chloroplast precursor, putative, expressed	**1.48**	down	**1.99**	up	**8.36**	down	**1.29**	down	**2.15**	down	**1.42**	up	3
Os.16327.1.S1_at	LOC_Os08g26230	expressed protein	**1.00**	down	**1.39**	down	**2.40**	down	**1.10**	down	**1.31**	up	**1.38**	up	ABA
Os.16333.1.S1_at	LOC_Os04g40310	dehydrogenase, putative, expressed	**1.36**	up	**1.01**	up	**1.82**	up	**1.23**	up	**2.43**	up	**1.57**	up	SA
Os.16334.1.S1_at	LOC_Os06g15380	acylphosphatase, putative	**1.30**	down	**1.00**	down	**2.08**	up	**1.38**	up	**1.36**	up	**1.29**	up	ABA
Os.16365.1.S1_at	LOC_Os09g32100	expressed protein	**1.28**	down	**1.29**	down	**16.01**	down	**1.06**	down	**1.69**	down	**1.06**	down	ABA
Os.1637.1.S1_at	LOC_Os01g02020	acetyl-CoA acetyltransferase, cytosolic, putative, expressed	**1.12**	up	**1.03**	down	**4.86**	up	**1.39**	up	**2.88**	up	**2.35**	up	3
Os.16429.1.S1_at	LOC_Os01g52630	regulator of chromosome condensation, putative, expressed	**1.05**	down	**1.01**	down	**4.36**	up	**1.04**	up	**1.09**	up	**1.13**	up	ABA
Os.16453.1.S1_at	LOC_Os12g39400	ZOS12-09 - C2H2 zinc finger protein, expressed	**1.05**	down	**1.03**	up	**12.58**	up	**1.20**	up	**1.31**	up	**1.19**	up	ABA
Os.16463.1.S1_at	LOC_Os04g58310	CBS domain-containing protein, putative, expressed	**1.08**	down	**1.35**	down	**20.96**	up	**1.14**	down	**1.00**	up	**1.14**	up	ABA
Os.16506.1.A1_at	LOC_Os12g01830	staphylococcal nuclease homologue, putative, expressed	**2.21**	down	**1.45**	down	**4.10**	down	**1.23**	up	**1.36**	down	**1.79**	down	2
Os.16532.1.S1_at	LOC_Os03g52370	PIII4 - Proteinase inhibitor II family protein precursor, expressed	**1.02**	down	**2.14**	up	**1.31**	up	**1.10**	down	**1.88**	up	**1.12**	down	BAP
Os.16558.1.S1_at	LOC_Os01g73200	peroxidase precursor, putative, expressed	**1.00**	up	**1.61**	up	**1.33**	down	**6.19**	up	**1.17**	up	**1.14**	up	ACC
Os.16582.1.S1_at	LOC_Os07g42910	cytochrome c oxidase subunit, putative, expressed	**1.37**	down	**1.05**	down	**6.80**	up	**1.37**	up	**1.55**	up	**1.26**	up	ABA
Os.16605.1.S1_at	LOC_Os10g30280	OsFBX386 - F-box domain containing protein, expressed	**1.37**	down	**1.23**	down	**5.50**	down	**1.07**	down	**1.49**	down	**1.62**	down	ABA
Os.16612.1.S1_at	AK100307	Oryza sativa Japonica Group cDNA clone:J023078G11, full insert sequence.	**1.13**	down	**1.10**	up	**2.11**	down	**1.03**	down	**1.21**	down	**1.23**	down	ABA
Os.16627.1.S1_at	AK102170	phytochelatin synthetase, putative	**1.42**	down	**1.06**	down	**2.18**	down	**1.22**	down	**1.30**	down	**1.38**	up	ABA
Os.1665.1.S1_a_at	LOC_Os01g07300	uncharacterized 50.6 kDa protein in the 5region of gyrA and gyrB, putative, expressed	**1.82**	up	**1.58**	up	**2.14**	up	**1.57**	up	**1.95**	up	**1.30**	down	ABA
Os.1665.2.S1_x_at	LOC_Os01g07300	uncharacterized 50.6 kDa protein in the 5region of gyrA and gyrB, putative, expressed	**1.40**	up	**1.45**	up	**2.02**	up	**1.63**	up	**1.87**	up	**1.17**	down	ABA
Os.16704.1.S1_at	LOC_Os07g42940	CAMK_CAMK_like.7 - CAMK includes calcium/calmodulin depedent protein kinases, ex	**1.03**	down	**1.32**	up	**2.42**	down	**1.06**	up	**1.37**	down	**1.03**	down	ABA
Os.16712.1.S1_at	LOC_Os03g02560	cyclin-like F-box, putative, expressed	**1.11**	up	**1.16**	down	**5.55**	up	**1.05**	up	**1.96**	up	**1.04**	up	ABA
Os.16743.1.S1_at	LOC_Os12g01930	lipase-related, putative, expressed	**1.28**	up	**1.23**	up	**2.27**	up	**1.07**	up	**1.19**	up	**1.08**	down	ABA
Os.16759.1.S1_at	CT836471	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN061M08, full insert sequenc	**1.00**	down	**1.01**	up	**4.77**	up	**1.01**	up	**1.03**	up	**1.02**	up	ABA
Os.16760.1.S1_at	LOC_Os07g47270	protein kinase APK1B, chloroplast precursor, putative, expressed	**1.04**	up	**1.12**	down	**4.15**	up	**1.02**	up	**1.04**	up	**1.28**	down	ABA
Os.1678.1.S1_at	LOC_Os01g07420	hydrolase, alpha/beta fold family protein, putative, expressed	**1.31**	down	**1.37**	up	**3.80**	down	**1.22**	down	**2.11**	down	**1.26**	down	2
Os.16797.1.S1_at	LOC_Os02g08320	haemolysin-III, putative, expressed	**1.16**	down	**1.28**	up	**5.02**	up	**1.17**	up	**1.19**	up	**1.15**	down	ABA
Os.16804.1.S1_at	LOC_Os10g23060	expressed protein	**1.23**	down	**1.41**	up	**7.44**	up	**1.04**	up	**1.76**	down	**2.69**	down	2
Os.16810.1.S1_at	LOC_Os03g11290	expressed protein	**1.06**	up	**1.06**	up	**2.92**	up	**1.02**	down	**1.09**	down	**1.05**	up	ABA
Os.16862.1.S1_at	LOC_Os03g02610	glycosyl hydrolases family 16 protein, protein, expressed	**1.13**	down	**1.15**	down	**2.49**	down	**1.11**	down	**1.29**	down	**1.14**	down	ABA
Os.16879.1.S1_at	LOC_Os06g20820	expressed protein	**1.05**	down	**1.09**	down	**1.80**	up	**1.01**	down	**2.27**	up	**1.45**	up	SA
Os.16889.1.S1_a_at	LOC_Os01g17320	PPR repeat domain containing protein, putative, expressed	**1.11**	down	**1.04**	up	**2.07**	down	**1.20**	up	**1.23**	down	**1.04**	down	ABA
Os.16899.1.S1_at	LOC_Os07g30150	phosphoribosyl transferase, putative, expressed	**1.09**	up	**2.95**	up	**8.65**	down	**1.38**	up	**2.57**	down	**1.49**	down	3
Os.16902.1.S1_at	LOC_Os02g41780	transporter-related, putative, expressed	**1.04**	up	**1.15**	down	**8.41**	down	**1.67**	down	**2.04**	down	**1.11**	down	2
Os.16912.1.A1_at	LOC_Os02g53994	DUF1771 domain containing protein, putative, expressed	**1.11**	up	**1.19**	down	**2.56**	up	**1.18**	down	**1.12**	down	**1.18**	down	ABA
Os.16914.1.S2_at	LOC_Os02g27400	OsFBX49 - F-box domain containing protein, expressed	**1.12**	up	**1.02**	down	**2.39**	up	**1.14**	up	**1.11**	up	**1.22**	up	ABA
Os.16922.1.S1_at	LOC_Os09g33530	expressed protein	**1.14**	down	**1.38**	up	**2.22**	up	**1.17**	up	**1.09**	up	**1.70**	up	ABA
Os.16968.1.S1_at	LOC_Os03g03990	signal recognition particle 43 kDa protein, chloroplast precursor, putative, expressed	**1.04**	down	**1.15**	up	**3.65**	down	**1.24**	down	**1.67**	down	**1.47**	down	ABA
Os.16973.1.S1_at	LOC_Os02g35830	extracellular ligand-gated ion channel, putative, expressed	**1.45**	up	**1.02**	up	**3.13**	up	**1.28**	down	**1.10**	up	**1.31**	down	ABA
Os.16987.1.S1_at	LOC_Os04g47700	expressed protein	**1.02**	up	**1.38**	up	**9.97**	up	**1.26**	down	**1.30**	up	**1.19**	down	ABA
Os.170.1.S1_at	LOC_Os01g64110	glycosyl hydrolase, putative, expressed	**1.49**	up	**1.07**	up	**4.51**	down	**1.28**	up	**1.17**	down	**1.40**	down	ABA
Os.17002.1.S1_at	LOC_Os01g26039	expressed protein	**1.10**	up	**1.05**	up	**8.55**	up	**1.11**	up	**1.09**	up	**1.63**	up	ABA
Os.17074.1.S1_at	LOC_Os03g44200	beclin-1, putative, expressed	**1.06**	up	**1.00**	down	**2.28**	up	**1.05**	down	**1.18**	up	**1.08**	down	ABA
Os.17076.1.S1_at	LOC_Os09g10340	cytochrome P450, putative, expressed	**1.34**	down	**1.65**	up	**30.76**	down	**6.91**	down	**1.56**	down	**3.48**	up	3
Os.17112.1.S1_at	LOC_Os03g18030	leucoanthocyanidin dioxygenase, putative, expressed	**1.24**	down	**1.11**	down	**2.07**	down	**1.06**	up	**1.64**	up	**18.46**	up	2
Os.17125.1.S1_at	LOC_Os08g41090	peroxidase precursor, putative, expressed	**1.17**	down	**1.03**	up	**3.35**	down	**1.08**	down	**1.20**	down	**1.60**	down	ABA
Os.17136.1.S1_at	LOC_Os03g51920	peptidase, M50 family, putative, expressed	**1.42**	down	**1.14**	down	**21.49**	up	**1.97**	down	**1.90**	up	**1.47**	up	ABA
Os.17144.1.A1_at	LOC_Os04g59000	protein kinase family protein, putative, expressed	**1.26**	down	**1.41**	down	**2.05**	down	**1.05**	down	**1.73**	down	**1.09**	up	ABA
Os.17147.1.S1_x_at	LOC_Os06g12310	aquaporin protein, putative, expressed	**1.06**	up	**1.13**	down	**4.70**	down	**1.34**	down	**1.98**	down	**1.26**	down	ABA
Os.17149.1.S1_at	LOC_Os03g60910	PPR repeat domain containing protein, putative, expressed	**1.06**	up	**1.16**	up	**2.01**	down	**1.12**	down	**1.46**	down	**1.44**	down	ABA

Os.17167.1.S1_at	LOC_Os06g03540	oligopeptide transporter, putative, expressed	**1.25**	down	**1.62**	down	**2.83**	up	**1.13**	up	**1.45**	up	**1.12**	down	ABA
Os.17173.1.S1_at	LOC_Os05g08640	transferase family protein, putative, expressed	**1.57**	down	**1.27**	down	**1.12**	down	**1.15**	up	**1.12**	up	**2.33**	up	JA
Os.17189.1.S1_at	LOC_Os05g44070	ras-related protein, putative, expressed	**1.29**	down	**1.02**	down	**3.87**	down	**1.06**	down	**1.42**	down	**1.40**	down	ABA
Os.17195.1.A1_at	AK068772	glycosyl hydrolase family 1 protein	**1.17**	down	**1.48**	down	**16.41**	up	**1.71**	down	**1.33**	up	**1.14**	up	ABA
Os.17210.1.S1_at	LOC_Os02g57750	protein binding protein, putative, expressed	**1.07**	down	**1.15**	down	**2.07**	up	**1.01**	down	**1.10**	up	**1.01**	down	ABA
Os.1723.1.S1_at	LOC_Os01g18220	expressed protein	**1.22**	down	**2.10**	down	**27.18**	up	**1.17**	down	**1.99**	up	**1.37**	up	2
Os.17250.1.S1_x_at	LOC_Os10g33170	POT domain containing peptide transporter, putative, expressed	**1.02**	up	**1.04**	down	**2.65**	down	**1.64**	down	**1.30**	down	**1.27**	down	ABA
Os.17280.1.A1_at	LOC_Os06g22080	diacylglycerol O-acyltransferase, putative, expressed	**1.01**	down	**1.01**	up	**2.09**	up	**1.17**	up	**1.56**	up	**1.06**	up	ABA
Os.17286.1.S1_at	LOC_Os03g21060	No apical meristem protein, putative, expressed	**1.09**	up	**1.25**	down	**14.16**	up	**1.47**	up	**1.58**	up	**1.08**	up	ABA
Os.17315.1.S1_at	LOC_Os03g04140	serine acetyltransferase protein, putative, expressed	**1.07**	up	**1.01**	down	**2.07**	down	**1.14**	down	**1.10**	down	**1.21**	down	ABA
Os.17323.2.S1_at	LOC_Os02g48190	expressed protein	**1.21**	up	**1.33**	down	**5.37**	up	**1.23**	up	**1.71**	up	**2.23**	up	2
Os.17334.1.S1_at	AK069265	Oryza sativa Japonica Group cDNA clone:J023012L05, full insert sequence.	**1.14**	down	**1.02**	down	**3.60**	up	**1.36**	up	**1.04**	down	**1.15**	up	ABA
Os.17334.1.S1_s_at	AK069265	Oryza sativa Japonica Group cDNA clone:J023012L05, full insert sequence.	**1.36**	down	**1.02**	down	**2.40**	up	**1.32**	up	**1.01**	up	**1.14**	up	ABA
Os.17334.2.S1_x_at	AK066992	Oryza sativa Japonica Group cDNA clone:J013089P17, full insert sequence.	**1.19**	down	**1.02**	down	**2.41**	up	**1.28**	up	**1.02**	down	**1.26**	up	ABA
Os.17348.1.S1_at	LOC_Os05g39070	NLI interacting factor-like phosphatase, putative, expressed	**1.12**	up	**1.04**	up	**2.51**	up	**1.06**	down	**1.24**	up	**1.02**	down	ABA
Os.17353.1.S1_at	LOC_Os06g45380	vacuolar-sorting receptor precursor, putative, expressed	**1.13**	down	**1.12**	up	**2.44**	down	**1.01**	down	**1.27**	down	**1.05**	up	ABA
Os.17359.1.S1_at	LOC_Os05g27780	expressed protein	**1.07**	down	**1.14**	up	**2.65**	up	**1.01**	up	**1.00**	up	**1.00**	down	ABA
Os.17368.1.S1_at	LOC_Os02g52420	peptidase, M24 family protein, putative, expressed	**1.07**	up	**1.09**	up	**2.13**	down	**1.16**	down	**1.30**	down	**1.18**	down	ABA
Os.1740.1.S1_at	LOC_Os01g26120	membrane associated DUF588 domain containing protein, putative, expressed	**1.25**	down	**1.11**	up	**5.38**	up	**1.28**	down	**1.51**	up	**1.22**	up	ABA
Os.17403.1.S1_a_at	LOC_Os03g42070	cyclin, putative, expressed	**1.66**	down	**1.60**	down	**3.52**	down	**1.18**	up	**1.21**	down	**1.62**	down	ABA
Os.17405.1.S1_a_at	LOC_Os12g31860	ureide permease, putative, expressed	**1.08**	down	**1.03**	down	**3.64**	up	**1.14**	up	**1.87**	up	**1.05**	down	ABA
Os.17419.1.S1_at	LOC_Os10g09850	EF hand family protein, putative, expressed	**1.05**	down	**1.04**	down	**15.53**	up	**1.10**	down	**1.13**	down	**1.03**	up	ABA
Os.17424.1.S1_at	LOC_Os03g24730	expressed protein	**1.21**	up	**1.13**	up	**4.28**	up	**1.34**	down	**1.34**	up	**1.57**	down	ABA
Os.17424.1.S1_x_at	LOC_Os03g24730	expressed protein	**1.37**	up	**1.24**	up	**3.98**	up	**1.35**	down	**1.22**	up	**1.67**	down	ABA
Os.17433.1.S1_at	LOC_Os09g33690	Os9bglu32 - beta-glucosidase homologue, similar to G. max hydroxyisourate hydrolase	**1.00**	up	**1.03**	down	**3.83**	up	**1.01**	down	**1.04**	up	**1.01**	up	ABA
Os.17437.1.S1_at	LOC_Os01g53390	glucosyltransferase, putative, expressed	**2.33**	down	**1.01**	up	**1.92**	down	**1.67**	up	**1.17**	up	**1.84**	up	IAA
Os.17446.1.S1_at	LOC_Os04g48270	OsFBX148 - F-box domain containing protein, expressed	**1.27**	up	**1.04**	up	**6.37**	up	**1.28**	down	**1.11**	up	**1.01**	up	ABA
Os.17446.2.S1_at	LOC_Os04g48270	OsFBX148 - F-box domain containing protein, expressed	**1.62**	up	**1.26**	up	**9.69**	up	**1.44**	down	**1.16**	up	**1.08**	up	ABA
Os.17484.1.S1_at	LOC_Os04g35280	neutral/alkaline invertase, putative, expressed	**1.16**	up	**1.11**	up	**2.97**	up	**1.20**	down	**1.09**	up	**1.10**	down	ABA
Os.17491.1.S1_at	LOC_Os10g35070	alpha-galactosidase precursor, putative, expressed	**1.07**	down	**1.02**	down	**34.60**	up	**1.68**	down	**2.82**	up	**1.02**	down	2
Os.17494.2.S1_at	LOC_Os06g28194	expressed protein	**1.11**	up	**1.46**	up	**2.81**	down	**1.28**	down	**1.26**	down	**1.07**	down	ABA
Os.17496.1.S1_at	LOC_Os12g16080	expressed protein	**1.07**	up	**1.20**	down	**1.03**	down	**1.47**	down	**2.21**	up	**1.03**	down	SA
Os.17501.1.A1_at	LOC_Os09g38410	sialin, putative, expressed	**1.09**	up	**1.23**	down	**2.95**	up	**1.02**	up	**1.33**	up	**1.04**	up	ABA
Os.17502.1.S1_at	LOC_Os11g32880	DEAD-box ATP-dependent RNA helicase, putative, expressed	**1.19**	up	**1.32**	up	**2.54**	down	**1.03**	down	**1.53**	down	**1.41**	down	ABA
Os.17506.1.S1_at	LOC_Os10g32680	expressed protein	**1.05**	up	**1.08**	up	**6.51**	up	**1.96**	up	**3.67**	up	**1.95**	up	2
Os.17522.1.S1_s_at	LOC_Os10g37290	DEFL6 - Defensin and Defensin-like DEFL family, expressed	**2.08**	down	**1.24**	up	**20.46**	down	**1.03**	down	**1.42**	up	**1.37**	down	2
Os.17554.1.S1_at	LOC_Os08g37760	zinc finger, C3HC4 type domain containing protein, expressed	**2.06**	down	**1.04**	down	**1.36**	down	**1.50**	up	**1.30**	up	**1.26**	up	IAA
Os.17584.1.S1_at	LOC_Os02g56860	3-ketoacyl-CoA synthase, putative, expressed	**1.51**	up	**1.55**	up	**3.90**	up	**1.37**	up	**1.59**	up	**1.58**	up	ABA
Os.17619.1.S1_at	LOC_Os02g17534	xyloglucan fucosyltransferase, putative, expressed	**1.23**	down	**1.05**	down	**2.66**	down	**1.08**	up	**1.31**	down	**1.07**	down	ABA
Os.17623.1.S1_at	LOC_Os07g49310	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed	**1.26**	up	**1.19**	up	**7.07**	down	**1.06**	down	**2.45**	down	**1.63**	down	2
Os.17652.1.S1_s_at	LOC_Os03g43720	transporter family protein, putative, expressed	**1.30**	up	**1.10**	down	**17.29**	up	**1.50**	up	**2.83**	up	**1.21**	up	2
Os.17652.1.S2_s_at	LOC_Os03g43720	transporter family protein, putative, expressed	**1.11**	up	**1.02**	down	**15.78**	up	**1.41**	up	**2.98**	up	**1.27**	up	2
Os.17653.1.S1_at	LOC_Os03g55870	membrane associated DUF588 domain containing protein, putative, expressed	**1.89**	up	**1.05**	down	**14.64**	up	**1.37**	down	**1.03**	up	**1.17**	down	ABA
Os.17655.1.S1_at	LOC_Os02g49160	OsIAA8 - Auxin-responsive Aux/IAA gene family member, expressed	**1.26**	down	**1.03**	down	**2.68**	down	**1.50**	up	**1.25**	up	**1.04**	down	ABA
Os.17663.1.S1_at	LOC_Os01g64860	OsSub11 - Putative Subtilisin homologue, expressed	**1.03**	up	**1.08**	up	**5.43**	down	**1.32**	down	**2.30**	down	**1.22**	down	2
Os.17691.1.S1_at	LOC_Os08g35620	HD domain containing protein, putative, expressed	**1.02**	up	**1.07**	down	**2.42**	up	**1.01**	down	**1.17**	down	**1.14**	down	ABA
Os.17718.1.S1_at	LOC_Os05g39410	expressed protein	**1.13**	up	**1.24**	down	**4.66**	up	**1.32**	up	**1.81**	up	**1.27**	up	ABA
Os.17722.1.S1_at	LOC_Os01g22249	peroxidase precursor, putative, expressed	**1.06**	down	**1.18**	up	**7.08**	down	**2.55**	up	**1.49**	down	**1.32**	up	2
Os.17746.1.S1_s_at	LOC_Os01g64540	anthocyanidin 3-O-glucosyltransferase, putative, expressed	**1.09**	down	**1.29**	up	**3.66**	down	**1.79**	down	**1.34**	up	**1.03**	down	ABA
Os.17761.1.S1_a_at	LOC_Os04g32110	ACT domain containing protein, expressed	**1.44**	down	**1.09**	up	**2.11**	down	**1.28**	up	**1.69**	down	**1.97**	up	ABA
Os.17762.1.S1_at	LOC_Os06g29844	MATE efflux family protein, putative, expressed	**1.10**	up	**1.39**	down	**3.64**	up	**1.05**	down	**1.32**	up	**1.04**	down	ABA
Os.17765.1.A1_at	LOC_Os05g37160	tubulin/FtsZ domain containing protein, putative, expressed	**1.10**	down	**1.03**	down	**2.31**	down	**1.10**	down	**1.50**	down	**1.20**	down	ABA
Os.17787.1.S1_at	LOC_Os07g48090	CAMK_KIN1/SNF1/Nim1_like.30 - CAMK includes calcium/calmodulin depedent protein	**1.18**	down	**1.28**	down	**2.10**	up	**1.06**	down	**1.05**	up	**1.60**	up	ABA
Os.17805.1.S1_at	LOC_Os01g63930	cytochrome P450, putative, expressed	**1.28**	up	**1.30**	up	**5.50**	up	**1.08**	down	**1.25**	down	**2.68**	up	2
Os.17841.2.S1_x_at	LOC_Os07g06940	valyl-tRNA synthetase, putative, expressed	**1.12**	up	**1.01**	down	**2.45**	down	**1.16**	down	**1.52**	down	**1.26**	down	ABA

Os.17890.1.S1_at	LOC_Os03g22120	sucrose synthase, putative, expressed	**1.10**	up	**1.08**	up	**8.54**	up	**1.20**	up	**1.34**	up	**1.33**	down	ABA
Os.17895.1.S1_a_at	LOC_Os10g30860	nicotiana lesion-inducing like, putative, expressed	**1.03**	down	**1.22**	down	**2.28**	down	**1.19**	down	**1.46**	down	**1.17**	up	ABA
Os.17895.1.S1_at	LOC_Os10g30870	expressed protein	**1.13**	down	**1.09**	down	**2.10**	down	**1.12**	down	**1.29**	down	**1.02**	up	ABA
Os.17895.2.S1_x_at	LOC_Os10g30860	nicotiana lesion-inducing like, putative, expressed	**1.02**	down	**1.14**	down	**2.21**	down	**1.25**	down	**1.24**	down	**1.20**	up	ABA
Os.17902.1.S1_at	LOC_Os05g02420	expressed protein	**1.50**	down	**1.92**	down	**3.25**	down	**1.03**	down	**1.46**	down	**1.47**	down	ABA
Os.17921.1.S1_at	LOC_Os05g47540	CPuORF26 - conserved peptide uORF-containing transcript, expressed	**2.26**	down	**5.61**	up	**47.08**	down	**1.29**	down	**13.79**	down	**5.55**	down	5
Os.17961.1.S1_a_at	LOC_Os02g20560	fasciclin domain containing protein, expressed	**1.03**	down	**1.27**	down	**5.76**	down	**1.20**	down	**1.50**	down	**1.12**	down	ABA
Os.17994.1.S1_at	LOC_Os04g41300	ribosome recycling factor, putative, expressed	**1.10**	up	**1.12**	up	**2.25**	down	**1.06**	up	**1.63**	down	**1.29**	down	ABA
Os.17997.1.S1_at	LOC_Os10g26570	phosphofructokinase, putative, expressed	**1.07**	up	**1.32**	down	**1.55**	up	**1.07**	up	**2.87**	up	**2.10**	up	2
Os.17997.2.S1_x_at	LOC_Os10g26570	phosphofructokinase, putative, expressed	**1.31**	up	**1.41**	down	**1.51**	up	**1.14**	down	**2.69**	up	**2.28**	up	2
Os.18019.1.S1_at	LOC_Os08g18150	WD domain, G-beta repeat domain containing protein, expressed	**1.41**	down	**1.07**	down	**2.96**	up	**1.08**	down	**1.36**	down	**1.52**	down	ABA
Os.18064.1.S1_at	LOC_Os08g40320	retrotransposon protein, putative, unclassified	**1.77**	down	**2.04**	down	**4.49**	up	**1.31**	down	**14.82**	up	**1.17**	up	3
Os.18078.1.S1_at	AK241601	Oryza sativa Japonica Group cDNA, clone: J065183I15, full insert sequence.	**1.07**	down	**1.04**	down	**1.77**	up	**1.46**	up	**40.89**	up	**1.08**	up	SA
Os.18082.1.S1_at	LOC_Os03g51330	GRAS family transcription factor domain containing protein, expressed	**1.35**	down	**1.06**	down	**2.08**	up	**1.25**	up	**1.10**	up	**1.03**	down	ABA
Os.18087.1.S1_at	LOC_Os03g30570	protein of unknown function DUF1675 domain containing protein, expressed	**1.12**	up	**1.13**	up	**3.74**	up	**1.28**	up	**1.09**	down	**1.02**	up	ABA
Os.18094.2.S1_a_at	LOC_Os05g46040	protein phosphatase 2C, putative, expressed	**1.67**	up	**1.38**	down	**16.96**	up	**1.24**	down	**1.71**	up	**1.03**	up	ABA
Os.18105.1.S1_at	LOC_Os12g13640	glycosyltransferase, putative, expressed	**1.52**	up	**1.09**	up	**4.10**	up	**1.08**	up	**1.27**	up	**1.25**	up	ABA
Os.18109.1.S1_at	LOC_Os10g34420	lysM domain containing protein, putative, expressed	**1.06**	down	**1.18**	down	**2.53**	up	**1.21**	up	**1.34**	up	**1.49**	up	ABA
Os.18122.1.S1_at	LOC_Os03g07790	zinc finger, C3HC4 type domain containing protein, expressed	**1.14**	down	**1.18**	up	**2.14**	down	**1.06**	down	**1.25**	down	**1.44**	down	ABA
Os.1814.1.S1_a_at	LOC_Os05g06670	gibberellin 2-oxidase, putative, expressed	**4.39**	up	**2.10**	down	**2.82**	down	**6.74**	up	**1.86**	down	**1.42**	up	4
Os.18157.1.S2_at	LOC_Os01g18360	OsIAA4 - Auxin-responsive Aux/IAA gene family member, expressed	**1.01**	down	**1.00**	up	**2.54**	up	**1.01**	up	**1.13**	up	**1.02**	up	ABA
Os.18169.1.S1_at	LOC_Os01g18360	OsIAA4 - Auxin-responsive Aux/IAA gene family member, expressed	**9.29**	up	**1.13**	down	**1.01**	down	**1.05**	up	**1.11**	up	**1.49**	up	IAA
Os.18169.2.S1_at	LOC_Os01g18360	OsIAA4 - Auxin-responsive Aux	**46.49**	up	**1.00**	up	**1.01**	down	**1.00**	up	**1.00**	down	**1.01**	up	IAA
Os.18169.2.S1_x_at	LOC_Os01g18360	OsIAA4 - Auxin-responsive Aux/IAA gene family member, expressed	**28.09**	up	**1.38**	down	**1.09**	up	**1.00**	up	**1.03**	up	**1.01**	up	IAA
Os.18177.1.S1_at	LOC_Os11g04104	major facilitator superfamily antiporter, putative, expressed	**1.07**	up	**1.30**	down	**3.79**	up	**1.12**	up	**4.68**	up	**3.00**	up	3
Os.18196.1.S1_at	LOC_Os07g42700	paramyosin, putative, expressed	**1.11**	down	**1.18**	down	**2.18**	up	**1.29**	down	**1.16**	up	**1.19**	down	ABA
Os.18229.1.S1_at	LOC_Os01g72610	glycosyltransferase, putative, expressed	**1.01**	up	**1.59**	down	**2.64**	up	**1.36**	up	**1.90**	up	**1.58**	up	ABA
Os.18235.1.S1_at	LOC_Os04g37550	aspartic proteinase nepenthesin-2 precursor, putative, expressed	**1.14**	up	**1.14**	up	**2.01**	up	**1.43**	down	**1.00**	down	**1.35**	down	ABA
Os.18241.2.A1_x_at	LOC_Os05g44570	histidine-containing phosphotransfer protein, putative, expressed	**1.19**	up	**1.05**	up	**7.61**	up	**1.05**	up	**1.16**	up	**1.15**	up	ABA
Os.18257.1.S1_at	LOC_Os07g10840	uncharacterized glycosyltransferase, putative, expressed	**1.01**	down	**1.08**	up	**7.10**	up	**1.09**	down	**1.92**	up	**1.13**	down	ABA
Os.18267.1.S1_at	LOC_Os08g05630	expressed protein	**1.11**	up	**1.04**	up	**2.31**	up	**1.14**	down	**1.04**	up	**1.09**	down	ABA
Os.18296.1.S1_x_at	LOC_Os01g10440	xylosyltransferase, putative, expressed	**1.38**	up	**1.18**	up	**7.06**	up	**1.36**	up	**5.38**	up	**1.21**	up	2
Os.18299.1.S1_at	LOC_Os07g07410	oxidoreductase, 2OG-Fe oxygenase family protein, putative, expressed	**1.27**	up	**1.07**	down	**3.65**	up	**1.03**	up	**1.68**	up	**1.24**	up	ABA
Os.18302.1.S1_at	LOC_Os01g06920	resistance protein SlVe1 precursor, putative, expressed	**1.00**	down	**1.00**	up	**5.59**	up	**1.01**	down	**1.01**	down	**1.02**	up	ABA
Os.18305.1.S1_at	LOC_Os05g50550	polyprenyl synthetase, putative, expressed	**1.23**	up	**1.02**	down	**2.15**	down	**1.05**	down	**1.13**	down	**1.13**	up	ABA
Os.18305.1.S2_at	LOC_Os05g50550	polyprenyl synthetase, putative, expressed	**1.19**	up	**1.05**	up	**2.13**	down	**1.02**	up	**1.12**	down	**1.04**	up	ABA
Os.18307.1.S1_at	LOC_Os07g38950	expressed protein	**1.22**	up	**1.12**	up	**2.60**	down	**1.22**	down	**1.47**	down	**1.13**	down	ABA
Os.18318.1.S1_at	LOC_Os03g10240	DUF677 domain containing protein, putative, expressed	**1.09**	up	**1.13**	up	**2.20**	up	**1.15**	up	**1.31**	down	**1.07**	up	ABA
Os.18323.1.S1_at	LOC_Os04g52590	protein kinase domain containing protein, expressed	**1.15**	down	**1.18**	down	**1.32**	down	**1.79**	up	**1.14**	down	**8.77**	up	JA
Os.18349.1.A1_s_at	LOC_Os11g08090	expressed protein	**1.14**	down	**1.06**	down	**2.32**	down	**1.05**	down	**1.33**	down	**1.22**	down	ABA
Os.18355.1.A1_at	C99457	---	**1.44**	up	**1.06**	up	**2.03**	down	**1.12**	up	**1.11**	up	**1.47**	down	ABA
Os.18364.1.S1_at	LOC_Os04g48760	leucine-rich repeat family protein, putative, expressed	**1.54**	up	**1.34**	down	**2.01**	down	**1.10**	up	**1.61**	down	**1.08**	down	ABA
Os.18374.1.A1_at	CT835882	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSA026A15, full insert sequence	**1.15**	up	**1.55**	down	**5.66**	up	**1.13**	down	**1.35**	up	**1.08**	down	ABA
Os.18376.1.S1_at	LOC_Os11g29780	plant-specific domain TIGR01627 family protein, expressed	**1.15**	down	**1.13**	down	**32.66**	up	**1.02**	up	**1.04**	down	**1.01**	up	ABA
Os.18381.1.S1_at	LOC_Os04g19740	transketolase, chloroplast precursor, putative, expressed	**1.03**	down	**1.20**	down	**28.81**	up	**1.21**	down	**1.18**	up	**1.14**	up	ABA
Os.18383.1.A1_at	LOC_Os08g37115	expressed protein	**1.08**	up	**1.54**	down	**6.21**	up	**1.56**	down	**1.07**	down	**1.72**	down	ABA
Os.18383.1.A1_x_at	LOC_Os08g37115	expressed protein	**1.25**	up	**1.17**	down	**4.28**	up	**1.09**	down	**1.12**	up	**1.40**	down	ABA
Os.18395.1.S1_s_at	LOC_Os06g15620	GASR7 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed	**1.33**	up	**1.01**	down	**8.15**	down	**1.43**	up	**1.04**	down	**1.27**	down	ABA
Os.18397.1.S1_at	LOC_Os02g46640	heat shock protein DnaJ, putative, expressed	**1.06**	down	**1.01**	up	**2.19**	up	**1.08**	down	**1.10**	up	**1.00**	down	ABA
Os.18406.1.S1_at	LOC_Os07g40220	expressed protein	**1.07**	up	**1.39**	down	**2.01**	up	**1.46**	down	**1.51**	up	**2.18**	down	2
Os.18418.1.S1_at	LOC_Os07g06600	glutaredoxin, putative, expressed	**1.14**	down	**1.23**	down	**2.01**	up	**1.08**	up	**1.15**	up	**1.08**	up	ABA
Os.18419.1.S1_at	LOC_Os03g63450	snRK1-interacting protein 1, putative, expressed	**1.10**	down	**1.06**	up	**1.36**	down	**1.01**	down	**1.09**	down	**2.10**	up	JA
Os.18421.1.S1_a_at	LOC_Os03g01800	glycosyl hydrolases family 16, putative, expressed	**1.06**	up	**1.04**	down	**21.11**	down	**1.30**	up	**1.71**	down	**1.07**	up	ABA
Os.18430.1.S1_at	LOC_Os04g35380	expressed protein	**1.02**	down	**1.00**	up	**2.79**	up	**1.07**	up	**1.41**	up	**1.03**	up	ABA
Os.18458.1.S1_at	LOC_Os01g57150	SR protein related family member, putative, expressed	**1.21**	up	**1.47**	up	**2.33**	down	**1.24**	down	**1.62**	down	**1.43**	down	ABA

Os.18486.1.S1_at	LOC_Os09g32670	UDP-glucuronate 4-epimerase, putative, expressed	1.37	down	1.14	down	3.40	down	1.07	down	1.19	up	1.11	up	ABA
Os.1849.1.S1_at	LOC_Os01g02390	protein kinase domain containing protein, expressed	1.41	up	1.28	down	3.73	up	1.02	up	2.14	up	1.28	up	2
Os.18490.1.S1_x_at	LOC_Os03g47610	thiamine biosynthesis protein thiC, putative, expressed	1.74	up	1.07	up	2.75	down	1.22	down	1.23	down	1.48	down	ABA
Os.18490.3.S1_at	LOC_Os03g47610	thiamine biosynthesis protein thiC, putative, expressed	1.46	up	1.26	up	2.20	down	1.15	down	1.35	down	1.41	down	ABA
Os.18493.1.S1_at	LOC_Os09g37480	OsSAUR53 - Auxin-responsive SAUR gene family member, expressed	1.65	up	1.13	down	3.19	down	1.10	down	1.24	up	1.68	down	ABA
Os.18513.1.S1_at	LOC_Os05g32820	peptide-N4-asparagine amidase A, putative, expressed	1.14	down	1.00	up	4.09	down	1.64	down	1.43	down	1.10	down	ABA
Os.1852.1.S1_at	LOC_Os09g23150	monoglyceride lipase, putative, expressed	1.22	down	1.23	down	3.65	up	1.26	up	1.57	up	1.19	up	ABA
Os.18552.1.S1_at	LOC_Os11g31980	OsSCP63 - Putative Serine Carboxypeptidase homologue, expressed	1.14	down	1.33	down	3.24	down	1.15	down	1.06	up	1.60	down	ABA
Os.18556.1.S1_x_at	LOC_Os03g64030	receptor protein kinase, putative, expressed	1.00	down	1.00	down	2.93	down	1.10	down	1.65	down	1.28	down	ABA
Os.18566.1.S1_at	LOC_Os01g37490	dynein light chain type 1 domain containing protein, expressed	1.23	down	1.15	down	3.10	down	1.07	down	1.78	down	1.67	down	ABA
Os.18572.1.S1_at	LOC_Os04g52310	metal cation transporter, putative, expressed	1.07	down	1.82	down	32.56	down	1.88	down	1.17	up	1.42	up	ABA
Os.18573.1.S1_at	LOC_Os07g43390	4-alpha-glucanotransferase, chloroplast precursor, putative, expressed	1.23	up	1.13	up	2.41	up	1.28	up	1.10	up	1.15	up	ABA
Os.18583.1.S1_at	LOC_Os01g07260	expressed protein	1.45	down	1.08	down	4.40	down	1.03	down	1.72	down	1.65	down	ABA
Os.18583.2.S1_at	LOC_Os01g07260	expressed protein	1.42	down	1.09	down	9.15	down	1.14	down	2.31	down	1.68	down	2
Os.18583.2.S1_x_at	LOC_Os01g07260	expressed protein	1.18	down	1.09	down	4.51	down	1.04	up	1.60	down	1.18	down	ABA
Os.18587.1.S1_at	LOC_Os07g08140	heat stress transcription factor, putative, expressed	1.09	down	1.14	down	2.26	up	1.91	down	1.28	down	1.35	down	ABA
Os.18595.1.A1_at	LOC_Os07g48450	no apical meristem protein, putative, expressed	1.53	down	1.38	down	5.61	up	2.05	up	1.15	up	1.02	up	2
Os.18597.1.S1_at	LOC_Os03g09930	sulfate transporter, putative, expressed	1.43	up	1.17	up	1.75	up	2.04	down	1.13	down	1.70	down	ACC
Os.18598.1.S1_at	LOC_Os03g49260	lipoxygenase, putative, expressed	1.83	down	1.04	down	15.66	down	1.39	up	4.49	down	1.37	up	2
Os.18599.1.S1_at	LOC_Os03g57970	LTPL73 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.05	up	1.20	up	2.11	up	1.49	down	1.08	up	1.14	down	ABA
Os.18612.1.S1_s_at	LOC_Os04g36050	cleft lip and palate transmembrane protein 1, putative, expressed	1.15	up	1.12	up	2.38	down	1.09	down	1.58	down	1.19	down	ABA
Os.18612.1.S1_x_at	LOC_Os04g36050	cleft lip and palate transmembrane protein 1, putative, expressed	1.06	up	1.08	up	2.10	down	1.00	down	1.42	down	1.04	down	ABA
Os.18615.1.S1_at	LOC_Os03g41390	ZOS3-15 - C2H2 zinc finger protein, expressed	1.27	up	1.04	down	4.08	up	1.10	up	1.26	down	1.45	down	ABA
Os.18615.1.S1_x_at	LOC_Os03g41390	ZOS3-15 - C2H2 zinc finger protein, expressed	1.20	up	1.06	down	4.76	up	1.24	up	1.08	down	1.17	down	ABA
Os.18623.1.S1_at	LOC_Os03g04530	cytochrome P450, putative, expressed	1.16	down	1.18	down	69.34	down	1.20	down	1.63	down	1.08	down	ABA
Os.18627.1.S1_at	LOC_Os03g53950	strictosidine synthase, putative, expressed	1.02	up	1.05	up	2.45	down	1.15	down	1.34	down	1.18	up	ABA
Os.18633.1.S1_at	LOC_Os04g43710	CAMK_CAMK_like.3 - CAMK includes calcium/calmodulin depedent protein kinases, ex	1.07	up	1.84	down	3.63	up	1.07	down	1.17	down	2.43	down	2
Os.18648.1.S1_at	AK108823	Oryza sativa (japonica cultivar-group) Os07g0142300 (Os07g0142300) mRNA, comple	1.03	down	1.03	up	2.93	up	1.24	down	1.17	up	1.25	down	ABA
Os.18653.1.S1_at	LOC_Os03g24844	expressed protein	1.21	up	1.20	up	2.19	down	1.09	down	1.43	down	1.39	down	ABA
Os.18654.1.S1_x_at	LOC_Os08g36630	bifunctional monodehydroascorbate reductase and carbonic anhydrasenectarin-3 precu	1.26	down	1.60	up	2.74	up	1.18	up	1.17	down	1.79	up	ABA
Os.18664.1.S1_a_at	LOC_Os01g71810	glycosyl hydrolases family 17, putative, expressed	1.57	down	1.23	up	8.29	up	1.42	up	1.42	up	2.68	up	2
Os.18664.1.S1_x_at	LOC_Os01g71820	glycosyl hydrolases family 17, putative, expressed	1.17	down	1.45	up	10.09	up	1.62	up	1.50	up	2.66	up	2
Os.18664.2.S1_x_at	LOC_Os01g71810	glycosyl hydrolases family 17, putative, expressed	1.03	up	1.48	up	4.49	up	1.63	up	1.66	up	2.97	up	2
Os.18692.1.S1_at	LOC_Os02g43290	protein kinase domain containing protein, expressed	2.18	down	1.34	down	3.80	down	1.17	up	1.19	down	1.33	up	2
Os.18712.1.S1_at	LOC_Os08g40940	expressed protein	1.36	up	2.04	down	7.63	down	1.01	up	2.22	up	2.95	up	4
Os.18714.1.S1_a_at	LOC_Os10g14920	integral membrane protein DUF6 containing protein, expressed	1.16	up	1.15	down	2.71	down	1.05	up	1.47	down	1.93	down	ABA
Os.18718.1.S1_at	LOC_Os05g32530	mannosylglycoprotein endo-beta-mannosidase, putative, expressed	1.08	down	1.11	up	2.78	up	1.02	down	1.13	down	1.17	down	ABA
Os.18723.1.S1_at	LOC_Os08g37210	patatin, putative, expressed	1.72	down	1.29	down	2.06	up	2.49	up	2.03	up	40.46	up	4
Os.18724.1.S1_a_at	LOC_Os01g54620	CESA4 - cellulose synthase, expressed	1.12	up	1.06	up	3.59	down	1.33	down	2.28	down	1.10	up	2
Os.18724.1.S1_at	LOC_Os01g54620	CESA4 - cellulose synthase, expressed	1.08	up	1.05	up	3.72	down	1.31	down	2.09	down	1.06	down	2
Os.18724.2.S1_x_at	LOC_Os01g54620	CESA4 - cellulose synthase, expressed	1.10	up	1.14	up	3.29	down	1.38	down	2.32	down	1.09	up	2
Os.18725.1.S1_at	LOC_Os03g56090	MYB family transcription factor, putative, expressed	1.48	up	1.53	up	3.04	up	1.46	down	3.39	up	1.34	down	2
Os.18734.1.S1_at	LOC_Os03g01700	expressed protein	1.51	down	3.53	down	155.65	down	1.10	up	3.79	down	1.06	down	3
Os.18736.1.S1_at	LOC_Os01g70200	exostosin family domain containing protein, expressed	1.08	up	1.06	down	2.94	down	1.32	down	1.74	down	1.20	up	ABA
Os.18742.1.A1_at	LOC_Os05g30010	WD domain, G-beta repeat domain containing protein, expressed	1.72	down	1.36	down	3.14	down	1.08	down	1.43	down	1.15	down	ABA
Os.18744.1.S1_at	LOC_Os01g59570	senescence-induced receptor-like serine/threonine-protein kinase precursor, putative, e	1.38	down	1.30	up	7.76	down	1.30	up	1.57	down	4.24	down	2
Os.1880.1.A1_at	AK068081	Yippee-like protein	1.00	up	1.63	up	3.24	up	1.12	up	1.27	up	1.08	down	ABA
Os.18818.1.S1_a_at	LOC_Os01g12710	oxidoreductase, short chain dehydrogenase/reductase family domain containing protei	1.40	up	1.12	up	9.86	up	1.12	down	1.07	up	1.09	up	ABA
Os.18819.1.S1_at	LOC_Os05g06660	OsSCP26 - Putative Serine Carboxypeptidase homologue, expressed	1.08	up	1.06	up	3.34	down	1.18	down	1.78	down	1.34	down	ABA
Os.18826.1.S1_at	LOC_Os03g15850	josephin, putative, expressed	1.18	up	1.03	down	2.75	up	1.01	down	1.26	up	1.20	down	ABA
Os.18830.1.S1_at	LOC_Os03g44150	aminotransferase, putative, expressed	1.18	down	1.29	down	3.38	up	1.26	up	1.93	up	1.43	up	ABA
Os.18830.1.S2_at	LOC_Os03g44150	aminotransferase, putative, expressed	1.03	up	1.10	down	2.87	up	1.30	up	1.81	up	1.31	up	ABA
Os.18847.1.S1_at	LOC_Os01g63180	laccase-6 precursor, putative, expressed	2.52	down	1.54	down	6.10	down	1.09	up	2.46	down	3.00	down	4
Os.18861.1.S1_a_at	LOC_Os06g35910	FYVE zinc finger domain containing protein, expressed	1.09	up	1.28	down	2.51	up	1.08	up	1.25	up	1.14	up	ABA
Os.18879.1.S1_at	LOC_Os12g37840	boron transporter protein, putative, expressed	1.24	up	1.06	down	1.42	up	1.10	up	2.46	up	1.08	up	SA

Os.18879.1.S2_at	LOC_Os12g37840	boron transporter protein, putative, expressed	**1.07**	down	**1.21**	down	**1.50**	up	**1.11**	up	**2.29**	up	**1.03**	down	SA
Os.18881.1.S1_at	LOC_Os05g37700	periplasmic beta-glucosidase precursor, putative, expressed	**1.09**	up	**1.34**	down	**5.52**	up	**1.36**	down	**1.85**	up	**1.69**	up	ABA
Os.18919.1.A1_at	LOC_Os03g49620	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative	**1.02**	down	**1.11**	down	**3.62**	down	**1.07**	up	**1.11**	down	**1.00**	up	ABA
Os.18922.2.S1_at	LOC_Os01g72530	OsCML31 - Calmodulin-related calcium sensor protein, expressed	**1.84**	up	**1.15**	up	**1.95**	up	**1.20**	down	**2.84**	up	**1.11**	down	SA
Os.18927.1.S1_at	LOC_Os05g25450	TKL_IRAK_CrRLK1L-1.3 - The CrRLK1L-1 subfamily has homology to the CrRLK1L ho	**1.22**	up	**1.15**	down	**2.18**	down	**1.12**	up	**1.08**	up	**1.26**	up	ABA
Os.18933.1.S1_at	LOC_Os02g12680	cytochrome P450, putative, expressed	**1.13**	down	**1.12**	down	**65.05**	up	**3.71**	up	**2.98**	up	**4.16**	up	4
Os.18941.1.S1_at	LOC_Os07g03050	expressed protein	**1.53**	up	**1.29**	up	**2.76**	up	**1.04**	up	**1.14**	up	**1.04**	down	ABA
Os.18946.1.S1_at	LOC_Os06g06050	OsFBL27 - F-box domain and LRR containing protein, expressed	**1.06**	up	**1.39**	up	**6.55**	up	**1.04**	up	**1.03**	down	**1.23**	up	ABA
Os.18946.2.S1_at	AK107102	F-box family protein	**1.14**	down	**1.17**	up	**2.86**	up	**1.01**	down	**1.10**	up	**1.08**	up	ABA
Os.18948.1.S1_at	LOC_Os02g04840	GHMP kinases ATP-binding protein, putative, expressed	**1.05**	up	**1.06**	down	**4.96**	up	**1.14**	down	**1.34**	up	**1.47**	down	ABA
Os.18954.1.S1_at	LOC_Os04g48230	dehydration response related protein, putative, expressed	**1.10**	down	**1.10**	down	**2.01**	down	**1.15**	down	**1.39**	down	**1.05**	up	ABA
Os.18955.1.S1_at	LOC_Os06g51260	MYB family transcription factor, putative, expressed	**1.40**	down	**1.28**	down	**3.33**	up	**1.11**	down	**1.03**	down	**1.27**	down	ABA
Os.19003.1.S1_a_at	LOC_Os01g21160	2-oxo acid dehydrogenases acyltransferase domain containing protein, expressed	**1.11**	up	**1.01**	down	**3.44**	up	**1.68**	up	**2.38**	up	**3.92**	up	3
Os.19019.1.S1_a_at	LOC_Os08g02850	zinc finger family protein, putative, expressed	**1.11**	up	**1.17**	down	**2.40**	up	**1.12**	up	**1.04**	up	**1.33**	up	ABA
Os.19021.1.S1_at	LOC_Os06g34040	DJ-1 family protein, putative, expressed	**1.13**	up	**1.12**	up	**2.28**	up	**1.00**	up	**1.06**	down	**1.06**	up	ABA
Os.19026.1.S1_at	LOC_Os07g08210	cytidylyltransferase domain containing protein, expressed	**1.43**	up	**1.02**	up	**3.31**	up	**1.16**	down	**1.35**	up	**1.10**	up	ABA
Os.19034.1.S1_at	LOC_Os05g51620	expressed protein	**1.03**	down	**1.18**	down	**3.95**	down	**1.24**	down	**1.19**	down	**1.25**	down	ABA
Os.19044.1.S1_at	LOC_Os10g04520	expressed protein	**1.02**	up	**1.48**	down	**2.46**	up	**1.04**	up	**1.47**	up	**1.15**	up	ABA
Os.19070.1.S1_at	LOC_Os11g09020	amino acid transporter, putative, expressed	**1.23**	down	**1.13**	down	**5.72**	up	**1.07**	up	**1.82**	up	**1.08**	down	ABA
Os.19131.1.A1_at	LOC_Os09g28910	carbonic anhydrase, chloroplast precursor, putative, expressed	**1.03**	up	**1.02**	down	**3.79**	up	**1.03**	up	**1.12**	up	**1.29**	up	ABA
Os.19134.1.S1_at	LOC_Os07g29224	expressed protein	**1.43**	up	**1.04**	up	**3.03**	up	**1.01**	down	**1.25**	up	**1.21**	up	ABA
Os.19165.1.S1_at	LOC_Os11g29900	expressed protein	**1.02**	up	**1.04**	down	**3.28**	up	**1.25**	up	**1.15**	up	**1.38**	up	ABA
Os.19187.1.S1_at	LOC_Os02g10470	EF hand family protein, putative, expressed	**1.10**	down	**1.10**	down	**4.94**	up	**1.16**	down	**1.12**	up	**1.09**	up	ABA
Os.19230.2.S1_at	LOC_Os06g40050	mitochondrial carrier protein, putative, expressed	**1.41**	up	**1.09**	up	**2.06**	up	**1.31**	up	**1.56**	up	**1.28**	up	ABA
Os.19307.1.S1_at	LOC_Os08g03430	extracellular ligand-gated ion channel, putative, expressed	**1.13**	up	**1.05**	up	**7.63**	up	**1.06**	down	**1.11**	up	**1.15**	up	ABA
Os.19350.1.S1_at	LOC_Os04g45290	glycosyl hydrolases, putative, expressed	**1.02**	up	**1.11**	up	**9.61**	down	**1.20**	up	**1.58**	down	**1.26**	down	ABA
Os.19361.1.S1_at	LOC_Os04g45290	glycosyl hydrolases, putative, expressed	**1.21**	up	**1.25**	up	**1.37**	up	**1.15**	down	**1.13**	down	**3.10**	up	JA
Os.19361.1.S2_at	LOC_Os04g45290	glycosyl hydrolases, putative, expressed	**1.22**	up	**1.29**	up	**1.43**	up	**1.08**	down	**1.02**	up	**2.29**	up	JA
Os.19366.1.S1_a_at	AK100298	Oryza sativa Japonica Group cDNA clone:J023077J24, full insert sequence.	**1.32**	down	**1.20**	down	**2.30**	up	**1.17**	up	**1.16**	up	**1.01**	up	ABA
Os.19366.1.S2_at	AK100298	Oryza sativa Japonica Group cDNA clone:J023077J24, full insert sequence.	**1.17**	up	**1.02**	up	**2.12**	up	**1.41**	down	**1.17**	down	**1.44**	down	ABA
Os.19366.4.A1_a_at	AK100298	Oryza sativa Japonica Group cDNA clone:J023077J24, full insert sequence.	**1.23**	down	**1.27**	down	**2.31**	up	**1.06**	up	**1.23**	up	**1.11**	up	ABA
Os.19375.1.S1_at	LOC_Os08g34780	adenylyl cyclase-associated protein, putative, expressed	**1.18**	up	**1.61**	up	**2.53**	down	**1.62**	up	**1.29**	down	**2.75**	up	2
Os.19385.1.S1_at	LOC_Os01g52730	DUF584 domain containing protein, putative, expressed	**1.66**	up	**1.04**	down	**28.93**	up	**1.37**	up	**1.99**	up	**1.05**	down	ABA
Os.19465.1.S1_at	NM_001060676	Oryza sativa (japonica cultivar-group) Os04g0660100 (Os04g0660100) mRNA, comple	**2.03**	up	**1.06**	up	**1.02**	down	**1.09**	up	**1.18**	up	**1.59**	up	IAA
Os.19472.1.S1_at	LOC_Os01g03330	BBTI3 - Bowman-Birk type bran trypsin inhibitor precursor, expressed	**1.13**	down	**1.25**	up	**3.42**	up	**2.31**	up	**2.30**	up	**6.28**	up	4
Os.19480.1.S1_at	LOC_Os03g20870	zinc finger, C3HC4 type domain containing protein, expressed	**1.36**	up	**1.12**	down	**4.85**	up	**1.35**	up	**2.51**	up	**1.17**	up	2
Os.19493.1.S1_at	LOC_Os08g01940	non-lysosomal glucosylceramidase, putative, expressed	**1.60**	down	**1.33**	up	**5.64**	down	**1.02**	down	**1.09**	down	**2.78**	up	2
Os.19539.1.S1_at	LOC_Os02g47560	DNA-binding protein, putative, expressed	**2.09**	up	**1.09**	down	**2.45**	up	**1.22**	up	**2.00**	up	**1.88**	up	3
Os.19547.1.S1_at	LOC_Os08g02030	transferase family protein, putative, expressed	**1.40**	up	**1.25**	up	**9.25**	up	**1.15**	up	**10.73**	up	**1.19**	up	2
Os.19553.1.S1_at	LOC_Os05g49420	transcription factor, putative, expressed	**1.17**	down	**1.10**	down	**5.39**	up	**1.46**	up	**1.57**	up	**2.43**	up	2
Os.19586.1.S1_at	LOC_Os12g12934	peptide transporter PTR3-A, putative, expressed	**2.74**	down	**1.28**	up	**12.58**	down	**1.12**	down	**1.67**	down	**1.35**	down	2
Os.19593.1.S1_s_at	NM_001056753	Oryza sativa (japonica cultivar-group) Os03g0375900 (Os03g0375900) mRNA, comple	**1.57**	down	**1.10**	up	**2.88**	down	**1.34**	up	**1.24**	down	**2.28**	up	2
Os.19608.1.S1_at	LOC_Os09g38130	auxin efflux carrier component, putative, expressed	**2.18**	up	**1.57**	down	**3.49**	up	**1.60**	up	**2.48**	up	**2.27**	up	4
Os.19617.1.S1_at	LOC_Os01g66760	inactive receptor kinase At2g26730 precursor, putative, expressed	**1.11**	down	**1.20**	up	**1.89**	down	**1.77**	up	**1.04**	down	**2.12**	up	JA
Os.19626.1.S1_at	LOC_Os02g39600	outer envelope protein, putative, expressed	**1.28**	up	**1.10**	up	**2.58**	down	**1.20**	down	**1.42**	down	**1.47**	down	ABA
Os.19632.1.S1_at	LOC_Os03g46470	metal cation transporter, putative, expressed	**1.59**	down	**2.97**	down	**7.24**	down	**1.33**	down	**1.24**	down	**1.01**	down	2
Os.19740.1.S2_at	LOC_Os03g02874	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	**1.02**	down	**1.18**	down	**9.00**	up	**2.79**	up	**137.60**	up	**1.81**	up	3
Os.1977.1.S1_a_at	LOC_Os01g02400	protein kinase domain containing protein, expressed	**1.03**	up	**1.39**	down	**2.15**	up	**1.06**	down	**2.32**	up	**1.02**	up	2
Os.1977.3.S1_x_at	LOC_Os01g02600	Ser/Thr receptor-like kinase, putative, expressed	**1.22**	up	**1.37**	down	**2.09**	up	**1.12**	down	**1.77**	up	**1.15**	up	ABA
Os.19771.1.S1_at	LOC_Os01g51360	lipase, putative, expressed	**1.12**	down	**1.30**	up	**3.79**	down	**1.24**	up	**1.66**	down	**1.25**	down	ABA
Os.19851.1.S1_at	LOC_Os03g13520	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	**1.57**	down	**1.28**	down	**5.19**	down	**1.08**	up	**1.69**	down	**1.49**	down	ABA
Os.19863.1.S1_a_at	LOC_Os04g36560	chloride channel protein, putative, expressed	**2.26**	up	**1.02**	down	**8.76**	up	**1.13**	down	**1.83**	up	**1.14**	up	2
Os.19895.1.S1_at	LOC_Os11g46860	wall-associated receptor kinase-like 4 precursor, putative, expressed	**2.03**	down	**1.18**	up	**3.32**	down	**1.09**	up	**2.02**	down	**1.14**	up	3
Os.19951.1.A1_at	AJ494928	Oryza sativa Z226 snoRNA	**1.10**	up	**1.83**	up	**2.70**	down	**1.71**	up	**3.30**	up	**1.66**	up	2
Os.19951.1.S1_at	AJ494928	Oryza sativa Z226 snoRNA.	**1.00**	up	**1.16**	up	**2.45**	down	**1.27**	up	**1.88**	up	**1.49**	up	ABA

Os.19951.1.S1_x_at	AJ494928	Oryza sativa Z226 snoRNA.	**1.01**	up	**1.16**	up	**2.31**	down	**1.21**	up	**1.95**	up	**1.42**	up	ABA
Os.19954.1.S1_at	LOC_Os09g28690	gibberellin receptor GID1L2, putative, expressed	**2.02**	up	**1.21**	up	**1.70**	down	**1.09**	up	**1.11**	up	**1.27**	up	IAA
Os.20001.1.S1_at	LOC_Os04g32080	11-beta-hydroxysteroid dehydrogenase, putative, expressed	**1.00**	down	**1.02**	up	**27.44**	up	**1.02**	down	**1.02**	down	**1.01**	up	ABA
Os.20067.1.S1_at	LOC_Os04g38530	aldose 1-epimerase, putative, expressed	**1.20**	down	**1.04**	down	**2.47**	down	**1.16**	up	**1.28**	down	**1.60**	down	ABA
Os.20079.1.S2_at	LOC_Os11g25160	tropinone reductase 2, putative, expressed	**1.33**	down	**1.89**	down	**1.90**	up	**1.17**	down	**1.30**	up	**2.38**	down	JA
Os.20120.1.S1_at	LOC_Os01g18670	MDR-like ABC transporter, putative, expressed	**1.02**	down	**1.03**	down	**2.49**	down	**1.13**	up	**1.07**	up	**1.83**	up	ABA
Os.20154.1.S1_at	LOC_Os02g56700	dehydrogenase, putative, expressed	**10.92**	up	**1.51**	down	**1.10**	up	**1.07**	up	**65.90**	up	**1.28**	up	2
Os.20163.1.S1_at	LOC_Os03g02860	heavy metal-associated domain containing protein, expressed	**1.06**	up	**1.58**	down	**3.29**	down	**1.15**	down	**1.48**	down	**1.64**	down	ABA
Os.20169.1.S1_at	LOC_Os06g34730	expressed protein	**1.66**	down	**2.01**	up	**2.95**	down	**1.16**	down	**2.12**	down	**1.12**	down	3
Os.20175.1.A1_x_at	LOC_Os04g47780	transmembrane amino acid transporter protein, putative, expressed	**1.69**	up	**1.46**	up	**1.92**	down	**2.64**	up	**1.37**	down	**1.17**	down	ACC
Os.2019.1.S1_at	LOC_Os01g50460	nodulin MtN3 family protein, putative, expressed	**1.73**	up	**1.51**	down	**4.98**	down	**1.80**	up	**2.80**	down	**2.27**	up	3
Os.2019.2.S1_x_at	LOC_Os01g50460	nodulin MtN3 family protein, putative, expressed	**1.84**	up	**1.66**	down	**2.81**	down	**1.50**	up	**1.66**	down	**1.50**	up	ABA
Os.20203.1.S1_at	LOC_Os01g10210	lachrymatory factor synthase, putative, expressed	**1.32**	down	**1.00**	up	**7.32**	down	**1.29**	down	**1.31**	down	**3.24**	up	2
Os.20203.1.S1_s_at	LOC_Os01g10210	lachrymatory factor synthase, putative, expressed	**1.37**	down	**1.06**	up	**4.99**	down	**1.13**	down	**1.09**	down	**3.57**	up	2
Os.20204.2.S1_a_at	LOC_Os02g12350	histone deacetylase, putative, expressed	**1.31**	down	**1.22**	down	**2.85**	up	**1.48**	up	**4.99**	up	**1.82**	up	2
Os.20206.1.S1_at	LOC_Os02g41840	DUF584 domain containing protein, putative, expressed	**1.50**	up	**2.19**	up	**17.72**	up	**1.23**	up	**1.20**	up	**1.04**	up	2
Os.20210.1.S1_at	LOC_Os02g13890	FYVE zinc finger domain containing protein, expressed	**1.26**	up	**1.03**	up	**2.01**	up	**1.00**	down	**1.18**	up	**1.02**	up	ABA
Os.20211.1.S1_at	LOC_Os10g36710	CAMK_CAMK_like.40 - CAMK includes calcium/calmodulin depedent protein kinases, e	**2.01**	up	**1.06**	down	**1.64**	up	**1.01**	up	**1.17**	up	**1.08**	up	IAA
Os.20221.1.S1_at	LOC_Os09g21710	AN1-like zinc finger domain containing protein, expressed	**3.77**	up	**1.05**	up	**1.89**	up	**1.76**	down	**5.01**	up	**1.70**	down	2
Os.20224.1.S1_at	LOC_Os12g37690	MYB family transcription factor, putative, expressed	**1.12**	up	**1.15**	down	**3.56**	up	**1.25**	down	**1.15**	up	**3.32**	up	2
Os.20230.1.S1_at	LOC_Os11g37950	WIP3 - Wound-induced protein precursor, expressed	**1.21**	down	**2.70**	up	**4.37**	up	**1.04**	up	**1.19**	up	**1.12**	up	2
Os.20234.2.S1_at	LOC_Os11g14570	expressed protein	**1.07**	up	**1.06**	down	**2.70**	down	**1.32**	down	**1.74**	down	**1.38**	down	ABA
Os.20237.1.S1_at	LOC_Os09g04710	GDSL-like lipase/acylhydrolase, putative, expressed	**1.18**	up	**1.05**	down	**3.44**	down	**1.10**	down	**1.13**	down	**1.14**	down	ABA
Os.20246.1.S1_at	LOC_Os10g32444	expressed protein	**1.06**	up	**1.06**	up	**2.99**	up	**1.08**	down	**1.12**	up	**1.15**	down	ABA
Os.20262.1.S1_at	LOC_Os05g03174	glycosyltransferase family 43 protein, putative, expressed	**1.12**	down	**1.20**	down	**2.98**	down	**1.19**	down	**1.48**	down	**1.62**	up	ABA
Os.20283.1.S1_at	LOC_Os04g49900	ABC transporter family protein, putative, expressed	**1.77**	down	**2.94**	down	**12.73**	up	**1.19**	up	**2.23**	down	**1.59**	up	3
Os.20289.1.S1_at	LOC_Os11g37960	WIP4 - Wound-induced protein precursor, expressed	**1.15**	down	**2.54**	up	**1.59**	up	**1.64**	up	**1.11**	down	**1.32**	down	BAP
Os.20290.1.S1_at	LOC_Os07g01410	peroxidase precursor, putative, expressed	**1.15**	down	**1.04**	down	**5.15**	down	**1.29**	up	**2.46**	down	**3.34**	down	3
Os.20300.1.S1_at	LOC_Os12g05180	avr9/Cf-9 rapidly elicited protein, putative, expressed	**1.36**	up	**1.04**	up	**2.74**	up	**1.05**	down	**1.07**	down	**1.36**	down	ABA
Os.20327.1.S1_at	LOC_Os06g44080	ubiquitin family protein, putative, expressed	**1.28**	down	**1.10**	down	**2.64**	down	**1.03**	up	**1.42**	down	**1.27**	down	ABA
Os.20341.1.S1_s_at	LOC_Os03g52040	OsSCP19 - Putative Serine Carboxypeptidase homologue, expressed	**1.20**	down	**1.01**	down	**2.58**	down	**1.18**	down	**1.31**	down	**1.83**	up	ABA
Os.20341.2.S1_at	LOC_Os03g52040	OsSCP19 - Putative Serine Carboxypeptidase homologue, expressed	**1.30**	down	**1.05**	down	**3.60**	down	**1.29**	down	**1.58**	down	**1.84**	up	ABA
Os.20342.1.S1_at	LOC_Os03g02710	hydroxymethylglutaryl-CoA synthase, putative, expressed	**1.15**	down	**1.05**	up	**5.12**	up	**1.23**	down	**2.14**	up	**1.83**	up	2
Os.20354.1.S1_at	LOC_Os03g45370	sodium/calcium exchanger protein, putative, expressed	**1.08**	up	**1.52**	down	**5.82**	up	**1.63**	up	**1.05**	up	**1.25**	up	ABA
Os.20355.1.S1_at	LOC_Os01g72100	OsCML10 - Calmodulin-related calcium sensor protein, expressed	**1.39**	up	**1.00**	up	**3.17**	down	**1.12**	up	**1.33**	down	**1.34**	down	ABA
Os.20404.1.S1_at	LOC_Os01g16146	phenazine biosynthesis protein, putative, expressed	**2.09**	up	**1.15**	down	**2.21**	up	**1.12**	up	**2.78**	up	**1.91**	up	3
Os.20408.1.S1_at	LOC_Os04g44980	short-chain dehydrogenase/reductase, putative, expressed	**1.77**	up	**2.54**	up	**1.42**	up	**1.31**	down	**1.21**	up	**2.10**	down	2
Os.20441.1.A1_at	AK240960	Oryza sativa Japonica Group cDNA, clone: J065045M09, full insert sequence.	**1.23**	down	**2.07**	up	**1.51**	down	**1.02**	up	**1.43**	down	**1.42**	down	BAP
Os.20447.1.S1_at	LOC_Os04g38620	NAP domain containing protein, putative, expressed	**1.13**	up	**1.25**	up	**2.44**	down	**1.17**	up	**1.08**	down	**1.07**	down	ABA
Os.20482.1.S1_at	LOC_Os03g02550	OsFBX76 - F-box domain containing protein, expressed	**1.45**	up	**1.37**	down	**2.38**	down	**1.56**	down	**1.03**	up	**2.00**	up	ABA
Os.20501.1.S1_at	LOC_Os07g47670	hypoxia-responsive family protein, putative, expressed	**2.09**	up	**1.05**	up	**11.17**	up	**2.49**	up	**2.54**	up	**1.58**	up	3
Os.20504.1.A1_at	LOC_Os12g12880	expressed protein	**1.11**	down	**1.55**	down	**2.88**	up	**1.06**	up	**1.07**	up	**1.21**	up	ABA
Os.20531.1.S1_at	LOC_Os04g54010	serine/threonine-protein kinase receptor precursor, putative, expressed	**1.08**	down	**1.69**	down	**3.00**	up	**1.42**	down	**1.53**	up	**1.35**	down	ABA
Os.20548.1.S1_at	AK066753	expressed protein	**1.45**	up	**1.56**	up	**1.23**	down	**1.44**	up	**1.96**	up	**5.48**	up	JA
Os.20557.1.S1_s_at	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	**1.26**	up	**1.27**	up	**5.00**	up	**1.08**	up	**1.63**	up	**1.01**	up	ABA
Os.20570.1.S1_x_at	LOC_Os06g02500	superoxide dismutase, chloroplast, putative, expressed	**1.10**	up	**1.20**	up	**3.33**	down	**1.07**	down	**1.71**	down	**1.33**	down	ABA
Os.20579.1.S1_at	LOC_Os01g52750	OsSub3 - Putative Subtilisin homologue, expressed	**1.04**	down	**1.22**	down	**2.00**	up	**1.03**	up	**1.28**	down	**1.83**	down	ABA
Os.20617.1.S1_at	LOC_Os07g46280	Os7bglu26 - beta-mannosidase/glucosidase/exoglucanase, expressed	**2.08**	down	**1.07**	down	**5.45**	up	**1.28**	down	**1.76**	up	**1.40**	up	2
Os.20617.2.S1_s_at	LOC_Os03g20710	beta-glucosidase, putative	**1.44**	down	**1.07**	down	**5.63**	up	**1.28**	down	**1.65**	up	**1.55**	up	ABA
Os.20617.2.S1_x_at	LOC_Os07g46280	Os7bglu26 - beta-mannosidase/glucosidase/exoglucanase, expressed	**1.53**	down	**1.04**	down	**5.57**	up	**1.36**	down	**1.65**	up	**1.51**	up	ABA
Os.20697.1.S1_at	LOC_Os09g34070	RNA recognition motif containing protein, expressed	**1.06**	up	**1.04**	up	**2.22**	up	**1.02**	up	**1.15**	up	**1.10**	down	ABA
Os.20701.1.S1_at	LOC_Os02g52560	xyloglucan fucosyltransferase, putative, expressed	**1.03**	up	**1.17**	down	**2.00**	up	**1.07**	up	**1.05**	up	**1.19**	up	ABA
Os.20712.2.A1_at	LOC_Os01g54030	NADP-dependent malic enzyme, putative, expressed	**1.20**	down	**1.19**	down	**8.14**	up	**1.15**	down	**1.15**	down	**1.09**	up	ABA
Os.20717.1.S1_at	LOC_Os01g61460	leaf senescence related protein, putative, expressed	**2.10**	up	**1.20**	down	**1.06**	up	**1.28**	up	**1.10**	up	**1.61**	up	IAA
Os.2075.1.S1_at	LOC_Os01g19220	beta-D-xylosidase, putative, expressed	**1.43**	down	**1.10**	up	**4.36**	down	**1.07**	down	**1.57**	down	**1.05**	down	ABA

Os.20750.1.S1_at	LOC_Os01g72970	DUF630/DUF632 domains containing protein, putative, expressed	**1.09**	up	**1.35**	up	**3.03**	up	**1.27**	up	**2.55**	up	**1.23**	down	2
Os.20755.1.S1_at	LOC_Os04g42690	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**2.04**	down	**1.55**	down	**3.49**	down	**1.01**	up	**1.23**	down	**1.84**	down	2
Os.20773.1.S1_at	LOC_Os06g10280	CDP-alcohol phosphatidyltransferase, putative, expressed	**1.06**	up	**1.11**	down	**3.26**	up	**1.27**	down	**1.28**	up	**1.02**	up	ABA
Os.20853.1.S1_at	LOC_Os09g38920	thiol protease SEN102 precursor, putative, expressed	**1.20**	down	**1.13**	down	**2.52**	up	**1.41**	up	**1.35**	up	**1.64**	up	ABA
Os.20863.1.S1_at	LOC_Os01g62970	expressed protein	**1.05**	down	**1.47**	up	**8.57**	up	**1.18**	down	**1.03**	up	**1.55**	down	ABA
Os.20863.2.S1_x_at	LOC_Os01g62970	expressed protein	**1.14**	down	**1.18**	up	**7.57**	up	**1.05**	up	**1.06**	down	**1.12**	down	ABA
Os.20884.1.S1_at	LOC_Os05g01760	lysine ketoglutarate reductase trans-splicing related 1, putative, expressed	**1.05**	up	**1.25**	down	**2.40**	up	**1.09**	up	**1.53**	up	**1.48**	up	ABA
Os.20885.1.S1_at	LOC_Os03g08170	protein kinase APK1B, chloroplast precursor, putative, expressed	**1.80**	down	**1.09**	down	**5.33**	down	**1.08**	down	**1.52**	down	**1.77**	down	ABA
Os.209.1.S1_at	LOC_Os01g16920	embryonic protein DC-8, putative, expressed	**1.04**	up	**1.03**	up	**15.39**	up	**1.04**	up	**1.03**	up	**1.01**	down	ABA
Os.20902.1.A1_at	LOC_Os11g01010	autophagy-related protein 8D, putative, expressed	**1.15**	up	**1.06**	down	**2.02**	up	**1.02**	up	**1.42**	up	**1.07**	up	ABA
Os.20931.1.S1_s_at	LOC_Os02g13300	mitochondrial carrier protein, putative, expressed	**1.15**	up	**1.05**	down	**5.43**	up	**1.04**	up	**1.99**	up	**1.69**	up	ABA
Os.20934.1.A1_at	LOC_Os03g07190	expressed protein	**1.01**	down	**1.01**	down	**2.54**	up	**1.01**	down	**1.01**	down	**1.00**	up	ABA
Os.20936.1.S1_a_at	LOC_Os07g05365	photosystem II 10 kDa polypeptide, chloroplast precursor, putative, expressed	**1.68**	down	**1.66**	down	**150.22**	up	**4.53**	down	**7.43**	up	**1.30**	down	3
Os.20973.1.S1_s_at	LOC_Os05g44760	hexokinase, putative, expressed	**1.27**	down	**1.03**	up	**2.15**	down	**1.03**	down	**1.33**	down	**1.00**	down	ABA
Os.20980.1.S1_at	LOC_Os01g56180	expressed protein	**1.29**	down	**1.00**	up	**4.11**	up	**1.08**	down	**1.14**	up	**1.23**	up	ABA
Os.20982.1.S1_at	LOC_Os11g45400	glycerol-3-phosphate acyltransferase, putative, expressed	**1.18**	down	**1.06**	down	**1.07**	up	**1.34**	up	**1.05**	up	**3.75**	up	JA
Os.21044.1.S1_at	LOC_Os07g29220	Cyclopropane-fatty-acyl-phospholipid synthase, putative, expressed	**1.16**	down	**1.19**	up	**2.45**	down	**1.10**	up	**1.34**	down	**1.44**	up	ABA
Os.21066.1.S1_at	LOC_Os03g56250	LRR receptor-like protein kinase, putative, expressed	**1.49**	up	**1.26**	down	**2.01**	up	**1.27**	up	**1.64**	up	**1.31**	up	ABA
Os.21108.1.S1_at	LOC_Os05g50890	OsGH3.5 - Probable indole-3-acetic acid-amido synthetase, expressed	**1.59**	up	**1.01**	down	**3.58**	down	**1.14**	down	**1.06**	down	**1.76**	up	ABA
Os.2117.1.S1_at	LOC_Os01g33000	expressed protein	**1.05**	up	**1.09**	down	**3.39**	up	**1.03**	up	**1.27**	up	**1.18**	up	ABA
Os.2117.1.S1_s_at	LOC_Os01g33000	expressed protein	**1.17**	up	**1.11**	up	**2.70**	up	**1.02**	up	**1.14**	up	**1.00**	up	ABA
Os.2117.2.S1_x_at	LOC_Os01g33000	expressed protein	**1.37**	up	**1.05**	down	**3.75**	up	**1.28**	down	**1.17**	up	**1.05**	down	ABA
Os.21192.1.S1_at	LOC_Os01g48820	expressed protein	**1.00**	up	**1.01**	up	**3.52**	up	**1.01**	down	**1.01**	down	**1.00**	down	ABA
Os.21193.2.S1_x_at	LOC_Os10g27980	transmembrane amino acid transporter protein, putative, expressed	**1.25**	down	**1.14**	down	**2.95**	down	**1.43**	down	**1.56**	down	**2.49**	up	2
Os.2123.1.S1_at	LOC_Os01g54300	OsMan02 - Endo-Beta-Mannanase	**1.15**	up	**1.03**	down	**4.10**	down	**1.22**	down	**1.91**	down	**1.53**	up	ABA
Os.21230.1.S1_at	LOC_Os12g07190	CBS domain-containing protein, putative, expressed	**1.27**	up	**1.11**	up	**3.25**	down	**1.19**	down	**1.30**	down	**1.03**	up	ABA
Os.21243.1.S1_at	LOC_Os02g36490	expressed protein	**1.05**	up	**1.12**	down	**2.66**	up	**1.25**	down	**1.28**	down	**1.10**	down	ABA
Os.21280.1.S1_at	LOC_Os12g25490	O-methyltransferase, putative, expressed	**1.48**	down	**1.51**	down	**2.55**	down	**1.05**	down	**1.74**	down	**7.23**	up	2
Os.21282.1.S1_at	LOC_Os03g13600	ZOS3-07 - C2H2 zinc finger protein, expressed	**1.20**	down	**1.09**	up	**2.47**	down	**1.05**	down	**1.04**	up	**1.34**	down	ABA
Os.21289.1.S1_at	LOC_Os11g05540	rhoGAP domain containing protein, expressed	**1.28**	down	**1.00**	down	**3.03**	down	**1.18**	down	**1.42**	down	**1.57**	down	ABA
Os.21323.1.S1_at	LOC_Os04g38885	expressed protein	**2.08**	up	**1.00**	up	**4.83**	up	**1.11**	up	**1.09**	up	**1.26**	up	2
Os.21380.1.S1_at	AK120358	Oryza sativa Japonica Group cDNA clone:J013067F13, full insert sequence.	**1.03**	up	**1.08**	up	**3.68**	up	**1.15**	down	**1.19**	down	**1.13**	down	ABA
Os.21410.1.S1_at	LOC_Os07g46780	tyrosine-specific transport protein, putative, expressed	**1.98**	up	**1.24**	up	**4.11**	down	**2.07**	down	**1.88**	down	**1.81**	down	3
Os.21442.1.S1_at	LOC_Os02g03960	CPuORF1 - conserved peptide uORF-containing transcript, expressed	**1.44**	down	**1.07**	down	**2.01**	down	**1.19**	up	**1.11**	down	**1.30**	down	ABA
Os.21442.1.S1_x_at	LOC_Os02g03960	CPuORF1 - conserved peptide uORF-containing transcript, expressed	**1.35**	down	**1.03**	down	**2.23**	down	**1.11**	up	**1.17**	down	**1.34**	down	ABA
Os.21454.1.S1_at	LOC_Os02g04810	auxin response factor 5, putative, expressed	**1.53**	up	**1.34**	down	**2.63**	up	**1.71**	up	**1.50**	up	**1.91**	down	ABA
Os.21461.1.S1_at	LOC_Os03g15430	Ser/Thr protein phosphatase family protein, putative, expressed	**1.06**	up	**1.01**	down	**2.33**	up	**1.20**	up	**1.30**	up	**1.06**	down	ABA
Os.21563.1.S1_a_at	LOC_Os01g07120	AP2 domain containing protein, expressed	**1.01**	down	**1.11**	down	**4.25**	up	**1.35**	up	**1.56**	up	**1.68**	up	ABA
Os.21629.1.S1_at	LOC_Os09g39940	plastocyanin-like domain containing protein, putative, expressed	**1.21**	down	**1.66**	down	**4.25**	up	**1.10**	down	**1.52**	up	**1.53**	up	ABA
Os.21635.1.S1_at	LOC_Os12g03860	major facilitator superfamily antiporter, putative, expressed	**1.56**	down	**1.28**	down	**4.04**	up	**1.07**	up	**1.54**	up	**1.68**	down	ABA
Os.21636.2.S1_a_at	LOC_Os09g36250	MYB family transcription factor, putative, expressed	**1.29**	down	**1.79**	down	**3.52**	down	**1.35**	down	**1.38**	down	**1.19**	down	ABA
Os.21764.1.S1_at	LOC_Os04g56710	GTP cyclohydrolase I 1, putative, expressed	**1.09**	up	**1.15**	down	**2.35**	down	**1.39**	up	**1.11**	down	**1.02**	up	ABA
Os.21792.1.S1_at	LOC_Os04g14790	FAD dependent oxidoreductase domain containing protein, expressed	**1.00**	up	**1.04**	down	**2.84**	up	**1.06**	up	**1.67**	up	**1.28**	up	ABA
Os.21806.1.S1_at	AK063130	Oryza sativa Japonica Group cDNA clone:001-111-F06, full insert sequence.	**1.25**	up	**1.22**	down	**5.75**	up	**1.05**	down	**1.40**	down	**1.39**	down	ABA
Os.21817.1.S1_at	LOC_Os01g21650	plant protein of unknown function domain containing protein, expressed	**4.87**	down	**1.03**	down	**16.67**	down	**1.35**	up	**1.03**	down	**4.81**	down	3
Os.21858.2.S1_x_at	AK071600	Oryza sativa Japonica Group cDNA clone:J023105E08, full insert sequence.	**1.46**	up	**1.17**	up	**2.10**	down	**1.29**	up	**1.30**	up	**1.11**	up	ABA
Os.21870.1.S1_at	LOC_Os02g45750	protein kinase domain containing protein, expressed	**1.47**	down	**1.11**	down	**2.58**	down	**1.29**	up	**1.25**	down	**1.35**	down	ABA
Os.21893.1.S1_x_at	LOC_Os04g59160	peroxidase precursor, putative, expressed	**2.09**	up	**1.91**	up	**2.61**	down	**1.81**	up	**5.29**	down	**2.22**	down	4
Os.2202.2.S1_x_at	BGIOSSBCE000693	Oryza sativa (japonica cultivar-group) Os01g0198100 (Os01g0198100) mRNA, partial	**1.02**	down	**1.01**	down	**2.12**	up	**1.07**	down	**1.09**	down	**1.06**	down	ABA
Os.2202.3.S1_x_at	LOC_Os01g10140	RNA-dependent RNA polymerase, putative, expressed	**1.14**	up	**1.07**	down	**2.48**	up	**1.00**	down	**1.06**	up	**1.02**	up	ABA
Os.22169.1.S1_a_at	LOC_Os06g51084	1,4-alpha-glucan-branching enzyme, chloroplast precursor, putative, expressed	**1.13**	down	**1.02**	up	**2.28**	up	**1.08**	down	**1.02**	up	**1.06**	down	ABA
Os.22169.2.S2_a_at	LOC_Os06g51084	1,4-alpha-glucan-branching enzyme, chloroplast precursor, putative, expressed	**1.04**	down	**1.14**	down	**2.07**	up	**1.10**	down	**1.01**	down	**1.06**	up	ABA
Os.2219.1.S1_at	LOC_Os03g58980	Cupin domain containing protein, expressed	**1.03**	down	**1.20**	up	**4.46**	down	**1.65**	up	**1.43**	down	**1.19**	down	ABA
Os.22241.1.S1_s_at	LOC_Os11g41150	nitrilase-associated protein, putative, expressed	**1.51**	down	**1.18**	up	**4.40**	down	**1.00**	down	**1.88**	down	**1.19**	up	ABA
Os.22263.1.S1_a_at	LOC_Os07g40550	IBS1, putative, expressed	**1.05**	up	**1.09**	up	**2.17**	down	**1.07**	up	**1.08**	down	**1.08**	down	ABA

Os.22271.2.S1_x_at	AK103312	transcriptional factor B3 family protein / auxin-responsive factor	2.72	up	1.05	down	1.32	down	1.21	down	1.41	up	1.39	up	IAA
Os.22278.1.S1_at	LOC_Os09g38320	phytoene synthase, chloroplast precursor, putative, expressed	1.51	up	1.36	down	23.72	up	1.26	down	2.13	up	1.60	up	2
Os.2230.1.S1_at	LOC_Os02g50960	auxin efflux carrier component, putative, expressed	2.55	up	1.15	down	1.65	down	1.08	up	1.23	up	1.20	up	IAA
Os.22312.2.S1_at	AK063864	Oryza sativa Japonica Group cDNA clone:001-122-E02, full insert sequence.	1.09	up	1.25	up	3.83	up	1.16	up	1.14	up	1.12	down	ABA
Os.22312.3.A1_a_at	LOC_Os05g28740	universal stress protein domain containing protein, putative, expressed	1.13	up	1.02	up	2.37	up	1.14	down	1.38	up	1.96	down	ABA
Os.2235.1.S1_a_at	LOC_Os12g06010	retrotransposon protein, putative, unclassified, expressed	1.04	up	1.08	up	39.94	up	1.20	down	1.45	up	1.17	up	ABA
Os.2239.1.S1_at	LOC_Os03g02050	LTPL151 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	2.76	up	1.63	up	101.58	up	2.21	up	2.09	up	1.28	up	4
Os.22415.1.S1_s_at	LOC_Os06g43430	cytochrome P450, putative, expressed	1.73	down	1.43	up	3.69	down	1.10	up	1.40	down	1.66	down	ABA
Os.2243.1.S1_a_at	LOC_Os05g03610	phospholipase C, putative, expressed	1.32	down	1.76	up	4.56	down	1.12	down	2.27	down	1.31	up	2
Os.22478.2.S1_at	LOC_Os01g60650	non-green plastid inner envelope membrane protein, putative, expressed	1.94	down	1.90	down	2.84	up	1.01	down	1.21	down	1.26	down	ABA
Os.22485.1.A1_at	LOC_Os11g29720	cytochrome P450, putative, expressed	1.37	down	2.38	down	3.10	down	2.27	down	3.18	down	2.18	up	5
Os.2250.1.S1_a_at	LOC_Os05g49440	DUF1264 domain containing protein, putative, expressed	1.05	up	1.00	up	436.61	up	1.01	down	1.00	up	1.05	up	ABA
Os.2254.1.S1_at	LOC_Os07g03770	Homeobox domain containing protein, expressed	1.01	up	1.18	down	2.06	down	1.29	up	1.14	up	1.09	down	ABA
Os.22563.1.S1_at	LOC_Os03g61030	transcription termination factor nusG family protein, expressed	1.11	up	1.39	up	4.12	down	1.26	down	1.83	down	1.23	down	ABA
Os.22571.1.S1_at	AF022734	Oryza sativa zinc inducible protein mRNA, complete cds.	1.04	up	1.48	up	10.22	up	1.17	up	2.66	up	1.54	up	2
Os.22577.2.S1_x_at	LOC_Os01g32770	DUF260 domain containing protein, putative, expressed	1.40	down	1.02	up	2.92	down	1.51	up	1.80	down	1.40	down	ABA
Os.22594.1.S1_at	LOC_Os01g03390	BBTI7 - Bowman-Birk type bran trypsin inhibitor precursor, expressed	1.26	down	1.29	up	4.89	up	1.13	up	2.00	up	2.20	up	3
Os.2260.1.S1_at	LOC_Os06g05690	cysteine synthase, chloroplast/chromoplast precursor, putative, expressed	1.75	down	2.85	up	19.55	down	1.14	down	2.09	down	1.46	down	3
Os.22624.1.A1_at	LOC_Os02g43920	cell division cycle protein 23, putative, expressed	1.04	down	1.18	down	17.41	up	1.92	down	1.11	down	1.75	down	ABA
Os.22631.1.S1_a_at	LOC_Os07g42960	phospho-2-dehydro-3-deoxyheptonate aldolase, chloroplast precursor, putative, expres	1.01	down	1.02	up	2.79	down	1.24	up	1.15	down	2.01	up	2
Os.22640.1.A1_at	LOC_Os01g10830	carnitine racemase like protein, putative, expressed	1.07	up	1.49	up	1.56	up	1.20	up	1.33	up	3.42	up	JA
Os.22651.1.S1_at	LOC_Os04g56230	polyprenyl synthetase, putative, expressed	1.05	down	2.00	up	7.68	down	1.37	down	2.32	down	1.80	down	3
Os.22660.2.S1_at	LOC_Os02g06640	ubiquitin family protein, putative, expressed	1.16	down	1.15	down	2.57	up	1.17	up	1.62	up	1.08	up	ABA
Os.22667.1.S1_at	LOC_Os04g40910	OsFBX146 - F-box domain containing protein, expressed	1.09	up	1.21	down	3.22	up	1.05	up	1.28	up	1.16	up	ABA
Os.22711.1.A1_at	LOC_Os03g06350	DUF623 domain containing protein, expressed	1.23	up	1.38	down	5.89	up	1.26	down	1.22	up	1.07	up	ABA
Os.22726.1.A1_at	LOC_Os10g37110	transposon protein, putative, unclassified, expressed	1.21	up	1.40	down	3.22	up	1.01	down	1.86	up	1.46	up	ABA
Os.22730.1.S1_at	AK069547	heat shock protein, low molecular weight	1.15	down	1.01	up	1.25	down	1.17	down	2.83	up	1.20	down	SA
Os.22731.1.S1_at	D12635	Oryza sativa Japonica Group mRNA for low molecular weight heat shock protein, comp	1.45	down	1.01	up	2.12	up	1.06	up	18.01	up	1.12	up	2
Os.22735.1.S1_at	LOC_Os06g47150	auxin response factor 18, putative, expressed	1.17	up	1.05	down	2.34	up	1.02	down	1.06	up	1.10	down	ABA
Os.22744.1.A1_at	LOC_Os08g01370	expressed protein	1.01	down	1.00	up	88.85	up	1.00	up	1.00	down	1.01	up	ABA
Os.22783.1.S1_s_at	LOC_Os05g31750	annexin, putative, expressed	1.10	up	1.07	down	3.27	down	1.25	down	1.34	down	2.56	up	2
Os.22812.1.S1_a_at	LOC_Os01g57720	expressed protein	1.05	up	1.19	down	2.06	up	1.08	up	1.24	up	1.09	up	ABA
Os.22819.1.S1_at	LOC_Os08g37060	gibberellin receptor GID1L2, putative, expressed	1.39	down	1.03	down	2.30	down	1.05	up	1.39	down	1.01	up	ABA
Os.22827.1.A1_x_at	LOC_Os12g06280	expressed protein	1.50	up	1.27	down	2.02	up	1.86	down	1.09	down	1.39	down	ABA
Os.22832.1.S1_at	LOC_Os09g24620	expressed protein	1.22	down	1.36	up	6.03	down	1.93	down	2.78	down	1.84	down	2
Os.22839.1.S1_at	LOC_Os06g48200	glycosyl hydrolases family 16, putative, expressed	1.39	up	1.13	up	14.69	up	1.30	down	2.86	up	1.36	up	2
Os.22839.1.S2_at	LOC_Os06g48200	glycosyl hydrolases family 16, putative, expressed	1.11	up	1.01	up	2.86	up	1.12	down	1.82	up	1.10	up	ABA
Os.22908.1.S1_at	LOC_Os06g50400	expansin precursor, putative, expressed	1.05	up	1.14	down	2.51	down	1.09	down	1.20	up	3.84	down	2
Os.22910.1.S1_at	LOC_Os04g39880	Os4bglu12 - beta-glucosidase, exo-beta-glucanase, expressed	1.35	down	1.32	up	2.44	down	1.39	up	1.34	down	1.46	up	ABA
Os.22910.2.S1_at	AK105375	glycosyl hydrolase family 1 protein	1.84	down	1.58	up	4.01	down	1.62	up	1.12	down	1.80	up	ABA
Os.22911.1.S1_a_at	LOC_Os06g01630	2-oxo acid dehydrogenases acyltransferase domain containing protein, expressed	1.13	up	1.05	down	2.68	up	1.00	down	2.00	up	1.62	up	ABA
Os.22928.2.S1_at	LOC_Os02g37040	peptide transporter PTR3-A, putative, expressed	1.40	down	1.35	down	3.66	up	1.01	up	1.59	up	1.03	up	ABA
Os.22932.1.S1_at	AK120355	Oryza sativa (japonica cultivar-group) Os04g0540500 (Os04g0540500) mRNA, comple	1.09	down	1.07	down	2.94	up	1.26	up	1.25	up	1.19	up	ABA
Os.22957.1.S1_at	LOC_Os01g72140	glutathione S-transferase, putative, expressed	1.41	up	1.18	down	2.99	down	1.79	up	5.14	up	1.85	down	2
Os.22966.1.S1_at	LOC_Os03g17350	white-brown complex homolog protein, putative, expressed	1.40	up	1.20	up	8.08	up	1.20	down	1.50	up	1.22	down	ABA
Os.23021.1.S1_at	LOC_Os03g62480	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	1.62	up	1.21	up	1.10	up	1.36	up	9.78	up	1.43	up	SA
Os.23028.1.S1_s_at	LOC_Os03g08490	AP2 domain containing protein, expressed	2.71	up	1.07	down	2.44	up	1.57	up	1.84	up	1.13	down	2
Os.23033.1.S1_s_at	LOC_Os01g09020	WD domain, G-beta repeat domain containing protein, expressed	1.01	down	1.09	down	2.39	up	1.00	down	1.50	up	1.14	down	ABA
Os.23043.1.A1_x_at	LOC_Os10g39720	homeobox domain containing protein	5.09	up	1.60	up	10.54	up	1.03	down	1.03	up	1.01	up	2
Os.23059.1.S1_s_at	CA754790		2.49	down	1.39	down	14.57	down	1.01	down	1.48	down	3.44	down	3
Os.23067.1.S1_at	LOC_Os04g55600	expressed protein	1.19	down	1.21	up	9.87	up	1.07	up	1.14	down	3.66	down	2
Os.2307.1.S1_at	LOC_Os05g50360	anaphase-promoting complex subunit 10, putative, expressed	1.18	up	1.14	up	2.24	down	1.11	down	1.85	down	1.40	down	ABA
Os.23084.1.S1_at	LOC_Os03g49270	THION36 - Plant thionin family protein precursor, expressed	1.06	down	1.06	up	2.42	down	1.17	down	1.67	down	2.54	down	2
Os.23087.1.S1_at	LOC_Os05g10690	Myb transcription factor, putative, expressed	1.01	down	1.00	up	4.63	up	1.56	down	1.75	down	1.12	down	ABA
Os.23100.1.S1_at	LOC_Os07g37310	uncharacterized secreted protein, putative, expressed	1.25	up	1.02	down	4.07	up	1.06	down	1.14	down	1.11	up	ABA

Os.23154.1.S1_at	LOC_Os02g50690	GDSL-like lipase/acylhydrolase, putative, expressed	1.02	up	1.53	down	4.12	up	1.64	up	5.69	up	1.72	up	2
Os.23164.1.S1_a_at	LOC_Os07g39980	GA22009-PA, putative, expressed	1.08	up	1.53	up	3.70	down	1.12	down	1.43	down	1.15	down	ABA
Os.23174.1.S1_at	LOC_Os08g14200	glycosyl hydrolases family 16, putative, expressed	3.80	down	2.25	down	3.57	down	1.47	down	1.78	up	2.30	down	4
Os.23179.1.S1_at	LOC_Os06g49990	UPF0183 protein, putative, expressed	1.19	up	1.03	up	2.03	up	1.07	down	1.20	up	1.12	down	ABA
Os.23181.1.S1_at	LOC_Os01g03530	multicopper oxidase domain containing protein, expressed	1.48	up	1.10	up	3.25	up	4.41	up	5.16	up	1.37	down	3
Os.23183.1.S1_at	LOC_Os09g28160	phosphate carrier protein, mitochondrial precursor, putative, expressed	2.27	up	1.17	up	2.54	up	1.45	up	5.32	up	2.23	up	4
Os.23185.1.S1_at	NM_001070757	Oryza sativa (japonica cultivar-group) Os10g0167200 (Os10g0167200) mRNA, comple	1.77	up	1.32	down	2.56	up	1.07	down	4.38	up	2.68	up	3
Os.23215.1.S1_at	LOC_Os06g24404	GDSL-like lipase/acylhydrolase, putative, expressed	1.09	down	1.02	down	2.44	down	1.48	down	1.15	down	1.09	up	ABA
Os.23217.1.S1_s_at	LOC_Os05g03830	aminotransferase, putative, expressed	1.20	up	1.12	up	1.06	up	1.23	up	1.35	up	2.21	up	JA
Os.23219.1.S1_at	LOC_Os01g52690	retrotransposon protein, putative, unclassified, expressed	1.40	up	1.23	down	9.05	up	1.21	up	1.09	up	1.04	down	ABA
Os.23222.1.S1_at	AU225797		1.21	down	1.01	up	1.70	down	1.44	up	1.54	down	4.85	down	JA
Os.23231.1.A1_at	LOC_Os03g09090	expressed protein	1.02	up	1.03	down	3.75	up	1.02	up	1.06	up	1.22	up	ABA
Os.23252.1.S1_at	LOC_Os10g40620	expressed protein	1.09	up	1.14	up	2.84	down	1.13	down	1.52	down	1.16	down	ABA
Os.23256.1.S1_at	LOC_Os02g56120	OsIAA9 - Auxin-responsive Aux/IAA gene family member, expressed	33.47	up	1.28	up	2.63	up	1.25	down	1.73	up	1.10	up	2
Os.23290.2.S1_x_at	LOC_Os10g40960	oxidoreductase, 2OG-Fe oxygenase family protein, putative, expressed	1.12	up	1.48	up	2.19	down	1.12	down	1.10	down	1.20	down	ABA
Os.23297.1.S1_at	LOC_Os03g56860	expressed protein	1.43	up	1.16	up	4.95	up	1.05	down	3.50	up	1.19	down	2
Os.23303.1.A1_at	LOC_Os03g26044	CSLA5 - cellulose synthase-like family A; mannan synthase, expressed	1.04	up	1.12	down	29.04	up	1.04	down	1.26	up	1.03	down	ABA
Os.23359.1.S1_at	LOC_Os05g39850	MCM3 - Putative minichromosome maintenance MCM complex subunit 3, expressed	1.44	down	1.06	down	4.10	down	1.08	down	2.18	down	1.86	down	2
Os.23381.1.A1_at	LOC_Os09g19710	hypersensitive-induced response protein, putative, expressed	1.15	down	1.07	down	3.89	up	4.13	up	1.11	up	2.03	down	3
Os.23397.1.S1_at	LOC_Os08g37874	2-nitropropane dioxygenase family, putative, expressed	1.96	up	1.00	down	8.28	up	1.14	up	12.75	up	5.21	up	3
Os.23397.1.S2_at	LOC_Os08g37874	2-nitropropane dioxygenase family, putative, expressed	2.11	up	1.14	down	24.00	up	2.11	up	18.76	up	6.60	up	5
Os.23411.1.S1_at	LOC_Os02g42660	sphingolipid delta desaturase, putative, expressed	1.06	down	1.14	down	2.39	down	1.06	up	1.34	down	1.11	down	ABA
Os.23416.2.S1_at	LOC_Os07g39270	polyprenyl synthetase, putative, expressed	1.06	down	1.07	up	2.12	up	1.18	up	1.08	down	1.75	up	ABA
Os.2344.1.S1_at	LOC_Os10g28230	Core histone H2A/H2B/H3/H4 domain containing protein, putative, expressed	1.29	down	1.11	down	3.51	down	1.27	down	1.79	down	1.72	down	ABA
Os.23454.1.A1_at	LOC_Os12g07810	aldehyde dehydrogenase, putative, expressed	1.07	down	1.05	down	1.14	down	1.08	down	1.05	up	2.18	up	JA
Os.23468.1.A1_at	LOC_Os09g27940	aspartic proteinase nepenthesin-1 precursor, putative, expressed	2.18	up	1.22	down	6.53	up	1.16	up	2.50	up	1.94	up	3
Os.23471.2.S1_x_at	LOC_Os11g18366	cycloartenol synthase, putative, expressed	1.01	down	1.00	up	2.86	up	1.00	up	1.00	down	1.04	up	ABA
Os.23482.1.S1_at	LOC_Os08g19420	O-methyltransferase, putative, expressed	1.23	down	1.48	up	45.97	up	1.06	down	1.36	down	1.24	down	ABA
Os.23492.1.A1_at	LOC_Os07g37820	expressed protein	3.64	up	1.35	up	1.72	up	1.00	down	1.09	down	2.33	down	2
Os.23504.1.A1_at	LOC_Os01g10530	expressed protein	1.03	up	1.21	up	2.75	up	1.11	up	1.01	down	1.26	up	ABA
Os.23544.1.S1_at	LOC_Os02g48740	fimbrin-like protein 2, putative, expressed	1.24	up	1.11	up	2.12	up	1.16	down	1.20	up	1.07	down	ABA
Os.23551.1.S1_at	LOC_Os02g05900	ternary complex factor MIP1, putative, expressed	1.03	up	1.10	down	2.47	down	1.04	down	1.05	down	1.30	down	ABA
Os.2357.1.S1_at	LOC_Os07g36190	hydrolase, NUDIX family, domain containing protein, expressed	1.11	down	1.08	up	2.19	down	1.18	down	1.55	down	1.17	down	ABA
Os.2362.1.S1_a_at	LOC_Os02g35770	homeobox associated leucine zipper, putative, expressed	1.07	up	1.08	down	24.27	up	1.12	up	1.11	up	1.63	up	ABA
Os.2362.2.S1_x_at	LOC_Os02g35770	homeobox associated leucine zipper, putative, expressed	1.02	up	1.00	down	27.58	up	1.08	up	1.03	up	1.20	up	ABA
Os.2363.1.S1_a_at	LOC_Os09g35910	homeobox associated leucine zipper, putative, expressed	1.16	down	1.53	down	3.76	up	1.03	down	1.24	up	1.14	down	ABA
Os.23632.1.A1_s_at	LOC_Os06g20610	seven in absentia protein family domain containing protein, expressed	1.01	down	1.03	up	2.87	up	1.11	up	1.23	up	1.01	up	ABA
Os.2365.1.S1_at	LOC_Os06g04870	homeobox associated leucine zipper, putative, expressed	2.17	up	1.10	up	2.41	down	1.14	down	1.43	up	1.45	down	2
Os.23656.1.A1_at	LOC_Os04g57650	expressed protein	1.08	down	1.37	down	2.28	down	1.30	down	1.13	up	1.11	down	ABA
Os.2367.1.S1_at	LOC_Os03g21820	expansin precursor, putative, expressed	1.94	up	1.07	down	2.08	down	1.77	up	1.82	up	1.01	up	ABA
Os.23678.1.A1_at	LOC_Os12g21789	expressed protein	1.43	down	1.40	down	2.71	up	1.28	up	1.29	up	1.18	up	ABA
Os.23695.2.S1_at	LOC_Os01g70950	spermatogenesis-associated protein 20 precursor, putative, expressed	1.14	down	1.01	down	4.17	up	1.21	down	1.39	up	1.07	down	ABA
Os.23695.3.S1_x_at	LOC_Os01g70950	spermatogenesis-associated protein 20 precursor, putative, expressed	1.11	up	1.14	down	4.43	up	1.31	down	1.18	up	1.05	up	ABA
Os.23700.1.A1_at	AK243128	phox (PX) domain-containing protein	1.30	down	1.23	down	2.15	up	1.34	up	1.50	up	1.37	up	ABA
Os.23712.2.S1_at	LOC_Os08g17784	purple acid phosphatase, putative, expressed	1.06	up	1.02	up	10.24	up	1.04	down	1.40	up	1.15	down	ABA
Os.2373.1.S1_at	LOC_Os10g40710	expansin precursor, putative, expressed	1.23	down	1.27	up	2.49	down	1.07	up	2.94	down	1.51	down	2
Os.2375.1.S1_at	LOC_Os04g41980	ATOZI1, putative, expressed	1.14	down	1.00	down	1.09	down	1.11	down	1.28	down	10.91	up	JA
Os.2376.1.S1_at	LOC_Os03g17480	IN2-1 protein, putative, expressed	7.32	up	1.46	down	17.21	up	1.68	up	21.71	up	9.22	up	4
Os.23770.1.A1_s_at	LOC_Os01g49280	zinc finger family protein, putative, expressed	1.97	down	2.12	down	7.84	up	1.37	down	1.30	up	1.00	down	2
Os.23778.1.S1_at	LOC_Os02g32590	HSF-type DNA-binding domain containing protein, expressed	1.63	up	1.13	down	2.50	up	1.27	down	1.83	up	1.39	down	ABA
Os.23802.1.A1_at	LOC_Os04g39540	expressed protein	1.31	up	1.05	up	2.17	up	1.23	up	1.61	up	1.25	down	ABA
Os.23942.1.A1_at	LOC_Os02g35180	OsRR2 type-A response regulator, expressed	1.95	down	6.67	up	13.59	down	1.05	up	3.72	down	2.20	down	4
Os.23950.1.A1_at	LOC_Os07g07310	polynucleotide phosphorylase, putative, expressed	1.16	up	1.09	up	4.23	down	1.22	down	1.94	down	1.30	down	ABA
Os.23978.1.A1_at	LOC_Os04g41460	transporter family protein, putative, expressed	1.12	up	1.11	up	2.47	up	1.31	down	1.07	down	1.05	up	ABA
Os.24025.1.S1_at	LOC_Os11g03160	glycosyl transferase, family 8, putative, expressed	1.16	down	1.55	up	2.06	down	1.05	up	1.15	down	1.35	down	ABA

Os.24032.1.S1_at	AK100879	Oryza sativa Japonica Group cDNA clone:J023127D23, full insert sequence.	2.71	up	1.04	up	3.76	up	1.14	down	2.40	up	1.10	up	3
Os.24032.2.S1_at	LOC_Os02g50805	transposon protein, putative, CACTA, En/Spm sub-class, expressed	1.54	up	1.37	down	3.84	up	1.59	up	2.44	up	1.44	up	2
Os.24034.2.S1_x_at	LOC_Os01g65400	DNA polymerase I, putative, expressed	1.06	down	1.11	up	2.62	down	1.10	down	1.45	down	1.12	down	ABA
Os.2404.1.S1_at	LOC_Os10g40700	expansin precursor, putative, expressed	1.03	up	1.77	up	6.45	down	1.04	up	1.77	down	1.32	down	ABA
Os.24051.2.S1_at	LOC_Os04g33640	glycosyl hydrolases family 17, putative, expressed	1.72	up	1.01	up	2.17	up	1.02	up	1.08	down	1.10	down	ABA
Os.24059.1.A1_at	LOC_Os04g10380	glycine-rich protein, putative, expressed	1.03	down	1.16	down	2.55	up	1.05	up	1.21	up	1.01	down	ABA
Os.2406.2.S1_a_at	LOC_Os02g44360	scarecrow transcription factor family protein, putative, expressed	1.06	up	1.03	down	2.08	down	1.07	up	1.06	up	1.15	down	ABA
Os.2407.1.S1_at	LOC_Os09g31200	AN1-like zinc finger domain containing protein, expressed	1.72	up	1.19	up	4.06	up	1.29	up	1.31	up	1.69	up	ABA
Os.24103.1.A1_at	LOC_Os07g18990	LTPL40 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.29	up	1.07	up	5.26	down	1.07	down	1.01	up	1.39	down	ABA
Os.24106.3.S1_at	LOC_Os03g49464	tetratricopeptide-like helical, putative, expressed	1.40	down	1.19	down	2.47	up	1.06	down	1.01	up	1.39	down	ABA
Os.24115.1.A1_at	AK062932	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI025D23, full insert sequence	1.60	down	3.26	up	1.03	up	1.12	down	1.66	down	1.67	down	BAP
Os.24154.1.A1_at	LOC_Os11g02640	expressed protein	1.15	up	1.01	up	2.05	up	1.13	down	1.16	up	1.08	down	ABA
Os.24190.1.A1_at	LOC_Os07g08320	RNA recognition motif containing protein, expressed	1.17	down	1.18	up	7.41	up	1.23	up	2.10	up	1.54	up	2
Os.24338.1.A1_at	AK111667	Oryza sativa Japonica Group cDNA clone:J013155L06, full insert sequence.	2.09	up	1.85	up	1.03	down	1.11	down	1.13	down	1.10	down	IAA
Os.24363.1.A1_at	LOC_Os08g33740	CSLA11 - cellulose synthase-like family A, expressed	1.49	down	1.21	down	3.21	down	1.25	down	1.20	down	1.14	up	ABA
Os.24379.1.A1_at	LOC_Os02g44900	expressed protein	1.62	down	1.04	up	2.06	up	1.33	down	1.15	down	1.38	down	ABA
Os.24403.1.A1_at	LOC_Os03g17660	expressed protein	1.07	up	1.19	down	13.59	up	1.36	down	1.09	down	1.32	down	ABA
Os.24424.1.S1_at	LOC_Os08g41270	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	1.05	up	1.23	up	2.98	up	1.47	down	1.05	down	1.24	down	ABA
Os.24469.1.A1_at	CA761866	---	1.05	down	1.02	down	2.94	up	1.04	down	1.12	down	1.03	down	ABA
Os.24493.1.A1_at	LOC_Os08g37500	expressed protein	1.14	up	1.07	down	2.94	up	1.31	up	1.56	up	1.05	up	ABA
Os.24495.1.S1_at	LOC_Os03g29980	ACT domain containing protein, expressed	1.11	up	1.26	up	4.53	down	1.05	up	1.06	down	1.83	up	ABA
Os.24495.2.S1_x_at	LOC_Os03g29980	ACT domain containing protein, expressed	1.45	up	1.41	up	4.88	down	1.04	down	1.04	down	1.64	up	ABA
Os.24545.2.S1_at	LOC_Os03g30300	6-phosphogluconolactonase, putative, expressed	1.06	down	1.24	up	4.90	up	1.25	down	1.79	up	1.03	down	ABA
Os.24548.1.A1_at	LOC_Os02g07480	transglycosylase SLT domain containing protein, expressed	1.31	up	1.16	down	3.28	up	1.40	down	1.54	up	1.13	down	ABA
Os.24577.1.S1_at	LOC_Os12g39320	DUF221 domain containing protein, expressed	1.30	down	1.07	down	3.38	up	1.04	up	1.04	up	1.10	down	ABA
Os.24599.1.A1_at	LOC_Os02g15870	molybdenum cofactor biosynthesis protein 1, putative, expressed	1.17	up	1.10	down	3.35	up	1.02	up	1.56	up	1.19	up	ABA
Os.24683.1.A1_s_at	LOC_Os09g14520	integral membrane protein, putative, expressed	1.11	up	1.06	up	2.04	down	1.08	down	1.14	down	1.17	down	ABA
Os.24690.1.A1_s_at	LOC_Os04g55210	chloride channel protein, putative, expressed	1.31	up	1.33	down	2.59	up	1.22	up	1.38	up	1.08	up	ABA
Os.24690.2.S1_s_at	LOC_Os04g55210	chloride channel protein, putative, expressed	1.33	up	1.07	down	3.21	up	1.26	up	1.41	up	1.29	up	ABA
Os.24691.1.A1_s_at	LOC_Os04g49320	tRNA-splicing endonuclease positive effector-related, putative, expressed	1.07	up	2.04	up	1.80	down	1.14	down	1.19	down	1.38	down	BAP
Os.24698.1.S1_at	LOC_Os11g37260	SEY1, putative, expressed	1.47	down	1.02	down	25.45	up	1.23	down	1.04	up	1.20	down	ABA
Os.24698.2.S1_x_at	LOC_Os11g37260	SEY1, putative, expressed	1.11	up	1.28	down	32.41	up	1.02	down	1.12	up	1.05	up	ABA
Os.24889.1.S1_at	LOC_Os01g55040	1,3-beta-glucan synthase component, putative, expressed	1.69	down	1.12	up	2.15	up	1.11	up	1.09	up	1.01	up	ABA
Os.24890.1.S2_at	LOC_Os01g72130	glutathione S-transferase, putative, expressed	2.75	up	1.07	down	1.61	up	1.15	up	13.11	up	1.34	up	2
Os.24913.1.A1_at	LOC_Os04g48260	zinc RING finger protein, putative, expressed	1.07	down	1.06	down	4.06	up	1.00	up	1.13	up	1.15	down	ABA
Os.24917.1.S1_at	LOC_Os01g36790	TKL_IRAK_DUF26-lf.2 - DUF26 kinases have homology to DUF26 containing loci, expr	1.52	up	1.06	down	3.59	up	1.99	up	2.00	up	1.75	up	3
Os.24927.1.S1_at	LOC_Os03g56160	lectin-like receptor kinase 7, putative, expressed	1.33	down	1.21	up	2.55	down	1.12	down	1.47	down	1.17	down	ABA
Os.24943.1.S1_at	LOC_Os01g72230	stromal membrane-associated protein, putative, expressed	1.10	up	1.13	down	2.36	down	1.02	down	1.30	down	1.25	down	ABA
Os.24951.1.S1_at	LOC_Os12g37400	MCM7 - Putative minichromosome maintenance MCM complex subunit 7, expressed	1.44	down	1.09	down	9.99	down	1.12	down	2.29	down	1.51	down	2
Os.24952.1.S1_at	LOC_Os04g57720	OsRR6 type-A response regulator, expressed	1.09	down	8.48	up	2.12	down	1.15	up	2.17	down	2.11	down	4
Os.24965.1.S1_at	AK070313	Oryza sativa Japonica Group cDNA clone:J023049J12, full insert sequence.	1.05	down	1.25	up	2.22	down	1.89	down	1.20	down	1.40	down	ABA
Os.24993.1.A1_s_at	LOC_Os02g07044	rhodanese-like domain containing protein, putative, expressed	1.39	up	1.18	down	2.13	down	1.01	down	1.96	up	1.58	up	ABA
Os.24995.1.S1_a_at	LOC_Os07g47250	lipase precursor, putative, expressed	1.17	up	1.19	up	3.52	up	1.22	up	1.16	up	1.16	down	ABA
Os.25027.1.S1_a_at	LOC_Os07g46700	zinc finger, RING-type, putative, expressed	1.00	down	1.05	down	3.77	up	1.85	up	1.09	down	1.42	down	ABA
Os.25027.3.S1_at	LOC_Os07g46700	zinc finger, RING-type, putative, expressed	1.04	up	1.04	up	3.79	up	1.44	up	1.07	down	1.03	up	ABA
Os.25027.3.S1_x_at	LOC_Os07g46700	zinc finger, RING-type, putative, expressed	1.08	up	1.00	up	3.45	up	1.71	up	1.11	down	1.41	down	ABA
Os.25065.3.S1_at	LOC_Os01g60309	retrotransposon protein, putative, Ty1-copia subclass	1.18	up	1.16	down	2.05	up	1.03	down	1.16	up	1.12	down	ABA
Os.25097.1.S1_at	LOC_Os02g02750	CDP-alcohol phosphatidyltransferase, putative, expressed	1.02	up	1.10	down	2.02	down	1.01	down	1.18	down	1.00	down	ABA
Os.25102.1.S1_at	AK064481	Oryza sativa Japonica Group cDNA clone:002-111-A10, full insert sequence.	1.09	up	1.06	up	3.09	up	1.09	up	1.41	up	1.07	down	ABA
Os.25107.1.S1_at	LOC_Os01g08750	expressed protein	1.03	down	1.04	down	2.05	up	1.06	down	1.03	up	1.31	down	ABA
Os.25128.1.S1_at	LOC_Os02g09810	amino acid transporter, putative, expressed	1.24	up	1.06	down	3.26	up	1.01	up	2.25	up	1.50	up	2
Os.25130.1.S1_at	LOC_Os08g02450	ATCHX, putative, expressed	1.06	up	1.07	down	2.91	up	1.09	up	1.54	up	1.02	down	ABA
Os.25142.1.A1_at	LOC_Os10g40490	U-box domain containing protein, expressed	1.01	down	1.37	down	4.05	up	1.39	down	3.83	up	2.18	up	3
Os.25168.2.A1_at	CA759316		1.16	down	1.15	down	3.56	down	1.01	down	1.23	down	1.08	down	ABA
Os.25266.1.S1_at	LOC_Os01g71690	recA protein, expressed	1.00	up	1.53	down	4.44	up	1.33	down	1.04	down	1.04	up	ABA

Os.25309.2.A1_a_at	CB682760	MI0006974 Oryza sativa miR444b stem-loop	**1.08**	up	**1.06**	up	**2.05**	up	**1.06**	up	**1.25**	down	**1.07**	down	ABA
Os.25414.1.S1_at	LOC_Os07g30810	nucleobase-ascorbate transporter, putative, expressed	**1.20**	down	**1.14**	down	**2.51**	down	**1.23**	down	**1.42**	down	**1.05**	up	ABA
Os.25432.1.S1_at	LOC_Os02g22260	fruit protein PKIWI502, putative, expressed	**1.16**	up	**1.03**	up	**2.10**	down	**1.23**	down	**1.53**	down	**1.21**	down	ABA
Os.2544.1.S1_s_at	LOC_Os10g35050	aquaporin protein, putative, expressed	**1.07**	down	**1.06**	down	**31.96**	up	**1.06**	down	**1.79**	up	**1.26**	down	ABA
Os.25452.1.S1_s_at	LOC_Os04g20070	tropinone reductase 2, putative, expressed	**1.37**	up	**1.14**	up	**7.54**	up	**1.08**	down	**1.78**	up	**1.21**	up	ABA
Os.25496.1.S1_at	LOC_Os11g07930	oxidoreductase, short chain dehydrogenase/reductase family domain containing family,	**1.17**	down	**1.31**	up	**2.00**	up	**1.93**	down	**1.04**	up	**1.05**	down	ABA
Os.25497.1.S1_at	AB027421	Oryza sativa mRNA for class III chitinase homologue (OsChib3H-b), complete cds, clor	**1.81**	down	**1.04**	down	**6.85**	up	**1.03**	up	**3.15**	up	**1.19**	up	2
Os.25497.1.S1_x_at	AB027421	Oryza sativa mRNA for class III chitinase homologue (OsChib3H-b), complete cds, clor	**1.65**	down	**1.06**	down	**8.69**	up	**1.04**	up	**3.42**	up	**1.17**	up	2
Os.25529.1.S1_at	LOC_Os05g44330	DJ-1 family protein, putative, expressed	**1.22**	up	**1.09**	up	**3.35**	down	**1.23**	down	**1.59**	down	**1.23**	down	ABA
Os.25544.1.S1_at	LOC_Os07g19444	regulatory protein, putative, expressed	**1.22**	up	**1.37**	down	**3.19**	up	**1.18**	up	**1.32**	up	**1.14**	up	ABA
Os.25546.1.S1_at	LOC_Os05g22730	expressed protein	**1.14**	down	**2.65**	up	**2.29**	down	**1.25**	up	**1.76**	down	**2.60**	down	3
Os.25561.1.S1_at	LOC_Os05g48270	auxin-responsive protein, putative, expressed	**1.37**	up	**1.19**	up	**2.91**	down	**1.24**	down	**1.50**	down	**1.36**	down	ABA
Os.25562.1.S1_at	LOC_Os10g33920	transporter-related, putative, expressed	**1.21**	down	**1.19**	up	**3.87**	down	**1.90**	down	**2.00**	down	**1.20**	down	2
Os.2558.1.S1_a_at	AK066452	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA019J09, full insert sequence	**1.75**	down	**1.46**	down	**2.62**	down	**1.15**	down	**1.35**	down	**1.99**	up	ABA
Os.25589.1.S1_at	CT829769	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA019J09, full insert sequence	**1.12**	up	**1.03**	up	**3.60**	up	**1.02**	up	**1.72**	up	**1.51**	down	ABA
Os.25589.3.S1_at	LOC_Os11g25780	PB1 domain containing protein, expressed	**1.14**	up	**1.02**	down	**4.41**	up	**1.29**	down	**1.29**	up	**1.24**	down	ABA
Os.25589.3.S1_x_at	LOC_Os11g25780	PB1 domain containing protein, expressed	**1.01**	up	**1.06**	down	**4.45**	up	**1.15**	down	**1.34**	up	**1.23**	down	ABA
Os.25621.2.S1_at	LOC_Os12g16720	cytochrome P450 71A1, putative, expressed	**1.35**	down	**1.12**	up	**2.88**	up	**1.10**	down	**1.77**	up	**1.16**	up	ABA
Os.25651.1.S1_at	LOC_Os01g27360	glutathione S-transferase, putative, expressed	**1.07**	up	**1.01**	up	**1.07**	down	**1.78**	down	**1.50**	up	**2.30**	up	JA
Os.25677.1.S1_at	LOC_Os03g28330	sucrose synthase, putative, expressed	**1.06**	up	**1.01**	down	**2.69**	down	**1.09**	down	**1.31**	down	**1.04**	up	ABA
Os.25687.1.S1_x_at	LOC_Os02g41680	phenylalanine ammonia-lyase, putative, expressed	**1.04**	down	**1.60**	up	**2.83**	down	**1.12**	down	**1.84**	down	**1.19**	up	ABA
Os.257.1.S1_at	LOC_Os04g59380	ZOS4-14 - C2H2 zinc finger protein, expressed	**1.13**	down	**1.20**	down	**2.71**	down	**1.11**	up	**1.09**	down	**1.02**	down	ABA
Os.25748.1.S1_at	AF216530	Oryza sativa ubiquitin RiP-20 mRNA, partial cds.	**1.02**	up	**1.06**	up	**2.70**	up	**1.12**	up	**1.39**	up	**1.03**	up	ABA
Os.2580.1.S1_at	LOC_Os10g33350	endo-beta-N-acetylglucosaminidase, putative, expressed	**1.05**	down	**1.15**	down	**4.13**	up	**1.11**	up	**1.04**	up	**1.11**	down	ABA
Os.25825.1.S1_at	LOC_Os03g22880	nucleolar protein 5A, putative, expressed	**1.02**	up	**1.14**	up	**2.00**	down	**1.17**	up	**1.27**	down	**1.18**	down	ABA
Os.25870.2.S1_a_at	LOC_Os02g12870	expressed protein	**1.14**	up	**1.07**	down	**2.38**	up	**1.08**	up	**1.10**	up	**1.19**	up	ABA
Os.2611.1.S1_a_at	LOC_Os10g36060	protein transport protein-related, putative, expressed	**1.33**	down	**1.30**	down	**2.96**	down	**1.47**	down	**1.66**	down	**1.11**	down	ABA
Os.2612.1.S1_at	AF309378	Oryza sativa (japonica cultivar-group) clone C12112_1A putative glutathione S-transfe	**18.83**	up	**1.63**	up	**7.64**	up	**1.04**	down	**30.03**	up	**4.45**	up	4
Os.26133.1.S1_at	LOC_Os02g47650	universal stress protein domain containing protein, putative, expressed	**1.53**	down	**1.07**	up	**2.81**	up	**1.00**	up	**2.68**	up	**1.47**	up	2
Os.2615.1.S1_at	LOC_Os03g01260	expansin precursor, putative, expressed	**1.88**	down	**1.04**	up	**2.05**	down	**1.07**	up	**1.11**	down	**1.12**	down	ABA
Os.2617.2.S1_a_at	LOC_Os06g48810	OsHKT2;1 - Na+ transporter, expressed	**1.40**	down	**2.67**	down	**16.29**	up	**1.87**	up	**5.02**	up	**1.58**	down	3
Os.26261.1.S1_at	LOC_Os01g65520	Sad1 / UNC-like C-terminal domain containing protein, putative, expressed	**1.37**	up	**1.03**	up	**6.91**	up	**1.02**	up	**1.49**	up	**1.14**	up	ABA
Os.26353.1.S1_at	LOC_Os12g44380	sucrose transporter, putativ, expressed	**1.24**	up	**1.33**	down	**3.61**	up	**1.07**	up	**1.98**	up	**1.48**	up	ABA
Os.26359.1.S1_a_at	LOC_Os02g53520	kinesin motor domain containing protein, putative, expressed	**1.03**	up	**1.01**	down	**2.18**	down	**1.03**	up	**1.17**	down	**1.11**	down	ABA
Os.26367.1.S1_at	LOC_Os01g58740	glycerol-3-phosphate dehydrogenase, putative, expressed	**1.33**	up	**1.23**	up	**2.81**	up	**1.07**	up	**1.24**	up	**1.95**	up	ABA
Os.26381.1.S1_x_at	LOC_Os07g29600	zinc finger, C3HC4 type, domain containing protein, expressed	**1.24**	up	**1.15**	up	**2.04**	down	**1.15**	down	**1.08**	up	**1.15**	up	ABA
Os.264.1.S1_at	LOC_Os04g59260	peroxidase precursor, putative, expressed	**1.26**	up	**1.08**	down	**1.52**	down	**1.29**	up	**2.33**	down	**5.13**	up	2
Os.26437.1.A1_s_at	LOC_Os12g40920	bZIP transcription factor domain containing protein, expressed	**1.86**	up	**1.04**	down	**5.02**	down	**1.19**	up	**1.67**	down	**1.74**	down	ABA
Os.26443.1.S1_at	LOC_Os01g73040	CBS domain-containing protein, putative, expressed	**1.11**	up	**1.13**	down	**2.91**	up	**1.08**	down	**1.50**	up	**1.08**	down	ABA
Os.26447.1.A1_at	LOC_Os01g48390	expressed protein	**1.35**	up	**1.46**	up	**3.03**	down	**1.28**	up	**1.20**	down	**1.39**	up	ABA
Os.26458.1.A1_at	LOC_Os04g58570	C2 domain containing protein, putative, expressed	**1.09**	down	**1.02**	up	**3.18**	down	**1.17**	up	**1.55**	down	**1.46**	down	ABA
Os.26471.1.S1_at	LOC_Os10g39760	WD domain, G-beta repeat domain containing protein, expressed	**1.20**	down	**1.04**	down	**2.67**	up	**1.07**	up	**1.45**	up	**1.00**	up	ABA
Os.26471.2.S1_x_at	LOC_Os10g39760	WD domain, G beta repeat domain containing protein	**1.00**	up	**1.00**	down	**2.70**	up	**1.04**	up	**1.20**	up	**1.03**	up	ABA
Os.26472.1.S1_at	LOC_Os04g40630	BTBZ4 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with TAZ zinc finger and	**1.10**	up	**1.06**	down	**3.91**	down	**1.38**	up	**1.46**	up	**1.82**	up	ABA
Os.26483.1.S1_at	LOC_Os04g55850	nuclease PA3, putative, expressed	**1.49**	down	**1.25**	down	**1.11**	up	**1.24**	up	**1.57**	down	**2.31**	up	JA
Os.26484.1.S1_at	LOC_Os01g65440	universal stress protein domain containing protein, putative, expressed	**1.26**	up	**1.05**	down	**2.18**	down	**1.22**	down	**1.26**	down	**1.51**	down	ABA
Os.26512.1.S1_at	LOC_Os03g58350	OsIAA14 - Auxin-responsive Aux/IAA gene family member, expressed	**3.29**	up	**1.11**	up	**3.70**	down	**1.77**	down	**1.15**	down	**1.13**	down	2
Os.26517.1.S1_at	LOC_Os02g44990	OsFBDUF13 - F-box and DUF domain containing protein, expressed	**1.05**	up	**2.68**	up	**33.12**	up	**1.35**	up	**2.14**	up	**1.10**	down	3
Os.26543.1.S1_at	LOC_Os03g58110	uncharacterized protein At4g06744 precursor, putative, expressed	**1.94**	down	**1.43**	up	**4.20**	down	**1.18**	up	**1.42**	down	**1.36**	down	ABA
Os.26565.3.S1_at	LOC_Os01g10320	class III HD-Zip protein 8, putative, expressed	**1.09**	down	**1.08**	up	**6.32**	up	**1.02**	up	**1.02**	up	**1.05**	down	ABA
Os.26592.1.S2_at	LOC_Os06g14370	caleosin related protein, putative, expressed	**1.06**	up	**1.09**	up	**2.80**	up	**1.48**	down	**1.34**	down	**1.49**	down	ABA
Os.26629.1.S1_a_at	LOC_Os11g14190	ARGOS, putative, expressed	**1.26**	up	**1.44**	up	**1.65**	down	**2.02**	up	**1.02**	down	**1.61**	down	ACC
Os.26684.1.S1_at	LOC_Os02g49760	potassium transporter, putative, expressed	**1.01**	down	**1.31**	down	**4.18**	up	**1.07**	up	**1.23**	up	**1.21**	up	ABA
Os.26695.1.S1_at	LOC_Os03g60080	NAC domain-containing protein 67, putative, expressed	**1.61**	up	**1.14**	up	**4.82**	up	**1.37**	up	**1.51**	up	**3.08**	up	2
Os.26698.2.S1_at	LOC_Os08g43300	UBX domain-containing protein, putative, expressed	**1.23**	down	**1.06**	down	**2.30**	up	**1.12**	down	**1.39**	up	**1.01**	down	ABA

Os.26706.1.S1_at	LOC_Os07g48229	vacuolar-sorting receptor precursor, putative, expressed	**1.01**	down	**1.14**	up	**2.70**	up	**1.22**	up	**1.03**	up	**1.02**	up	ABA
Os.26713.1.S1_at	LOC_Os06g04780	coiled-coil domain-containing protein 97, putative, expressed	**1.02**	up	**1.13**	up	**2.02**	up	**1.14**	up	**1.34**	up	**1.15**	up	ABA
Os.26716.1.S1_at	LOC_Os05g34320	beta-hexosaminidase precursor, putative, expressed	**1.07**	up	**1.16**	down	**5.26**	down	**1.17**	down	**1.37**	down	**1.10**	down	ABA
Os.26735.1.S1_at	LOC_Os11g06440	expressed protein	**1.27**	up	**1.11**	up	**2.31**	up	**1.01**	down	**1.02**	down	**1.47**	down	ABA
Os.26767.1.A1_at	LOC_Os11g28104	TKL_IRAK_DUF26-lf.4 - DUF26 kinases have homology to DUF26 containing loci, expr	**1.03**	up	**1.13**	up	**3.31**	down	**1.06**	down	**1.35**	down	**1.08**	down	ABA
Os.2677.1.S1_at	LOC_Os07g48830	glycosyl transferase 8 domain containing protein, putative, expressed	**1.45**	up	**1.30**	up	**3.55**	up	**1.45**	down	**1.73**	up	**1.09**	down	ABA
Os.26775.1.A1_at	CB656527	---	**1.18**	down	**1.36**	down	**10.81**	down	**1.27**	up	**1.28**	down	**1.67**	down	ABA
Os.26787.3.S1_at	LOC_Os06g36270	receptor-like protein kinase 5 precursor, putative, expressed	**1.17**	down	**1.20**	down	**2.29**	down	**1.21**	up	**1.25**	down	**1.11**	down	ABA
Os.26799.1.A1_at	LOC_Os07g47590	expressed protein	**1.27**	up	**1.11**	up	**3.77**	up	**1.08**	down	**2.40**	up	**1.06**	up	2
Os.26802.1.S1_at	LOC_Os12g08130	amino acid transporter, putative, expressed	**1.58**	down	**1.63**	up	**2.04**	down	**1.56**	up	**1.18**	down	**1.25**	down	ABA
Os.26816.1.A1_s_at	LOC_Os07g35410	TKL_IRAK_DUF26-lc.18 - DUF26 kinases have homology to DUF26 containing loci, ex	**1.17**	down	**1.04**	down	**1.95**	down	**1.42**	up	**1.03**	up	**2.55**	up	JA
Os.26823.1.S1_at	LOC_Os01g11880	DJ-1 family protein, putative, expressed	**1.15**	down	**1.03**	up	**2.89**	up	**1.17**	up	**1.14**	up	**1.17**	up	ABA
Os.26827.1.A1_at	LOC_Os01g21420	pre-mRNA-splicing factor SF2, putative, expressed	**1.23**	down	**1.10**	down	**6.50**	up	**1.04**	up	**1.83**	up	**1.03**	down	ABA
Os.26827.2.A1_x_at	LOC_Os01g21420	pre-mRNA-splicing factor SF2, putative, expressed	**1.03**	up	**1.05**	down	**4.53**	up	**1.26**	down	**1.30**	up	**1.01**	up	ABA
Os.26830.1.S1_at	LOC_Os07g33440	cytochrome P450, putative, expressed	**1.27**	down	**1.22**	up	**3.37**	down	**1.45**	up	**1.34**	up	**1.49**	up	ABA
Os.26831.1.A1_a_at	AK241507	ceramide kinase-related	**1.25**	up	**1.17**	down	**4.92**	up	**1.07**	up	**1.81**	up	**1.30**	up	ABA
Os.26835.1.A1_at	LOC_Os10g16930	hypothetical protein	**1.24**	up	**1.00**	down	**2.82**	up	**1.16**	down	**1.13**	up	**1.10**	down	ABA
Os.2685.1.S1_at	LOC_Os01g68790	RNA recognition motif containing protein, putative, expressed	**1.08**	up	**1.02**	up	**2.34**	down	**1.09**	up	**1.31**	down	**1.08**	down	ABA
Os.26856.1.S1_at	LOC_Os07g16970	rab GDP dissociation inhibitor alpha, putative, expressed	**1.15**	up	**1.12**	up	**8.75**	up	**1.00**	down	**1.48**	up	**1.25**	up	ABA
Os.26859.1.S1_at	LOC_Os10g11354	MATE efflux family protein, putative, expressed	**1.43**	up	**1.16**	down	**1.22**	up	**1.44**	up	**3.01**	up	**2.00**	up	SA
Os.26864.1.S1_at	LOC_Os01g56350	PTAC12, putative, expressed	**1.05**	down	**1.08**	down	**2.53**	down	**1.17**	down	**1.40**	down	**1.31**	down	ABA
Os.26864.2.S1_x_at	LOC_Os01g56350	PTAC12, putative, expressed	**1.17**	up	**1.02**	down	**2.14**	down	**1.06**	down	**1.41**	down	**1.01**	down	ABA
Os.26868.1.A1_at	LOC_Os03g10100	transporter family protein, putative, expressed	**1.09**	down	**1.29**	up	**2.21**	up	**1.82**	down	**1.15**	down	**1.53**	down	ABA
Os.26907.1.S1_at	LOC_Os02g17710	receptor-like protein kinase 5 precursor, putative, expressed	**1.34**	down	**1.05**	down	**2.52**	down	**1.32**	up	**1.40**	down	**1.22**	down	ABA
Os.26908.1.A1_at	LOC_Os04g54500	POLGAMMA2, putative, expressed	**1.13**	up	**1.02**	up	**2.02**	down	**1.09**	down	**1.34**	down	**1.20**	down	ABA
Os.26914.1.S1_at	LOC_Os07g35330	TKL_IRAK_DUF26-lc.13 - DUF26 kinases have homology to DUF26 containing loci, ex	**1.19**	up	**1.19**	down	**4.24**	down	**2.77**	up	**2.11**	up	**2.72**	up	4
Os.26915.1.A1_at	LOC_Os11g45050	NBS-LRR disease resistance protein, putative, expressed	**1.02**	down	**1.09**	down	**2.43**	down	**1.48**	up	**1.06**	down	**1.06**	up	ABA
Os.26930.1.S1_x_at	LOC_Os04g06590	expressed protein	**1.02**	up	**1.00**	down	**1.01**	down	**1.04**	up	**3.13**	up	**1.04**	up	SA
Os.26933.1.S1_x_at	LOC_Os10g34840	RIPER6 - Ripening-related family protein precursor, expressed	**1.47**	down	**1.20**	up	**14.73**	down	**2.59**	up	**2.59**	down	**1.65**	down	3
Os.26933.2.S1_x_at	LOC_Os10g34840	RIPER6 - Ripening-related family protein precursor, expressed	**1.63**	down	**1.28**	up	**12.36**	down	**2.47**	up	**2.58**	down	**1.54**	down	3
Os.26938.1.A1_at	LOC_Os02g42150	OsWAK14 - OsWAK receptor-like protein kinase, expressed	**2.50**	up	**1.11**	up	**6.23**	down	**1.42**	down	**1.13**	down	**1.06**	up	2
Os.2694.1.S1_at	LOC_Os04g43200	caleosin related protein, putative, expressed	**1.04**	up	**1.05**	down	**28.46**	up	**1.07**	down	**1.66**	up	**1.20**	up	ABA
Os.26941.1.A1_at	LOC_Os05g07420	S-domain receptor-like protein kinase, putative, expressed	**1.68**	down	**1.49**	up	**15.22**	down	**1.48**	up	**2.06**	down	**1.99**	down	2
Os.26945.1.S1_at	LOC_Os12g17090	stripe rust resistance protein Yr10, putative, expressed	**1.52**	up	**1.41**	up	**3.56**	down	**1.05**	down	**1.40**	down	**1.25**	down	ABA
Os.2696.1.S1_at	LOC_Os04g15840	expansin precursor, putative, expressed	**1.57**	up	**1.29**	up	**1.52**	up	**2.51**	down	**2.03**	down	**1.10**	down	2
Os.26967.1.S1_a_at	LOC_Os01g50616	phosphatidylinositol transfer, putative, expressed	**1.21**	up	**1.20**	down	**7.96**	up	**1.06**	down	**1.38**	up	**1.14**	up	ABA
Os.26967.1.S2_at	LOC_Os01g50616	phosphatidylinositol transfer, putative, expressed	**1.14**	down	**1.37**	down	**14.02**	up	**1.22**	down	**1.34**	up	**1.11**	up	ABA
Os.26968.1.S1_at	LOC_Os06g30179	cytochrome P450, putative, expressed	**1.19**	up	**1.06**	down	**11.83**	up	**1.58**	down	**1.79**	up	**1.58**	down	ABA
Os.26972.1.S1_at	LOC_Os09g38960	potassium transporter, putative, expressed	**1.13**	up	**1.04**	up	**2.49**	up	**1.07**	down	**1.14**	up	**1.51**	up	ABA
Os.26979.1.S1_x_at	LOC_Os12g29950	nodulin, putative, expressed	**1.46**	down	**1.82**	up	**2.47**	down	**1.17**	down	**1.42**	down	**1.01**	down	ABA
Os.27019.1.S1_at	LOC_Os04g43410	Os4bglu18 - monolignol beta-glucoside homologue, expressed	**1.12**	up	**1.45**	up	**2.62**	up	**1.39**	down	**1.04**	up	**1.18**	up	ABA
Os.27027.1.S1_at	LOC_Os09g32010	ternary complex factor MIP1, putative, expressed	**1.05**	down	**1.04**	down	**3.01**	up	**1.17**	down	**1.21**	up	**1.04**	down	ABA
Os.27028.1.A1_at	LOC_Os05g41580	calcium-transporting ATPase, plasma membrane-type, putative, expressed	**1.01**	down	**1.14**	down	**3.48**	down	**1.47**	up	**1.24**	down	**1.51**	down	ABA
Os.27035.1.S1_s_at	LOC_Os01g38229	peptidyl-prolyl isomerase, putative, expressed	**1.22**	up	**1.07**	down	**4.74**	down	**1.14**	up	**1.35**	down	**1.05**	down	ABA
Os.27035.2.S1_s_at	LOC_Os01g38229	peptidyl-prolyl isomerase, putative, expressed	**1.53**	up	**1.07**	up	**4.69**	down	**1.04**	up	**1.35**	down	**1.03**	up	ABA
Os.27041.1.S1_at	LOC_Os02g54580	serine esterase family protein, putative, expressed	**1.00**	down	**1.05**	down	**2.19**	up	**1.12**	up	**1.20**	up	**1.33**	up	ABA
Os.27043.1.A1_at	LOC_Os05g03920	TKL_IRAK_DUF26-lf.3 - DUF26 kinases have homology to DUF26 containing loci, expr	**1.38**	up	**1.32**	up	**24.27**	up	**2.93**	up	**1.86**	up	**3.25**	up	3
Os.27053.3.A1_s_at	LOC_Os11g07200	receptor protein kinase CLAVATA1 precursor, putative, expressed	**1.00**	up	**1.16**	down	**1.74**	down	**2.35**	up	**1.28**	down	**1.13**	down	ACC
Os.27067.2.A1_at	LOC_Os08g02230	FAD-binding and arabino-lactone oxidase domains containing protein, putative, express	**1.43**	down	**1.03**	up	**3.22**	down	**1.09**	up	**1.20**	down	**1.71**	up	ABA
Os.27081.1.A1_at	LOC_Os02g06570	CAMK_KIN1/SNF1/Nim1_like.13 - CAMK includes calcium/calmodulin depedent protein	**1.08**	up	**1.05**	up	**2.71**	up	**1.20**	down	**1.24**	up	**1.05**	down	ABA
Os.27084.1.A1_a_at	LOC_Os04g52640	SHR5-receptor-like kinase, putative, expressed	**2.07**	down	**1.17**	down	**3.26**	down	**1.28**	up	**1.28**	down	**1.42**	down	2
Os.27084.2.S1_a_at	LOC_Os04g52640	SHR5-receptor-like kinase, putative, expressed	**1.62**	down	**1.22**	down	**7.00**	down	**1.33**	up	**1.48**	down	**1.45**	down	ABA
Os.27095.1.A1_at	LOC_Os02g21460	uncharacterized protein yqjG, putative, expressed	**1.33**	up	**1.05**	up	**1.26**	down	**1.37**	up	**2.40**	up	**1.80**	up	SA
Os.27112.1.S1_at	LOC_Os01g09800	BTBA1 - Bric-a-Brac,Tramtrack, Broad Complex BTB domain with Ankyrin repeat region	**1.01**	up	**1.21**	down	**1.91**	down	**1.36**	up	**1.24**	up	**4.51**	up	JA
Os.27118.1.A1_at	LOC_Os06g44050	methyladenine glycosylase, putative, expressed	**2.24**	up	**1.04**	up	**1.63**	down	**1.03**	down	**1.18**	down	**1.07**	up	IAA

Os.27119.1.S1_at	LOC_Os02g55120	translation initiation factor IF-3, putative, expressed	1.11	up	1.03	up	2.94	down	1.22	down	1.58	down	1.46	down	ABA
Os.27144.1.S1_at	AK065548	leucine-rich repeat family protein	1.15	up	1.10	up	4.33	down	1.07	down	1.12	down	1.19	down	ABA
Os.27145.1.S1_at	LOC_Os01g59100	cytokinin-N-glucosyltransferase 1, putative, expressed	1.18	down	1.10	up	6.99	up	1.01	up	3.56	up	1.27	up	2
Os.27161.1.S1_at	LOC_Os01g47460	expressed protein	1.27	up	1.08	down	3.93	up	1.10	up	2.09	up	1.40	up	2
Os.27166.1.A1_s_at	LOC_Os03g04130	AMP-binding domain containing protein, expressed	1.37	down	1.03	down	2.74	up	1.08	up	1.02	down	1.28	down	ABA
Os.27169.1.S1_s_at	LOC_Os01g68740	keratin, type I cytoskeletal 9, putative, expressed	1.77	down	1.38	up	40.28	down	1.14	down	3.21	down	1.34	down	2
Os.27170.1.S1_at	LOC_Os01g50400	STE_MEKK_ste11_MAP3K.5 - STE kinases include homologs to sterile 7, sterile 11 an	1.46	up	1.09	up	56.64	up	1.40	up	1.33	up	1.84	up	ABA
Os.27176.1.S1_at	LOC_Os09g28354	CPuORF39 - conserved peptide uORF-containing transcript, expressed	1.02	up	1.08	up	4.27	up	1.13	down	1.35	up	1.13	up	ABA
Os.27178.1.S1_s_at	LOC_Os04g54474	transcription factor, putative, expressed	1.24	up	3.27	down	1.28	up	1.02	down	1.20	up	1.07	down	BAP
Os.27182.1.A1_at	LOC_Os02g43150	GATA zinc finger domain containing protein, expressed	1.02	up	1.05	up	2.29	up	1.20	up	1.01	down	1.04	up	ABA
Os.27185.1.S1_x_at	LOC_Os07g35750	TKL_IRAK_DUF26-ld.3 - DUF26 kinases have homology to DUF26 containing loci, exp	1.39	down	1.13	down	2.81	down	1.63	up	1.06	down	1.29	up	ABA
Os.27193.1.S1_at	LOC_Os02g58510	GHMP kinases ATP-binding protein, putative	1.03	up	1.02	down	2.01	down	1.22	up	1.04	down	1.35	up	ABA
Os.27198.1.S1_at	LOC_Os02g15690	polygalacturonase, putative, expressed	1.05	down	1.11	up	3.29	down	1.25	down	1.37	down	1.50	down	ABA
Os.27205.1.S1_at	LOC_Os06g48180	glycosyl hydrolases family 16, putative, expressed	1.06	down	1.24	down	3.70	up	1.44	down	1.08	up	1.81	down	ABA
Os.27207.1.S1_at	LOC_Os12g25200	chloride transporter, chloride channel family, putative, expressed	1.10	down	1.23	up	1.92	up	1.39	down	1.31	down	2.03	down	JA
Os.27218.1.A1_at	LOC_Os05g49940	expressed protein	1.04	down	1.36	up	19.91	up	1.17	up	1.39	up	1.27	down	ABA
Os.27220.2.A1_a_at	EU563917	Oryza sativa Japonica Group Pri-miR1850_1, complete sequence.	1.04	up	1.01	down	2.20	down	1.18	up	1.07	up	1.00	down	ABA
Os.27227.1.S1_at	LOC_Os09g16510	OsWRKY74 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.65	down	2.40	up	7.35	down	1.87	up	1.62	down	1.56	up	2
Os.27230.1.A1_at	LOC_Os12g05330	protein of unknown function containing protein, expressed	1.38	up	1.07	down	39.34	up	1.01	down	1.17	up	1.03	up	ABA
Os.27232.1.S1_at	LOC_Os01g68650	plant-specific domain TIGR01615 family protein, expressed	1.17	up	1.64	up	5.36	up	1.41	up	1.36	up	1.59	up	ABA
Os.27238.1.S1_at	LOC_Os10g28970	BTB6 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain, expressed	2.25	down	2.78	up	1.79	down	1.52	up	2.95	down	2.15	down	4
Os.27247.1.S1_at	LOC_Os06g50950	GDSL-like lipase/acylhydrolase, putative, expressed	1.06	up	1.92	up	7.28	down	1.41	up	2.99	down	3.07	up	3
Os.27251.1.S1_at	LOC_Os04g10350	1-aminocyclopropane-1-carboxylate oxidase homolog 2, putative, expressed	1.14	down	2.41	up	1.06	down	1.31	up	1.11	down	3.54	up	2
Os.27255.2.S1_x_at	LOC_Os06g50390	eukaryotic aspartyl protease domain containing protein, expressed	1.14	up	1.22	down	2.96	up	1.20	up	1.16	up	1.23	down	ABA
Os.27277.1.A1_at	AK241848	expressed protein	1.02	down	1.06	up	2.72	up	1.13	up	1.54	up	1.30	up	ABA
Os.27292.1.A1_at	LOC_Os04g44354	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	1.16	down	1.18	down	19.14	down	2.55	up	1.35	down	7.17	up	3
Os.27299.1.A1_at	LOC_Os01g04800	B3 DNA binding domain containing protein, expressed	1.72	down	1.11	down	3.13	down	1.84	up	1.02	up	1.42	up	ABA
Os.27307.1.S1_at	AK241912	Oryza sativa Japonica Group cDNA, clone: J075062C10, full insert sequence.	1.21	down	1.12	up	5.23	up	1.19	down	1.01	up	1.03	up	ABA
Os.27323.1.S1_at	LOC_Os01g22600	mitochondrial carrier protein, putative, expressed	1.32	up	1.04	up	3.33	up	1.01	up	1.40	up	1.14	up	ABA
Os.27323.2.S1_x_at	LOC_Os01g22600	mitochondrial carrier protein, putative, expressed	1.29	up	1.04	up	3.10	up	1.02	down	1.28	up	1.25	up	ABA
Os.27330.1.A1_at	LOC_Os04g49160	zinc finger, C3HC4 type domain containing protein, expressed	1.07	up	1.40	down	2.08	down	1.77	up	1.03	up	4.23	up	2
Os.27354.1.S1_at	LOC_Os09g17600	membrane protein, putative, expressed	1.35	down	1.03	up	3.48	down	1.47	down	1.52	down	1.13	up	ABA
Os.27355.1.A1_at	LOC_Os02g39400	isochorismatase family protein, putative, expressed	1.05	down	1.10	down	2.10	down	1.52	up	1.12	up	1.02	up	ABA
Os.27359.1.S1_at	LOC_Os08g20660	sucrose-phosphate synthase, putative, expressed	1.03	down	1.13	down	2.90	up	1.04	up	1.15	up	1.05	down	ABA
Os.27382.2.S1_at	LOC_Os02g02110	Alg9-like mannosyltransferase protein, putative, expressed	1.02	down	1.05	down	16.75	down	1.49	up	1.78	down	2.79	down	2
Os.27383.2.S1_at	LOC_Os03g48710	expressed protein	1.22	down	1.07	down	3.30	up	1.10	up	1.89	up	1.50	up	ABA
Os.27395.1.S1_a_at	LOC_Os04g57760	expressed protein	1.30	up	1.53	up	3.52	up	1.10	up	1.44	up	1.40	up	ABA
Os.27414.2.S1_x_at	LOC_Os07g39590	spotted leaf 11, putative, expressed	1.28	up	1.02	down	2.24	up	1.07	down	1.03	down	1.04	down	ABA
Os.27417.1.S1_at	LOC_Os01g52170	expressed protein	1.28	up	1.18	down	7.34	down	1.51	down	2.71	down	1.88	down	2
Os.27430.1.S1_at	AK240684	probable cinnamoyl-CoA reductase	1.40	up	1.21	down	4.01	up	1.38	down	1.23	up	1.22	down	ABA
Os.27431.1.A1_at	LOC_Os07g35310	TKL_IRAK_DUF26-lc.12 - DUF26 kinases have homology to DUF26 containing loci, ex	1.07	down	1.01	down	3.33	down	2.49	up	1.13	up	2.29	up	3
Os.27438.1.S1_a_at	LOC_Os08g05320	expressed protein	1.04	up	1.15	down	5.68	up	1.31	up	1.99	up	1.15	up	ABA
Os.27438.2.S1_x_at	LOC_Os08g05320	expressed protein	1.06	down	1.11	down	3.73	up	1.10	up	1.40	up	1.14	up	ABA
Os.27439.2.S1_at	LOC_Os05g34854	gibberellin 20 oxidase 2, putative, expressed	1.04	down	1.27	up	4.60	down	1.65	up	3.80	down	2.28	down	3
Os.27446.1.S1_a_at	LOC_Os03g62580	vacuolar sorting protein, putative, expressed	1.05	up	1.11	down	2.72	up	1.09	down	1.28	up	1.01	up	ABA
Os.27446.2.S1_at	AK065755	vacuolar sorting protein 9 domain-containing protein	1.12	down	1.02	down	3.39	up	1.40	up	1.30	up	1.15	up	ABA
Os.27446.3.S1_x_at	AK065755	vacuolar sorting protein 9 domain-containing protein	1.03	down	1.15	down	2.61	up	1.02	up	1.16	up	1.08	up	ABA
Os.27451.1.S1_at	LOC_Os06g46670	glutamate receptor, putative, expressed	1.41	down	1.33	down	3.25	down	1.16	down	1.49	down	1.56	up	ABA
Os.27489.1.A1_at	LOC_Os01g11120	CID11, putative, expressed	1.00	up	1.06	up	2.09	down	1.05	down	1.32	down	1.15	up	ABA
Os.27494.1.S1_at	LOC_Os07g41200	expressed protein	2.80	up	1.12	up	2.70	down	1.20	up	1.47	up	1.28	down	2
Os.27497.1.S1_at	LOC_Os12g12390	transposon protein, putative, CACTA, En	4.87	down	5.65	up	6.54	down	1.23	up	6.30	down	6.06	down	5
Os.27502.1.S1_at	AK067679	Oryza sativa Japonica Group cDNA clone:J013114G19, full insert sequence.	1.00	down	1.08	up	2.38	up	1.37	up	1.43	up	1.34	up	ABA
Os.27506.1.A1_at	LOC_Os11g15340	SAM dependent carboxyl methyltransferase family protein, putative, expressed	2.17	down	1.14	down	2.73	down	1.00	down	1.50	down	1.16	up	2
Os.27507.1.S1_at	LOC_Os06g35700	reticuline oxidase-like protein precursor, putative, expressed	1.46	down	1.52	up	1.99	down	1.79	up	1.46	up	3.04	up	JA
Os.27522.2.S1_at	LOC_Os03g58330	BHLH transcription factor, putative, expressed	1.16	up	1.19	up	3.19	down	1.43	down	1.42	down	1.83	down	ABA

Os.27524.2.S1_at	LOC_Os09g16920	desaturase/cytochrome b5 protein, putative, expressed	**1.17**	up	**1.02**	down	**3.95**	down	**1.61**	down	**1.81**	down	**1.52**	down	ABA
Os.27525.1.A1_at	LOC_Os09g27500	cytochrome P450, putative, expressed	**1.17**	up	**1.93**	up	**10.71**	down	**1.13**	up	**4.15**	down	**4.00**	down	3
Os.27538.1.S1_at	LOC_Os12g17430	NBS-LRR disease resistance protein, putative, expressed	**1.01**	down	**1.66**	up	**1.78**	down	**1.02**	down	**1.55**	down	**3.21**	up	JA
Os.27552.1.S1_a_at	LOC_Os08g06230	nucleolar GTP-binding protein 1, putative, expressed	**1.16**	up	**1.11**	up	**2.49**	down	**1.19**	down	**1.34**	down	**1.17**	down	ABA
Os.27564.1.S1_a_at	LOC_Os01g52540	B3 DNA binding domain containing protein, expressed	**1.16**	down	**1.28**	up	**5.90**	down	**1.03**	up	**1.88**	down	**1.60**	up	ABA
Os.27569.1.S2_at	LOC_Os09g30490	EF hand family protein, expressed	**1.56**	up	**1.40**	up	**2.31**	up	**1.06**	up	**5.72**	up	**1.93**	up	2
Os.27573.1.S1_at	LOC_Os11g35320	BSD domain-containing protein, putative, expressed	**1.08**	up	**1.13**	down	**2.45**	up	**1.19**	up	**1.23**	up	**1.07**	up	ABA
Os.27577.1.S1_at	LOC_Os01g04880	retrotransposon protein, putative, unclassified, expressed	**1.08**	up	**1.02**	up	**2.42**	down	**1.13**	down	**1.39**	down	**1.35**	down	ABA
Os.27580.1.S1_at	LOC_Os07g37230	inositol-1-monophosphatase, putative, expressed	**1.03**	up	**1.86**	up	**21.55**	down	**1.71**	down	**4.07**	down	**1.15**	down	2
Os.27587.1.S1_at	LOC_Os10g40740	helix-loop-helix DNA-binding domain containing protein, expressed	**1.03**	up	**1.28**	up	**2.93**	down	**1.20**	up	**1.16**	down	**1.00**	up	ABA
Os.2759.1.S1_s_at	LOC_Os10g42299	mitochondrial carrier protein, putative, expressed	**1.37**	up	**1.14**	down	**5.45**	down	**1.28**	down	**1.76**	down	**1.37**	down	ABA
Os.27591.1.A1_at	LOC_Os04g12499	amino acid transporter protein, putative, expressed	**1.34**	up	**1.51**	down	**5.65**	up	**1.54**	down	**1.15**	up	**1.41**	down	ABA
Os.27606.1.S1_at	LOC_Os03g63330	aspartokinase, chloroplast precursor, putative, expressed	**1.19**	down	**1.09**	up	**5.43**	down	**1.26**	down	**1.25**	down	**1.09**	down	ABA
Os.27611.1.S1_s_at	LOC_Os04g10214	expressed protein	**1.34**	down	**1.13**	down	**2.80**	down	**1.19**	up	**1.48**	down	**1.02**	down	ABA
Os.27612.1.S1_at	LOC_Os08g01150	DTA2, putative, expressed	**1.04**	down	**1.11**	down	**3.37**	up	**1.20**	down	**1.56**	up	**1.17**	up	ABA
Os.27624.1.S1_at	LOC_Os03g14590	calcium-binding EF hand family protein, putative, expressed	**1.12**	up	**1.22**	down	**2.37**	up	**1.32**	down	**1.12**	down	**1.20**	up	ABA
Os.27640.1.A1_s_at	LOC_Os12g36680	expressed protein	**1.15**	down	**1.04**	up	**5.13**	up	**1.29**	up	**1.06**	up	**2.61**	up	2
Os.27660.1.S1_at	LOC_Os05g48210	expressed protein	**2.15**	down	**1.40**	down	**4.89**	down	**1.16**	down	**1.67**	down	**1.76**	down	2
Os.27671.1.S1_at	LOC_Os03g17470	IN2-1 protein, putative, expressed	**2.27**	up	**1.02**	down	**1.50**	up	**1.08**	up	**2.98**	up	**1.78**	up	2
Os.27673.1.S1_at	LOC_Os03g14730	gibberellin receptor GID1L2, putative, expressed	**1.00**	up	**1.04**	down	**5.24**	down	**1.29**	up	**1.23**	down	**1.49**	up	ABA
Os.27694.1.S1_at	LOC_Os02g46750	expressed protein	**1.05**	up	**1.10**	up	**2.46**	down	**1.21**	down	**1.36**	down	**1.36**	down	ABA
Os.27696.1.S1_at	LOC_Os11g25260	nucleoside-triphosphatase, putative, expressed	**1.11**	down	**1.01**	up	**2.64**	down	**1.03**	up	**1.38**	down	**1.56**	up	ABA
Os.27701.1.A1_at	LOC_Os07g45000	cytochrome P450, putative, expressed	**1.05**	down	**1.20**	down	**4.54**	up	**1.12**	down	**1.52**	up	**1.39**	up	ABA
Os.27703.1.S1_a_at	LOC_Os09g13650	microtubule-associated protein, putative, expressed	**1.01**	down	**1.13**	down	**12.15**	down	**1.14**	down	**1.34**	down	**1.41**	up	ABA
Os.27703.1.S1_s_at	LOC_Os09g13650	microtubule-associated protein, putative, expressed	**1.26**	up	**1.01**	up	**11.78**	down	**1.20**	down	**1.39**	down	**1.14**	up	ABA
Os.27712.2.S1_x_at	LOC_Os06g48510	choline monooxygenase, chloroplast precursor, putative, expressed	**1.02**	up	**1.06**	up	**2.16**	up	**1.09**	up	**1.33**	up	**1.35**	down	ABA
Os.27730.1.S1_at	LOC_Os08g37700	RNA recognition motif containing protein, putative, expressed	**1.18**	up	**1.17**	up	**2.37**	down	**1.33**	down	**1.71**	down	**1.40**	down	ABA
Os.27755.1.S1_at	LOC_Os07g35560	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	**1.90**	down	**1.45**	up	**2.94**	down	**1.55**	up	**1.85**	down	**1.57**	up	ABA
Os.27756.1.S1_at	LOC_Os06g49640	uncharacterized UPF0114 domain containing protein, expressed	**1.43**	up	**1.62**	down	**2.37**	up	**1.51**	up	**1.30**	up	**1.45**	down	ABA
Os.27767.1.A1_s_at	LOC_Os04g29680	OsWAK38 - OsWAK receptor-like protein kinase, expressed	**1.13**	down	**1.26**	down	**2.82**	down	**2.49**	up	**1.94**	up	**1.69**	down	2
Os.27773.1.S1_at	LOC_Os04g52600	SHR5-receptor-like kinase, putative, expressed	**1.23**	down	**1.17**	down	**2.39**	down	**1.45**	up	**1.04**	down	**1.43**	up	ABA
Os.27788.1.S1_at	LOC_Os06g41450	VQ domain containing protein, putative, expressed	**1.10**	down	**1.51**	down	**3.27**	down	**1.56**	up	**1.24**	up	**1.38**	down	ABA
Os.27789.1.A1_at	LOC_Os06g20150	peroxidase precursor, putative, expressed	**1.82**	down	**1.34**	down	**9.04**	down	**1.43**	up	**2.21**	down	**2.30**	down	3
Os.27796.1.A1_at	LOC_Os07g26210	non-lysosomal glucosylceramidase, putative, expressed	**1.22**	up	**1.18**	up	**3.16**	up	**1.19**	up	**1.11**	up	**1.18**	up	ABA
Os.27802.1.S1_s_at	LOC_Os02g43850	serine esterase family protein, putative, expressed	**1.04**	up	**1.11**	up	**2.80**	up	**1.04**	down	**1.09**	up	**1.14**	down	ABA
Os.27804.1.S1_at	LOC_Os08g10310	SHR5-receptor-like kinase, putative, expressed	**1.02**	down	**1.93**	up	**9.09**	down	**2.62**	up	**1.75**	down	**1.01**	down	2
Os.27820.1.S1_at	LOC_Os01g43410	CAMK_CAMK_like.9 - CAMK includes calcium/calmodulin depedent protein kinases, ex	**1.10**	down	**1.19**	down	**2.63**	down	**1.02**	up	**1.50**	down	**1.46**	down	ABA
Os.27822.2.S1_at	LOC_Os04g47520	growth regulator related protein, putative, expressed	**1.24**	down	**1.09**	down	**3.33**	up	**1.04**	down	**1.17**	up	**1.37**	up	ABA
Os.27837.1.S1_at	LOC_Os06g37450	GATA zinc finger domain containing protein, expressed	**1.06**	down	**1.81**	up	**3.97**	down	**1.13**	down	**2.07**	down	**3.38**	down	3
Os.27837.2.S1_x_at	LOC_Os06g37450	GATA zinc finger domain containing protein, expressed	**1.02**	down	**1.75**	up	**3.79**	down	**1.11**	up	**1.46**	down	**1.72**	down	ABA
Os.27860.1.A1_at	LOC_Os01g53710	dual specificity protein phosphatase, putative, expressed	**1.30**	down	**1.28**	down	**1.97**	up	**1.09**	up	**1.18**	up	**3.02**	up	JA
Os.27874.2.S1_x_at	LOC_Os05g48840	expressed protein	**1.00**	down	**1.16**	up	**4.88**	up	**1.06**	down	**1.52**	down	**1.40**	down	ABA
Os.27875.1.S1_at	LOC_Os10g28120	glycosyl hydrolase, putative, expressed	**1.47**	down	**2.74**	up	**3.58**	up	**1.11**	down	**1.15**	up	**1.58**	down	2
Os.27906.1.S1_a_at	LOC_Os01g62760	protein phosphatase 2C, putative, expressed	**2.21**	up	**1.20**	down	**25.53**	up	**1.38**	down	**3.43**	up	**1.63**	up	3
Os.27914.1.S1_at	LOC_Os08g02390	RNA recognition motif containing protein, putative, expressed	**1.22**	up	**1.27**	up	**3.58**	down	**1.14**	down	**1.49**	down	**1.07**	down	ABA
Os.27918.1.A1_at	LOC_Os03g05530	nodulin, putative, expressed	**1.62**	down	**1.02**	down	**28.27**	down	**1.22**	down	**3.39**	down	**1.60**	down	2
Os.27926.1.A1_s_at	LOC_Os07g48460	stress responsive protein, putative, expressed	**1.12**	up	**1.10**	up	**3.37**	up	**1.05**	down	**1.03**	up	**1.14**	down	ABA
Os.27932.1.S1_at	LOC_Os01g68580	LTPL38 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.65**	down	**1.33**	down	**13.57**	down	**1.82**	down	**3.92**	down	**3.85**	down	3
Os.27943.1.S1_a_at	LOC_Os01g50030	CPuORF25 - conserved peptide uORF-containing transcript, expressed	**1.24**	down	**1.88**	up	**4.53**	up	**1.24**	down	**1.42**	down	**1.41**	down	ABA
Os.27943.1.S1_s_at	LOC_Os01g50030	CPuORF25 - conserved peptide uORF-containing transcript, expressed	**1.06**	up	**2.09**	up	**3.87**	up	**1.08**	down	**1.40**	down	**1.62**	down	2
Os.27956.1.S1_at	LOC_Os03g06360	late embryogenesis abundant protein D-34, putative, expressed	**1.74**	up	**1.29**	down	**34.05**	up	**1.00**	down	**1.01**	down	**1.02**	up	ABA
Os.27967.1.A1_at	LOC_Os01g63620	expressed protein	**1.19**	up	**1.01**	down	**4.69**	down	**1.39**	down	**1.50**	down	**1.06**	down	ABA
Os.27979.1.S1_at	LOC_Os03g50120	zinc finger family protein, putative, expressed	**1.06**	up	**1.01**	up	**2.15**	down	**1.21**	up	**1.33**	down	**1.35**	down	ABA
Os.27990.1.S1_at	LOC_Os07g01620	dirigent, putative, expressed	**1.28**	down	**1.30**	down	**4.17**	down	**1.47**	down	**1.67**	up	**1.16**	up	ABA
Os.27991.1.S1_at	LOC_Os09g17850	acetyltransferase type B catalytic subunit, putative, expressed	**1.03**	up	**1.13**	up	**3.68**	down	**1.08**	down	**1.95**	down	**1.77**	down	ABA

Os.280.1.S1_at	LOC_Os04g32670	exostosin family domain containing protein, expressed	1.10	up	1.09	up	2.14	up	1.03	down	1.22	up	1.13	down	ABA
Os.280.1.S2_at	LOC_Os04g32680	POEI20 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.11	down	1.13	down	4.32	up	1.01	up	1.16	up	1.57	down	ABA
Os.28002.1.S1_at	LOC_Os08g35710	expressed protein	1.04	up	1.06	down	3.77	down	1.42	down	1.96	down	1.76	up	ABA
Os.28030.1.S1_at	LOC_Os06g48160	glycosyl hydrolases family 16, putative, expressed	1.12	up	1.21	down	3.07	up	1.41	down	1.19	up	1.26	down	ABA
Os.28030.1.S1_s_at	LOC_Os06g48160	glycosyl hydrolases family 16, putative, expressed	1.08	up	1.05	down	2.52	up	1.24	down	1.32	up	1.03	down	ABA
Os.28030.2.A1_at	LOC_Os06g48160	glycosyl hydrolases family 16, putative, expressed	1.45	up	1.26	down	4.32	up	1.07	up	1.06	up	1.49	down	ABA
Os.28032.1.A1_at	LOC_Os01g21070	endoglucanase, putative, expressed	1.33	down	1.40	down	2.65	down	1.06	down	1.34	down	1.48	down	ABA
Os.28042.1.S1_a_at	LOC_Os04g35560	glutathione S-transferase, putative, expressed	1.15	up	1.12	down	2.88	up	1.01	up	1.26	up	1.14	up	ABA
Os.28078.1.S1_at	LOC_Os01g71050	MSP domain containing protein, putative, expressed	1.20	down	1.15	down	2.18	down	1.21	down	1.31	down	1.04	down	ABA
Os.28080.1.A1_at	AK060371	probable (S)-2-hydroxy-acid oxidase (EC 1.1.3.15), peroxisomal	1.13	down	1.16	down	2.76	up	1.05	down	1.02	down	1.01	down	ABA
Os.28087.1.S1_s_at	LOC_Os10g39440	transporter family protein, putative, expressed	1.50	down	1.18	down	2.62	up	1.03	down	1.10	up	1.20	down	ABA
Os.28096.1.S1_at	LOC_Os05g43170	calreticulin precursor protein, putative, expressed	1.11	down	1.01	up	2.42	down	1.13	up	1.01	down	1.03	down	ABA
Os.28098.1.S1_at	LOC_Os10g32810	beta-amylase, putative, expressed	1.17	up	1.15	down	83.38	up	1.15	up	1.74	up	3.47	down	2
Os.28110.4.S1_x_at	AK068693	L-asparaginase, putative	3.30	up	1.54	up	1.65	down	1.42	down	1.60	up	1.51	up	IAA
Os.28127.1.S1_at	LOC_Os03g12900	squalene monooxygenase, putative, expressed	1.05	down	1.22	down	1.25	up	1.12	up	1.51	down	2.73	down	JA
Os.28129.1.S1_at	LOC_Os05g42040	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	1.10	up	1.45	down	4.57	up	1.28	down	1.07	down	1.13	down	ABA
Os.28148.1.S1_at	LOC_Os03g11440	protein transport protein Sec61 subunit alpha, putative, expressed	1.20	down	1.05	down	2.21	down	1.23	up	1.28	down	1.22	up	ABA
Os.28176.1.S1_at	LOC_Os01g61680	expressed protein	1.09	up	1.03	up	5.06	up	1.05	up	1.80	up	1.10	up	ABA
Os.28192.1.S1_at	LOC_Os12g42850	amino acid permease, putative, expressed	1.15	up	1.17	down	2.26	up	1.04	up	1.27	up	1.40	up	ABA
Os.2820.1.A1_at	LOC_Os03g56900	reticulon domain containing protein, putative, expressed	1.02	down	1.10	up	3.15	down	1.14	down	1.51	down	2.14	up	2
Os.28200.1.S1_x_at	LOC_Os03g61160	expressed protein	3.03	up	1.33	up	194.40	up	1.31	up	16.04	up	1.73	down	3
Os.28217.1.S1_at	LOC_Os01g62810	regulator of chromosome condensation, putative, expressed	1.36	down	1.09	down	2.06	up	1.48	up	1.25	up	1.01	down	ABA
Os.28229.2.S1_x_at	LOC_Os01g52770	GDSL-like lipase/acylhydrolase, putative, expressed	1.28	up	1.06	down	2.73	down	1.51	down	1.13	down	1.58	up	ABA
Os.28320.1.S1_at	LOC_Os05g38710	lipin, N-terminal conserved region family protein, expressed	1.01	up	1.11	down	4.51	up	1.16	up	1.67	up	1.52	up	ABA
Os.28385.1.S1_x_at	LOC_Os11g02300	CPuORF36 - conserved peptide uORF-containing transcript, expressed	1.13	up	1.00	up	2.38	up	1.44	down	1.49	up	1.10	down	ABA
Os.28385.2.S1_a_at	LOC_Os11g02300	CPuORF36 - conserved peptide uORF-containing transcript, expressed	1.20	down	1.13	down	2.92	up	1.44	down	1.60	up	1.13	down	ABA
Os.28394.2.S1_s_at	LOC_Os05g38680	plant-specific domain TIGR01589 family protein, expressed	1.23	down	1.19	up	4.76	up	1.06	down	2.45	down	1.02	down	2
Os.28404.1.A1_at	LOC_Os03g07190	expressed protein	1.12	up	1.08	down	3.64	up	1.10	up	1.45	up	1.38	up	ABA
Os.28406.1.S1_at	LOC_Os09g11480	AP2 domain containing protein, expressed	1.22	down	1.30	up	2.66	down	2.97	up	1.33	down	2.12	down	3
Os.28409.20.A1_a_at	LOC_Os05g03480	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed	1.10	up	1.13	down	2.95	up	1.26	up	1.90	up	1.30	up	ABA
Os.28409.4.S1_s_at	LOC_Os03g29830	expressed protein	1.07	down	1.08	down	2.02	down	1.31	up	1.00	up	1.17	up	ABA
Os.28418.1.S1_a_at	LOC_Os06g41360	phosphoribosyl transferase, putative, expressed	1.20	up	1.11	up	2.77	up	1.11	up	1.42	up	1.67	up	ABA
Os.28421.1.S1_at	LOC_Os09g36240	deoxyribodipyrimidine photolyase family protein, expressed	1.26	up	1.14	up	4.59	down	1.53	down	1.95	down	1.70	down	ABA
Os.28422.1.S1_at	LOC_Os04g51610	calcium-transporting ATPase, plasma membrane-type, putative, expressed	1.09	down	1.09	up	20.08	up	1.23	down	1.48	up	1.06	down	ABA
Os.28427.1.S1_x_at	LOC_Os05g12640	BURP domain containing protein, expressed	1.80	up	3.73	up	5.77	down	5.70	down	4.25	down	7.60	down	5
Os.28435.4.S1_at	LOC_Os10g40934	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	2.45	down	1.03	down	1.64	down	1.50	up	1.11	up	1.18	up	IAA
Os.28441.1.S1_at	LOC_Os03g60560	ZOS3-21 - C2H2 zinc finger protein, expressed	1.19	down	1.50	down	16.50	up	1.06	down	1.76	up	1.02	up	ABA
Os.28450.1.S1_at	LOC_Os01g70730	flowering promoting factor-like 1, putative, expressed	1.19	down	1.13	up	5.54	down	1.07	up	1.46	down	1.02	down	ABA
Os.28457.1.S1_at	LOC_Os11g48070	GDSL-like lipase/acylhydrolase, putative, expressed	1.03	up	1.09	up	2.02	down	1.15	down	1.18	down	1.20	down	ABA
Os.28489.1.S1_at	LOC_Os01g52030	zinc finger A20 and AN1 domain-containing stress-associated protein, putative, express	1.11	up	1.07	down	3.88	up	1.75	up	1.36	up	1.06	down	ABA
Os.28539.1.S1_at	LOC_Os05g25040	expressed protein	1.47	down	1.63	down	30.27	up	1.30	up	1.92	up	1.12	up	ABA
Os.28617.1.S1_at	LOC_Os02g57840	remorin C-terminal domain containing protein, putative, expressed	1.42	down	1.49	down	305.56	up	2.47	down	1.29	up	1.60	down	2
Os.2867.1.A1_at	LOC_Os11g45740	MYB family transcription factor, putative, expressed	1.21	down	2.34	down	2.05	up	1.47	up	1.64	up	6.97	up	3
Os.28679.1.S1_at	LOC_Os07g45370	expressed protein	1.46	up	1.23	down	11.01	up	1.39	up	1.75	up	1.08	down	ABA
Os.28773.1.S1_at	LOC_Os01g14650	expansin precursor, putative, expressed	1.77	down	1.44	up	9.99	down	1.15	down	1.15	down	1.72	down	ABA
Os.28798.1.S1_at	CT833215	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSA047I02, full insert sequence.	1.07	up	1.28	up	4.59	up	1.08	down	1.02	down	1.36	down	ABA
Os.2881.1.S1_at	LOC_Os10g40360	proline oxidase, mitochondrial precursor, putative, expressed	1.36	up	1.24	up	3.87	down	1.33	up	2.08	up	4.62	up	3
Os.28823.1.S1_at	LOC_Os01g37750	glutathione S-transferase, putative, expressed	1.22	down	1.25	down	3.33	up	1.25	down	1.08	up	1.07	up	ABA
Os.28909.1.S1_at	LOC_Os01g45460	serine esterase, putative, expressed	1.18	up	1.00	down	3.59	up	1.00	down	1.00	down	1.01	up	ABA
Os.28952.1.S1_at	LOC_Os01g08810	cytochrome P450, putative, expressed	1.21	down	1.14	down	2.45	up	1.24	down	1.21	up	1.02	down	ABA
Os.28964.1.S1_at	LOC_Os01g42790	xylem cysteine proteinase 2 precursor, putative, expressed	1.03	down	1.33	down	3.14	down	1.17	down	1.08	down	1.34	down	ABA
Os.28988.1.S1_at	LOC_Os01g73530	ABC transporter, ATP-binding protein, putative, expressed	1.00	down	1.19	down	2.07	up	1.18	up	1.72	up	1.17	up	ABA
Os.28994.1.S1_at	LOC_Os01g67390	POEI32 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.22	down	1.12	down	1.45	down	1.36	up	2.56	down	1.42	up	SA
Os.29062.1.S1_at	LOC_Os01g05150	expressed protein	1.01	down	1.11	down	3.81	up	1.36	up	1.03	up	1.11	up	ABA
Os.29084.1.S1_at	LOC_Os01g53650	zinc finger CCCH type family protein, putative, expressed	1.01	down	1.00	up	138.72	up	1.19	up	1.49	up	1.03	up	ABA

Os.29093.1.S1_at	LOC_Os07g14600	hydrolase, putative, expressed	1.04	up	1.07	up	7.89	up	1.01	down	1.69	up	1.12	up	ABA
Os.29115.1.S1_at	LOC_Os01g02120	osMFT2 MFT-Like2 homologous to Mother of FT and TFL1 gene; contains Pfam profil	1.01	down	1.00	up	17.10	up	1.01	up	1.67	up	1.12	up	ABA
Os.2914.1.S1_at	LOC_Os07g44330	kinase, putative, expressed	1.32	up	1.37	down	3.28	up	1.08	down	1.07	down	1.06	down	ABA
Os.2915.1.S1_at	AK243113	Oryza sativa Japonica Group cDNA, clone: J100027C20, full insert sequence.	1.69	up	1.08	down	4.51	up	1.18	down	2.15	up	2.07	up	2
Os.2919.1.S1_s_at	LOC_Os05g05830	bifunctional protein folD, putative, expressed	1.04	up	1.01	up	2.43	down	1.23	down	1.37	down	1.19	down	ABA
Os.29290.1.S1_at	LOC_Os01g08780	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	1.88	down	1.32	down	12.26	up	2.15	down	1.38	up	4.77	up	3
Os.29377.1.S1_at	LOC_Os06g22290	legume lectins beta domain containing protein, expressed	2.09	down	1.11	down	4.61	down	1.60	up	1.11	down	1.04	down	2
Os.2938.1.S1_at	LOC_Os10g39640	expansin precursor, putative, expressed	1.05	up	1.55	up	13.50	up	1.29	down	1.30	down	2.28	down	2
Os.2938.1.S1_x_at	LOC_Os10g39640	expansin precursor, putative, expressed	1.13	up	1.27	up	9.46	up	1.09	up	1.01	down	1.37	down	ABA
Os.2957.1.S1_at	LOC_Os03g25330	peroxidase precursor, putative, expressed	1.42	down	1.30	down	13.01	down	1.49	up	2.09	down	1.84	up	2
Os.29815.1.S1_at	NM_001052010	Oryza sativa (japonica cultivar-group) Os01g0962100 (Os01g0962100) mRNA, comple	1.02	up	1.00	up	41.02	up	1.04	up	3.39	up	1.56	down	2
Os.29815.2.S1_x_at	LOC_Os01g73110	expressed protein	1.58	up	1.30	down	25.19	up	1.02	up	1.33	up	1.02	up	ABA
Os.29823.2.S1_x_at	LOC_Os01g04160	expressed protein	1.21	down	1.45	down	6.83	up	1.51	down	1.21	down	1.02	up	ABA
Os.29823.3.S1_at	LOC_Os01g04160	expressed protein	1.23	down	1.21	down	6.56	up	1.04	down	1.03	down	1.69	up	ABA
Os.29826.2.S1_at	LOC_Os01g53990	pectinesterase, putative, expressed	1.31	up	1.14	down	3.01	down	1.06	up	2.56	down	1.13	down	2
Os.29842.1.S1_x_at	LOC_Os01g50820	transporter, major facilitator family, putative, expressed	1.35	down	1.85	down	6.40	down	1.12	down	2.43	down	6.75	down	3
Os.29865.1.S1_at	LOC_Os01g56570	xylosyltransferase, putative, expressed	9.89	up	1.82	up	5.02	up	1.23	down	5.08	up	1.49	up	3
Os.29933.1.S1_at	LOC_Os07g44910	gibberellin receptor GID1L2, putative, expressed	1.05	down	1.01	down	1.34	up	1.06	down	1.00	down	4.08	up	JA
Os.29958.1.S1_at	LOC_Os07g36400	expressed protein	1.32	up	1.03	up	5.16	up	1.06	down	1.02	up	1.20	down	ABA
Os.29959.1.S1_at	LOC_Os07g01810	potassium channel protein, putative, expressed	1.15	up	1.22	down	9.09	up	1.24	down	1.19	down	1.10	up	ABA
Os.29979.1.S1_at	LOC_Os01g09100	OsWRKY10 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.65	down	1.00	up	1.12	down	2.36	up	1.54	up	13.19	up	2
Os.30033.1.S1_at	LOC_Os01g65260	amidophosphoribosyltransferase, chloroplast precursor, putative, expressed	1.13	up	1.00	down	3.47	down	1.76	up	1.27	down	1.05	down	ABA
Os.30044.1.S1_a_at	LOC_Os01g01870	helix-loop-helix DNA-binding domain containing protein, expressed	1.30	up	1.10	down	2.07	down	1.43	down	1.38	down	4.54	up	2
Os.30049.1.S1_at	LOC_Os03g25960	RNA recognition motif containing protein, putative, expressed	1.21	up	1.11	up	3.46	down	1.15	down	1.79	down	1.13	down	ABA
Os.30054.1.S1_at	AK109381	probable peroxidase [imported] - Arabidopsis thaliana	1.05	up	1.16	down	3.40	down	1.13	down	1.79	down	1.46	down	ABA
Os.30063.1.S1_at	LOC_Os05g45450	DUF584 domain containing protein, putative, expressed	1.49	up	1.21	up	4.91	up	1.02	down	1.58	up	1.00	down	ABA
Os.30245.1.S1_at	LOC_Os08g06320	DNA binding protein, putative, expressed	1.20	down	1.16	down	2.67	down	1.14	up	1.49	up	1.07	up	ABA
Os.30324.2.S1_x_at	LOC_Os01g44250	CBS domain containing membrane protein, putative, expressed	1.00	down	1.00	up	157.91	up	1.00	up	1.00	up	1.02	up	ABA
Os.30428.1.S1_at	AK108858	Oryza sativa (japonica cultivar-group) Os01g0288800 (Os01g0288800) mRNA, comple	1.01	down	1.01	up	5.28	up	1.00	up	1.00	down	1.03	up	ABA
Os.30473.1.S1_at	LOC_Os01g11150	gibberellin 2-beta-dioxygenase, putative, expressed	1.21	down	2.19	up	6.73	up	3.39	up	1.52	up	3.06	up	4
Os.3048.1.S1_at	LOC_Os10g40600	peptide transporter PTR2, putative, expressed	1.45	up	1.02	up	6.93	up	1.33	down	2.09	up	1.42	down	2
Os.3048.2.S1_x_at	LOC_Os10g40600	peptide transporter PTR2, putative, expressed	1.18	up	1.17	down	4.89	up	1.10	down	1.63	up	1.10	down	ABA
Os.30512.1.S1_at	LOC_Os01g43650	OsWRKY11 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.51	up	2.42	up	1.06	up	1.26	up	3.59	up	3.32	up	3
Os.30516.1.S1_at	LOC_Os01g67360	methyltransferase, putative, expressed	1.35	down	1.55	down	13.01	down	1.37	down	1.40	down	1.67	down	ABA
Os.30528.1.S1_at	LOC_Os08g31860	expressed protein	1.01	down	1.00	down	15.69	up	1.02	down	1.50	up	1.14	up	ABA
Os.30567.1.S1_at	AK108658	probable zinc finger protein	1.88	down	1.17	up	5.04	down	1.11	down	1.89	down	1.07	down	ABA
Os.30593.1.S1_at	LOC_Os01g71070	xylanase inhibitor, putative, expressed	1.05	down	1.19	down	1.54	up	2.08	down	1.67	down	6.42	up	2
Os.30608.1.S1_at	LOC_Os10g10180	methyltransferase domain containing protein, putative, expressed	1.02	down	1.00	up	2.29	down	1.04	down	1.30	down	1.25	down	ABA
Os.30670.2.S1_x_at	LOC_Os07g22730	AP2 domain containing protein, expressed	12.66	up	1.96	up	1.03	up	1.07	down	3.19	up	1.13	up	2
Os.30866.1.S1_at	LOC_Os07g02460	expressed protein	1.23	down	1.11	up	1.42	up	2.08	down	1.53	up	1.73	up	ACC
Os.30886.1.S1_at	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed	1.36	up	1.05	up	3.08	up	1.42	up	10.30	up	2.79	up	3
Os.30886.1.S1_x_at	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed	2.55	up	1.05	up	2.63	up	1.45	up	14.24	up	2.94	up	4
Os.30886.2.S1_x_at	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed	2.65	up	1.03	up	2.95	up	1.80	up	14.39	up	3.81	up	4
Os.30886.3.S1_x_at	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed	2.76	up	1.12	up	2.27	up	1.33	up	9.40	up	2.95	up	4
Os.30962.1.S1_at	LOC_Os02g35000	chaperone protein dnaJ 10, putative, expressed	1.06	down	1.33	down	2.06	up	1.22	down	1.04	up	1.68	down	ABA
Os.31021.1.S1_at	LOC_Os07g36430	expressed protein	11.04	up	1.10	down	12.48	up	1.07	down	1.63	up	1.26	down	2
Os.31022.1.S1_at	LOC_Os06g02040	late embryogenesis abundant group 1, putative, expressed	1.00	up	1.01	up	664.16	up	1.26	up	1.01	up	1.04	up	ABA
Os.31089.1.S1_at	LOC_Os03g02400	plastocyanin-like domain containing protein, putative, expressed	1.32	down	1.48	up	2.12	down	1.18	down	2.06	down	1.74	down	2
Os.31128.1.S1_x_at	LOC_Os01g60350	hypothetical protein	1.02	down	1.18	down	3.84	up	1.11	up	1.02	up	1.06	down	ABA
Os.31128.2.S1_at	LOC_Os01g60350	hypothetical protein	1.02	up	1.06	down	7.16	up	1.18	up	1.19	up	1.37	up	ABA
Os.31147.1.S1_at	LOC_Os03g06610	expressed protein	1.40	down	1.27	down	1.77	down	1.35	up	1.03	up	2.94	down	JA
Os.31151.2.S1_at	LOC_Os03g59180	expressed protein	1.66	up	1.45	down	2.56	up	1.31	up	1.04	up	1.11	up	ABA
Os.31171.1.S1_at	LOC_Os01g40290	expressed protein	1.31	up	1.80	up	1.20	up	4.13	up	3.48	up	2.78	down	3
Os.31185.1.S1_at	LOC_Os01g13950	OsGrx_A1 - glutaredoxin subgroup III, expressed	1.48	up	1.17	down	5.06	up	1.01	down	4.90	up	2.79	up	3
Os.3121.1.S1_at	LOC_Os10g28050	chitinase 2, putative, expressed	1.01	up	1.48	up	2.47	down	1.12	down	1.25	down	1.08	down	ABA

Os.31293.1.S1_at	LOC_Os01g70500	expressed protein	**1.01**	up	**1.31**	down	**9.18**	up	**1.10**	down	**1.05**	down	**1.73**	down	ABA
Os.31303.1.S1_at	LOC_Os03g08930	helix-loop-helix DNA-binding protein, putative, expressed	**1.67**	down	**3.47**	up	**2.74**	down	**1.28**	up	**1.07**	down	**1.95**	down	2
Os.31379.1.S1_s_at	LOC_Os10g41560	expressed protein	**1.13**	down	**1.03**	down	**5.71**	up	**1.04**	up	**1.30**	up	**1.12**	down	ABA
Os.31415.1.S1_at	LOC_Os10g13810	glycosyltransferase family 43 protein, putative, expressed	**1.07**	down	**1.26**	down	**4.43**	up	**1.24**	up	**1.16**	up	**1.02**	up	ABA
Os.31430.1.S1_at	LOC_Os07g13830	OsFBX228 - F-box domain containing protein, expressed	**1.00**	up	**1.00**	up	**3.77**	up	**1.00**	down	**1.02**	down	**1.01**	up	ABA
Os.31464.1.S1_a_at	LOC_Os04g44530	expressed protein	**1.47**	down	**1.04**	up	**11.38**	up	**1.04**	down	**1.70**	up	**1.07**	up	ABA
Os.315.1.S1_at	LOC_Os03g39710	transporter family protein, putative, expressed	**1.07**	down	**1.18**	down	**2.34**	up	**1.53**	down	**1.42**	up	**1.26**	down	ABA
Os.31636.1.S1_at	LOC_Os08g32960	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	**1.01**	down	**1.08**	down	**7.23**	up	**1.09**	down	**1.30**	down	**1.38**	down	ABA
Os.31693.2.S1_at	LOC_Os01g48830	expressed protein	**1.03**	up	**1.01**	up	**3.87**	up	**1.08**	up	**1.05**	up	**1.04**	up	ABA
Os.31693.3.S1_at	LOC_Os01g48830	expressed protein	**1.01**	down	**1.09**	down	**2.49**	up	**1.01**	down	**1.09**	up	**1.03**	up	ABA
Os.31716.2.A1_at	LOC_Os06g01620	scarecrow, putative, expressed	**1.36**	down	**1.17**	down	**5.48**	down	**1.31**	down	**1.20**	down	**1.17**	down	ABA
Os.31771.2.S1_at	LOC_Os03g51479	maf, putative, expressed	**1.34**	down	**1.12**	up	**1.97**	up	**1.81**	up	**4.11**	up	**1.18**	up	SA
Os.31771.2.S1_x_at	LOC_Os03g51479	maf, putative, expressed	**1.26**	down	**1.21**	down	**1.51**	up	**1.63**	up	**4.82**	up	**1.22**	down	SA
Os.31838.1.S1_at	LOC_Os03g24870	transporter family protein, putative, expressed	**1.15**	up	**1.12**	down	**3.63**	down	**1.22**	down	**1.74**	down	**1.56**	up	ABA
Os.31867.1.S1_at	LOC_Os09g39020	N-rich protein, putative, expressed	**1.22**	down	**1.31**	down	**6.21**	up	**1.20**	up	**1.35**	up	**1.29**	down	ABA
Os.31908.1.S1_at	LOC_Os01g12440	AP2 domain containing protein, expressed	**3.31**	up	**1.19**	up	**1.01**	up	**1.36**	up	**1.51**	up	**1.08**	up	IAA
Os.31975.1.S1_at	LOC_Os05g10670	zinc finger CCCH type family protein, putative, expressed	**1.29**	up	**1.25**	down	**13.98**	up	**1.07**	down	**1.06**	up	**1.24**	down	ABA
Os.31975.1.S1_x_at	LOC_Os05g10670	zinc finger CCCH type family protein, putative, expressed	**1.27**	up	**1.16**	down	**10.73**	up	**1.06**	down	**1.04**	up	**1.37**	down	ABA
Os.31991.1.S1_s_at	LOC_Os11g02290	expressed protein	**1.24**	up	**1.44**	up	**5.70**	up	**1.27**	down	**1.70**	up	**2.51**	down	2
Os.32022.1.S1_x_at	LOC_Os07g37620	fiber expressed protein, putative, expressed	**1.04**	up	**1.27**	up	**2.27**	up	**1.09**	up	**1.35**	down	**1.31**	down	ABA
Os.3206.1.S1_at	LOC_Os10g32980	CESA7 - cellulose synthase, expressed	**1.02**	up	**1.22**	up	**2.61**	down	**1.32**	down	**1.91**	down	**1.07**	down	ABA
Os.32078.1.S1_at	LOC_Os01g51140	helix-loop-helix DNA-binding domain containing protein, expressed	**1.58**	down	**2.42**	up	**2.21**	down	**1.77**	up	**2.30**	down	**2.08**	down	4
Os.32115.1.S1_at	LOC_Os01g71350	glycosyl hydrolases family 17, putative, expressed	**1.40**	down	**1.63**	down	**3.06**	down	**1.26**	up	**1.61**	down	**1.80**	up	ABA
Os.32126.1.S1_x_at	LOC_Os03g54050	anther-specific proline-rich protein APG precursor, putative, expressed	**1.04**	up	**1.18**	down	**2.02**	up	**1.01**	up	**1.06**	up	**1.40**	up	ABA
Os.32153.1.S1_at	LOC_Os01g61440	expressed protein	**2.44**	up	**1.19**	down	**1.68**	up	**1.11**	up	**1.63**	up	**1.66**	up	IAA
Os.32192.1.S1_at	LOC_Os01g67090	IQ calmodulin-binding motif domain containing protein, expressed	**1.17**	up	**1.06**	down	**2.18**	down	**1.59**	down	**1.24**	down	**1.10**	down	ABA
Os.32252.1.S1_at	LOC_Os01g48446	no apical meristem protein, putative, expressed	**1.06**	down	**1.09**	down	**2.45**	up	**1.14**	up	**1.51**	up	**1.15**	up	ABA
Os.32272.1.S1_s_at	LOC_Os01g28690	nucleoporin autopeptidase domain containing protein, expressed	**1.06**	down	**1.19**	up	**2.87**	up	**1.25**	down	**1.02**	down	**1.59**	down	ABA
Os.32272.1.S1_x_at	LOC_Os01g28690	nucleoporin autopeptidase domain containing protein, expressed	**1.25**	up	**1.09**	up	**3.15**	up	**1.03**	up	**1.08**	up	**1.05**	down	ABA
Os.32279.1.S1_at	LOC_Os01g63400	PPR repeat containing protein, expressed	**1.04**	up	**1.24**	down	**2.67**	up	**1.20**	up	**1.14**	up	**1.04**	up	ABA
Os.32292.1.S1_at	LOC_Os01g36240	peroxidase precursor, putative, expressed	**1.14**	down	**2.29**	up	**1.11**	down	**1.15**	down	**1.28**	down	**1.35**	up	BAP
Os.32314.1.S1_at	LOC_Os08g32910	expressed protein	**1.27**	down	**1.11**	down	**3.62**	down	**1.09**	down	**1.75**	down	**1.15**	down	ABA
Os.32357.1.S1_at	LOC_Os07g46950	ligA, putative, expressed	**1.01**	up	**1.03**	down	**47.66**	up	**1.02**	up	**2.33**	up	**1.24**	up	2
Os.32357.1.S1_x_at	LOC_Os07g46950	ligA, putative, expressed	**1.00**	up	**1.02**	up	**11.54**	up	**1.00**	down	**1.02**	up	**1.04**	up	ABA
Os.3241.1.S1_at	AK068326	Oryza sativa (japonica cultivar-group) Os10g0522700 (Os10g0522700) mRNA, comple	**1.01**	down	**1.61**	up	**12.67**	down	**1.33**	down	**1.95**	down	**1.81**	up	ABA
Os.32439.1.S1_at	LOC_Os01g56610	homocysteine S-methyltransferase protein, putative, expressed	**1.01**	down	**1.00**	up	**78.48**	up	**1.00**	up	**1.00**	up	**1.01**	up	ABA
Os.32455.1.S1_at	LOC_Os01g54670	coiled-coil domain-containing protein 25, putative, expressed	**1.71**	down	**1.37**	up	**5.50**	down	**1.11**	up	**1.28**	down	**1.66**	up	ABA
Os.32465.1.S1_at	LOC_Os02g54710	expressed protein	**1.18**	up	**1.31**	up	**4.00**	down	**1.25**	down	**1.75**	down	**1.44**	down	ABA
Os.32471.1.S1_at	LOC_Os03g55410	peroxidase precursor, putative, expressed	**1.06**	down	**1.07**	up	**5.67**	up	**1.68**	down	**1.21**	down	**2.22**	down	2
Os.32492.1.S1_at	LOC_Os03g14040	expressed protein	**1.09**	up	**1.03**	up	**3.93**	down	**1.24**	down	**1.58**	down	**1.40**	down	ABA
Os.32504.2.S1_at	LOC_Os07g02100	flavin-containing monooxygenase family protein, putative, expressed	**1.39**	down	**1.15**	up	**4.39**	down	**1.14**	down	**1.71**	down	**1.55**	down	ABA
Os.32568.1.S1_at	LOC_Os01g07200	staphylococcal nuclease homologue, putative, expressed	**1.08**	down	**1.06**	down	**3.59**	up	**1.19**	down	**1.07**	up	**1.16**	down	ABA
Os.32597.1.S1_at	LOC_Os01g47300	retrotransposon protein, putative, unclassified, expressed	**1.01**	down	**1.00**	down	**1.04**	down	**1.00**	up	**15.40**	up	**1.03**	up	SA
Os.32597.1.S1_x_at	LOC_Os01g47300	retrotransposon protein, putative, unclassified, expressed	**1.01**	down	**1.00**	up	**1.03**	down	**1.00**	up	**11.57**	up	**1.04**	up	SA
Os.32622.1.S1_at	LOC_Os01g01170	expressed protein	**1.15**	down	**1.21**	up	**4.66**	down	**1.20**	down	**1.73**	down	**2.41**	down	2
Os.32630.1.S1_at	LOC_Os10g32700	hypersensitive-induced response protein, putative, expressed	**1.05**	down	**1.31**	up	**1.99**	down	**2.86**	up	**1.62**	up	**10.32**	down	3
Os.32659.1.S1_at	LOC_Os03g20020	plant neutral invertase domain containing protein, expressed	**1.19**	up	**1.04**	down	**4.41**	up	**1.18**	up	**1.71**	up	**1.32**	up	ABA
Os.32667.1.S1_at	LOC_Os01g12070	endoglucanase precursor, putative, expressed	**1.67**	up	**2.57**	down	**6.51**	down	**1.36**	down	**2.95**	down	**4.64**	down	4
Os.32668.1.S1_at	LOC_Os01g08090	flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed	**2.21**	up	**1.03**	up	**1.19**	down	**1.14**	down	**1.67**	up	**1.03**	up	IAA
Os.32680.1.S1_at	LOC_Os07g05190	leucine-rich repeat family protein, putative, expressed	**1.17**	down	**1.14**	down	**2.86**	down	**1.09**	down	**1.28**	down	**1.49**	down	ABA
Os.32687.1.S1_at	LOC_Os01g12720	protein kinase domain containing protein, expressed	**1.14**	up	**1.18**	down	**2.53**	up	**1.02**	down	**1.04**	up	**1.05**	down	ABA
Os.32727.1.S1_at	LOC_Os01g43480	AAA-type ATPase family protein, putative, expressed	**3.27**	up	**1.39**	down	**2.14**	down	**1.02**	up	**1.56**	down	**1.25**	down	2
Os.32752.2.S1_s_at	LOC_Os01g60910	CAMK_KIN1/SNF1/Nim1_like.12 - CAMK includes calcium/calmodulin depedent protein	**1.25**	up	**1.00**	down	**2.45**	up	**1.05**	down	**1.14**	down	**1.10**	down	ABA
Os.32753.1.S1_at	LOC_Os01g49030	expressed protein	**1.30**	up	**1.30**	down	**9.93**	up	**1.37**	up	**1.47**	up	**1.40**	down	ABA
Os.32760.1.S1_at	LOC_Os01g07130	expressed protein	**1.00**	down	**1.92**	down	**1.32**	up	**1.11**	up	**2.56**	up	**3.31**	up	2

Os.32770.1.S1_at	LOC_Os01g09990	helix-loop-helix DNA-binding domain containing protein, expressed	**1.08**	down	**1.99**	up	**1.15**	up	**2.25**	up	**1.50**	down	**6.33**	up	2
Os.32770.1.S1_x_at	LOC_Os01g09990	helix-loop-helix DNA-binding domain containing protein, expressed	**1.31**	down	**1.45**	up	**1.09**	down	**1.89**	up	**1.64**	down	**5.78**	up	JA
Os.32770.2.S1_x_at	LOC_Os01g09990	helix-loop-helix DNA-binding domain containing protein, expressed	**1.14**	down	**1.12**	up	**1.55**	down	**1.78**	up	**1.51**	down	**7.67**	up	JA
Os.3278.1.S1_at	LOC_Os10g40130	Mur ligase family protein, putative, expressed	**1.03**	down	**1.15**	up	**2.93**	down	**1.18**	down	**1.61**	down	**1.11**	down	ABA
Os.32782.1.S1_at	LOC_Os08g43170	hydroxymethylglutaryl-CoA synthase, putative, expressed	**1.10**	up	**1.22**	down	**2.50**	up	**1.10**	up	**1.39**	up	**1.27**	up	ABA
Os.3280.1.S1_at	LOC_Os10g40040	expressed protein	**1.04**	down	**1.10**	up	**267.99**	up	**1.75**	down	**2.88**	up	**1.27**	up	2
Os.32822.1.S1_at	LOC_Os01g05960	receptor kinase, putative, expressed	**1.25**	up	**1.76**	up	**7.57**	up	**2.22**	up	**3.03**	up	**1.07**	up	3
Os.32827.1.S1_at	LOC_Os01g46290	lipase, putative, expressed	**1.46**	down	**1.17**	down	**2.71**	up	**1.00**	up	**1.14**	up	**1.15**	up	ABA
Os.32856.1.S1_at	LOC_Os01g55450	CAMK_KIN1/SNF1/Nim1_like.11 - CAMK includes calcium/calmodulin depedent protei	**1.24**	down	**1.20**	down	**9.73**	up	**1.19**	up	**1.12**	up	**1.02**	up	ABA
Os.32856.1.S2_at	LOC_Os01g55450	CAMK_KIN1/SNF1/Nim1_like.11 - CAMK includes calcium/calmodulin depedent protei	**1.62**	down	**1.65**	down	**15.57**	up	**1.06**	down	**1.04**	up	**1.01**	down	ABA
Os.32890.1.S1_at	LOC_Os11g47600	glycosyl hydrolase, putative, expressed	**1.86**	down	**1.01**	down	**4.50**	up	**1.46**	up	**2.61**	up	**1.54**	up	2
Os.32943.1.S1_at	LOC_Os01g12660	AAA-type ATPase family protein, putative, expressed	**1.02**	up	**1.02**	up	**151.29**	up	**2.35**	up	**1.32**	up	**1.01**	up	2
Os.32943.2.S1_x_at	LOC_Os01g12660	AAA-type ATPase family protein, putative, expressed	**1.01**	down	**1.03**	up	**107.00**	up	**1.03**	up	**1.00**	up	**1.02**	up	ABA
Os.33007.1.S1_x_at	LOC_Os07g27480	ELMO/CED-12 family protein, putative, expressed	**1.07**	up	**1.11**	down	**2.03**	up	**1.10**	down	**1.12**	up	**1.01**	up	ABA
Os.33038.1.S1_a_at	LOC_Os01g52100	DUF581 domain containing protein, expressed	**1.30**	up	**1.34**	down	**3.73**	up	**1.70**	down	**1.01**	down	**1.09**	up	ABA
Os.33087.1.S1_at	LOC_Os07g35060	OsFBX238 - F-box domain containing protein, expressed	**2.69**	down	**1.04**	down	**1.83**	up	**1.08**	down	**1.08**	down	**1.63**	down	IAA
Os.33102.1.S1_at	LOC_Os01g43740	cytochrome P450 72A1, putative, expressed	**1.11**	down	**1.01**	up	**2.04**	down	**1.16**	down	**19.26**	up	**2.00**	down	3
Os.33106.1.S1_at	LOC_Os01g57730	peroxidase precursor, putative, expressed	**1.55**	up	**1.22**	down	**3.12**	down	**1.49**	down	**1.43**	up	**1.86**	down	ABA
Os.33110.1.S1_at	LOC_Os01g45900	OsFBX20 - F-box domain containing protein, expressed	**1.09**	down	**1.02**	up	**2.55**	up	**1.20**	down	**1.63**	up	**1.32**	down	ABA
Os.33170.1.S1_x_at	LOC_Os01g45550	auxin efflux carrier component, putative, expressed	**1.42**	up	**1.27**	down	**2.76**	down	**1.20**	up	**1.14**	down	**1.33**	up	ABA
Os.33184.1.S1_at	LOC_Os01g51870	methyltransferase, putative, expressed	**1.32**	down	**1.02**	down	**1.45**	up	**1.25**	down	**2.71**	up	**1.28**	up	SA
Os.33210.1.S1_at	LOC_Os01g68570	expressed protein	**1.00**	down	**1.72**	down	**2.18**	up	**1.17**	up	**2.02**	up	**1.19**	down	2
Os.33210.2.S1_x_at	LOC_Os01g68570	expressed protein	**1.49**	up	**2.00**	down	**2.44**	up	**1.07**	up	**2.03**	up	**1.03**	down	3
Os.33212.2.S1_at	LOC_Os01g67580	multidrug resistance-associated protein, putative, expressed	**1.45**	down	**1.18**	down	**3.08**	up	**1.13**	down	**1.03**	up	**1.22**	down	ABA
Os.33238.2.S1_at	AK101258	C2 domain-containing protein	**1.14**	up	**1.31**	up	**3.13**	up	**1.42**	up	**2.63**	up	**1.40**	up	2
Os.33244.1.S1_at	LOC_Os01g62900	amino acid kinase, putative, expressed	**1.01**	up	**1.10**	down	**5.23**	up	**1.19**	down	**1.14**	down	**1.01**	up	ABA
Os.33244.1.S2_at	LOC_Os01g62910	CRR2, putative, expressed	**1.02**	down	**1.01**	down	**3.09**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
Os.33309.1.S1_at	LOC_Os01g56810	cytokinin dehydrogenase precursor, putative, expressed	**1.14**	up	**5.77**	up	**1.83**	down	**1.00**	up	**1.30**	down	**1.89**	up	BAP
Os.33316.1.S1_at	LOC_Os01g34560	3-ketoacyl-CoA synthase, putative, expressed	**1.21**	down	**1.01**	up	**4.01**	down	**1.11**	up	**1.07**	down	**1.26**	up	ABA
Os.33336.1.S1_at	LOC_Os01g11350	bZIP transcription factor domain containing protein, expressed	**1.26**	down	**1.20**	down	**2.59**	down	**1.09**	down	**1.12**	down	**1.29**	down	ABA
Os.33341.1.S1_at	LOC_Os01g45830	sulfate transporter, putative, expressed	**1.17**	up	**1.06**	up	**2.10**	up	**1.02**	down	**1.34**	up	**1.10**	up	ABA
Os.33373.1.S1_x_at	LOC_Os01g44069	glycerol-3-phosphate acyltransferase, putative, expressed	**2.47**	up	**1.35**	down	**1.00**	down	**1.00**	up	**1.05**	up	**1.01**	down	IAA
Os.33373.1.S2_x_at	LOC_Os01g44069	glycerol-3-phosphate acyltransferase, putative, expressed	**2.01**	up	**1.00**	up	**1.01**	down	**1.00**	down	**1.00**	down	**1.01**	up	IAA
Os.33471.1.A1_at	LOC_Os08g38700	C3-BTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with C3 subfamily cons	**1.02**	up	**1.20**	up	**3.14**	up	**1.31**	up	**1.98**	down	**2.47**	down	3
Os.33529.1.S1_at	LOC_Os01g62500	OsFtsH3 FtsH protease, homologue of AtFtsH3/10, expressed	**1.23**	up	**1.00**	up	**3.14**	up	**1.80**	down	**1.48**	up	**1.10**	down	ABA
Os.33605.2.S1_x_at	LOC_Os01g50750	zinc finger, C3HC4 type domain containing protein, expressed	**1.10**	down	**1.04**	up	**3.80**	up	**1.22**	down	**1.19**	down	**1.17**	down	ABA
Os.33613.1.S1_at	LOC_Os01g06280	TKL_IRAK_CrRLK1L-1.4 - The CrRLK1L-1 subfamily has homology to the CrRLK1L ho	**1.39**	down	**1.06**	up	**2.44**	down	**1.24**	down	**1.37**	down	**1.06**	up	ABA
Os.33625.4.S1_at	LOC_Os01g70850	esterase, putative, expressed	**3.21**	up	**2.63**	up	**1.33**	up	**1.15**	up	**5.64**	up	**1.56**	up	3
Os.33625.5.S1_x_at	LOC_Os01g70840	esterase, putative, expressed	**1.07**	down	**2.49**	up	**2.17**	down	**1.20**	down	**1.06**	down	**1.38**	down	2
Os.33676.2.S1_at	LOC_Os03g32790	expressed protein	**1.78**	up	**1.40**	down	**5.40**	down	**1.32**	down	**1.28**	down	**1.95**	down	ABA
Os.33676.3.S1_x_at	LOC_Os03g32790	expressed protein	**2.53**	up	**1.42**	down	**4.24**	down	**1.36**	down	**1.38**	down	**2.12**	down	3
Os.33687.1.S1_at	LOC_Os01g19800	zinc finger, C3HC4 type, putative, expressed	**1.08**	down	**1.07**	down	**10.56**	up	**1.43**	down	**1.04**	up	**1.22**	down	ABA
Os.33696.1.S1_at	LOC_Os01g50050	polyprenyl synthetase, putative, expressed	**1.45**	up	**1.55**	down	**4.99**	up	**2.83**	down	**2.86**	up	**1.01**	up	3
Os.33704.3.S1_x_at	LOC_Os01g20110	expressed protein	**1.11**	up	**1.15**	down	**3.10**	down	**1.25**	down	**1.86**	down	**1.27**	down	ABA
Os.33747.1.S1_at	LOC_Os08g30810	puromycin-sensitive aminopeptidase, putative, expressed	**1.19**	up	**1.14**	down	**3.09**	up	**1.12**	down	**1.12**	up	**1.03**	up	ABA
Os.33755.1.S1_at	LOC_Os03g05280	ras-related protein, putative, expressed	**1.09**	down	**1.12**	down	**4.33**	up	**1.03**	down	**1.06**	down	**1.11**	down	ABA
Os.3376.1.S1_at	LOC_Os02g56130	PCNA - Putative DNA replicative polymerase clamp, expressed	**1.47**	down	**1.05**	up	**8.26**	down	**1.16**	down	**2.39**	down	**2.29**	down	3
Os.33762.1.S1_at	LOC_Os01g11160	amino acid permease family protein, putative, expressed	**2.02**	down	**1.83**	up	**3.76**	down	**1.19**	up	**1.40**	down	**1.41**	down	2
Os.33770.1.S1_at	LOC_Os01g59510	chloroplast ribonuclease III domain protein, putative, expressed	**1.53**	down	**1.18**	down	**3.76**	down	**1.20**	down	**1.68**	down	**1.34**	down	ABA
Os.33786.1.S1_at	LOC_Os02g58450	uncharacterized ACR, COG1399 family protein, expressed	**1.42**	up	**1.33**	up	**3.49**	down	**1.65**	down	**1.64**	down	**1.65**	down	ABA
Os.33834.1.S1_at	AK073863	Oryza sativa Japonica Group cDNA clone:J033071F17, full insert sequence.	**1.05**	down	**1.33**	down	**2.09**	down	**1.06**	down	**1.08**	down	**1.22**	down	ABA
Os.3386.1.S1_x_at	LOC_Os06g10350	MYB family transcription factor, putative, expressed	**1.19**	up	**1.04**	down	**7.69**	down	**1.69**	up	**1.18**	down	**2.50**	up	2
Os.3387.1.S1_at	LOC_Os10g33810	myb-related protein Myb4, putative, expressed	**1.03**	up	**1.31**	up	**1.07**	down	**1.27**	up	**1.22**	up	**3.09**	up	JA
Os.3389.2.S1_at	LOC_Os11g03440	myb-like DNA-binding domain containing protein, putative, expressed	**1.08**	down	**1.11**	down	**2.45**	down	**1.15**	up	**1.17**	down	**1.19**	up	ABA
Os.3390.1.S1_at	LOC_Os07g37210	MYB family transcription factor, putative, expressed	**1.15**	down	**1.16**	down	**12.78**	up	**1.14**	down	**1.00**	down	**1.05**	down	ABA

Os.33939.1.A1_at	LOC_Os01g04590	expressed protein	1.12	down	1.36	down	3.66	up	1.06	down	1.04	down	1.08	down	ABA
Os.3396.1.S1_at	LOC_Os06g49880	B-box zinc finger family protein, putative, expressed	2.42	down	1.02	down	3.29	down	1.59	up	1.30	down	1.29	up	2
Os.33968.1.S1_at	LOC_Os01g28840	C4-dicarboxylate transporter/malic acid transport protein, expressed	1.54	up	1.21	up	31.31	up	1.49	down	2.31	up	1.21	down	2
Os.3406.1.S1_at	LOC_Os04g51160	transposon protein, putative, unclassified, expressed	5.13	up	2.11	up	4.44	up	1.38	down	6.29	up	1.34	down	4
Os.3408.1.A1_x_at	LOC_Os01g64660	fructose-1,6-bisphosphatase, putative, expressed	1.46	up	1.09	down	2.31	down	1.37	down	1.15	down	1.47	down	ABA
Os.3408.2.S1_at	LOC_Os01g64670	soluble inorganic pyrophosphatase, putative, expressed	1.02	down	1.05	down	11.19	up	1.07	down	1.05	down	1.38	down	ABA
Os.3409.1.S1_at	LOC_Os03g59040	squalene synthetase, putative, expressed	1.16	up	1.11	down	2.46	up	1.07	up	1.00	up	1.26	down	ABA
Os.34118.1.S1_at	AK072776	Oryza sativa Japonica Group cDNA clone:J023137P05, full insert sequence.	1.17	down	1.12	up	3.91	down	1.40	down	1.81	down	1.49	up	ABA
Os.34130.1.S1_at	LOC_Os01g66510	MLO domain containing protein, putative, expressed	1.04	up	1.14	down	2.45	down	1.34	up	1.38	down	2.69	down	2
Os.3416.2.S1_x_at	AY324880	Oryza sativa (japonica cultivar-group) putative EPSP1 mRNA, partial cds.	1.03	up	1.06	up	1.05	down	1.30	up	1.29	up	2.02	up	JA
Os.34167.1.S1_at	LOC_Os01g26970	expressed protein	1.29	up	1.06	down	2.82	up	1.17	up	1.06	down	1.08	up	ABA
Os.3417.1.S1_at	LOC_Os01g70860	esterase, putative, expressed	1.45	up	1.11	up	4.52	up	1.27	down	1.57	up	1.44	down	ABA
Os.3419.1.S1_a_at	LOC_Os01g50700	dehydrin family protein, expressed	1.15	down	1.00	up	452.71	up	1.25	up	1.59	up	1.04	up	ABA
Os.34191.1.S1_at	LOC_Os07g46630	AMP deaminase, putative, expressed	1.10	down	1.78	up	6.31	up	1.03	down	1.05	up	1.37	down	ABA
Os.34258.1.S1_at	LOC_Os01g57450	universal stress protein domain containing protein, putative, expressed	1.26	up	1.13	down	7.89	up	1.00	down	1.65	up	1.05	down	ABA
Os.3428.1.S1_x_at	LOC_Os02g03060	cyclin-dependent kinase A-2, putative, expressed	1.04	down	1.16	down	3.29	down	1.06	up	1.29	down	1.16	down	ABA
Os.3428.2.S1_at	LOC_Os02g03060	cyclin-dependent kinase A-2, putative, expressed	1.64	down	1.31	down	2.87	down	1.06	down	1.13	down	1.25	down	ABA
Os.34310.1.S1_at	LOC_Os01g61160	laccase precursor protein, putative, expressed	1.03	down	1.27	up	4.25	up	1.19	down	1.31	up	1.22	down	ABA
Os.34356.1.S1_at	LOC_Os07g45260	glycosyl transferase 8 domain containing protein, putative, expressed	1.02	down	1.05	down	5.12	up	1.05	down	1.71	up	1.46	up	ABA
Os.34358.1.S1_at	LOC_Os07g42924	dehydrogenase, putative, expressed	1.29	up	1.34	down	1.10	down	1.18	down	6.09	up	2.27	up	2
Os.34372.1.S1_at	LOC_Os06g48300	protein phosphatase 2C, putative, expressed	1.03	up	1.22	down	149.06	up	1.23	down	2.44	up	1.21	up	2
Os.34373.1.S1_at	LOC_Os12g12580	NADP-dependent oxidoreductase, putative, expressed	1.27	down	1.21	down	1.24	down	1.86	down	1.08	up	2.25	up	JA
Os.34438.1.S1_x_at	LOC_Os07g39740	GDSL-like lipase/acylhydrolase, putative, expressed	1.03	down	1.11	up	13.96	up	1.09	down	1.11	down	1.08	down	ABA
Os.34438.2.A1_x_at	LOC_Os07g39740	GDSL-like lipase/acylhydrolase, putative, expressed	1.01	down	1.02	up	3.82	up	1.00	down	1.00	down	1.03	up	ABA
Os.34471.1.S1_at	LOC_Os01g64310	no apical meristem protein, putative, expressed	2.78	up	1.11	up	1.60	down	1.07	up	1.25	up	1.06	up	IAA
Os.34493.1.A1_at	AK071189	Oryza sativa Japonica Group cDNA clone:J023086G16, full insert sequence.	1.02	down	1.01	up	8.02	up	1.02	up	1.92	up	1.05	up	ABA
Os.34496.1.S1_at	AK071173	Oryza sativa Japonica Group cDNA clone:J023082F07, full insert sequence.	1.31	down	1.05	up	3.36	down	2.96	up	1.16	up	5.98	up	3
Os.34521.1.S1_at	LOC_Os03g29810	OsClp6 - Putative Clp protease homologue, expressed	1.06	up	1.11	up	2.53	down	1.28	down	1.53	down	1.20	down	ABA
Os.34523.1.S1_at	LOC_Os11g30500	HVA22, putative, expressed	1.11	up	1.10	up	25.65	up	1.83	down	1.88	up	1.39	down	ABA
Os.34537.1.S1_at	LOC_Os01g52160	heavy metal-associated domain containing protein, expressed	1.16	down	1.59	down	2.57	down	1.40	down	1.51	down	2.19	down	2
Os.34537.2.S1_x_at	LOC_Os01g52160	heavy metal-associated domain containing protein, expressed	1.25	down	1.67	down	2.05	down	1.26	down	1.24	down	1.63	down	ABA
Os.34549.1.S1_at	LOC_Os07g43530	helix-loop-helix DNA-binding domain containing protein, expressed	2.03	down	1.52	down	3.70	down	1.06	down	1.27	up	1.05	up	2
Os.34596.1.S1_at	LOC_Os01g52980	OsFBX23 - F-box domain containing protein, expressed	1.09	up	1.07	up	6.17	up	1.33	up	1.10	up	1.20	up	ABA
Os.34673.1.S1_at	LOC_Os05g34000	POT family protein, expressed	1.69	down	1.33	up	2.89	down	1.10	down	1.98	down	1.96	down	ABA
Os.34701.1.S1_s_at	LOC_Os03g07130	RING finger protein 13, putative, expressed	1.12	up	1.19	down	2.36	up	1.01	up	1.10	up	1.05	down	ABA
Os.34737.2.S1_x_at	LOC_Os07g46820	CUG-BP- and ETR-3-like factor 5, putative, expressed	1.24	down	3.07	up	1.04	down	1.08	up	1.01	down	1.01	up	BAP
Os.34741.1.S1_at	LOC_Os01g19130	protein phosphatase 2C, putative, expressed	1.60	up	1.07	down	8.42	up	1.06	down	2.05	up	1.19	up	2
Os.34767.2.S1_s_at	LOC_Os03g12530	cation efflux family protein, putative, expressed	1.28	up	1.02	down	3.29	down	1.31	down	1.01	down	1.14	down	ABA
Os.34773.1.S1_at	LOC_Os10g30520	ras-related protein, putative, expressed	1.12	down	1.02	up	2.00	up	1.04	down	1.15	up	1.04	up	ABA
Os.34789.1.S1_at	LOC_Os07g11300	expressed protein	1.07	up	1.21	down	4.76	up	1.02	up	1.13	up	1.04	up	ABA
Os.34873.1.S1_at	LOC_Os07g46510	expressed protein	1.28	up	1.08	up	3.46	down	1.17	up	1.32	down	1.14	down	ABA
Os.34913.1.S1_at	LOC_Os01g55160	expressed protein	2.22	up	1.25	down	2.74	up	4.49	up	2.84	up	1.29	up	4
Os.34962.1.S1_at	LOC_Os01g38110	cytochrome P450, putative, expressed	1.17	down	1.71	up	9.69	up	2.13	down	15.91	up	1.76	up	3
Os.34998.1.S1_x_at	LOC_Os01g48850	auxin-responsive protein, putative, expressed	1.14	down	1.12	down	1.64	down	1.33	down	2.25	down	1.04	up	SA
Os.35005.1.S1_at	AK069318	Oryza sativa partial mRNA for putative metallothionein-like protein	1.00	up	1.02	up	2.05	up	1.01	down	1.03	down	1.01	down	ABA
Os.35013.1.S1_at	LOC_Os03g16170	protein phosphatase 2C, putative, expressed	2.36	up	1.09	down	148.27	up	2.02	down	1.21	up	1.11	up	3
Os.35020.1.S1_at	LOC_Os11g03300	NAC domain transcription factor, putative, expressed	1.42	up	1.58	down	19.30	up	1.31	up	1.28	up	2.62	up	2
Os.35154.1.S1_x_at	LOC_Os04g43390	Os4bglu16 - monolignol beta-glucoside homologue, expressed	1.10	down	1.41	down	18.67	up	1.93	down	1.57	up	1.16	up	ABA
Os.35247.1.S1_at	LOC_Os05g32610	required to maintain repression 1, putative, expressed	1.05	up	1.03	up	4.16	down	1.50	up	1.17	down	1.12	down	ABA
Os.35273.1.S1_at	LOC_Os07g29240	expressed protein	1.10	up	1.14	up	4.08	down	1.28	down	1.57	down	1.14	down	ABA
Os.353.1.S1_at	LOC_Os04g08350	cysteine synthase, chloroplast/chromoplast precursor, putative, expressed	1.17	up	1.07	up	2.24	down	1.21	down	1.28	up	1.09	down	ABA
Os.35300.1.S1_at	LOC_Os07g40700	RNA methyltransferase, TrmH family protein, putative, expressed	1.26	down	1.04	up	3.53	down	1.12	up	1.49	down	1.12	down	ABA
Os.35365.1.S1_at	LOC_Os06g30950	transporter-related, putative, expressed	1.23	up	1.02	up	3.04	down	1.15	down	1.63	down	1.16	up	ABA
Os.35425.1.S1_at	LOC_Os01g61940	white-brown complex homolog protein, putative, expressed	1.03	up	1.04	down	5.30	up	1.02	up	1.81	up	1.14	down	ABA
Os.35451.1.S1_at	LOC_Os03g19930	adenylosuccinate lyase, putative, expressed	1.01	up	1.12	up	2.47	down	1.15	up	1.36	down	1.11	down	ABA

Os.35495.1.S1_at	LOC_Os01g16030	ADP-ribosylation factor, putative, expressed	1.22	down	1.04	down	2.13	down	1.12	down	1.61	down	1.36	up	ABA
Os.35495.1.S1_s_at	LOC_Os01g16030	ADP-ribosylation factor, putative, expressed	1.11	down	1.05	down	2.29	down	1.27	down	2.03	down	1.34	up	2
Os.35510.1.S1_at	LOC_Os02g01220	rhodanese-like domain containing protein, putative, expressed	1.94	up	1.40	down	2.14	up	1.12	up	1.92	up	1.23	up	ABA
Os.35524.1.S1_at	LOC_Os01g65130	peptide transporter, putative, expressed	1.08	down	1.76	down	3.09	down	1.24	up	1.13	down	1.82	down	ABA
Os.35559.1.S1_at	AK066880	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	1.02	up	1.02	up	2.48	up	1.07	up	1.50	up	1.14	up	ABA
Os.35561.1.S1_x_at	LOC_Os03g01550	expressed protein	1.37	up	1.39	down	3.72	up	1.40	down	1.21	up	1.01	up	ABA
Os.35573.1.S1_at	LOC_Os01g41240	hydrolase, alpha/beta fold family domain containing protein, expressed	1.08	down	1.55	up	1.96	up	1.32	up	2.53	up	1.55	up	SA
Os.35606.1.S1_at	LOC_Os01g01610	IscA-like iron-sulfur assembly protein, mitochondrial precursor, putative, expressed	1.12	down	1.05	up	2.32	up	1.00	down	1.02	up	1.35	down	ABA
Os.3568.1.S1_at	LOC_Os06g04889	expressed protein	1.09	down	1.10	down	10.21	up	1.01	up	1.17	up	1.30	down	ABA
Os.35681.1.S1_at	LOC_Os01g53220	HSF-type DNA-binding domain containing protein, expressed	1.67	up	3.05	up	15.23	up	1.02	down	1.01	down	1.27	down	2
Os.35704.2.S1_at	LOC_Os01g60940	expressed protein	1.06	down	1.35	down	5.62	down	1.38	down	1.82	down	1.18	up	ABA
Os.35707.1.S1_at	LOC_Os09g33580	BEE 1, putative, expressed	2.70	up	1.19	up	1.99	down	1.06	down	1.02	up	1.12	down	IAA
Os.35710.1.S1_at	AK066176	Oryza sativa Japonica Group cDNA clone:J013056E23, full insert sequence.	1.02	down	1.19	up	2.31	up	1.03	up	1.08	up	1.17	up	ABA
Os.35718.1.S1_at	LOC_Os12g39220	ZOS12-08 - C2H2 zinc finger protein, expressed	1.12	up	1.49	up	3.65	down	1.19	down	1.42	down	1.35	down	ABA
Os.35785.1.S1_at	LOC_Os01g35160	TKL_IRAK_DUF26-lh.4 - DUF26 kinases have homology to DUF26 containing loci, exp	1.43	down	1.08	down	2.25	up	1.02	down	1.00	up	1.10	up	ABA
Os.35787.1.S1_at	LOC_Os03g63150	powdery mildew resistance protein PM3b, putative, expressed	1.06	down	1.01	down	4.63	up	1.04	down	1.05	down	1.06	down	ABA
Os.35787.1.S1_x_at	LOC_Os03g63150	powdery mildew resistance protein PM3b, putative, expressed	1.01	down	1.00	up	3.77	up	1.00	up	1.00	down	1.01	up	ABA
Os.35808.1.S1_at	LOC_Os01g42190	heat shock protein DnaJ, putative, expressed	1.56	up	1.17	up	3.77	up	1.36	down	1.18	down	1.16	down	ABA
Os.3582.1.S1_at	LOC_Os06g05090	methyltransferase domain containing protein, expressed	1.16	up	1.30	up	2.93	down	1.14	up	1.26	down	1.28	down	ABA
Os.35827.1.S1_at	LOC_Os01g14510	BRASSINOSTEROID INSENSITIVE 1 precursor, putative, expressed	1.28	down	1.44	down	11.52	up	1.76	down	1.42	up	1.73	up	ABA
Os.35919.1.S1_s_at	LOC_Os03g60340	leaf senescence related protein, putative, expressed	1.08	down	1.03	up	2.08	down	1.36	down	1.26	down	1.13	down	ABA
Os.35921.1.S1_at	LOC_Os01g60730	RING-H2 finger protein, putative, expressed	1.51	up	4.01	up	5.81	up	1.06	up	1.22	down	1.58	down	2
Os.36149.1.S1_x_at	LOC_Os11g23080	retrotransposon protein, putative, unclassified, expressed	1.02	up	1.02	up	1.02	up	1.04	up	27.17	up	1.22	up	SA
Os.36152.1.S1_at	LOC_Os01g63980	ZOS1-17 - C2H2 zinc finger protein, expressed	1.29	up	1.05	up	4.75	up	1.76	up	3.87	up	1.11	down	2
Os.36161.1.S1_at	LOC_Os01g58960	cytochrome P450, putative, expressed	1.01	down	1.78	up	2.06	down	7.82	up	1.18	down	1.84	down	2
Os.36278.1.S1_x_at	LOC_Os03g03724	expressed protein	1.20	up	1.26	down	1.58	down	1.54	down	1.36	down	2.12	down	JA
Os.36280.1.S1_at	LOC_Os05g45320	ubiquitin domain-containing protein 1, putative, expressed	1.19	down	1.19	down	3.74	up	1.01	up	1.23	up	1.18	down	ABA
Os.36307.1.S1_at	LOC_Os04g35490	expressed protein	1.00	down	1.00	up	1139.85	up	1.00	up	1.00	up	1.02	up	ABA
Os.3634.1.S1_a_at	LOC_Os01g13280	ubiquitin conjugating enzyme protein, putative, expressed	1.01	up	1.09	down	5.18	up	1.07	down	1.07	up	1.09	down	ABA
Os.36409.1.S1_x_at	AK063499	Oryza sativa Japonica Group cDNA clone:001-116-E02, full insert sequence.	1.02	down	1.04	down	20.60	up	1.01	down	1.03	up	1.04	up	ABA
Os.36435.1.S1_at	LOC_Os11g48080	SOR/SNZ family protein, putative, expressed	1.15	down	1.01	down	3.00	down	1.05	up	1.57	down	1.32	down	ABA
Os.36449.1.S1_at	LOC_Os01g57610	OsGH3.1 - Probable indole-3-acetic acid-amido synthetase, expressed	6.11	up	2.17	down	1.12	up	1.06	down	1.52	down	2.55	down	3
Os.36458.1.S1_at	LOC_Os01g14080	lipase class 3 family protein, putative, expressed	1.01	down	1.03	down	2.37	up	1.00	up	1.17	up	1.04	up	ABA
Os.36458.2.S1_x_at	LOC_Os01g14080	lipase class 3 family protein, putative, expressed	1.01	up	1.10	down	5.10	up	1.05	up	1.55	up	1.11	up	ABA
Os.36470.1.S1_at	LOC_Os07g15320	leaf senescence related protein, putative, expressed	2.29	down	2.15	down	1.11	down	1.01	up	1.22	up	1.02	down	2
Os.36549.1.S1_at	CT829079	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA043F20, full insert sequence	1.93	up	1.67	down	7.59	down	1.16	up	1.15	down	1.66	down	ABA
Os.3655.1.S1_at	LOC_Os01g18744	transferase family protein, putative, expressed	2.27	down	1.61	down	11.51	down	1.01	down	2.27	down	1.23	up	3
Os.36558.1.S1_x_at	NM_001072512	Oryza sativa (japonica cultivar-group) Os12g0114000 (Os12g0114000) mRNA, comple	1.18	up	1.19	up	6.14	up	1.01	up	1.56	up	1.41	down	ABA
Os.36651.1.S1_at	LOC_Os04g43560	no apical meristem protein, putative, expressed	2.97	down	3.40	up	1.73	up	1.79	up	1.05	down	13.01	down	3
Os.36663.1.S1_at	LOC_Os01g27390	glutathione S-transferase, putative, expressed	1.56	down	1.51	up	15.83	down	1.06	up	6.85	down	2.02	down	3
Os.36687.1.A1_at	LOC_Os09g10730	expressed protein	1.00	down	1.25	up	3.22	down	1.14	down	1.08	down	1.08	down	ABA
Os.36706.1.S1_at	LOC_Os07g33660	expressed protein	1.09	up	1.16	up	3.15	down	1.07	down	1.61	down	1.19	down	ABA
Os.36709.1.S1_at	LOC_Os01g48710	heavy metal-associated domain containing protein, expressed	2.77	down	1.04	down	7.41	down	1.18	down	1.98	down	2.27	down	4
Os.36709.1.S1_x_at	LOC_Os01g48710	heavy metal-associated domain containing protein, expressed	1.85	down	1.01	up	6.47	down	1.05	up	1.67	down	1.92	down	ABA
Os.36756.1.S1_at	LOC_Os08g06540	expressed protein	1.09	down	1.09	down	1.13	down	1.28	down	2.05	up	1.24	down	SA
Os.36767.1.S1_at	LOC_Os01g04330	OsCML16 - Calmodulin-related calcium sensor protein, expressed	1.11	up	1.11	up	7.09	up	1.52	down	1.35	up	1.29	down	ABA
Os.36913.1.S1_at	LOC_Os10g40530	LTPL146 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.25	down	1.11	up	3.51	down	1.09	down	1.65	down	1.54	down	ABA
Os.36925.1.A1_at	LOC_Os12g37370	DNA-directed RNA polymerase II subunit RPB9, putative, expressed	1.12	down	1.08	up	2.11	down	1.01	up	1.33	down	1.36	down	ABA
Os.36969.1.S1_at	LOC_Os04g02880	expressed protein	2.01	up	1.62	up	10.02	down	1.49	down	1.70	down	2.70	down	3
Os.37006.1.S1_at	LOC_Os06g11660	phosphate-induced protein 1 conserved region domain containing protein, expressed	1.09	up	1.42	up	2.65	up	1.54	up	1.77	up	1.49	down	ABA
Os.37062.2.S1_x_at	LOC_Os01g29280	expressed protein	1.04	up	1.05	up	1.14	down	1.12	up	1.05	up	3.09	up	JA
Os.37066.1.S1_at	LOC_Os01g07500	alliin lyase precursor, putative, expressed	1.32	up	2.03	up	3.23	down	1.02	down	1.09	up	1.56	down	2
Os.37089.1.S1_at	LOC_Os07g04040	expressed protein	1.00	down	1.19	down	2.70	up	1.05	up	1.06	up	1.03	up	ABA
Os.372.1.S1_a_at	LOC_Os04g40874	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform, putative, expressed	1.05	up	1.21	up	2.34	down	1.16	up	1.30	down	1.05	down	ABA
Os.3721.1.S1_at	LOC_Os01g03980	expressed protein	1.39	down	1.28	down	2.25	down	1.75	up	1.33	up	1.06	down	ABA

Os.37217.1.S1_at	AK070075	Oryza sativa Japonica Group cDNA clone:J023044P22, full insert sequence.	**1.67**	down	**1.70**	down	**6.75**	up	**2.24**	down	**2.60**	down	**1.85**	down	3
Os.37225.1.S1_at	LOC_Os07g27810	fiber protein Fb34, putative, expressed	**1.01**	up	**1.10**	down	**3.11**	down	**1.29**	down	**1.88**	down	**1.17**	up	ABA
Os.37229.1.S1_at	LOC_Os02g46210	DUF581 domain containing protein, expressed	**2.05**	up	**2.25**	up	**9.29**	up	**1.10**	down	**1.28**	down	**1.06**	down	3
Os.37247.1.S1_at	LOC_Os11g02450	elongation factor P, putative, expressed	**1.17**	up	**1.16**	up	**3.99**	down	**1.25**	down	**1.87**	down	**1.00**	up	ABA
Os.37285.1.S1_at	LOC_Os05g03530	tetraspanin family protein, putative, expressed	**1.63**	down	**1.01**	down	**1.35**	down	**1.28**	down	**1.10**	down	**2.00**	down	JA
Os.37303.1.S1_at	LOC_Os07g48100	CAMK_KIN1	**1.44**	up	**1.00**	up	**2.61**	up	**1.07**	up	**1.17**	up	**1.18**	up	ABA
Os.37318.1.S1_at	AK059315	Oryza sativa Japonica Group cDNA clone:001-025-H02, full insert sequence.	**1.15**	down	**1.57**	down	**2.08**	down	**1.03**	up	**1.15**	up	**1.40**	down	ABA
Os.37320.1.S1_at	LOC_Os03g62950	expressed protein	**1.14**	up	**1.08**	up	**3.53**	down	**1.16**	down	**1.59**	down	**1.46**	down	ABA
Os.37320.2.S1_at	LOC_Os03g62950	expressed protein	**1.23**	up	**1.14**	up	**3.64**	down	**1.15**	down	**1.58**	down	**1.37**	down	ABA
Os.37320.2.S1_x_at	LOC_Os03g62950	expressed protein	**1.25**	up	**1.14**	up	**3.56**	down	**1.19**	down	**1.62**	down	**1.46**	down	ABA
Os.37328.1.S1_at	LOC_Os01g72740	cytochrome P450, putative, expressed	**1.06**	down	**1.45**	down	**2.63**	down	**1.26**	down	**1.33**	up	**1.86**	up	ABA
Os.3738.1.S1_s_at	LOC_Os11g08314	methyltransferase, putative, expressed	**1.03**	down	**1.03**	down	**3.72**	down	**1.22**	down	**2.05**	down	**1.96**	down	3
Os.37430.1.S1_at	LOC_Os11g04720	OsRR10 type-A response regulator, expressed	**2.81**	down	**12.09**	up	**15.69**	down	**1.31**	down	**4.65**	down	**3.33**	down	5
Os.37438.1.S1_at	LOC_Os01g65420	expressed protein	**1.90**	up	**2.74**	up	**4.04**	down	**1.39**	down	**1.08**	down	**1.38**	down	2
Os.37457.1.S1_at	LOC_Os07g44780	GDSL-like lipase/acylhydrolase, putative, expressed	**1.18**	down	**2.55**	up	**4.62**	down	**1.68**	down	**1.21**	down	**1.84**	up	2
Os.37509.1.S1_at	LOC_Os01g50040	DNA binding protein, putative, expressed	**1.39**	up	**1.21**	up	**2.65**	up	**1.28**	up	**1.29**	up	**1.45**	up	ABA
Os.37531.1.S1_at	LOC_Os06g33330	powdery mildew resistant protein 5, putative, expressed	**1.91**	up	**1.08**	up	**11.42**	up	**1.91**	down	**1.14**	down	**1.37**	down	ABA
Os.37548.1.S1_at	LOC_Os05g34830	No apical meristem protein, putative, expressed	**1.52**	up	**1.40**	down	**25.88**	up	**1.36**	up	**3.06**	up	**2.49**	up	3
Os.37558.1.S1_at	LOC_Os01g06630	small hydrophilic plant seed protein, putative, expressed	**1.03**	down	**1.01**	up	**24.57**	up	**1.00**	up	**1.03**	up	**1.01**	up	ABA
Os.37562.1.A1_x_at	D85512	Oryza sativa Japonica Group CP26 mRNA, partial sequence.	**1.12**	up	**1.02**	up	**2.78**	down	**1.12**	down	**1.14**	down	**1.12**	down	ABA
Os.37565.1.S1_at	LOC_Os05g25770	OsWRKY45 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**1.46**	up	**1.07**	up	**5.84**	down	**1.19**	down	**2.19**	up	**1.20**	up	2
Os.37565.2.S1_at	LOC_Os05g25770	OsWRKY45 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**1.10**	down	**1.02**	up	**4.40**	down	**1.16**	up	**1.63**	up	**1.07**	up	ABA
Os.37571.1.S1_at	LOC_Os08g37660	plastocyanin-like domain containing protein, putative, expressed	**1.57**	up	**1.54**	up	**4.46**	down	**2.69**	up	**2.21**	up	**2.56**	up	4
Os.37603.1.S1_at	LOC_Os01g63480	transferase family protein, putative, expressed	**1.12**	up	**1.68**	down	**3.43**	up	**6.47**	up	**1.11**	up	**2.45**	up	3
Os.37617.1.S1_at	LOC_Os01g39860	1-aminocyclopropane-1-carboxylate oxidase protein, putative, expressed	**1.22**	down	**2.36**	up	**4.26**	down	**3.31**	up	**3.58**	down	**2.58**	down	5
Os.37620.1.S1_at	LOC_Os01g55820	X8 domain containing protein, expressed	**2.98**	up	**1.44**	down	**1.39**	up	**1.05**	down	**1.47**	down	**1.10**	up	IAA
Os.3766.1.S1_at	LOC_Os01g58420	AP2 domain containing protein, expressed	**1.59**	up	**1.03**	up	**2.99**	up	**1.11**	down	**1.13**	up	**1.00**	up	ABA
Os.37668.1.S1_at	LOC_Os01g43844	cytochrome P450 72A1, putative, expressed	**1.30**	up	**1.03**	up	**6.58**	down	**1.35**	up	**1.81**	down	**1.92**	up	ABA
Os.37687.1.A1_at	LOC_Os05g04150	expressed protein	**1.02**	up	**1.18**	up	**6.34**	up	**1.15**	down	**1.01**	up	**1.06**	down	ABA
Os.37699.2.S1_at	LOC_Os03g16334	fringe-related protein, putative, expressed	**1.33**	up	**1.39**	down	**4.22**	up	**1.04**	down	**1.02**	down	**1.05**	down	ABA
Os.37710.1.S1_at	AK066299	Oryza sativa Japonica Group cDNA clone:J013059M19, full insert sequence.	**1.22**	down	**1.35**	down	**2.80**	down	**1.25**	up	**1.25**	down	**1.24**	up	ABA
Os.37717.1.A2_s_at	LOC_Os05g15770	glycosyl hydrolase, putative, expressed	**1.17**	up	**2.06**	up	**1.71**	up	**1.08**	down	**1.18**	up	**1.58**	up	BAP
Os.37718.1.S1_at	LOC_Os10g26940	BURP domain containing protein, expressed	**1.12**	up	**1.05**	down	**2.29**	down	**1.37**	up	**1.20**	down	**1.11**	up	ABA
Os.37728.1.S1_x_at	LOC_Os08g38170	methyladenine glycosylase, putative, expressed	**1.17**	up	**1.16**	up	**4.80**	down	**1.25**	down	**1.86**	down	**1.30**	down	ABA
Os.37754.1.S1_at	AK058554	probable peroxidase (EC 1.11.1.7), cationic	**2.26**	down	**1.35**	down	**9.37**	down	**1.34**	down	**4.12**	down	**1.19**	up	3
Os.37773.1.S1_at	LOC_Os03g16030	hsp20/alpha crystallin family protein, putative, expressed	**1.24**	up	**1.45**	down	**1.26**	up	**1.02**	up	**85.50**	up	**2.53**	up	2
Os.37773.1.S1_x_at	LOC_Os03g16030	hsp20/alpha crystallin family protein, putative, expressed	**1.02**	up	**1.06**	down	**1.37**	up	**1.05**	down	**79.45**	up	**1.99**	up	SA
Os.37872.1.S1_at	LOC_Os06g08280	protein kinase domain containing protein, expressed	**1.34**	up	**1.20**	down	**6.42**	up	**1.07**	up	**2.07**	up	**1.08**	up	2
Os.37876.1.S1_at	LOC_Os10g39920	expressed protein	**2.21**	up	**1.21**	up	**10.75**	up	**1.60**	up	**2.11**	up	**1.13**	up	3
Os.37902.1.S1_at	LOC_Os03g30250	COBRA-like protein precursor, putative, expressed	**1.05**	down	**1.34**	up	**6.75**	down	**1.24**	down	**2.58**	down	**1.13**	up	2
Os.37909.1.S1_at	LOC_Os05g27780	expressed protein	**1.05**	up	**1.23**	up	**3.10**	up	**1.21**	up	**1.27**	up	**1.26**	down	ABA
Os.37967.1.S1_at	LOC_Os07g42420	3-oxoacyl-synthase, putative, expressed	**1.03**	down	**1.24**	up	**2.16**	down	**1.18**	down	**1.72**	down	**1.12**	down	ABA
Os.38014.1.S1_at	LOC_Os01g14100	BT1 family protein, putative, expressed	**1.12**	up	**1.26**	down	**4.43**	up	**1.09**	up	**1.58**	up	**1.45**	up	ABA
Os.38017.1.S1_s_at	LOC_Os05g31750	annexin, putative, expressed	**1.18**	up	**1.10**	down	**3.72**	down	**1.48**	down	**1.35**	down	**4.31**	up	2
Os.38021.1.S1_at	LOC_Os07g43950	RNA recognition motif containing protein, putative, expressed	**1.07**	down	**1.13**	up	**11.60**	up	**1.12**	up	**1.47**	up	**1.08**	up	ABA
Os.38022.1.S1_at	LOC_Os01g49710	glutathione S-transferase, putative, expressed	**1.12**	up	**1.00**	up	**4.81**	up	**1.23**	down	**3.17**	up	**1.09**	up	2
Os.38022.2.S1_x_at	LOC_Os01g49710	glutathione S-transferase, putative, expressed	**1.50**	up	**1.29**	up	**2.97**	up	**1.05**	down	**1.80**	up	**1.03**	up	ABA
Os.38045.1.S1_at	LOC_Os12g08810	VTC2, putative, expressed	**1.15**	up	**1.25**	down	**2.28**	down	**1.02**	down	**1.60**	up	**1.75**	up	ABA
Os.38090.1.S1_at	LOC_Os01g37820	oxidoreductase/ transition metal ion binding protein, putative, expressed	**1.01**	down	**1.21**	up	**2.65**	down	**1.13**	down	**1.64**	down	**1.24**	down	ABA
Os.38090.2.S1_x_at	LOC_Os01g37820	oxidoreductase/ transition metal ion binding protein, putative, expressed	**1.05**	up	**1.18**	up	**2.23**	down	**1.01**	down	**1.63**	down	**1.15**	down	ABA
Os.38099.1.S1_at	LOC_Os03g61270	OsMan04 - Endo-Beta-Mannanase, expressed	**1.47**	down	**1.23**	up	**36.38**	up	**1.09**	down	**1.16**	down	**1.41**	down	ABA
Os.38099.2.S1_x_at	LOC_Os03g61270	OsMan04 - Endo-Beta-Mannanase, expressed	**1.01**	down	**1.00**	down	**35.06**	up	**1.02**	up	**1.13**	down	**1.03**	down	ABA
Os.38152.1.S1_x_at	LOC_Os10g42780	IrgB-like family protein, expressed	**1.21**	up	**1.15**	down	**2.56**	down	**1.06**	up	**1.45**	down	**1.06**	up	ABA
Os.38157.1.S1_at	LOC_Os09g39910	ABC transporter, ATP-binding protein, putative, expressed	**1.04**	up	**1.06**	down	**9.17**	up	**1.06**	up	**1.38**	up	**1.42**	up	ABA
Os.38157.1.S1_s_at	LOC_Os09g39910	ABC transporter, ATP-binding protein, putative, expressed	**1.24**	up	**1.34**	down	**14.55**	up	**1.26**	up	**2.12**	up	**1.90**	up	2

Os.38169.1.S1_a_at	LOC_Os02g43110	sodium/calcium exchanger 1 precursor, putative, expressed	1.24	up	1.08	down	1.54	down	2.11	down	1.03	down	2.24	up	2
Os.38169.1.S1_at	LOC_Os02g43100	hypothetical protein	1.27	up	1.05	up	1.65	down	2.06	down	1.05	up	2.25	up	2
Os.38179.2.S1_at	LOC_Os12g42070	OsWAK129b - OsWAK receptor-like protein kinase, expressed	1.12	down	1.14	up	2.73	down	1.10	up	1.66	down	1.26	down	ABA
Os.38258.1.S1_x_at	LOC_Os01g56070	RING finger protein, putative, expressed	1.09	up	1.18	down	2.41	up	1.19	up	1.16	up	1.18	up	ABA
Os.38258.2.S1_at	LOC_Os01g56070	RING finger protein, putative, expressed	1.23	down	1.18	down	2.34	up	1.08	up	1.21	up	1.13	down	ABA
Os.38269.1.S1_x_at	AK060977	Oryza sativa Japonica Group cDNA clone:006-202-F05, full insert sequence.	1.01	up	1.01	up	3.08	up	1.06	down	1.08	down	1.09	down	ABA
Os.38283.1.S1_a_at	LOC_Os05g41550	expressed protein	1.63	up	1.01	down	2.19	up	1.22	down	1.36	up	1.04	down	ABA
Os.38283.1.S2_a_at	LOC_Os05g41550	expressed protein	1.16	up	1.12	down	2.28	up	1.12	up	1.57	up	1.26	up	ABA
Os.38285.1.A1_at	LOC_Os07g36820	uncharacterized Cys-rich domain containing protein, putative, expressed	1.18	down	1.00	down	2.33	up	1.06	up	1.43	up	1.33	up	ABA
Os.38309.1.S1_at	LOC_Os06g36390	expressed protein	1.06	up	2.59	up	3.06	up	1.24	up	1.79	up	2.07	down	3
Os.38312.2.S1_x_at	LOC_Os01g04860	DUF647 domain containing protein, putative, expressed	1.38	up	1.14	up	2.70	down	1.09	down	1.29	down	1.23	down	ABA
Os.38330.2.S1_at	LOC_Os01g56010	serpin domain containing protein, putative, expressed	1.02	up	1.20	down	46.93	up	1.01	down	1.62	up	1.76	down	ABA
Os.38339.1.S1_at	LOC_Os05g33960	peptide transporter PTR2, putative, expressed	1.49	down	1.23	down	17.96	up	1.67	up	2.76	up	1.33	up	2
Os.38340.1.S1_at	LOC_Os03g55990	homeobox domain containing protein, expressed	1.23	down	1.17	down	4.83	up	1.02	down	1.17	up	1.11	down	ABA
Os.38367.1.S1_s_at	LOC_Os03g51050	peptide transporter PTR2, putative, expressed	1.13	down	1.10	down	2.56	up	1.03	down	1.11	up	1.05	down	ABA
Os.38381.1.S1_at	LOC_Os01g20830	heavy metal-associated domain containing protein, expressed	1.21	down	2.21	up	16.31	down	1.14	up	4.20	down	2.72	down	4
Os.38399.1.S1_at	LOC_Os03g02685	lysM domain containing protein, putative, expressed	1.31	up	1.30	down	4.38	up	1.07	down	1.04	up	1.20	up	ABA
Os.38447.1.S1_s_at	LOC_Os06g07030	AP2 domain containing protein, expressed	1.12	down	1.48	down	4.41	up	1.27	up	1.35	up	1.25	up	ABA
Os.38485.1.S1_at	LOC_Os03g26910	uncharacterized glycosyl hydrolase Rv2006/MT2062, putative, expressed	1.59	up	1.10	up	2.69	up	1.31	up	1.22	up	1.03	up	ABA
Os.38581.1.S1_s_at	LOC_Os05g38530	DnaK family protein, putative, expressed	1.24	down	1.02	down	15.66	up	1.19	up	4.78	up	1.14	down	2
Os.38599.3.S1_a_at	LOC_Os05g03460	protein kinase, putative, expressed	1.16	up	1.03	up	6.26	up	1.28	up	1.92	up	1.54	up	ABA
Os.38638.1.S1_at	LOC_Os06g04990	early nodulin 93 ENOD93 protein, putative, expressed	2.42	down	1.36	up	4.83	up	1.42	up	1.77	up	1.62	down	2
Os.38638.3.S1_x_at	LOC_Os06g04990	early nodulin 93 ENOD93 protein, putative, expressed	2.15	down	1.15	up	3.16	up	1.00	up	2.28	up	1.00	down	3
Os.38638.4.S1_s_at	LOC_Os06g05020	early nodulin 93 ENOD93 protein, putative, expressed	3.00	down	1.11	up	1.19	down	1.36	up	2.16	up	1.64	down	2
Os.38806.1.A1_x_at	LOC_Os06g04230	expressed protein	4.13	up	1.23	up	5.53	up	1.02	up	1.08	down	1.14	up	2
Os.38848.1.S1_at	LOC_Os06g15330	CCT/B-box zinc finger protein, putative, expressed	1.11	down	1.26	up	10.15	down	1.04	down	1.87	down	1.47	down	ABA
Os.38849.1.S1_at	LOC_Os02g51620	glycosyl hydrolase family 3 protein, putative, expressed	1.04	up	1.14	down	2.76	down	1.49	down	1.47	down	1.09	down	ABA
Os.38856.1.A1_s_at	LOC_Os01g67950	ubiquitin family protein, putative, expressed	3.22	up	1.18	up	2.46	down	1.00	down	1.02	up	1.06	up	2
Os.3887.1.S1_at	LOC_Os05g02820	protein transport protein-related, putative, expressed	1.07	down	1.18	down	2.31	down	1.16	down	1.45	down	1.04	up	ABA
Os.38985.1.S1_at	LOC_Os07g02060	OsWRKY29 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.69	down	1.19	up	5.07	down	1.07	up	1.24	down	1.46	down	ABA
Os.38992.1.A1_x_at	LOC_Os08g45120	hypothetical protein	1.67	down	1.90	down	3.03	up	1.28	up	28.11	up	1.40	up	2
Os.38999.1.S1_at	LOC_Os12g27830	dehydrogenase/reductase, putative, expressed	1.01	down	1.00	down	12.55	up	1.00	down	1.01	down	1.02	up	ABA
Os.39000.1.S1_at	CF314194	---	1.13	up	1.09	down	3.38	up	1.15	down	1.28	up	1.10	down	ABA
Os.39043.1.S1_s_at	LOC_Os10g42960	urea active transporter, putative, expressed	1.08	down	1.65	down	20.51	down	1.33	down	9.30	down	1.52	down	2
Os.39055.2.A1_x_at	LOC_Os06g51150	catalase isozyme B, putative, expressed	2.04	down	1.30	down	1.41	up	1.27	up	1.26	up	1.22	up	IAA
Os.39069.1.A1_at	LOC_Os07g08669	expressed protein	1.58	down	1.52	down	5.01	up	1.04	down	1.13	up	1.01	up	ABA
Os.39087.1.S1_at	LOC_Os01g14550	pathogen-related protein, putative, expressed	1.06	up	1.18	up	1.94	down	1.94	up	1.35	up	7.48	up	JA
Os.39128.1.A1_at	CT836262	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRA117L16, full insert sequence	1.23	up	1.10	up	2.19	down	1.13	down	1.80	down	1.45	down	ABA
Os.39129.1.S1_at	LOC_Os10g33760	No apical meristem protein, putative, expressed	1.41	down	1.48	up	5.02	up	1.15	up	1.38	down	1.52	down	ABA
Os.39214.1.S1_at	LOC_Os10g38090	cytochrome P450, putative, expressed	1.02	up	1.41	up	4.20	up	1.45	down	1.81	up	1.09	down	ABA
Os.3927.1.S1_x_at	LOC_Os01g15000	lipase, putative, expressed	1.14	up	1.05	down	8.16	up	1.05	down	1.42	up	1.00	up	ABA
Os.3927.2.S1_s_at	LOC_Os01g15000	lipase, putative, expressed	1.17	down	1.03	up	7.54	up	1.06	down	1.50	up	1.08	up	ABA
Os.3927.3.S1_x_at	LOC_Os01g15000	lipase, putative, expressed	1.20	up	1.05	down	15.34	up	1.05	up	1.76	up	1.49	up	ABA
Os.39552.1.A1_s_at	LOC_Os06g48300	protein phosphatase 2C, putative, expressed	1.00	down	1.14	down	53.72	up	1.01	up	1.49	up	1.08	up	ABA
Os.39617.1.S1_at	LOC_Os09g29660	white-brown complex homolog protein 11, putative, expressed	1.05	down	1.04	down	1.50	up	1.36	up	1.22	up	7.17	up	JA
Os.39725.1.S1_at	LOC_Os12g30680	retrotransposon protein, putative, unclassified	1.03	up	1.06	down	1.10	up	1.17	up	12.87	up	1.20	up	SA
Os.39973.1.S1_s_at	LOC_Os03g60580	actin-depolymerizing factor, putative, expressed	1.50	down	1.23	down	39.78	up	1.71	down	5.16	up	1.28	up	2
Os.39994.1.S1_at	LOC_Os01g39136	retrotransposon protein, putative, unclassified, expressed	1.00	down	1.00	up	1.04	down	1.00	up	22.79	up	1.14	up	SA
Os.39995.1.S1_x_at	AK241103	Oryza sativa Japonica Group cDNA, clone: J065079A13, full insert sequence.	1.05	down	1.03	down	2.31	up	1.00	down	7.82	up	1.03	up	2
Os.39998.1.A1_x_at	LOC_Os04g53970	hypothetical protein	1.53	up	1.65	up	2.20	up	1.57	up	1.02	up	1.51	down	ABA
Os.40007.1.S1_x_at	CB636581		1.02	down	1.03	down	1.04	up	1.04	up	22.33	up	1.21	up	SA
Os.40015.1.S1_at	LOC_Os01g43590	HSF-type DNA-binding domain containing protein, expressed	2.57	up	2.04	up	6.11	up	1.79	down	1.36	up	1.35	up	3
Os.40106.1.A1_s_at	LOC_Os08g42600	retinoblastoma-related protein-like, putative, expressed	1.52	down	1.14	down	4.70	down	1.03	up	1.88	down	1.45	down	ABA
Os.40139.1.A1_x_at	AF022734	Oryza sativa zinc inducible protein mRNA, complete cds.	1.02	up	1.14	up	3.28	up	1.02	down	1.64	up	1.51	up	ABA
Os.40244.1.S1_at	LOC_Os11g31940	GDSL-like lipase/acylhydrolase, putative, expressed	1.17	up	1.37	up	3.48	up	1.10	down	1.30	up	1.08	down	ABA

Os.40342.1.A1_s_at	LOC_Os06g18900	cadmium tolerance factor, putative, expressed	**1.12**	down	**1.11**	down	**3.25**	down	**1.44**	up	**1.13**	down	**1.17**	up	ABA
Os.40388.2.S1_s_at	LOC_Os03g01110	RNA methyltransferase, TrmH family protein, putative, expressed	**1.20**	down	**1.13**	down	**1.76**	up	**1.61**	up	**1.32**	up	**2.30**	up	JA
Os.40417.1.A1_at	LOC_Os07g14740	harpin-induced protein 1 domain containing protein, expressed	**1.46**	down	**1.20**	down	**13.32**	down	**1.36**	up	**1.06**	down	**1.71**	down	ABA
Os.40419.1.S1_at	LOC_Os03g12230	caleosin related protein, putative, expressed	**1.01**	down	**1.02**	up	**28.77**	up	**1.03**	up	**1.00**	down	**1.03**	up	ABA
Os.40426.1.S1_x_at	LOC_Os08g06280	LSD1 zinc finger domain containing protein, expressed	**1.29**	down	**1.08**	down	**2.78**	down	**1.01**	up	**1.15**	down	**1.17**	down	ABA
Os.40947.1.A1_at	LOC_Os01g36660	carboxyl-terminal peptidase, putative, expressed	**1.01**	up	**1.02**	up	**2.23**	down	**1.07**	down	**1.00**	up	**1.19**	up	ABA
Os.411.1.S1_a_at	LOC_Os01g64730	bZIP transcription factor domain containing protein, expressed	**1.11**	down	**1.36**	down	**9.90**	up	**2.05**	up	**1.29**	up	**1.12**	up	2
Os.411.1.S1_at	LOC_Os01g64730	bZIP transcription factor domain containing protein, expressed	**1.44**	down	**1.40**	down	**13.67**	up	**2.02**	up	**1.32**	up	**1.07**	down	2
Os.411.2.S1_x_at	LOC_Os01g64730	bZIP transcription factor domain containing protein, expressed	**1.16**	down	**1.14**	down	**9.11**	up	**1.48**	up	**1.19**	up	**1.01**	down	ABA
Os.41257.1.S1_at	LOC_Os01g43040	amino acid transporter, putative, expressed	**1.14**	down	**1.04**	down	**2.21**	down	**1.04**	up	**1.13**	down	**1.13**	down	ABA
Os.413.1.S1_at	LOC_Os01g46970	transcription factor, putative, expressed	**1.11**	up	**1.46**	down	**33.92**	up	**1.21**	down	**1.44**	up	**1.17**	down	ABA
Os.41516.1.S1_at	NM_192393	---	**1.01**	up	**1.01**	down	**2.53**	up	**1.01**	up	**1.00**	up	**1.03**	down	ABA
Os.4154.1.S1_at	LOC_Os02g56850	glutathione reductase, putative, expressed	**1.39**	up	**1.01**	up	**1.95**	up	**1.23**	up	**2.70**	up	**1.36**	up	SA
Os.4159.1.S1_at	LOC_Os01g51570	glycosyl hydrolases family 17, putative, expressed	**1.12**	down	**1.09**	down	**4.60**	down	**1.30**	up	**1.35**	down	**1.41**	up	ABA
Os.4161.1.S1_at	LOC_Os05g46580	polyprenyl synthetase, putative, expressed	**1.24**	down	**1.12**	down	**2.05**	down	**1.06**	down	**1.41**	down	**1.04**	up	ABA
Os.4166.1.S1_at	LOC_Os05g50380	glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative,	**1.22**	up	**1.10**	up	**7.54**	up	**1.01**	up	**1.13**	down	**1.37**	up	ABA
Os.41694.1.S1_at	LOC_Os01g49120	MATE efflux family protein, putative, expressed	**1.05**	up	**1.07**	up	**2.22**	down	**1.06**	down	**1.14**	down	**1.71**	up	ABA
Os.4170.1.S1_at	LOC_Os02g13380	early nodulin 93 ENOD93 protein, putative, expressed	**1.78**	up	**1.02**	down	**1.61**	up	**1.21**	up	**2.99**	up	**2.16**	up	2
Os.41771.1.S1_at	LOC_Os01g47900	S-locus-like receptor protein kinase, putative, expressed	**1.42**	down	**1.74**	down	**2.85**	down	**1.28**	up	**1.21**	down	**1.10**	down	ABA
Os.4179.1.S1_at	AB023498	Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.	**1.15**	up	**1.09**	down	**2.39**	up	**1.66**	down	**1.23**	down	**1.39**	down	ABA
Os.41790.1.S1_x_at	LOC_Os01g47490	Lg106, putative, expressed	**1.01**	up	**1.18**	down	**4.32**	up	**1.06**	down	**1.55**	up	**1.01**	down	ABA
Os.41841.1.S1_at	LOC_Os01g52130	sulfate transporter, putative, expressed	**1.01**	up	**1.32**	down	**8.92**	up	**1.47**	up	**1.44**	up	**2.80**	up	2
Os.4186.1.S1_a_at	LOC_Os01g55340	dof zinc finger domain containing protein, putative, expressed	**1.03**	up	**1.17**	up	**3.63**	up	**1.28**	up	**1.03**	up	**1.15**	down	ABA
Os.41891.1.S1_at	CT836526	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA048M01, full insert sequence	**1.00**	up	**1.06**	down	**2.93**	up	**1.14**	up	**1.16**	up	**1.34**	up	ABA
Os.4194.1.S1_at	LOC_Os10g40430	LTPL139 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.18**	down	**1.59**	down	**3.39**	down	**1.23**	up	**1.41**	down	**4.13**	down	2
Os.4198.1.S1_at	LOC_Os06g06980	caffeoyl-CoA O-methyltransferase, putative, expressed	**1.39**	up	**1.07**	down	**2.78**	down	**1.13**	down	**1.36**	down	**1.13**	up	ABA
Os.4198.1.S1_x_at	LOC_Os06g06980	caffeoyl-CoA O-methyltransferase, putative, expressed	**1.36**	up	**1.13**	down	**2.71**	down	**1.13**	down	**1.40**	down	**1.12**	up	ABA
Os.42024.1.S1_at	LOC_Os01g56420	ctr copper transporter family protein, putative, expressed	**1.11**	down	**1.08**	down	**5.11**	down	**1.21**	up	**1.23**	down	**1.71**	down	ABA
Os.42067.1.S1_at	LOC_Os01g55560	ABIL3, putative, expressed	**1.00**	up	**1.53**	down	**2.13**	up	**1.42**	down	**2.04**	down	**1.42**	down	2
Os.4208.1.S1_at	LOC_Os06g07070	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative	**1.50**	up	**1.03**	up	**2.84**	up	**1.03**	down	**2.01**	up	**1.23**	up	2
Os.4222.1.S1_at	LOC_Os06g07210	ribonucleoside-diphosphate reductase large subunit, putative, expressed	**1.33**	down	**1.04**	down	**4.02**	down	**1.18**	down	**1.62**	down	**1.56**	down	ABA
Os.4223.1.S1_s_at	LOC_Os06g07220	LTPL128 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.25**	down	**1.35**	down	**8.63**	up	**1.06**	down	**1.30**	down	**1.55**	down	ABA
Os.42285.1.S1_x_at	LOC_Os01g58550	methyladenine glycosylase, putative, expressed	**2.12**	up	**1.13**	down	**1.24**	down	**1.05**	up	**1.04**	up	**1.42**	down	IAA
Os.42305.1.S1_s_at	LOC_Os01g58194	protein disulfide isomerase, putative, expressed	**1.52**	up	**1.72**	down	**30.36**	up	**1.15**	up	**1.84**	up	**1.03**	up	ABA
Os.42305.2.S1_x_at	LOC_Os01g58194	protein disulfide isomerase, putative, expressed	**1.62**	up	**1.42**	down	**37.97**	up	**1.07**	down	**1.29**	up	**1.20**	down	ABA
Os.4264.1.S1_at	LOC_Os02g10070	citrate synthase, putative, expressed	**1.01**	up	**1.08**	up	**2.41**	up	**1.09**	up	**2.02**	up	**1.68**	up	2
Os.42681.1.S1_at	LOC_Os01g65560	snRK1-interacting protein 1, putative, expressed	**1.13**	down	**1.02**	down	**2.32**	down	**1.10**	up	**1.45**	down	**1.48**	down	ABA
Os.42759.1.S1_at	LOC_Os01g68830	expressed protein	**1.27**	down	**1.02**	up	**2.44**	down	**1.10**	down	**1.17**	down	**1.08**	up	ABA
Os.42796.1.S1_at	NM_189846	---	**1.18**	up	**1.31**	up	**2.52**	down	**1.18**	up	**1.25**	down	**1.15**	down	ABA
Os.42801.1.S1_at	LOC_Os07g42626	STRUBBELIG-RECEPTOR FAMILY 6 precursor, putative, expressed	**2.00**	up	**1.58**	up	**4.42**	up	**1.27**	down	**1.18**	up	**2.12**	down	3
Os.4281.1.S1_x_at	LOC_Os06g03830	retinol dehydrogenase, putative, expressed	**1.59**	down	**3.62**	up	**3.97**	down	**1.14**	up	**1.35**	down	**1.46**	down	2
Os.42812.1.A1_at	LOC_Os07g42520	dirigent, putative, expressed	**1.12**	down	**1.09**	up	**2.71**	down	**1.05**	down	**1.26**	down	**1.21**	down	ABA
Os.4324.1.S1_at	LOC_Os03g03670	expressed protein	**1.20**	up	**1.13**	up	**6.00**	down	**1.30**	down	**1.72**	down	**1.22**	down	ABA
Os.43375.1.S1_at	AK241759	glutathione transferase (EC 2.5.1.18) 27K chain - maize	**1.08**	down	**1.06**	down	**12.04**	up	**1.05**	down	**1.93**	up	**1.14**	up	ABA
Os.4338.1.S1_at	LOC_Os03g03820	adenylate kinase, putative, expressed	**1.11**	up	**1.07**	down	**2.36**	down	**1.13**	up	**1.07**	up	**1.08**	up	ABA
Os.43491.1.S1_x_at	LOC_Os01g11620	GDSL-like lipase/acylhydrolase, putative, expressed	**1.33**	up	**1.15**	down	**2.96**	up	**1.02**	up	**1.33**	up	**1.37**	up	ABA
Os.43596.1.S1_at	LOC_Os01g10110	cytokinin dehydrogenase precursor, putative, expressed	**1.01**	down	**727.12**	up	**4.17**	up	**1.00**	up	**1.00**	down	**1.06**	up	2
Os.4370.2.S1_x_at	LOC_Os06g06780	harpin-induced protein, putative, expressed	**1.16**	up	**1.01**	down	**2.34**	down	**1.57**	down	**1.45**	down	**1.11**	up	ABA
Os.4379.1.S1_at	LOC_Os08g36790	bZIP transcription factor, putative, expressed	**1.07**	down	**1.04**	down	**3.73**	up	**1.09**	down	**1.19**	up	**1.05**	up	ABA
Os.43896.1.S1_at	LOC_Os03g08900	MATE efflux family protein, putative, expressed	**2.28**	up	**1.34**	down	**2.16**	up	**1.07**	down	**7.35**	up	**2.79**	up	4
Os.4404.1.S1_at	LOC_Os06g01966	auxin-induced protein 5NG4, putative, expressed	**1.35**	up	**1.12**	up	**27.87**	down	**1.85**	down	**2.13**	down	**2.18**	down	3
Os.4404.1.S1_s_at	LOC_Os06g01966	auxin-induced protein 5NG4, putative, expressed	**1.51**	up	**1.10**	up	**16.33**	down	**1.70**	down	**2.01**	down	**1.84**	down	2
Os.44475.1.S1_at	LOC_Os07g37730	NADH-ubiquinone oxidoreductase, mitochondrial precursor, putative, expressed	**4.61**	up	**1.80**	up	**1.48**	up	**2.25**	down	**9.40**	up	**3.28**	up	4
Os.44475.1.S1_x_at	LOC_Os07g37730	NADH-ubiquinone oxidoreductase, mitochondrial precursor, putative, expressed	**4.88**	up	**1.53**	up	**1.22**	up	**2.21**	down	**8.06**	up	**2.87**	up	4
Os.4453.1.S1_at	LOC_Os06g03520	DUF581 domain containing protein, expressed	**1.25**	down	**1.45**	down	**7.11**	down	**1.33**	up	**1.16**	up	**1.04**	up	ABA

Os.4458.1.S1_at	LOC_Os06g03580	zinc RING finger protein, putative, expressed	**1.12**	down	**1.04**	down	**4.32**	down	**1.07**	down	**1.56**	up	**1.04**	down	ABA
Os.44613.1.S1_at	LOC_Os07g46610	cis-zeatin O-glucosyltransferase, putative, expressed	**1.03**	down	**1.46**	up	**2.34**	up	**1.37**	up	**1.88**	up	**2.95**	up	2
Os.44735.1.S1_at	LOC_Os06g07760	sulfiredoxin-1, putative, expressed	**1.13**	up	**1.05**	down	**3.02**	up	**1.08**	up	**1.42**	up	**1.08**	up	ABA
Os.44806.1.A1_x_at	LOC_Os06g03800	pollen ankyrin, putative, expressed	**1.14**	up	**1.14**	down	**7.95**	up	**1.22**	down	**1.33**	down	**1.09**	up	ABA
Os.44850.1.S1_at	LOC_Os06g01990	phosphoglycolate phosphatase, plasmid, putative, expressed	**1.25**	up	**1.08**	up	**2.43**	down	**1.11**	up	**1.41**	down	**1.41**	up	ABA
Os.44872.1.S1_at	LOC_Os06g01660	integral membrane protein DUF6 domain containing protein, expressed	**1.09**	down	**1.08**	up	**4.64**	up	**1.01**	up	**1.02**	up	**1.28**	down	ABA
Os.44872.2.S1_x_at	LOC_Os06g01660	integral membrane protein DUF6 domain containing protein, expressed	**1.08**	up	**1.15**	down	**5.41**	up	**1.08**	down	**1.01**	down	**1.20**	down	ABA
Os.44937.1.S1_at	LOC_Os03g60810	lectin-like receptor kinase, putative, expressed	**1.39**	down	**1.19**	down	**4.83**	down	**1.19**	down	**1.02**	up	**1.97**	up	ABA
Os.4506.3.S1_x_at	LOC_Os06g02370	expressed protein	**1.20**	up	**1.15**	down	**2.20**	down	**1.20**	down	**1.41**	down	**1.42**	down	ABA
Os.4509.1.S1_x_at	LOC_Os06g02410	expressed protein	**1.18**	up	**1.20**	up	**5.66**	up	**1.60**	down	**1.20**	down	**1.29**	down	ABA
Os.45250.1.S1_at	LOC_Os03g25460	OsRCI2-4 - Putative low temperature and salt responsive protein, expressed	**1.17**	up	**1.22**	up	**3.35**	up	**1.10**	down	**1.19**	down	**1.58**	down	ABA
Os.45427.1.A1_at	LOC_Os01g04120	ZOS1-03 - C2H2 zinc finger protein, expressed	**1.18**	up	**2.71**	up	**1.15**	down	**1.19**	up	**1.61**	down	**1.82**	down	BAP
Os.456.1.S1_a_at	LOC_Os05g18604	OsSCP28 - Putative Serine Carboxypeptidase homologue, expressed	**1.04**	down	**1.08**	up	**1.10**	down	**1.02**	down	**1.14**	up	**2.40**	up	JA
Os.456.3.S1_s_at	LOC_Os05g18604	OsSCP28 - Putative Serine Carboxypeptidase homologue, expressed	**1.05**	up	**1.04**	up	**1.01**	up	**1.06**	down	**1.03**	up	**2.03**	up	JA
Os.45878.1.S1_at	NM_001049410	Oryza sativa (japonica cultivar-group) Os01g0315700 (Os01g0315700) mRNA, partial	**1.11**	down	**1.34**	down	**3.27**	up	**1.04**	up	**1.21**	up	**1.21**	down	ABA
Os.459.1.S1_at	LOC_Os03g46070	thaumatin, putative, expressed	**1.90**	down	**1.53**	up	**1.43**	down	**1.41**	down	**1.19**	down	**2.23**	up	JA
Os.45902.1.A1_at	LOC_Os01g27270	retrotransposon protein, putative, unclassified	**1.12**	down	**1.32**	up	**1.12**	down	**1.12**	up	**1.06**	up	**4.84**	up	JA
Os.45916.1.S1_x_at	LOC_Os01g14850	MFS18 protein precursor, putative, expressed	**1.00**	up	**1.19**	down	**2.15**	down	**1.14**	down	**1.27**	down	**1.16**	down	ABA
Os.45920.1.S1_at	LOC_Os03g01530	tubulin/FtsZ domain containing protein, putative, expressed	**1.16**	down	**1.10**	down	**3.03**	down	**1.10**	down	**1.58**	down	**1.33**	down	ABA
Os.45923.1.S1_at	LOC_Os01g37590	peptide transporter PTR2, putative, expressed	**1.47**	up	**1.15**	up	**79.44**	up	**1.51**	down	**1.38**	up	**1.57**	down	ABA
Os.45926.1.S1_s_at	LOC_Os01g09700	aminotransferase, classes I and II, domain containing protein, expressed	**4.45**	up	**1.27**	up	**2.51**	up	**1.13**	up	**1.01**	down	**1.29**	down	2
Os.45928.1.S1_at	LOC_Os01g32460	expressed protein	**1.13**	up	**1.24**	down	**7.35**	down	**1.05**	down	**1.33**	down	**1.16**	up	ABA
Os.45929.1.S1_at	LOC_Os05g34170	tubulin/FtsZ domain containing protein, putative, expressed	**1.17**	up	**1.17**	up	**3.22**	down	**1.25**	down	**1.44**	down	**1.37**	down	ABA
Os.45957.1.S1_at	LOC_Os11g11694	retrotransposon protein, putative, unclassified, expressed	**2.12**	up	**1.05**	up	**3.47**	up	**1.14**	up	**1.68**	up	**1.44**	up	2
Os.45963.1.S1_at	LOC_Os01g11670	OsSCP2 - Putative Serine Carboxypeptidase homologue, expressed	**1.38**	down	**1.26**	down	**2.50**	down	**2.12**	up	**1.16**	down	**1.82**	up	2
Os.45975.1.S1_a_at	LOC_Os03g27250	OsFBO14 - F-box and other domain containing protein, expressed	**1.05**	up	**1.08**	down	**2.36**	up	**1.15**	down	**1.12**	up	**1.15**	down	ABA
Os.45991.1.S1_x_at	LOC_Os01g10440	xylosyltransferase, putative, expressed	**1.61**	up	**1.13**	up	**5.85**	up	**1.56**	up	**5.07**	up	**1.84**	up	2
Os.45998.1.S1_x_at	LOC_Os03g12620	glycosyl hydrolases family 17, putative, expressed	**1.38**	up	**1.18**	down	**6.07**	down	**1.39**	down	**2.84**	down	**1.42**	down	2
Os.46006.1.S1_at	LOC_Os07g47140	CCT/B-box zinc finger protein, putative, expressed	**1.05**	down	**1.03**	down	**4.28**	down	**1.08**	down	**1.16**	down	**1.02**	up	ABA
Os.46021.1.S1_at	LOC_Os01g46580	actin-related protein 2/3 complex subunit 2, putative, expressed	**1.35**	up	**1.91**	up	**22.12**	up	**1.45**	down	**1.23**	up	**1.39**	down	ABA
Os.46041.1.S1_at	LOC_Os01g18210	peptidyl-prolyl cis-trans isomerase, putative, expressed	**1.06**	up	**1.01**	down	**3.00**	down	**1.04**	down	**1.40**	down	**1.14**	up	ABA
Os.46049.1.S1_at	LOC_Os01g41870	protein kinase, putative, expressed	**1.01**	down	**1.04**	up	**3.19**	down	**1.07**	up	**1.19**	down	**1.02**	up	ABA
Os.4605.1.S1_at	LOC_Os10g41230	homeobox associated leucine zipper, putative, expressed	**2.73**	up	**1.43**	up	**4.27**	up	**1.08**	up	**1.11**	down	**1.31**	down	2
Os.46073.1.A1_at	LOC_Os04g33150	desiccation-related protein PCC13-62 precursor, putative, expressed	**4.13**	down	**1.15**	up	**3.25**	up	**1.05**	down	**3.41**	down	**8.74**	up	4
Os.46074.1.A1_at	LOC_Os10g05210	OsFBX368 - F-box domain containing protein, expressed	**1.19**	up	**1.02**	up	**2.14**	up	**1.00**	down	**1.15**	up	**1.10**	down	ABA
Os.4608.3.A1_a_at	LOC_Os06g43860	homeobox protein knotted-1, putative, expressed	**1.09**	up	**1.08**	up	**2.15**	down	**1.11**	down	**1.18**	down	**1.20**	down	ABA
Os.46093.1.S1_at	LOC_Os10g33900	possible lysine decarboxylase domain containing protein, expressed	**1.65**	up	**1.22**	down	**2.83**	down	**1.05**	up	**1.01**	down	**1.78**	down	ABA
Os.46160.2.S1_at	LOC_Os10g30790	inorganic phosphate transporter, putative, expressed	**1.61**	down	**1.07**	up	**1.01**	up	**1.33**	up	**2.95**	up	**1.13**	up	SA
Os.46160.2.S1_x_at	LOC_Os10g30790	inorganic phosphate transporter, putative, expressed	**1.22**	down	**1.10**	up	**1.25**	down	**1.23**	up	**2.46**	up	**1.01**	up	SA
Os.4618.1.S1_at	LOC_Os01g32670	expressed protein	**2.18**	up	**1.77**	up	**1.39**	down	**2.10**	up	**12.17**	up	**1.61**	down	3
Os.46187.1.S1_at	LOC_Os07g40940	X8 domain containing protein, expressed	**1.09**	down	**1.09**	down	**2.05**	down	**1.25**	down	**1.30**	down	**1.07**	down	ABA
Os.4619.1.S1_at	CT836472	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN061P16, full insert sequence	**1.18**	up	**1.07**	down	**2.64**	down	**1.29**	down	**1.50**	down	**1.25**	up	ABA
Os.46219.1.S1_at	LOC_Os02g16709	peptidase, putative, expressed	**1.01**	up	**1.15**	up	**3.57**	down	**1.14**	down	**1.54**	down	**1.27**	down	ABA
Os.46223.1.S1_s_at	LOC_Os09g33690	Os9bglu32 - beta-glucosidase homologue, similar to G. max hydroxyisourate hydrolase	**1.18**	up	**1.03**	down	**2.86**	up	**1.01**	down	**1.07**	up	**1.05**	up	ABA
Os.4633.1.S1_at	LOC_Os01g59970	expressed protein	**1.14**	up	**1.10**	down	**2.15**	up	**1.11**	down	**1.18**	down	**1.89**	down	ABA
Os.4634.1.S1_at	LOC_Os09g10274	expressed protein	**1.26**	down	**1.34**	down	**3.72**	down	**1.11**	up	**1.37**	down	**1.09**	up	ABA
Os.4644.1.S1_at	LOC_Os01g60770	expansin precursor, putative, expressed	**1.32**	up	**2.70**	up	**16.47**	down	**1.33**	up	**2.54**	down	**1.08**	down	3
Os.46443.1.S1_at	LOC_Os10g42430	transcription factor MYC7E, putative, expressed	**1.15**	down	**1.14**	up	**1.48**	down	**1.22**	up	**1.12**	down	**3.49**	up	JA
Os.46453.1.S1_a_at	LOC_Os10g13550	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	**2.43**	up	**1.09**	down	**2.05**	down	**1.16**	down	**1.18**	down	**1.13**	down	2
Os.46460.1.S1_at	LOC_Os10g04610	OsFBX360 - F-box domain containing protein, expressed	**1.00**	down	**1.12**	down	**3.08**	up	**1.06**	up	**1.22**	up	**1.03**	down	ABA
Os.46472.1.S1_at	LOC_Os10g07290	glycosyl hydrolases family 17, putative, expressed	**1.18**	down	**1.02**	down	**2.57**	down	**1.03**	down	**1.27**	down	**1.32**	down	ABA
Os.46477.1.S1_at	LOC_Os10g28060	3-ketoacyl-CoA synthase, putative, expressed	**1.17**	down	**1.07**	down	**2.40**	down	**1.04**	up	**1.08**	down	**1.03**	up	ABA
Os.46492.1.S1_at	LOC_Os10g04370	OsFBX357 - F-box domain containing protein, expressed	**1.02**	down	**1.00**	down	**2.45**	up	**1.01**	up	**1.03**	up	**1.02**	up	ABA
Os.46498.1.S1_at	LOC_Os10g11310	expressed protein	**1.10**	down	**1.19**	up	**3.00**	up	**1.05**	down	**1.20**	down	**1.14**	down	ABA
Os.46498.2.S1_x_at	LOC_Os10g11310	expressed protein	**1.04**	down	**1.02**	up	**2.70**	up	**1.06**	down	**1.38**	down	**1.03**	up	ABA

Os.46507.1.S1_at	LOC_Os10g39980	expressed protein	**1.14**	down	**1.27**	down	**8.03**	down	**1.07**	up	**3.14**	down	**4.04**	down	3
Os.46525.1.S1_at	LOC_Os10g12354	endonuclease, putative, expressed	**1.14**	up	**1.33**	up	**2.28**	down	**1.20**	down	**1.47**	down	**1.50**	down	ABA
Os.46540.1.S1_at	LOC_Os10g41060	expressed protein	**8.87**	up	**1.43**	down	**1.17**	up	**1.27**	down	**1.61**	up	**1.20**	down	IAA
Os.46576.1.S1_at	LOC_Os10g36100	LTPL157 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.10**	down	**2.28**	up	**1.04**	up	**1.03**	down	**1.04**	up	**1.82**	up	BAP
Os.46576.1.S1_x_at	LOC_Os10g36100	LTPL157 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.25**	up	**2.19**	up	**1.33**	up	**1.26**	up	**1.51**	up	**1.98**	up	BAP
Os.46580.1.S1_at	LOC_Os10g19200	vegetative cell wall protein gp1 precursor, putative, expressed	**1.10**	down	**1.09**	up	**3.41**	down	**1.33**	up	**1.35**	down	**1.27**	down	ABA
Os.46582.1.S1_at	LOC_Os10g36180	expressed protein	**1.38**	up	**1.39**	up	**335.68**	up	**1.05**	down	**2.45**	up	**1.08**	up	2
Os.46582.2.S1_x_at	LOC_Os10g36180	expressed protein	**1.01**	up	**1.01**	up	**32.58**	up	**1.14**	up	**1.04**	down	**1.13**	up	ABA
Os.46589.1.S1_at	LOC_Os10g17790	remorin C-terminal domain containing protein, putative, expressed	**1.02**	up	**1.19**	down	**2.02**	up	**1.06**	down	**1.08**	up	**1.12**	down	ABA
Os.4660.1.S1_s_at	LOC_Os03g10860	expressed protein	**1.20**	up	**1.20**	up	**2.81**	down	**1.16**	up	**1.34**	down	**1.57**	up	ABA
Os.46600.1.S1_at	LOC_Os10g23050	helix-loop-helix DNA-binding protein, putative, expressed	**1.06**	down	**1.35**	up	**1.30**	up	**3.91**	up	**4.20**	up	**1.83**	up	2
Os.46610.1.S1_x_at	LOC_Os12g43165	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	**2.05**	down	**1.18**	down	**1.11**	up	**1.34**	up	**1.16**	up	**1.05**	up	IAA
Os.46613.1.S1_s_at	LOC_Os10g42900	peptide transporter PTR2, putative, expressed	**1.13**	down	**1.42**	down	**4.49**	down	**1.39**	down	**1.69**	down	**1.26**	up	ABA
Os.46617.1.S1_at	LOC_Os10g41560	expressed protein	**1.16**	down	**1.11**	down	**5.48**	up	**1.01**	down	**1.20**	up	**1.20**	down	ABA
Os.46618.1.S1_at	LOC_Os10g41550	beta-amylase, putative, expressed	**1.74**	up	**1.28**	up	**15.29**	up	**1.42**	up	**2.17**	up	**3.67**	up	3
Os.46629.1.S1_s_at	LOC_Os10g40480	LTPL143 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.04**	down	**1.73**	up	**1.37**	down	**1.05**	down	**1.97**	down	**3.12**	down	JA
Os.46631.1.S1_x_at	LOC_Os10g39840	glycosyl hydrolases family 16, putative, expressed	**1.25**	down	**1.64**	up	**4.15**	down	**1.28**	up	**1.17**	down	**1.10**	up	ABA
Os.46633.1.A1_at	LOC_Os10g38940	fatty acid hydroxylase, putative, expressed	**2.52**	up	**1.67**	up	**3.29**	down	**1.82**	up	**3.15**	down	**2.01**	down	4
Os.46634.1.S1_x_at	AK241921	glutathione S-transferase, putative	**2.66**	up	**1.92**	up	**2.69**	up	**1.67**	up	**4.88**	up	**2.19**	up	4
Os.46635.1.S1_x_at	LOC_Os10g38350	glutathione S-transferase, putative, expressed	**2.64**	up	**1.10**	up	**4.92**	up	**1.11**	down	**7.72**	up	**1.58**	up	3
Os.46638.1.S1_at	LOC_Os10g37770	dehydration response related protein, putative, expressed	**1.11**	down	**1.16**	down	**2.70**	down	**1.13**	up	**1.31**	down	**1.07**	down	ABA
Os.46645.1.S1_at	LOC_Os10g36924	aquaporin protein, putative, expressed	**1.23**	down	**1.75**	down	**2.57**	down	**1.07**	down	**1.07**	up	**1.09**	down	ABA
Os.46687.1.S1_at	LOC_Os10g25550	tyrosine protein kinase domain containing protein, putative, expressed	**1.25**	down	**1.23**	down	**3.53**	down	**1.33**	up	**1.10**	down	**1.19**	down	ABA
Os.46687.1.S1_x_at	LOC_Os10g25550	tyrosine protein kinase domain containing protein, putative, expressed	**1.11**	down	**1.26**	down	**3.63**	down	**1.31**	up	**1.06**	down	**1.12**	down	ABA
Os.46689.1.S1_at	LOC_Os10g25210	OsFBX384 - F-box domain containing protein, expressed	**1.88**	up	**1.10**	down	**2.85**	up	**1.14**	up	**3.77**	up	**1.59**	up	2
Os.46695.1.S1_at	LOC_Os10g21790	dehydration stress-induced protein, putative, expressed	**1.23**	up	**1.42**	up	**15.61**	up	**1.60**	up	**1.29**	up	**1.48**	up	ABA
Os.467.1.S1_a_at	LOC_Os01g42380	pleiotropic drug resistance protein, putative, expressed	**1.17**	up	**2.17**	up	**3.81**	up	**1.56**	up	**6.24**	up	**8.51**	up	4
Os.4671.1.S1_a_at	LOC_Os01g24710	jacalin-like lectin domain containing protein, expressed	**1.11**	down	**1.07**	up	**3.42**	up	**1.39**	up	**1.58**	up	**1.70**	up	ABA
Os.4671.2.S1_a_at	LOC_Os04g42470	regulatory subunit, putative, expressed	**1.07**	up	**1.06**	down	**2.63**	up	**1.12**	down	**1.23**	up	**1.38**	down	ABA
Os.46718.1.S1_at	LOC_Os10g08319	cytochrome P450, putative, expressed	**1.76**	down	**1.17**	down	**4.46**	down	**1.34**	down	**1.47**	down	**3.72**	up	2
Os.46725.1.S1_at	LOC_Os10g05130	expressed protein	**1.39**	down	**1.23**	up	**9.93**	down	**1.11**	down	**2.52**	down	**1.01**	up	2
Os.46740.1.A1_at	LOC_Os10g01640	decarboxylase, putative	**3.55**	down	**5.51**	down	**3.61**	down	**1.21**	up	**3.72**	down	**2.74**	down	5
Os.46741.1.S1_at	LOC_Os10g01570	C-5 cytosine-specific DNA methylase, putative, expressed	**1.19**	down	**1.23**	down	**4.08**	down	**1.14**	down	**2.19**	down	**1.75**	down	2
Os.46741.2.S1_x_at	LOC_Os10g01570	C-5 cytosine-specific DNA methylase, putative, expressed	**1.15**	down	**1.13**	down	**3.96**	down	**1.29**	down	**2.58**	down	**1.48**	down	2
Os.46749.1.S1_x_at	LOC_Os09g27990	annexin, putative, expressed	**1.23**	up	**4.00**	up	**3.61**	down	**1.49**	down	**1.44**	up	**2.88**	down	3
Os.46758.1.S1_at	AK120868	phospholipase D zeta1	**1.20**	down	**1.09**	down	**5.02**	up	**1.10**	down	**1.03**	up	**1.68**	down	ABA
Os.46758.1.S1_s_at	AK120868	phospholipase D zeta1	**1.14**	down	**1.15**	down	**4.32**	up	**1.03**	down	**1.26**	up	**1.12**	down	ABA
Os.46767.1.S1_at	AK119988	Oryza sativa Japonica Group cDNA clone:002-184-G03, full insert sequence.	**1.02**	up	**1.10**	down	**4.43**	up	**1.03**	down	**1.03**	up	**1.00**	up	ABA
Os.46783.1.S1_a_at	LOC_Os10g26280	ORC3 - Putative origin recognition complex subunit 3, expressed	**1.57**	down	**1.36**	down	**4.60**	down	**1.08**	up	**2.98**	down	**1.82**	down	2
Os.4679.1.S1_at	AK108349	Oryza sativa Japonica Group cDNA clone:002-142-B10, full insert sequence.	**1.45**	up	**1.32**	up	**3.85**	down	**1.45**	up	**1.08**	down	**1.00**	down	ABA
Os.46791.1.S1_at	LOC_Os10g09240	expressed protein	**1.01**	down	**1.02**	up	**42.34**	up	**1.01**	up	**1.04**	down	**1.02**	up	ABA
Os.46793.1.S1_at	LOC_Os10g05660	thaumatin, putative, expressed	**1.66**	up	**2.15**	up	**3.52**	down	**1.46**	up	**1.12**	up	**2.72**	up	3
Os.4681.1.S1_at	LOC_Os08g40690	glycosyl hydrolase, putative, expressed	**1.35**	down	**1.46**	up	**6.85**	up	**2.98**	up	**2.75**	up	**1.04**	up	3
Os.46810.1.S1_at	LOC_Os03g19452	SMP-30/Gluconolaconase/LRE domain protein, putative, expressed	**1.25**	down	**1.14**	up	**2.71**	down	**1.11**	down	**1.38**	down	**1.38**	down	ABA
Os.46823.1.S1_at	LOC_Os10g41480	phospho-2-dehydro-3-deoxyheptonate aldolase, chloroplast precursor, putative, expres	**1.06**	up	**1.00**	up	**38.69**	up	**1.12**	up	**2.37**	up	**1.21**	up	2
Os.46823.2.S1_x_at	LOC_Os10g41480	phospho-2-dehydro-3-deoxyheptonate aldolase, chloroplast precursor, putative, expres	**1.09**	down	**1.09**	down	**8.88**	up	**1.01**	up	**1.03**	down	**1.03**	up	ABA
Os.4683.1.S1_at	AK100678	pyruvate decarboxylase, putative	**1.47**	down	**1.22**	up	**10.47**	up	**2.65**	up	**9.54**	up	**4.76**	up	4
Os.46836.1.S1_at	LOC_Os10g38820	bZIP family transcription factor, putative, expressed	**1.78**	up	**1.44**	up	**2.37**	up	**1.12**	down	**1.05**	up	**1.09**	down	ABA
Os.46842.1.S1_at	AK108440	Oryza sativa (japonica cultivar-group) Os10g0466800 (Os10g0466800) mRNA, comple	**1.42**	up	**2.59**	up	**1.13**	up	**1.58**	down	**2.55**	down	**2.32**	down	3
Os.46844.1.S1_at	LOC_Os10g25400	GDSL-like lipase/acylhydrolase, putative, expressed	**1.24**	down	**1.13**	down	**1.12**	down	**1.17**	up	**3.13**	up	**15.13**	up	2
Os.46846.1.S1_at	LOC_Os10g37540	OsFBDUF48 - F-box and DUF domain containing protein, expressed	**1.02**	up	**1.04**	down	**1.07**	up	**1.11**	up	**32.04**	up	**1.10**	up	SA
Os.46849.1.S1_at	LOC_Os10g25230	ZIM domain containing protein, putative, expressed	**1.44**	down	**2.16**	up	**1.81**	down	**1.33**	up	**1.10**	up	**14.09**	up	2
Os.46852.1.S1_at	LOC_Os10g41430	cyclin, putative, expressed	**1.22**	down	**1.12**	down	**3.07**	down	**1.24**	down	**1.27**	down	**1.33**	down	ABA
Os.46858.1.S1_at	LOC_Os10g38860	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.08**	up	**1.13**	up	**3.83**	up	**1.39**	down	**1.06**	down	**1.34**	down	ABA
Os.46872.1.S1_at	LOC_Os10g37160	transposon protein, putative, unclassified, expressed	**1.05**	down	**1.03**	down	**1.19**	down	**1.56**	down	**4.08**	up	**3.92**	up	2

Os.46881.1.S1_at	LOC_Os10g39770	zinc finger, C3HC4 type, domain containing protein, expressed	**1.73**	down	**1.06**	up	**2.17**	down	**1.51**	up	**1.41**	down	**1.42**	down	ABA
Os.46890.1.S1_s_at	LOC_Os10g37640	HIT zinc finger domain containing protein, expressed	**1.13**	down	**1.08**	up	**2.32**	up	**1.15**	down	**1.18**	up	**1.45**	down	ABA
Os.46890.1.S1_x_at	LOC_Os10g37640	HIT zinc finger domain containing protein, expressed	**1.14**	down	**1.16**	up	**2.39**	up	**1.01**	down	**1.31**	up	**1.15**	down	ABA
Os.46890.2.S1_at	LOC_Os10g37640	HIT zinc finger domain containing protein, expressed	**1.05**	up	**1.11**	up	**2.20**	up	**1.13**	down	**1.00**	up	**1.07**	down	ABA
Os.46895.1.S1_at	LOC_Os10g34230	cytokinin dehydrogenase precursor, putative, expressed	**1.23**	down	**7.67**	up	**2.60**	down	**1.23**	down	**1.37**	down	**1.23**	down	2
Os.46896.1.S1_at	LOC_Os10g39870	ATG1, putative, expressed	**1.23**	up	**1.06**	up	**1.10**	up	**1.45**	up	**2.82**	up	**1.44**	up	SA
Os.46924.1.S1_at	LOC_Os07g40690	NAD dependent epimerase/dehydratase family protein, putative, expressed	**1.28**	up	**1.27**	up	**15.78**	down	**1.15**	down	**1.63**	down	**1.57**	down	ABA
Os.4693.1.S1_at	LOC_Os04g52830	OsFBK15 - F-box domain and kelch repeat containing protein, expressed	**1.16**	down	**1.14**	down	**2.05**	down	**1.05**	down	**1.22**	down	**1.16**	up	ABA
Os.46941.1.S1_s_at	LOC_Os06g48500	expressed protein	**1.07**	down	**1.34**	up	**4.03**	up	**1.10**	up	**1.38**	up	**1.59**	down	ABA
Os.4695.1.S1_s_at	LOC_Os03g28940	ZIM domain containing protein, putative, expressed	**1.64**	up	**1.01**	down	**1.92**	down	**1.01**	up	**1.15**	down	**3.06**	up	JA
Os.4700.1.S1_at	LOC_Os07g47100	transporter, monovalent cation:proton antiporter-2 family, putative, expressed	**2.91**	up	**1.03**	down	**8.17**	up	**1.88**	down	**1.23**	up	**1.23**	down	2
Os.47000.1.S1_x_at	LOC_Os10g42220	enoyl-CoA hydratase/isomerase family protein, putative	**1.10**	up	**1.10**	down	**2.39**	up	**1.03**	up	**1.65**	up	**1.41**	up	ABA
Os.47251.1.S1_at	LOC_Os06g11600	growth regulator related protein, putative, expressed	**1.02**	up	**1.06**	down	**2.44**	up	**1.10**	down	**1.02**	down	**1.05**	down	ABA
Os.47290.1.S1_at	LOC_Os04g34240	histone H3, putative, expressed	**1.29**	down	**1.04**	down	**6.78**	down	**1.55**	down	**3.15**	down	**2.96**	down	3
Os.4730.1.S1_at	CT837944	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN025B22, full insert sequence	**1.11**	up	**1.08**	down	**2.41**	up	**1.01**	up	**1.01**	up	**1.12**	up	ABA
Os.47303.1.S1_at	LOC_Os01g54030	NADP-dependent malic enzyme, putative, expressed	**1.01**	up	**1.04**	up	**368.54**	up	**1.14**	down	**1.25**	down	**1.08**	down	ABA
Os.47303.1.S1_s_at	LOC_Os01g54030	NADP-dependent malic enzyme, putative, expressed	**1.02**	down	**1.06**	up	**386.31**	up	**1.48**	down	**1.51**	down	**1.46**	down	ABA
Os.47313.1.A1_at	LOC_Os01g64820	POLA1 - Putative DNA polymerase alpha catalytic subunit, expressed	**1.33**	down	**1.01**	down	**5.37**	down	**1.03**	down	**2.09**	down	**1.65**	down	2
Os.47314.1.S2_at	LOC_Os08g39100	protein phosphatase 2C, putative, expressed	**1.08**	down	**1.12**	up	**2.10**	down	**1.17**	down	**1.44**	down	**1.10**	down	ABA
Os.47327.1.S1_at	LOC_Os03g52380	PIII5 - Proteinase inhibitor II family protein precursor, expressed	**1.32**	down	**1.33**	up	**6.33**	up	**1.05**	up	**1.98**	up	**1.69**	up	ABA
Os.47327.1.S1_x_at	LOC_Os03g52380	PIII5 - Proteinase inhibitor II family protein precursor, expressed	**1.14**	down	**1.32**	up	**5.77**	up	**1.10**	down	**2.14**	up	**1.86**	up	2
Os.47333.1.S1_at	LOC_Os09g34000	expressed protein	**1.11**	up	**1.17**	up	**2.03**	down	**1.14**	down	**1.30**	down	**1.14**	down	ABA
Os.47344.1.A1_at	LOC_Os11g07440	plant neutral invertase domain containing protein, expressed	**1.52**	up	**1.25**	up	**2.27**	down	**1.02**	down	**2.12**	up	**1.30**	up	2
Os.47352.1.S1_s_at	LOC_Os05g29860	mitochondrial carrier protein, putative, expressed	**1.27**	up	**1.13**	up	**2.73**	down	**1.19**	down	**1.60**	down	**1.38**	down	ABA
Os.47373.1.S1_at	LOC_Os03g11110	zinc finger family protein, putative, expressed	**1.16**	down	**1.13**	down	**2.22**	down	**1.11**	down	**1.38**	down	**1.36**	down	ABA
Os.4738.2.S1_x_at	LOC_Os03g56800	CBS domain containing membrane protein, putative, expressed	**1.04**	down	**1.06**	up	**2.41**	down	**1.04**	up	**1.42**	down	**1.00**	down	ABA
Os.47381.1.S1_x_at	LOC_Os04g36800	3-oxoacyl-synthase, putative, expressed	**1.23**	up	**1.07**	up	**6.33**	down	**1.08**	down	**2.36**	down	**1.10**	down	2
Os.47381.2.S1_at	LOC_Os04g36800	3-oxoacyl-synthase, putative, expressed	**1.14**	up	**1.24**	up	**6.57**	down	**1.23**	down	**2.39**	down	**1.44**	down	2
Os.47401.1.A1_s_at	LOC_Os02g58550	chloroplast channel forming outer membrane protein, putative, expressed	**1.11**	up	**1.03**	up	**2.22**	down	**1.27**	down	**1.54**	down	**1.27**	down	ABA
Os.4741.2.S1_x_at	LOC_Os10g41930	haloacid dehalogenase-like hydrolase family protein, putative, expressed	**4.04**	up	**1.02**	up	**4.46**	up	**1.28**	up	**5.02**	up	**1.29**	up	3
Os.47413.1.S1_at	LOC_Os06g33100	peroxidase precursor, putative, expressed	**3.19**	down	**1.39**	up	**14.37**	down	**3.61**	up	**1.05**	up	**1.32**	up	3
Os.47413.1.S1_x_at	LOC_Os06g33100	peroxidase precursor, putative, expressed	**2.96**	down	**1.28**	up	**10.22**	down	**3.39**	up	**1.22**	down	**1.15**	up	3
Os.47438.1.A1_at	LOC_Os10g38470	glutathione S-transferase, putative, expressed	**1.15**	up	**1.09**	down	**3.06**	up	**1.60**	up	**2.26**	up	**1.44**	up	2
Os.47472.1.S1_at	LOC_Os09g39410	male sterility protein, putative, expressed	**1.06**	down	**1.03**	up	**2.15**	down	**1.25**	up	**1.07**	down	**1.31**	up	ABA
Os.47474.1.S1_at	LOC_Os06g44160	heat shock protein DnaJ, putative, expressed	**1.00**	down	**1.55**	up	**2.73**	up	**1.12**	up	**1.04**	up	**1.13**	down	ABA
Os.47490.1.S1_at	LOC_Os08g39550	polygalacturonase inhibitor 2 precursor, putative, expressed	**1.20**	up	**1.11**	up	**2.38**	down	**1.03**	up	**1.02**	down	**1.53**	down	ABA
Os.4750.1.S1_x_at	LOC_Os01g15970	expressed protein	**1.42**	down	**1.17**	down	**2.50**	down	**1.34**	down	**1.65**	down	**1.86**	down	ABA
Os.47560.1.S1_at	LOC_Os12g06660	actin, putative, expressed	**1.23**	down	**1.10**	up	**6.24**	down	**1.09**	up	**2.86**	down	**3.58**	down	3
Os.4759.1.S1_at	LOC_Os09g20220	glutathione S-transferase, putative, expressed	**33.75**	up	**1.38**	up	**33.43**	up	**2.18**	up	**102.03**	up	**9.17**	up	5
Os.4760.1.S1_at	LOC_Os04g39420	6-phosphofructokinase 2, putative, expressed	**1.05**	down	**1.19**	down	**9.60**	up	**1.13**	up	**1.79**	up	**1.19**	up	ABA
Os.47600.1.S1_s_at	LOC_Os02g54730	transmembrane amino acid transporter protein, putative, expressed	**1.12**	up	**1.41**	up	**2.29**	down	**1.17**	up	**1.24**	down	**1.63**	down	ABA
Os.47600.2.S1_x_at	LOC_Os02g54730	transmembrane amino acid transporter protein, putative, expressed	**1.19**	up	**1.39**	up	**2.24**	down	**1.32**	up	**1.20**	down	**1.33**	down	ABA
Os.47601.1.A1_at	LOC_Os12g12720	jasmonate-induced protein, putative, expressed	**1.60**	down	**1.57**	down	**3.01**	down	**1.55**	down	**4.19**	down	**13.79**	up	3
Os.4762.1.S1_at	LOC_Os10g38740	glutathione S-transferase, putative, expressed	**4.45**	up	**1.04**	up	**2.45**	up	**1.26**	up	**4.78**	up	**1.63**	up	3
Os.47660.1.S1_s_at	LOC_Os05g03480	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed	**1.04**	up	**1.04**	down	**2.39**	up	**1.24**	up	**1.70**	up	**1.44**	up	ABA
Os.4770.1.S1_a_at	LOC_Os01g06560	transcription factor HBP-1b, putative, expressed	**1.02**	up	**1.02**	down	**18.87**	up	**1.46**	up	**2.79**	up	**1.00**	up	2
Os.47717.1.A1_s_at	LOC_Os01g64670	soluble inorganic pyrophosphatase, putative, expressed	**1.01**	down	**1.04**	up	**20.32**	up	**1.04**	up	**1.03**	down	**1.01**	up	ABA
Os.47726.1.S1_at	LOC_Os12g34890	acyl carrier protein, putative, expressed	**1.16**	up	**1.11**	up	**3.76**	down	**1.24**	down	**1.90**	down	**1.25**	down	ABA
Os.4773.1.S1_at	LOC_Os06g04240	expressed protein	**1.24**	up	**1.09**	up	**3.28**	up	**1.32**	down	**2.10**	up	**1.02**	up	2
Os.47730.2.S1_x_at	AK072692	nucleoside triphosphatase precursor, chromatin-associated	**1.02**	up	**1.19**	down	**3.35**	down	**2.01**	down	**1.14**	up	**1.99**	up	3
Os.47732.1.S1_s_at	LOC_Os12g36640	universal stress protein domain containing protein, putative, expressed	**1.24**	up	**1.01**	up	**2.71**	up	**1.24**	up	**1.28**	up	**1.21**	down	ABA
Os.47735.1.S1_at	LOC_Os02g34970	no apical meristem protein, putative, expressed	**1.45**	up	**3.31**	down	**20.19**	up	**1.17**	up	**2.76**	up	**1.57**	up	3
Os.47750.1.A1_at	LOC_Os01g50900	Cupin domain containing protein, expressed	**1.06**	up	**1.01**	up	**2.52**	up	**1.01**	up	**1.00**	up	**1.05**	up	ABA
Os.47761.1.S1_at	LOC_Os03g13300	glutamate decarboxylase, putative, expressed	**1.08**	up	**1.23**	down	**3.95**	up	**1.32**	up	**4.07**	up	**1.08**	up	2
Os.47778.1.A1_s_at	LOC_Os04g33640	glycosyl hydrolases family 17, putative, expressed	**1.44**	up	**1.26**	up	**4.92**	up	**1.02**	up	**1.08**	up	**1.41**	down	ABA

Os.4780.1.S1_at	LOC_Os03g55290	GASR3 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expresse	**1.53**	up	**1.16**	down	**5.75**	up	**1.34**	up	**3.30**	up	**1.08**	down	2
Os.47814.1.A1_s_at	LOC_Os09g38130	auxin efflux carrier component, putative, expressed	**2.85**	up	**1.32**	down	**4.85**	up	**1.88**	up	**2.77**	up	**2.41**	up	4
Os.4782.1.S1_at	AK111769	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN048K14, full insert sequence	**1.09**	down	**1.16**	down	**4.57**	up	**1.12**	up	**1.81**	up	**1.16**	up	ABA
Os.4784.1.S1_at	LOC_Os09g31040	EF hand family protein, putative, expressed	**1.09**	down	**2.56**	up	**4.39**	up	**1.12**	up	**3.03**	up	**1.44**	up	3
Os.47854.1.S1_at	LOC_Os02g46780	MYB family transcription factor, putative, expressed	**1.32**	down	**1.40**	down	**2.35**	down	**1.26**	up	**1.16**	down	**4.13**	up	2
Os.47871.1.S1_at	LOC_Os06g51440	transposon protein, putative, CACTA, En/Spm sub-class, expressed	**1.01**	down	**1.04**	up	**34.70**	up	**1.05**	up	**1.07**	up	**1.09**	up	ABA
Os.47875.1.S1_s_at	LOC_Os05g34290	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	**1.04**	down	**1.05**	up	**1.10**	down	**1.05**	down	**2.50**	up	**1.30**	up	SA
Os.47879.1.A1_at	AK111367	Oryza sativa Japonica Group cDNA clone:002-182-A01, full insert sequence.	**1.27**	down	**1.30**	down	**3.80**	down	**1.64**	down	**1.61**	down	**1.40**	down	ABA
Os.47900.1.A1_at	AK106506	Oryza sativa Japonica Group cDNA clone:002-105-G01, full insert sequence.	**1.03**	up	**1.00**	down	**1.03**	up	**1.03**	up	**4.29**	up	**1.27**	up	SA
Os.47914.1.S1_at	LOC_Os06g11210	12-oxophytodienoate reductase, putative, expressed	**5.55**	up	**1.32**	up	**1.56**	down	**1.29**	up	**4.13**	up	**2.13**	up	3
Os.47938.1.S1_at	LOC_Os04g43290	ARPC2B, putative, expressed	**1.05**	down	**1.25**	up	**4.32**	down	**2.99**	down	**2.72**	down	**1.37**	down	3
Os.47958.1.A1_x_at	LOC_Os01g61410	NADH-ubiquinone oxidoreductase, mitochondrial precursor, putative, expressed	**1.14**	up	**1.04**	down	**3.25**	up	**1.11**	down	**1.22**	up	**1.23**	up	ABA
Os.47961.2.S1_x_at	LOC_Os01g38990	mitochondrial carrier protein, putative, expressed	**1.17**	down	**1.25**	down	**3.19**	up	**1.26**	up	**1.50**	up	**1.74**	up	ABA
Os.47962.1.S1_at	LOC_Os01g35160	TKL_IRAK_DUF26-lh.4 - DUF26 kinases have homology to DUF26 containing loci, exp	**1.23**	down	**1.01**	up	**2.87**	up	**1.11**	up	**1.15**	up	**1.04**	down	ABA
Os.47962.1.S1_x_at	LOC_Os01g35160	TKL_IRAK_DUF26-lh.4 - DUF26 kinases have homology to DUF26 containing loci, exp	**1.03**	down	**1.01**	up	**2.65**	up	**1.12**	down	**1.01**	down	**1.04**	down	ABA
Os.47971.1.A1_at	LOC_Os05g49350	DUF1645 domain containing protein, putative, expressed	**1.48**	up	**1.01**	up	**3.76**	up	**1.49**	down	**1.02**	up	**1.17**	down	ABA
Os.47976.1.S1_at	AK289245	Oryza sativa Japonica Group cDNA, clone: J100077H08, full insert sequence.	**1.18**	up	**1.15**	up	**1.99**	down	**1.66**	down	**3.21**	down	**2.49**	down	3
Os.47989.1.S1_at	LOC_Os04g57800	BTBN13 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hy	**1.50**	up	**1.15**	up	**2.73**	up	**1.46**	up	**1.00**	down	**1.69**	down	ABA
Os.4799.1.S1_at	LOC_Os06g23684	tyrosine aminotransferase, putative, expressed	**1.11**	down	**1.49**	down	**11.27**	up	**1.11**	up	**1.40**	up	**1.42**	up	ABA
Os.47996.1.A1_at	LOC_Os01g36390	MCM4 - Putative minichromosome maintenance MCM complex subunit 4, expressed	**1.35**	down	**1.19**	down	**8.60**	down	**1.01**	down	**2.37**	down	**1.58**	down	2
Os.47997.1.A1_at	LOC_Os01g43950	expressed protein	**1.33**	up	**1.30**	down	**2.84**	up	**1.00**	up	**1.37**	down	**2.98**	down	2
Os.48003.1.A1_at	LOC_Os01g47840	S-locus-like receptor protein kinase, putative, expressed	**1.83**	down	**2.83**	down	**1.70**	down	**2.98**	up	**2.24**	up	**12.16**	up	4
Os.48013.1.A1_at	LOC_Os03g12230	caleosin related protein, putative, expressed	**1.12**	down	**1.22**	up	**15.36**	up	**1.20**	down	**1.01**	down	**1.03**	up	ABA
Os.48017.1.S1_x_at	LOC_Os07g46420	expressed protein	**1.08**	down	**1.00**	down	**2.58**	up	**1.09**	up	**1.04**	up	**1.11**	up	ABA
Os.48018.1.S1_at	LOC_Os06g03570	pentatricopeptide, putative, expressed	**1.09**	down	**1.04**	up	**2.33**	down	**1.63**	up	**1.39**	down	**1.32**	up	ABA
Os.48038.1.S1_at	LOC_Os02g55340	WD domain and HEAT domain containing protein, putative, expressed	**1.07**	up	**1.06**	down	**2.17**	up	**1.03**	up	**1.16**	up	**1.19**	down	ABA
Os.4804.1.S1_at	LOC_Os06g07030	AP2 domain containing protein, expressed	**1.26**	down	**1.54**	down	**4.17**	up	**1.19**	up	**1.40**	up	**1.12**	up	ABA
Os.4806.1.S1_at	LOC_Os02g57250	OsIAA10 - Auxin-responsive Aux/IAA gene family member, expressed	**3.07**	up	**1.12**	up	**1.64**	down	**1.74**	down	**1.03**	down	**1.61**	down	IAA
Os.48061.1.A1_x_at	LOC_Os06g18670	anthocyanidin 3-O-glucosyltransferase, putative, expressed	**1.17**	up	**1.01**	up	**1.09**	down	**2.05**	down	**1.05**	down	**1.25**	up	ACC
Os.48064.1.S1_at	LOC_Os09g26780	zinc-finger protein, putative, expressed	**1.01**	down	**1.01**	down	**2.52**	down	**1.31**	down	**1.48**	down	**4.17**	up	2
Os.4807.1.S1_at	LOC_Os04g54200	diacylglycerol kinase, putative, expressed	**1.17**	down	**1.09**	up	**3.55**	down	**1.17**	up	**1.61**	down	**1.16**	up	ABA
Os.48072.1.S1_at	LOC_Os02g55410	MCM5 - Putative minichromosome maintenance MCM complex subunit 5, expressed	**1.57**	down	**1.21**	down	**6.17**	down	**1.06**	down	**2.13**	down	**1.71**	down	2
Os.48077.1.A1_at	LOC_Os12g26060	bifunctional dihydrofolate reductase-thymidylate synthase, putative, expressed	**1.27**	down	**1.12**	down	**6.43**	down	**1.37**	down	**2.54**	down	**2.60**	down	3
Os.48082.1.S1_at	LOC_Os09g25070	OsWRKY62 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**1.02**	down	**1.36**	down	**11.70**	down	**1.65**	up	**4.03**	up	**1.78**	up	2
Os.48095.1.S1_s_at	LOC_Os06g13830	endoglucanase, putative, expressed	**1.00**	down	**1.06**	up	**2.11**	down	**1.08**	up	**1.34**	down	**1.28**	up	ABA
Os.4810.1.S1_s_at	LOC_Os06g12740	expressed protein	**2.10**	down	**1.11**	up	**2.35**	down	**1.41**	down	**1.10**	down	**1.66**	up	2
Os.48101.1.S1_at	LOC_Os04g54810	beta-D-xylosidase, putative, expressed	**1.01**	up	**1.06**	down	**3.57**	down	**1.16**	down	**1.54**	down	**1.13**	down	ABA
Os.48105.1.A1_at	LOC_Os06g15620	GASR7 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expresse	**1.42**	up	**1.14**	up	**8.33**	down	**1.30**	up	**1.06**	down	**1.46**	down	ABA
Os.48131.1.S1_s_at	LOC_Os04g58890	expressed protein	**2.37**	up	**1.14**	up	**3.67**	up	**1.01**	down	**1.89**	up	**1.99**	up	3
Os.48215.1.A1_at	LOC_Os05g43940	O-methyltransferase, putative, expressed	**1.06**	down	**1.45**	up	**2.90**	down	**1.08**	down	**1.82**	down	**2.05**	up	2
Os.48216.1.S1_at	LOC_Os09g34250	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.17**	up	**1.23**	down	**2.00**	up	**1.05**	up	**3.31**	up	**1.92**	up	2
Os.4822.1.S1_at	LOC_Os05g08570	OsIAA15 - Auxin-responsive Aux/IAA gene family member, expressed	**2.77**	up	**1.01**	down	**1.05**	down	**1.13**	down	**1.19**	up	**1.06**	up	IAA
Os.48260.1.S2_at	LOC_Os02g52490	expressed protein	**1.11**	down	**1.07**	up	**5.20**	up	**1.36**	down	**1.41**	down	**1.79**	down	ABA
Os.48263.1.S1_at	LOC_Os04g55120	jp18, putative, expressed	**1.09**	up	**1.03**	down	**4.87**	down	**1.12**	down	**1.22**	down	**1.26**	down	ABA
Os.48278.2.S1_x_at	LOC_Os03g48600	domain of unknown function DUF966 domain containing protein, expressed	**1.44**	up	**1.30**	down	**2.14**	down	**1.38**	down	**1.26**	down	**1.37**	down	ABA
Os.48287.1.S1_at	LOC_Os04g38570	multidrug resistance protein, putative, expressed	**1.07**	up	**1.02**	down	**2.24**	down	**1.05**	up	**1.09**	down	**1.63**	down	ABA
Os.48291.1.S1_at	LOC_Os04g59580	zinc finger, C3HC4 type domain containing protein, expressed	**1.06**	down	**1.13**	down	**2.23**	up	**1.12**	down	**1.09**	up	**1.29**	down	ABA
Os.48328.1.S1_at	LOC_Os01g24560	fruit bromelain precursor, putative, expressed	**2.76**	down	**1.67**	up	**35.57**	down	**1.02**	down	**6.79**	down	**5.68**	down	4
Os.48353.1.S1_at	LOC_Os02g51130	glycosyl transferase 8 domain containing protein, putative, expressed	**1.32**	up	**1.22**	down	**2.76**	down	**1.12**	down	**1.02**	down	**1.18**	down	ABA
Os.48388.1.S1_at	LOC_Os12g34500	expressed protein	**1.02**	down	**1.03**	down	**3.86**	down	**1.10**	down	**1.59**	down	**1.24**	down	ABA
Os.48412.1.A1_at	LOC_Os08g38890	expressed protein	**1.09**	down	**1.07**	down	**2.75**	up	**1.05**	down	**1.02**	down	**1.28**	up	ABA
Os.48418.1.S1_at	LOC_Os11g24374	OsSCP55 - Putative Serine Carboxypeptidase homologue, expressed	**1.15**	down	**1.30**	up	**5.96**	down	**1.32**	down	**1.07**	up	**2.49**	up	2
Os.48429.1.S1_at	LOC_Os03g63970	gibberellin 20 oxidase 1, putative, expressed	**3.68**	down	**1.66**	up	**9.75**	down	**1.12**	up	**1.89**	down	**1.42**	down	2
Os.48438.1.S1_at	LOC_Os03g05806	pseudouridine synthase family protein, putative, expressed	**1.06**	down	**1.08**	up	**3.30**	down	**1.24**	down	**1.59**	down	**1.38**	down	ABA
Os.4844.1.S1_at	LOC_Os05g06970	peroxidase precursor, putative, expressed	**1.58**	down	**1.24**	down	**4.33**	down	**1.58**	up	**1.24**	down	**1.73**	down	ABA

Os.48443.1.S1_at	LOC_Os12g03130	CDC45A - Putative DNA replication initiation protein, expressed	1.52	down	1.05	down	3.87	down	1.32	down	2.11	down	1.51	down	2
Os.48498.1.S1_at	LOC_Os03g08110	hydrolase protein, putative, expressed	1.23	up	1.78	up	10.15	up	1.03	up	1.37	up	2.43	up	2
Os.48563.1.S1_x_at	LOC_Os01g45060	polygalacturonase, putative	1.09	up	1.42	down	2.47	down	1.03	down	2.02	down	1.05	down	2
Os.4862.1.S1_at	LOC_Os02g50350	dihydroorotate dihydrogenase protein, putative, expressed	1.09	down	1.06	up	5.04	up	1.12	up	1.35	up	1.58	up	ABA
Os.4863.1.S1_at	LOC_Os01g44050	siroheme synthase, putative, expressed	5.83	up	1.40	down	1.78	up	1.12	up	6.72	up	1.12	up	2
Os.4863.2.S1_at	LOC_Os01g44050	siroheme synthase, putative, expressed	7.37	up	1.62	down	1.96	up	1.05	up	7.80	up	1.29	up	2
Os.48636.1.S1_at	LOC_Os08g41400	expressed protein	1.10	up	1.06	down	3.00	down	1.35	down	1.39	down	1.47	down	ABA
Os.4866.1.S1_at	LOC_Os01g31980	MATE efflux family protein, putative, expressed	1.00	up	1.01	down	1.07	down	1.17	up	2.15	up	2.30	up	2
Os.4867.1.S1_at	LOC_Os08g40680	glycosyl hydrolase, putative, expressed	1.67	down	1.59	up	7.02	up	1.14	up	2.96	up	1.65	up	2
Os.48695.1.S1_s_at	EF575785	Oryza sativa (indica cultivar-group) clone OSE-97-192-C10 putative serine threonine k	2.05	down	1.06	down	8.58	down	1.68	up	1.05	up	1.13	up	2
Os.48695.1.S1_x_at	EF575785	Oryza sativa (indica cultivar-group) clone OSE-97-192-C10 putative serine threonine k	1.82	down	1.06	down	10.45	down	1.83	up	1.05	up	1.23	up	ABA
Os.48702.1.A1_at	LOC_Os07g31960	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	1.02	down	1.71	up	3.26	down	1.20	up	1.12	up	1.52	up	ABA
Os.48782.1.S1_at	LOC_Os12g10520	OsMADS33 - MADS-box family gene with MIKCc type-box, expressed	1.01	down	1.03	up	2.69	up	1.03	up	1.00	up	1.08	up	ABA
Os.4881.1.S1_s_at	LOC_Os07g41600	proline-rich protein, putative, expressed	1.09	up	1.01	up	3.14	up	1.10	up	1.61	up	2.23	up	2
Os.4882.1.S2_at	AK106599	Oryza sativa Japonica Group cDNA clone:002-112-B01, full insert sequence.	1.12	down	1.01	up	2.28	down	1.10	down	1.09	up	1.02	down	ABA
Os.48830.1.S1_at	LOC_Os07g38490	GDP-fucose protein-O-fucosyltransferase 2, putative, expressed	1.36	down	1.17	down	2.05	down	1.20	down	1.51	down	1.33	up	ABA
Os.48846.1.S1_at	LOC_Os09g24840	GASR10 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expresse	4.97	up	2.02	up	1.23	down	1.54	up	1.06	up	1.20	down	2
Os.48856.1.S1_at	LOC_Os08g04110	transporter, putative, expressed	1.11	down	1.04	down	1.70	down	1.08	down	1.05	up	2.40	up	JA
Os.48857.1.S1_a_at	LOC_Os01g51840	IQ calmodulin-binding motif family protein, putative, expressed	1.00	up	1.04	down	2.36	down	1.13	down	1.39	down	1.40	down	ABA
Os.48871.1.A1_at	LOC_Os05g27790	membrane associated DUF588 domain containing protein, putative, expressed	1.19	down	1.20	down	5.66	up	1.01	down	1.14	up	1.94	down	ABA
Os.4890.1.S1_at	LOC_Os07g05570	ERD4 protein, putative, expressed	1.07	down	1.12	down	2.07	down	1.05	down	1.28	down	1.06	down	ABA
Os.4891.1.S1_at	LOC_Os03g06200	aminotransferase, putative, expressed	1.39	up	1.16	up	1.55	down	1.36	up	2.49	up	1.65	up	SA
Os.4893.1.S1_at	LOC_Os05g29810	AP2 domain containing protein, expressed	1.18	up	1.27	up	8.34	up	3.36	up	1.62	up	2.96	up	3
Os.48981.1.S1_at	LOC_Os07g40240	GASR9 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expresse	1.02	up	1.40	down	10.71	up	1.68	up	1.38	up	1.27	up	ABA
Os.4900.2.A1_x_at	LOC_Os03g11550	protein of unknown function DUF1675 domain containing protein, expressed	1.07	up	1.01	up	4.86	up	1.12	up	1.11	up	1.18	down	ABA
Os.49023.1.S1_x_at	LOC_Os03g22680	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	1.09	down	1.05	up	6.01	up	1.30	up	1.01	up	1.01	down	ABA
Os.49030.1.A1_s_at	LOC_Os09g20220	glutathione S-transferase, putative, expressed	17.60	up	1.38	up	14.72	up	1.80	up	27.68	up	5.95	up	4
Os.49042.1.A1_s_at	LOC_Os01g09620	zinc finger/CCCH transcription factor, putative, expressed	1.17	up	1.09	down	2.14	up	1.00	up	1.20	down	1.19	down	ABA
Os.49050.1.S1_at	LOC_Os02g34580	ammonium transporter protein, putative, expressed	3.17	down	2.02	down	5.09	down	1.15	up	5.31	down	2.91	down	4
Os.49073.1.S1_at	LOC_Os01g12570	3-methyl-2-oxobutanoate hydroxymethyltransferase, putative, expressed	1.05	down	4.09	up	14.15	up	1.25	down	1.62	down	7.51	up	3
Os.49088.1.S1_at	LOC_Os04g44890	tRNA-dihydrouridine synthase, putative, expressed	1.08	down	1.04	up	2.44	up	1.17	up	1.69	up	1.32	up	ABA
Os.49088.2.S1_at	LOC_Os04g44890	tRNA-dihydrouridine synthase, putative, expressed	1.02	down	1.32	down	4.19	up	1.05	up	1.62	up	1.58	up	ABA
Os.49093.1.S1_a_at	LOC_Os02g02170	transporter, major facilitator family, putative, expressed	1.09	up	1.75	down	2.10	up	1.41	down	1.14	up	1.50	down	ABA
Os.49093.2.S1_x_at	LOC_Os02g02190	transporter, major facilitator family, putative, expressed	1.21	up	2.05	down	1.57	up	1.01	down	1.38	up	1.04	down	BAP
Os.49105.1.S1_at	LOC_Os02g44770	uncharacterized mscS family protein, putative, expressed	1.15	up	1.01	down	16.30	up	1.16	down	2.66	up	1.23	up	2
Os.49108.2.S1_x_at	LOC_Os04g32540	OsSCP24 - Putative Serine Carboxypeptidase homologue, expressed	1.01	down	1.05	up	2.99	down	1.21	down	1.39	down	1.54	down	ABA
Os.49109.1.S2_at	LOC_Os08g38850	phosphatidylinositol transfer, putative, expressed	1.56	up	1.15	up	2.22	down	1.03	down	1.18	down	1.13	down	ABA
Os.49114.1.S1_at	LOC_Os03g63550	expressed protein	1.13	down	1.09	down	2.11	down	1.02	up	1.29	down	1.01	down	ABA
Os.49117.2.A1_at	LOC_Os04g48830	DUF623 domain containing protein, expressed	1.10	down	1.16	down	2.53	up	1.02	up	1.01	up	1.04	up	ABA
Os.49120.1.S1_at	AK064156	membrane bound O-acyl transferase (MBOAT) family protein	2.18	down	1.44	up	3.86	down	1.30	down	1.19	down	1.19	down	2
Os.49135.1.S1_at	LOC_Os01g72520	phosphoesterase family protein, putative, expressed	1.04	up	1.40	up	4.70	up	1.21	down	1.61	up	1.12	down	ABA
Os.49146.1.S1_at	LOC_Os05g51240	hydrolase, alpha/beta fold family domain containing protein, expressed	1.25	down	1.15	up	2.26	down	1.20	down	2.60	down	1.80	down	2
Os.49149.1.S1_at	AK106080	plastid-lipid associated protein PAP / fibrillin family protein	1.56	up	1.39	up	5.90	down	1.34	down	1.60	down	1.22	down	ABA
Os.49151.1.S1_at	LOC_Os11g44800	expressed protein	1.51	down	1.69	up	13.46	up	1.46	down	1.31	down	1.68	down	ABA
Os.49153.1.A1_x_at	LOC_Os10g39440	transporter family protein, putative, expressed	1.06	down	1.15	down	3.08	up	1.23	down	1.09	down	1.21	down	ABA
Os.49160.1.S1_at	LOC_Os04g40300	transglutaminase, putative, expressed	1.14	up	1.05	down	2.26	up	1.05	down	1.10	up	1.09	down	ABA
Os.49194.1.S1_at	LOC_Os04g32840	formin-like protein 20, putative, expressed	1.75	down	1.36	down	4.31	down	1.68	up	1.37	down	1.89	down	ABA
Os.49201.1.S1_at	LOC_Os09g29820	bZIP transcription factor domain containing protein, expressed	1.83	down	1.16	down	3.09	down	1.46	up	1.01	up	1.16	up	ABA
Os.49208.1.S1_at	LOC_Os04g34270	serine/threonine-protein kinase receptor precursor, putative, expressed	1.29	up	1.99	down	11.40	down	3.92	up	2.84	down	1.01	up	3
Os.49242.1.S1_at	LOC_Os05g46220	mitochondrial carrier protein, putative, expressed	1.14	down	1.03	down	2.80	up	1.02	up	1.11	up	1.19	down	ABA
Os.49245.1.S1_at	LOC_Os02g43330	homeobox associated leucine zipper, putative, expressed	1.13	up	3.89	down	1298.28	up	1.10	down	2.24	up	1.12	down	3
Os.49252.1.S1_x_at	AK069129	Oryza sativa Japonica Group cDNA clone:J023007E02, full insert sequence.	1.04	up	1.01	up	2.18	up	1.01	down	1.01	down	1.01	up	ABA
Os.49255.1.S1_at	LOC_Os10g27300	expressed protein	1.03	down	1.30	up	2.54	up	1.13	up	1.55	up	1.03	up	ABA
Os.49259.1.S1_at	LOC_Os05g16824	SHR5-receptor-like kinase, putative, expressed	1.22	up	1.10	down	1.64	up	1.19	up	1.62	up	8.47	up	JA
Os.49290.1.S1_at	LOC_Os06g39590	OsIAA23 - Auxin-responsive Aux/IAA gene family member, expressed	1.54	up	1.88	up	3.55	down	1.28	down	1.18	up	1.27	down	ABA

Os.49290.1.S1_x_at	LOC_Os06g39590	OsIAA23 - Auxin-responsive Aux/IAA gene family member, expressed	**1.64**	up	**1.74**	up	**3.36**	down	**1.26**	down	**1.15**	up	**1.22**	down	ABA
Os.49313.1.S1_a_at	LOC_Os03g55100	cyclic nucleotide-gated ion channel 2, putative, expressed	**1.04**	down	**1.10**	down	**2.59**	up	**1.52**	down	**1.01**	up	**1.16**	down	ABA
Os.49324.1.S1_at	LOC_Os04g44354	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.01**	down	**1.00**	up	**1.03**	down	**1.07**	up	**1.00**	up	**8.86**	up	JA
Os.49352.1.S1_at	LOC_Os11g15570	Ser/Thr protein phosphatase family protein, putative, expressed	**1.93**	down	**1.44**	up	**4.35**	down	**1.12**	down	**1.02**	down	**1.46**	up	ABA
Os.4936.1.S1_at	LOC_Os09g21340	nucleobase-ascorbate transporter, putative, expressed	**1.35**	up	**1.14**	up	**2.95**	up	**1.01**	down	**1.10**	up	**1.14**	down	ABA
Os.49369.1.S1_at	LOC_Os06g42800	STRUBBELIG-RECEPTOR FAMILY 8 precursor, putative, expressed	**1.11**	down	**1.06**	down	**2.27**	down	**1.39**	down	**1.31**	down	**1.14**	up	ABA
Os.49381.1.S1_at	LOC_Os08g26820	plant protein of unknown function domain containing protein, expressed	**1.40**	down	**1.16**	down	**5.87**	down	**1.04**	up	**1.45**	down	**1.31**	down	ABA
Os.49410.1.A1_at	LOC_Os04g33240	sex determination protein tasselseed-2, putative, expressed	**1.23**	up	**1.10**	down	**2.09**	up	**1.42**	down	**2.83**	up	**8.53**	up	3
Os.49436.1.S1_x_at	LOC_Os04g45460	cysteine-rich repeat secretory protein precursor, putative, expressed	**1.93**	up	**1.03**	down	**1.11**	up	**1.13**	down	**1.89**	down	**2.22**	down	JA
Os.49442.2.S1_x_at	LOC_Os03g44760	SWI1, putative, expressed	**1.24**	up	**1.33**	up	**2.61**	up	**1.01**	up	**1.11**	up	**1.22**	down	ABA
Os.49448.1.S1_at	LOC_Os01g72210	early-responsive to dehydration protein-related, putative, expressed	**1.71**	up	**1.58**	up	**31.81**	up	**1.60**	up	**1.82**	up	**1.02**	down	ABA
Os.4945.1.S1_at	LOC_Os09g01960	MYB family transcription factor, putative, expressed	**1.19**	down	**1.74**	down	**2.64**	up	**1.11**	up	**1.05**	down	**1.39**	up	ABA
Os.49451.1.S1_at	LOC_Os08g34780	adenylyl cyclase-associated protein, putative, expressed	**1.01**	down	**1.04**	up	**13.55**	up	**1.02**	up	**1.00**	down	**1.02**	up	ABA
Os.49453.1.S1_at	LOC_Os02g08270	class I glutamine amidotransferase, putative, expressed	**2.23**	down	**1.00**	down	**19.77**	down	**1.64**	down	**1.91**	down	**3.93**	up	3
Os.49464.1.S1_at	LOC_Os04g58560	cysteine protease ATG4, putative, expressed	**1.01**	down	**1.03**	up	**2.11**	up	**1.02**	down	**1.13**	up	**1.03**	up	ABA
Os.49475.1.S1_at	LOC_Os03g25790	glycosyl hydrolases family 17 protein, expressed	**1.27**	up	**1.16**	up	**6.43**	up	**1.10**	up	**1.35**	up	**1.26**	down	ABA
Os.49479.1.S1_at	LOC_Os05g05020	expressed protein	**1.30**	down	**1.11**	up	**1.14**	up	**1.44**	down	**1.12**	up	**2.09**	up	JA
Os.49482.1.S1_at	LOC_Os01g12920	thioesterase family protein, putative, expressed	**1.00**	up	**1.01**	down	**3.67**	up	**1.27**	down	**1.33**	up	**1.00**	down	ABA
Os.49485.1.S1_at	LOC_Os09g25770	auxin-induced protein 5NG4, putative, expressed	**1.05**	down	**1.09**	down	**7.96**	up	**1.35**	down	**2.04**	up	**1.63**	up	2
Os.49489.1.S1_at	LOC_Os11g07950	expressed protein	**1.12**	up	**1.11**	up	**4.06**	down	**1.16**	up	**1.22**	up	**1.03**	up	ABA
Os.49496.1.S1_at	LOC_Os06g46500	monocopper oxidase, putative, expressed	**1.03**	down	**1.09**	up	**3.20**	down	**1.28**	up	**1.55**	down	**1.37**	up	ABA
Os.49506.1.S1_at	LOC_Os07g09010	nodulin, putative, expressed	**1.57**	down	**1.11**	down	**3.97**	up	**1.11**	down	**1.29**	up	**1.02**	down	ABA
Os.49514.1.S1_at	LOC_Os02g16680	bZIP transcription factor domain containing protein, expressed	**1.06**	up	**1.11**	down	**2.33**	up	**1.17**	down	**1.16**	up	**1.03**	down	ABA
Os.49521.1.S1_at	LOC_Os04g36040	peptide transporter PTR2, putative, expressed	**1.20**	down	**2.35**	up	**2.96**	up	**1.20**	up	**1.42**	up	**1.46**	down	2
Os.49524.1.S1_at	LOC_Os11g39990	patatin, putative, expressed	**1.15**	down	**1.10**	down	**1.23**	down	**1.12**	up	**1.53**	down	**2.71**	up	JA
Os.49526.1.S1_a_at	LOC_Os06g42560	tryptophan synthase beta chain 2, putative, expressed	**1.15**	up	**1.20**	up	**1.09**	up	**1.15**	down	**2.62**	up	**1.96**	up	SA
Os.49529.1.S1_at	LOC_Os06g43810	expressed protein	**1.34**	down	**1.49**	up	**4.68**	down	**1.12**	down	**1.65**	down	**1.85**	down	ABA
Os.49538.1.S1_at	LOC_Os03g43010	expressed protein	**1.32**	down	**1.57**	up	**4.35**	down	**1.20**	down	**1.88**	down	**2.23**	up	2
Os.49545.1.S1_at	LOC_Os11g32030	sex determination protein tasselseed-2, putative, expressed	**3.52**	up	**1.51**	down	**2.23**	down	**1.07**	up	**1.65**	up	**1.11**	up	2
Os.49550.1.S1_at	LOC_Os09g29120	GRAM domain containing protein, expressed	**1.20**	up	**1.06**	down	**6.38**	up	**1.25**	down	**1.26**	down	**1.23**	down	ABA
Os.49552.1.S1_at	LOC_Os09g36900	WD domain, G-beta repeat domain containing protein, expressed	**1.22**	down	**1.37**	down	**3.11**	down	**1.10**	down	**1.87**	down	**1.96**	down	ABA
Os.49568.1.S1_at	LOC_Os04g56900	transferase family protein, putative, expressed	**1.82**	down	**2.94**	up	**1.42**	down	**1.10**	down	**1.12**	up	**1.24**	up	BAP
Os.49572.1.A1_at	LOC_Os06g11090	CXE carboxylesterase, putative, expressed	**1.42**	down	**1.13**	up	**3.58**	up	**1.07**	down	**1.07**	down	**1.06**	down	ABA
Os.49577.1.S1_at	LOC_Os02g50340	membrane attack complex component/perforin/complement C9, putative, expressed	**1.38**	up	**1.22**	up	**5.66**	up	**1.11**	up	**2.66**	up	**1.53**	down	2
Os.4958.1.A1_at	LOC_Os01g68830	expressed protein	**1.16**	down	**1.05**	up	**2.00**	down	**1.11**	down	**1.12**	down	**1.14**	down	ABA
Os.49588.1.S1_at	AK287943	zinc finger (C2H2 type) family protein	**1.72**	up	**1.11**	down	**5.38**	up	**1.35**	up	**1.17**	down	**1.04**	down	ABA
Os.49601.1.S1_at	LOC_Os06g46940	Os6bglu25 - beta-glucosidase homologue, similar to Os3bglu6, expressed	**1.38**	up	**1.17**	up	**3.69**	up	**1.13**	down	**2.02**	down	**1.08**	down	2
Os.49608.1.S1_at	LOC_Os03g15340	plastocyanin-like domain containing protein, putative, expressed	**1.07**	down	**2.14**	up	**1.39**	up	**2.14**	down	**2.58**	down	**11.38**	down	4
Os.49621.1.S1_at	LOC_Os07g25590	decarboxylase, putative, expressed	**1.03**	down	**1.18**	down	**2.86**	down	**1.08**	down	**1.47**	down	**1.23**	down	ABA
Os.4963.1.S1_at	LOC_Os10g33240	expressed protein	**1.02**	down	**1.03**	up	**4.88**	up	**1.01**	up	**1.01**	up	**1.05**	up	ABA
Os.49631.2.S1_x_at	LOC_Os07g33350	hsp20/alpha crystallin family protein, putative, expressed	**1.25**	down	**1.16**	up	**10.57**	down	**1.03**	up	**1.60**	down	**1.26**	down	ABA
Os.49634.1.S1_x_at	LOC_Os01g55510	dynein light chain type 1 domain containing protein, expressed	**1.20**	up	**1.06**	up	**2.59**	down	**1.01**	down	**1.02**	down	**1.81**	up	ABA
Os.49639.1.S1_at	LOC_Os06g21910	late embryogenesis abundant group 1, putative, expressed	**1.01**	down	**1.01**	down	**1140.85**	up	**1.01**	up	**1.01**	up	**1.08**	up	ABA
Os.49648.1.S1_at	LOC_Os02g54140	hsp20/alpha crystallin family protein, putative, expressed	**1.01**	down	**1.16**	down	**54.09**	up	**1.10**	down	**3.43**	up	**1.03**	up	2
Os.49648.1.S1_s_at	LOC_Os02g54140	hsp20/alpha crystallin family protein, putative, expressed	**2.07**	down	**1.10**	down	**205.97**	up	**1.01**	down	**7.06**	up	**1.10**	up	3
Os.4965.1.S1_at	LOC_Os03g59440	dirigent, putative, expressed	**2.50**	down	**1.51**	up	**84.76**	down	**1.11**	up	**18.46**	down	**2.13**	down	4
Os.49655.1.S1_at	LOC_Os06g09420	B3 DNA binding domain containing protein, expressed	**1.10**	down	**1.01**	up	**2.79**	down	**1.16**	down	**1.52**	down	**1.04**	down	ABA
Os.49657.1.S1_at	LOC_Os09g28560	protein phosphotase protein, putative, expressed	**4.33**	up	**1.16**	down	**3.42**	up	**1.44**	up	**1.27**	up	**1.55**	down	2
Os.49658.1.S1_at	LOC_Os05g45810	calcineurin B, putative, expressed	**1.34**	up	**1.06**	down	**4.66**	up	**1.45**	down	**1.10**	down	**1.25**	down	ABA
Os.49662.1.S1_at	LOC_Os09g31000	EF hand family protein, expressed	**1.99**	down	**2.13**	up	**1.06**	up	**1.01**	up	**1.31**	up	**1.22**	up	BAP
Os.49664.1.S1_at	LOC_Os03g21160	RNA-binding zinc finger protein, putative, expressed	**1.07**	down	**1.11**	up	**8.45**	down	**1.09**	down	**2.19**	down	**3.56**	down	3
Os.49668.1.S1_at	LOC_Os03g16060	expressed protein	**1.67**	up	**1.12**	down	**2.01**	down	**1.19**	up	**1.13**	up	**1.17**	up	ABA
Os.49676.1.S1_at	AK105164	Oryza sativa (japonica cultivar-group) Os04g0649600 (Os04g0649600) mRNA, comple	**1.27**	up	**1.19**	up	**3.20**	up	**1.26**	up	**1.74**	down	**1.89**	down	ABA
Os.49677.1.S1_at	LOC_Os11g07600	ABC-2 type transporter domain containing protein, expressed	**1.22**	up	**1.16**	up	**7.92**	up	**1.27**	down	**1.06**	down	**1.20**	up	ABA
Os.4972.1.S1_at	LOC_Os07g42280	von Willebrand factor type A domain containing protein, expressed	**1.09**	down	**1.05**	down	**3.12**	up	**1.23**	down	**1.59**	up	**1.11**	down	ABA

Os.49726.1.S1_at	LOC_Os11g05470	RCN1 Centroradialis-like1 homogous to TFL1 gene; contains Pfam profile PF01161:	1.49	down	3.22	down	2.04	up	1.04	up	1.72	up	2.19	up	3
Os.49731.1.S1_at	LOC_Os02g21920	CPuORF24 - conserved peptide uORF-containing transcript, expressed	1.29	up	1.01	down	2.99	up	1.20	up	1.49	up	1.57	up	ABA
Os.49731.1.S1_s_at	LOC_Os02g21920	CPuORF24 - conserved peptide uORF-containing transcript, expressed	1.19	up	1.06	down	3.00	up	1.18	up	1.45	up	1.34	up	ABA
Os.4974.1.S1_at	LOC_Os11g31190	nodulin MtN3 family protein, putative, expressed	1.32	up	1.56	down	1.55	up	1.00	up	4.78	up	1.24	down	SA
Os.4974.1.S1_x_at	LOC_Os11g31190	nodulin MtN3 family protein, putative, expressed	1.25	up	1.68	down	1.27	up	1.06	down	3.97	up	1.40	down	SA
Os.49745.1.S1_at	LOC_Os03g41460	CAMK_CAMK_like.20 - CAMK includes calcium/calmodulin depedent protein kinases, e	1.23	up	1.14	down	2.98	up	1.05	down	1.03	up	1.18	down	ABA
Os.49755.1.S1_at	AF402802	Oryza sativa (japonica cultivar-group) clone S14087 putative glutathione S-transferase	4.27	up	1.02	down	1.34	up	1.02	up	4.13	up	2.19	up	3
Os.49762.1.S1_at	LOC_Os02g36924	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	2.07	up	1.43	down	2.01	up	1.15	up	1.74	up	1.04	down	2
Os.49764.1.S1_at	LOC_Os01g45659	hypothetical protein	1.18	down	1.51	up	1254.07	up	1.01	up	1.52	up	1.07	down	ABA
Os.49771.1.S1_at	LOC_Os08g07740	histone-like transcription factor and archaeal histone, putative, expressed	1.60	down	1.17	down	6.03	down	1.22	down	1.39	down	1.24	down	ABA
Os.49784.1.S1_at	LOC_Os11g12530	receptor-like protein kinase 5 precursor, putative, expressed	2.42	down	1.88	up	1.54	up	1.04	up	2.02	down	2.44	down	3
Os.49785.1.S1_at	LOC_Os03g51110	MYB family transcription factor, putative, expressed	1.21	up	1.06	down	2.69	up	1.05	up	1.04	down	1.31	up	ABA
Os.49786.1.S1_at	LOC_Os06g36320	receptor-like protein kinase 5 precursor, putative, expressed	1.02	up	1.00	up	3.40	up	1.00	up	1.01	up	1.02	up	ABA
Os.49787.1.S1_at	LOC_Os01g64360	MYB family transcription factor, putative, expressed	1.14	down	1.10	up	19.38	up	1.02	up	1.94	up	1.75	up	ABA
Os.49814.1.S1_at	LOC_Os09g37949	serine/threonine-protein kinase SRPK1, putative, expressed	1.15	up	1.16	down	2.39	up	1.00	down	1.02	up	1.28	up	ABA
Os.49816.1.S1_at	LOC_Os04g51040	OsWAK50 - OsWAK receptor-like protein kinase, expressed	1.30	down	1.16	down	1.33	down	1.07	up	1.03	up	2.11	up	JA
Os.49818.1.S1_s_at	LOC_Os07g35310	TKL_IRAK_DUF26-lc.12 - DUF26 kinases have homology to DUF26 containing loci, ex	1.07	down	1.14	down	4.75	down	2.42	up	1.18	up	2.58	up	3
Os.49829.1.S1_at	LOC_Os02g40530	MYB family transcription factor, putative, expressed	1.05	down	1.24	up	65.02	up	1.01	down	1.17	up	1.32	up	ABA
Os.4983.1.S1_at	CT831877	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRA102M02, full insert sequence	1.03	down	1.34	down	2.18	up	1.06	down	1.03	up	1.05	down	ABA
Os.49838.1.S1_at	LOC_Os04g47720	cis-zeatin O-glucosyltransferase, putative, expressed	1.24	up	1.12	up	13.23	up	1.62	down	4.58	up	2.87	up	3
Os.49844.1.S1_at	LOC_Os06g37750	S-locus-like receptor protein kinase, putative, expressed	1.75	down	1.24	down	7.91	down	1.55	up	3.40	down	1.22	down	2
Os.49849.1.S1_at	LOC_Os09g27010	tyrosine protein kinase domain containing protein, putative, expressed	1.78	up	1.02	up	2.29	up	1.19	down	1.57	down	1.34	up	ABA
Os.49865.1.S1_at	LOC_Os02g54780	CYPRO4, putative, expressed	1.42	up	1.03	down	2.87	up	1.15	down	1.28	up	1.37	down	ABA
Os.49891.1.S1_at	LOC_Os07g03060	expressed protein	1.04	down	1.15	down	2.32	up	1.01	up	1.04	up	1.03	down	ABA
Os.49920.2.S1_at	LOC_Os03g61780	glucan endo-1,3-beta-glucosidase-related, putative, expressed	1.29	down	1.37	up	5.56	down	1.13	down	1.00	up	1.45	down	ABA
Os.49940.1.S1_at	LOC_Os04g10650	CDT1A - Putative DNA replication initiation protein, expressed	1.24	down	1.12	down	5.19	down	1.10	up	1.40	down	1.47	down	ABA
Os.49950.1.S1_at	LOC_Os11g35450	leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed	1.22	down	1.22	down	12.93	down	1.96	up	2.95	down	2.30	down	4
Os.49964.1.S2_at	AK120918	Oryza sativa Japonica Group cDNA clone:J023034N15, full insert sequence.	1.02	down	1.01	down	5.75	up	1.04	up	1.02	down	1.02	down	ABA
Os.49981.1.A1_at	LOC_Os12g43000	retrotransposon protein, putative, unclassified, expressed	1.85	up	1.26	up	2.18	up	1.45	down	1.13	down	1.46	down	ABA
Os.49988.1.S1_at	LOC_Os12g40940	expressed protein	1.03	down	1.04	down	2.08	up	1.02	up	1.00	down	1.04	up	ABA
Os.49994.1.S1_at	LOC_Os03g14880	expressed protein	1.27	down	1.25	up	2.19	down	1.04	down	1.66	down	1.01	down	ABA
Os.49996.1.S1_at	LOC_Os06g49220	peptide transporter, putative, expressed	1.97	down	1.06	up	18.53	down	1.12	down	2.02	down	1.14	down	3
Os.50005.1.S1_at	LOC_Os08g36390	ZOS8-07 - C2H2 zinc finger protein, expressed	1.21	up	1.21	up	2.48	up	1.21	up	1.24	up	1.21	up	ABA
Os.50007.1.S1_at	LOC_Os05g38470	expressed protein	1.26	up	1.08	down	3.71	up	1.16	down	1.12	up	1.38	down	ABA
Os.50014.1.S1_at	LOC_Os03g38050	galactosyltransferase, putative, expressed	1.14	down	1.30	down	4.33	down	1.01	down	1.16	down	1.37	up	ABA
Os.50018.1.S1_at	LOC_Os07g47750	POEI49 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.17	down	1.50	down	7.04	down	1.27	down	1.22	down	1.76	down	ABA
Os.50019.1.S1_at	LOC_Os03g04080	expressed protein	1.75	up	1.63	up	94.99	up	1.02	up	1.67	up	1.23	down	ABA
Os.50023.1.S1_at	LOC_Os02g58740	expressed protein	1.36	up	1.25	down	2.52	down	1.05	down	1.05	up	1.04	down	ABA
Os.50023.1.S1_x_at	LOC_Os02g58740	expressed protein	1.23	up	1.26	down	2.44	down	1.03	up	1.07	up	1.08	down	ABA
Os.50053.1.A1_at	LOC_Os07g05940	9-cis-epoxycarotenoid dioxygenase 1, chloroplast precursor, putative, expressed	1.69	up	1.22	up	78.30	up	1.03	up	1.11	up	1.42	up	ABA
Os.50054.1.S1_x_at	LOC_Os06g04090	no apical meristem protein, putative, expressed	1.03	up	1.53	up	3.35	down	1.14	down	1.80	down	1.06	down	ABA
Os.50104.1.S1_at	LOC_Os06g40180	phospholipase D, putative, expressed	1.26	down	2.21	down	16.85	down	1.64	down	4.17	down	8.14	up	4
Os.50119.1.S1_at	LOC_Os02g36414	transporter family protein, putative, expressed	1.59	down	1.02	down	16.39	down	1.31	up	2.50	down	1.94	down	2
Os.50129.1.S1_at	AK119921	ankyrin repeat family protein	1.02	down	1.16	up	22.70	up	1.03	up	1.48	up	2.09	up	2
Os.50134.1.S1_at	LOC_Os05g49730	protein phosphatase 2C, putative, expressed	1.12	down	1.11	down	126.79	up	1.01	up	1.01	up	1.02	up	ABA
Os.50134.2.S1_at	AK119929	protein phosphatase 2C ABI1 / PP2C ABI1 / abscisic acid-insensitive 1	1.01	down	1.00	up	19.52	up	1.00	down	1.00	down	1.02	up	ABA
Os.50139.1.S1_at	LOC_Os09g08280	expressed protein	1.00	down	1.01	up	12.45	up	1.02	up	1.01	down	1.04	up	ABA
Os.50155.1.S1_at	LOC_Os06g12960	expressed protein	1.84	down	1.15	up	2.23	up	1.01	up	1.28	up	1.14	up	ABA
Os.5016.1.S1_at	LOC_Os03g55070	UDP-glucose 6-dehydrogenase, putative, expressed	1.00	up	1.13	down	2.11	down	1.28	up	1.35	down	2.41	up	2
Os.50175.2.S1_at	LOC_Os04g51820	OsHKT1;1 - Na+ transporter, expressed	1.09	down	1.33	down	9.92	up	1.07	down	1.01	down	1.16	down	ABA
Os.50222.1.S1_at	LOC_Os12g24800	9-cis-epoxycarotenoid dioxygenase 1, chloroplast precursor, putative, expressed	1.25	down	2.35	down	1.46	down	1.50	down	1.40	down	1.43	up	BAP
Os.50227.1.S1_at	LOC_Os08g04400	pentatricopeptide repeat domain containing protein, putative, expressed	1.22	up	1.55	up	2.23	down	1.55	down	1.24	down	1.41	down	ABA
Os.50234.1.S1_at	LOC_Os06g47930	expressed protein	1.04	down	1.24	up	3.16	down	1.98	down	1.76	down	1.92	down	ABA
Os.50236.1.S1_at	LOC_Os11g40540	transporter family protein, putative, expressed	1.01	down	1.16	down	2.56	up	1.05	down	1.05	down	1.11	down	ABA
Os.50249.1.S1_x_at	LOC_Os03g21640	expressed protein	1.49	up	1.18	up	2.48	up	1.03	up	1.62	up	1.14	down	ABA

Os.50251.1.S1_at	LOC_Os09g07660	ELMO/CED-12 family protein, putative, expressed	**1.05**	up	**1.01**	up	**2.21**	up	**1.22**	down	**1.29**	up	**1.19**	up	ABA
Os.50275.1.S1_at	LOC_Os01g58400	zinc finger C3HC4 type family protein, putative, expressed	**1.13**	up	**1.12**	down	**2.19**	up	**1.14**	down	**1.06**	up	**1.21**	down	ABA
Os.5028.1.S1_at	LOC_Os02g48870	aspartic proteinase nepenthesin-2 precursor, putative, expressed	**1.68**	down	**1.13**	down	**3.80**	down	**1.20**	up	**1.43**	down	**1.01**	up	ABA
Os.50285.2.S1_x_at	LOC_Os03g31180	diacylglycerol kinase 1, putative, expressed	**1.72**	up	**1.40**	down	**9.78**	up	**1.31**	down	**1.03**	up	**1.03**	down	ABA
Os.50287.1.S1_at	LOC_Os04g39010	heavy metal associated domain containing protein, expressed	**1.07**	down	**1.07**	down	**2.27**	up	**1.36**	down	**1.09**	down	**1.43**	up	ABA
Os.50295.1.S1_at	LOC_Os12g29740	expressed protein	**1.01**	down	**1.00**	up	**4.56**	up	**1.03**	up	**1.15**	down	**1.09**	down	ABA
Os.50299.1.S1_at	LOC_Os02g27070	PPR repeat domain containing protein, putative, expressed	**1.04**	down	**1.68**	up	**6.37**	down	**1.16**	down	**1.70**	down	**1.40**	down	ABA
Os.50300.1.S1_at	LOC_Os06g20040	aspartic proteinase nepenthesin-2 precursor, putative, expressed	**1.44**	up	**1.70**	down	**2.30**	up	**1.10**	down	**1.08**	up	**1.60**	up	ABA
Os.50329.1.S1_s_at	LOC_Os08g36860	cytochrome P450, putative, expressed	**1.05**	up	**1.69**	up	**30.66**	up	**1.41**	down	**2.89**	up	**1.37**	up	2
Os.50342.1.S1_at	LOC_Os04g52780	leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed	**1.09**	down	**1.03**	up	**2.70**	down	**1.68**	up	**1.69**	up	**1.48**	down	ABA
Os.50346.1.S1_at	LOC_Os05g04680	expressed protein	**1.69**	up	**1.36**	up	**12.36**	down	**1.47**	down	**1.18**	down	**1.44**	up	ABA
Os.50360.1.S1_at	LOC_Os05g45490	hydrolase, acting on carbon-nitrogen, putative, expressed	**1.10**	up	**1.00**	down	**2.30**	down	**1.00**	up	**1.41**	down	**1.72**	up	ABA
Os.50371.1.S1_x_at	LOC_Os05g05620	glutathione S-transferase, putative, expressed	**1.15**	down	**1.01**	down	**2.26**	down	**1.30**	down	**1.05**	down	**4.33**	up	2
Os.50381.1.S1_at	LOC_Os11g09150	expressed protein	**1.07**	up	**1.00**	up	**5.28**	up	**1.06**	down	**1.01**	down	**1.36**	down	ABA
Os.50384.1.S1_at	LOC_Os02g32760	60S acidic ribosomal protein, putative, expressed	**1.07**	down	**1.04**	down	**3.27**	down	**1.00**	down	**1.67**	down	**1.20**	down	ABA
Os.50386.1.S1_at	LOC_Os05g35010	cytochrome P450, putative, expressed	**1.12**	up	**1.02**	up	**2.64**	up	**1.07**	up	**1.42**	up	**1.04**	down	ABA
Os.50391.1.S1_at	LOC_Os03g13030	lecithin cholesterol acyltransferase, putative, expressed	**1.08**	up	**1.11**	up	**3.23**	down	**1.34**	down	**1.07**	down	**1.33**	down	ABA
Os.50393.1.S1_at	LOC_Os02g51680	uncharacterized glycosyl hydrolase Rv2006/MT2062, putative, expressed	**1.07**	up	**2.56**	down	**2.54**	up	**1.73**	down	**1.66**	up	**1.25**	down	2
Os.50395.1.S1_at	LOC_Os12g31000	pumilio-family RNA binding repeat domain containing protein, expressed	**2.60**	up	**1.36**	up	**25.37**	down	**1.09**	up	**1.99**	down	**1.45**	down	3
Os.50398.1.S1_at	LOC_Os02g44090	zinc finger protein, putative, expressed	**1.86**	up	**1.43**	up	**10.77**	up	**1.10**	up	**1.12**	up	**1.01**	up	ABA
Os.50399.1.S1_at	LOC_Os06g05420	expressed protein	**1.96**	up	**1.38**	down	**8.33**	up	**1.53**	down	**8.74**	up	**1.86**	up	3
Os.50400.1.S1_at	LOC_Os05g35060	DUF803 domain containing, putative, expressed	**1.02**	down	**1.06**	down	**2.02**	down	**1.18**	down	**1.72**	down	**1.17**	up	ABA
Os.50402.1.S1_at	LOC_Os03g03334	expressed protein	**1.65**	up	**6.22**	up	**2.41**	down	**1.16**	up	**1.22**	up	**1.07**	up	2
Os.50413.1.S1_at	LOC_Os04g01690	pyridoxal-dependent decarboxylase protein, putative, expressed	**1.94**	down	**1.01**	down	**1.38**	down	**1.96**	down	**2.50**	up	**20.22**	up	3
Os.50416.1.S1_at	LOC_Os08g42530	SFC, putative, expressed	**1.39**	down	**1.41**	down	**4.38**	down	**1.17**	down	**1.41**	down	**1.60**	down	ABA
Os.50438.1.S1_at	CT828313	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI012B19, full insert sequence.	**2.74**	up	**1.24**	up	**1.87**	up	**1.07**	up	**3.26**	up	**2.06**	up	3
Os.50455.1.S1_at	LOC_Os06g40170	phospholipase D, putative, expressed	**1.01**	up	**1.48**	down	**5.51**	down	**1.03**	up	**1.41**	down	**6.77**	up	2
Os.50460.1.S1_at	LOC_Os03g59620	phospholipase, patatin family, putative, expressed	**1.23**	down	**1.25**	up	**2.54**	up	**1.05**	up	**1.04**	up	**1.11**	down	ABA
Os.50466.1.S1_at	AK121303	Oryza sativa Japonica Group cDNA clone:J023111B15, full insert sequence.	**1.07**	down	**1.04**	down	**2.04**	down	**1.10**	up	**1.40**	down	**1.16**	up	ABA
Os.50468.1.S1_at	LOC_Os03g15320	glyoxal oxidase-related, putative, expressed	**1.22**	down	**1.11**	up	**9.00**	down	**1.08**	down	**4.02**	down	**2.93**	down	3
Os.50470.1.S1_at	LOC_Os01g71310	cytokinin dehydrogenase precursor, putative, expressed	**3.46**	up	**3.68**	up	**1.38**	up	**1.33**	down	**1.44**	down	**1.33**	down	2
Os.50478.1.S1_at	LOC_Os05g25350	TKL_IRAK_CrRLK1L-1.12 - The CrRLK1L-1 subfamily has homology to the CrRLK1L h	**1.06**	up	**1.02**	up	**15.52**	down	**1.20**	up	**1.90**	down	**28.60**	down	2
Os.50487.1.S1_at	LOC_Os03g21960	aminotransferase, putative, expressed	**1.36**	up	**4.40**	down	**15.30**	down	**1.32**	down	**2.03**	down	**4.06**	down	4
Os.5049.1.S1_at	LOC_Os10g20470	MATE efflux family protein, putative, expressed	**1.61**	up	**1.36**	down	**6.32**	up	**1.30**	up	**2.74**	up	**2.42**	up	3
Os.50494.1.A1_at	LOC_Os06g50180	DUF803 domain containing, putative, expressed	**1.25**	down	**1.16**	down	**2.08**	down	**1.24**	down	**1.09**	up	**1.09**	down	ABA
Os.50498.1.S1_at	LOC_Os01g03549	multi-copper oxidase type I family protein, putative, expressed	**1.54**	up	**1.22**	down	**5.12**	down	**1.36**	up	**1.74**	down	**1.18**	up	ABA
Os.50575.1.S1_at	LOC_Os04g40700	steroid nuclear receptor, ligand-binding, putative, expressed	**1.20**	up	**1.32**	down	**5.22**	up	**1.19**	down	**1.36**	up	**1.28**	down	ABA
Os.50575.2.S1_x_at	LOC_Os04g40700	steroid nuclear receptor, ligand-binding, putative, expressed	**1.41**	up	**1.24**	down	**5.49**	up	**1.69**	down	**1.31**	up	**1.24**	down	ABA
Os.50583.1.S1_at	LOC_Os03g60260	ANT1, putative, expressed	**1.02**	up	**1.05**	up	**2.37**	up	**1.08**	up	**1.08**	up	**1.29**	up	ABA
Os.50588.1.S1_at	LOC_Os11g34370	phospholipase, patatin family, putative, expressed	**1.29**	up	**1.13**	up	**2.58**	up	**1.16**	down	**1.41**	up	**1.02**	up	ABA
Os.50594.1.S1_at	LOC_Os04g46680	ZOS4-10 - C2H2 zinc finger protein, expressed	**1.00**	down	**1.00**	up	**3.00**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
Os.50596.1.S1_at	LOC_Os04g40680	expressed protein	**5.63**	up	**1.06**	down	**1.81**	up	**1.38**	down	**2.21**	up	**1.72**	up	2
Os.50598.1.S1_at	LOC_Os12g03370	harpin-induced protein 1 domain containing protein, expressed	**2.10**	down	**1.25**	down	**1.00**	down	**1.71**	up	**1.98**	up	**1.25**	up	IAA
Os.50606.1.S1_at	LOC_Os12g05394	protein kinase, putative, expressed	**4.95**	up	**1.34**	down	**1.46**	down	**1.48**	down	**1.31**	down	**1.43**	down	IAA
Os.50620.1.S1_at	LOC_Os12g44190	ATPase 3, putative, expressed	**1.71**	down	**1.69**	down	**9.15**	down	**1.34**	up	**2.38**	up	**1.74**	up	2
Os.50632.1.S1_x_at	LOC_Os10g35940	folylpolyglutamate synthetase, putative, expressed	**1.43**	up	**1.41**	up	**8.25**	down	**1.06**	down	**1.71**	down	**1.26**	down	ABA
Os.5064.1.S1_at	LOC_Os05g06440	dnaJ homolog subfamily B member 11 precursor, putative, expressed	**1.44**	down	**1.11**	up	**2.35**	down	**1.12**	up	**1.22**	down	**1.33**	up	ABA
Os.50640.1.S1_at	LOC_Os04g33740	glycosyl hydrolases, putative, expressed	**1.20**	down	**1.11**	up	**6.70**	down	**1.55**	up	**1.29**	down	**1.24**	up	ABA
Os.50642.1.S1_at	LOC_Os04g48030	heat stress transcription factor B-1, putative, expressed	**2.10**	down	**1.05**	down	**6.18**	up	**1.02**	up	**1.79**	up	**1.03**	up	2
Os.50659.1.S1_at	AJ490355	Oryza sativa z134b snoRNA.	**3.86**	down	**1.60**	down	**1.04**	down	**1.37**	up	**1.70**	down	**1.16**	up	IAA
Os.5066.1.S1_at	LOC_Os01g12000	expressed protein	**1.55**	up	**1.21**	down	**1.07**	up	**1.46**	up	**1.48**	up	**2.26**	up	JA
Os.50743.1.S1_at	LOC_Os02g43900	expressed protein	**1.24**	up	**1.01**	down	**2.98**	down	**1.85**	down	**1.16**	down	**1.14**	down	ABA
Os.50750.1.S1_at	LOC_Os03g02190	protein kinase domain containing protein, expressed	**1.37**	down	**1.01**	down	**7.70**	down	**1.17**	down	**1.45**	down	**1.08**	up	ABA
Os.50763.1.S1_at	LOC_Os03g30260	COBRA-like protein precursor, putative, expressed	**1.19**	down	**1.11**	down	**3.49**	down	**1.02**	down	**1.56**	down	**1.76**	down	ABA
Os.50771.1.S1_at	LOC_Os06g44320	expressed protein	**1.93**	up	**1.49**	up	**2.74**	down	**1.09**	up	**1.02**	down	**1.12**	down	ABA

Os.50776.1.S1_at	CT833789	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN032F14, full insert sequence	1.05	up	1.22	up	2.44	down	1.34	down	1.34	down	1.72	down	ABA
Os.50786.1.S1_at	NM_001052476	Oryza sativa (japonica cultivar-group) Os02g0156300 (Os02g0156300) mRNA, comple	1.34	up	1.28	up	3.84	up	1.21	up	1.57	up	1.41	up	ABA
Os.50788.1.A1_at	LOC_Os06g43044	GDSL-like lipase/acylhydrolase, putative, expressed	1.07	down	1.02	up	2.50	down	1.20	down	1.26	down	1.25	down	ABA
Os.50791.1.S1_at	LOC_Os02g53530	ZOS2-17 - C2H2 zinc finger protein, expressed	1.07	down	1.11	up	6.62	down	1.15	down	1.10	down	1.37	down	ABA
Os.50798.1.S1_at	LOC_Os08g01480	cytochrome P450, putative, expressed	1.34	down	5.30	up	1.18	up	1.04	down	2.97	up	2.73	up	3
Os.50799.1.S1_at	LOC_Os04g48130	OsRhmbd11 - Putative Rhomboid homologue, expressed	1.30	up	1.07	up	11.42	down	1.04	up	1.94	down	1.18	down	ABA
Os.50805.1.S1_at	LOC_Os08g20130	flavonol sulfotransferase, putative, expressed	1.88	down	1.29	down	4.04	down	2.41	down	1.36	down	2.49	up	3
Os.50813.1.S1_at	LOC_Os09g26570	CAAX amino terminal protease family protein, putative, expressed	1.12	down	1.18	down	7.22	up	1.17	down	1.43	up	1.13	down	ABA
Os.50825.1.S1_s_at	LOC_Os05g39990	expansin precursor, putative, expressed	1.80	up	3.04	up	8.68	down	1.68	up	1.40	down	1.48	down	2
Os.50831.1.S1_at	LOC_Os02g32580	expressed protein	1.17	up	1.80	down	7.15	up	1.01	up	1.09	up	1.20	up	ABA
Os.50846.1.S1_s_at	LOC_Os01g10490	keratin, type I cytoskeletal 9, putative, expressed	1.35	down	1.10	down	2.04	down	1.11	up	1.02	down	1.13	down	ABA
Os.50849.1.S1_at	LOC_Os03g15690	phosphate carrier protein, mitochondrial precursor, putative, expressed	1.20	down	1.27	up	2.90	down	1.01	down	1.33	down	1.13	down	ABA
Os.50858.1.S1_at	LOC_Os02g47780	hydrolase, alpha/beta fold family domain containing protein, expressed	2.34	up	1.47	up	5.00	up	1.30	down	1.83	up	1.35	down	2
Os.50861.1.S1_at	LOC_Os04g42700	receptor-like protein kinase precursor, putative, expressed	1.15	down	1.37	up	2.54	up	1.02	down	1.01	down	1.22	down	ABA
Os.5087.1.S1_at	LOC_Os11g03780	alpha-N-arabinofuranosidase, putative, expressed	1.03	down	1.09	down	14.20	up	1.01	up	1.05	up	1.14	down	ABA
Os.50876.1.S1_at	LOC_Os06g04150	magnesium-protoporphyrin O-methyltransferase, putative, expressed	1.44	up	1.17	up	6.77	down	1.10	down	2.44	down	1.35	down	2
Os.50879.1.S1_at	LOC_Os09g38510	purine permease, putative, expressed	1.47	up	1.61	down	6.58	up	1.68	down	1.45	up	1.39	down	ABA
Os.50883.1.S1_at	LOC_Os04g51520	glycosyl hydrolases family 16, putative, expressed	1.04	up	3.48	up	2.06	up	1.09	up	2.70	down	3.21	down	4
Os.50896.1.S1_at	LOC_Os01g66010	amino acid transporter, putative, expressed	1.87	up	1.27	down	14.81	down	1.41	up	1.38	down	1.15	up	ABA
Os.50909.1.S1_at	LOC_Os03g55120	plastocyanin-like domain containing protein, putative, expressed	1.08	down	1.12	down	5.04	down	1.02	down	1.66	down	2.05	down	2
Os.50909.2.S1_s_at	LOC_Os03g55120	plastocyanin-like domain containing protein, putative, expressed	1.05	up	1.20	down	3.44	down	1.09	up	1.44	down	1.59	down	ABA
Os.5091.1.S1_at	LOC_Os08g44750	auxin-induced protein 5NG4, putative, expressed	1.26	up	1.11	down	3.34	down	1.04	up	1.08	up	1.00	up	ABA
Os.50911.1.S1_at	LOC_Os05g32150	expressed protein	1.66	down	1.75	up	1.08	down	6.85	up	1.07	down	1.08	down	ACC
Os.50916.1.S1_at	LOC_Os11g04350	cell death associated protein, putative, expressed	1.61	down	1.25	up	12.66	down	1.26	down	1.52	down	1.92	down	ABA
Os.50919.1.S1_at	LOC_Os11g03580	expressed protein	2.31	up	1.52	down	2.05	down	1.14	up	1.23	down	1.34	down	2
Os.50922.1.S1_at	LOC_Os09g27890	lysM domain-containing GPI-anchored protein precursor, putative, expressed	1.25	down	1.15	down	2.92	down	1.07	up	1.30	down	1.52	down	ABA
Os.50939.1.S1_at	LOC_Os01g67870	expressed protein	1.16	up	1.10	up	2.44	up	1.05	down	1.06	up	1.27	down	ABA
Os.50941.1.S1_at	LOC_Os05g32680	PAC, putative, expressed	1.04	down	1.04	up	2.97	down	1.20	down	1.47	down	1.41	down	ABA
Os.5095.1.S1_at	LOC_Os07g40130	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	1.01	up	1.13	down	2.02	down	1.10	up	1.40	down	1.17	up	ABA
Os.50950.1.S1_x_at	LOC_Os02g44730	tetracycline transporter protein, putative, expressed	1.05	down	1.94	up	5.28	up	1.14	down	1.54	down	3.69	down	2
Os.50952.1.S1_at	LOC_Os07g03120	expressed protein	1.01	down	1.70	down	5.20	up	1.18	down	1.14	up	2.26	up	2
Os.50953.1.S1_at	LOC_Os06g49970	alpha-amylase precursor, putative, expressed	1.13	down	1.24	down	5.07	up	1.01	down	1.07	up	1.40	down	ABA
Os.50955.1.S1_at	AK059675	Oryza sativa Japonica Group cDNA clone:001-031-G07, full insert sequence.	1.37	down	1.21	down	2.55	up	1.01	up	1.35	up	1.04	down	ABA
Os.50958.1.S1_at	LOC_Os06g47820	protein kinase domain containing protein, expressed	1.06	up	1.00	down	4.76	up	1.00	up	1.01	up	1.02	down	ABA
Os.50970.1.S1_at	LOC_Os03g32230	ZOS3-12 - C2H2 zinc finger protein, expressed	1.09	up	2.35	up	1.02	up	1.04	up	1.04	up	2.76	up	2
Os.50978.1.S1_at	LOC_Os10g08026	lecithin:cholesterol acyltransferase, putative, expressed	1.56	down	1.65	up	9.41	down	1.47	up	1.97	down	1.70	down	ABA
Os.50990.1.S1_at	CT830381	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSA027G08, full insert sequence	1.47	down	1.16	down	9.88	down	1.11	down	1.75	down	1.63	up	ABA
Os.5100.1.S1_s_at	LOC_Os01g47635	expressed protein	1.71	down	2.02	up	10.47	down	1.35	down	3.60	down	7.28	down	4
Os.51009.1.S1_x_at	AK100528	DENN (AEX-3) domain-containing protein	1.00	up	1.05	down	6.62	up	2.21	down	1.68	down	2.47	down	3
Os.51023.1.S1_at	LOC_Os01g43851	cytochrome P450 72A1, putative, expressed	1.36	down	1.44	down	4.15	up	1.75	down	1.22	up	1.09	down	ABA
Os.51029.1.S1_at	LOC_Os09g02770	translation initiation factor IF-2, putative, expressed	1.02	down	1.12	up	4.79	up	1.01	up	1.59	up	1.06	up	ABA
Os.51035.1.S1_at	LOC_Os12g12260	diacylglycerol kinase 1, putative, expressed	1.01	down	1.10	down	2.86	up	1.06	down	1.04	up	1.35	up	ABA
Os.51053.1.S1_at	LOC_Os11g27400	glycosyl hydrolase, putative, expressed	1.12	up	1.20	down	3.56	down	1.21	down	1.28	down	1.02	down	ABA
Os.51063.1.S1_at	LOC_Os09g28210	bHelix-loop-helix transcription factor, putative, expressed	2.13	up	2.21	up	1.96	up	1.44	down	1.30	down	2.37	down	4
Os.51071.1.A1_x_at	LOC_Os12g44100	peptide transporter PTR2, putative, expressed	1.08	down	1.03	down	2.54	up	1.00	down	1.26	up	1.11	up	ABA
Os.51080.1.S1_at	LOC_Os05g19150	hydrolase, alpha/beta fold family domain containing protein, expressed	1.06	up	1.25	down	1.97	down	1.04	up	1.66	down	2.49	up	JA
Os.51088.1.S1_at	LOC_Os04g05050	pectate lyase precursor, putative, expressed	1.00	down	1.31	down	3.46	down	1.30	down	1.31	down	1.73	up	ABA
Os.51088.1.S1_x_at	LOC_Os08g43170	hydroxymethylglutaryl-CoA synthase, putative, expressed	1.19	up	1.18	down	2.31	up	1.05	up	1.32	up	1.27	up	ABA
Os.51091.1.S1_at	LOC_Os03g19670	GDSL-like lipase/acylhydrolase, putative, expressed	1.04	up	1.82	up	5.06	down	1.15	up	1.15	down	1.26	down	ABA
Os.51106.1.S1_at	LOC_Os06g14540	endoglucanase, putative, expressed	1.14	up	1.06	down	2.56	down	1.40	down	1.53	down	1.23	down	ABA
Os.51110.1.S1_at	AK060697	Oryza sativa (japonica cultivar-group) Os04g0687200 (Os04g0687200) mRNA, comple	1.06	down	1.02	up	2.38	down	1.00	up	1.50	down	1.44	down	ABA
Os.51112.1.S1_at	LOC_Os03g50860	histidine kinase, putative, expressed	1.08	up	2.20	up	5.98	down	1.01	down	1.74	down	1.48	down	2
Os.51115.1.S1_x_at	AK060839	Ras-related GTP-binding protein, putative	1.11	down	1.10	down	2.56	up	1.03	down	1.26	up	1.89	down	ABA
Os.51117.1.S1_at	AK060942	Oryza sativa Japonica Group cDNA clone:006-201-D03, full insert sequence.	1.12	up	1.00	down	1.24	down	1.42	down	1.64	down	2.19	down	JA
Os.5112.1.S1_at	LOC_Os04g57810	GA18008-PA, putative, expressed	1.44	up	1.04	down	2.33	up	1.20	up	2.57	up	1.42	up	3

Os.51120.1.S1_at	LOC_Os02g56600	no apical meristem protein, putative, expressed	**1.07**	down	**2.18**	up	**4.88**	up	**1.04**	up	**1.44**	down	**1.08**	up	2
Os.51127.1.S1_a_at	LOC_Os04g37820	cytokinin-O-glucosyltransferase 2, putative, expressed	**1.12**	up	**1.27**	up	**3.14**	down	**1.74**	up	**1.25**	down	**1.92**	up	ABA
Os.51142.1.S1_at	LOC_Os04g46660	cyclin, putative, expressed	**1.09**	down	**1.13**	up	**1.02**	down	**2.08**	down	**2.08**	down	**1.41**	down	2
Os.51144.1.S1_at	LOC_Os07g47210	GDSL-like lipase/acylhydrolase, putative, expressed	**1.07**	up	**1.10**	up	**3.94**	up	**2.19**	down	**1.18**	down	**1.45**	down	2
Os.51147.1.S1_at	LOC_Os03g16960	cysteine-rich repeat secretory protein 55 precursor, putative, expressed	**1.21**	down	**1.15**	up	**5.55**	down	**1.79**	up	**2.26**	up	**2.02**	up	3
Os.51152.1.S1_at	LOC_Os03g18680	membrane associated DUF588 domain containing protein, putative, expressed	**1.22**	up	**1.31**	down	**4.94**	up	**1.10**	down	**1.31**	up	**1.14**	down	ABA
Os.5117.1.S1_at	AK111124	Oryza sativa Japonica Group cDNA clone:002-176-C05, full insert sequence.	**1.37**	down	**1.22**	up	**7.24**	up	**1.15**	down	**1.11**	up	**2.53**	up	2
Os.51174.1.S1_at	LOC_Os03g13570	glycosyl hydrolases family 16, putative, expressed	**1.26**	up	**1.16**	down	**2.25**	down	**1.06**	up	**1.02**	up	**1.41**	down	ABA
Os.51176.1.S1_at	LOC_Os10g31320	retrotransposon protein, putative, unclassified, expressed	**1.08**	up	**1.26**	down	**3.67**	up	**1.04**	down	**1.18**	up	**2.00**	up	2
Os.51184.1.S1_at	LOC_Os05g10370	acid phosphatase, putative, expressed	**1.86**	down	**1.12**	up	**8.73**	down	**1.48**	down	**1.52**	down	**2.36**	up	2
Os.51206.1.S1_at	LOC_Os04g49620	DUF581 domain containing protein, expressed	**1.56**	up	**1.62**	up	**2.51**	down	**1.89**	down	**1.87**	down	**1.75**	down	ABA
Os.51212.1.S1_at	LOC_Os04g42800	photosystem-II repair protein, putative, expressed	**1.24**	up	**1.21**	down	**4.33**	down	**1.06**	down	**1.47**	down	**1.14**	down	ABA
Os.51213.1.S1_at	LOC_Os03g18370	MRH1, putative, expressed	**1.17**	up	**1.11**	down	**3.07**	down	**1.18**	down	**1.41**	down	**1.16**	down	ABA
Os.51223.1.S1_at	LOC_Os04g57690	expressed protein	**1.30**	up	**1.15**	up	**2.11**	up	**1.06**	down	**1.28**	up	**1.12**	down	ABA
Os.51228.2.A1_at	LOC_Os03g14120	dihydrodipicolinate reductase, putative, expressed	**1.02**	up	**1.34**	down	**5.55**	down	**2.11**	down	**1.50**	down	**1.44**	down	2
Os.51228.3.S1_at	LOC_Os03g14120	dihydrodipicolinate reductase, putative, expressed	**1.68**	down	**1.08**	down	**3.19**	down	**1.05**	down	**1.44**	down	**1.33**	down	ABA
Os.51228.3.S1_x_at	LOC_Os03g14120	dihydrodipicolinate reductase, putative, expressed	**1.05**	down	**1.01**	up	**2.59**	down	**1.05**	up	**1.26**	down	**1.02**	down	ABA
Os.5124.1.S1_at	LOC_Os05g49770	CTP synthase, putative, expressed	**3.21**	up	**1.90**	up	**3.87**	up	**1.10**	down	**1.73**	up	**1.39**	down	2
Os.5124.1.S1_s_at	LOC_Os05g49770	CTP synthase, putative, expressed	**2.50**	up	**1.68**	up	**3.34**	up	**1.15**	down	**1.42**	up	**1.74**	down	2
Os.51245.1.S1_at	LOC_Os02g32450	expressed protein	**1.26**	up	**1.34**	down	**4.13**	up	**1.15**	down	**1.82**	up	**1.14**	down	ABA
Os.51258.1.S1_at	LOC_Os02g03250	expressed protein	**1.05**	down	**1.10**	up	**2.10**	down	**1.17**	down	**1.42**	down	**1.26**	down	ABA
Os.51260.1.S1_at	LOC_Os04g47840	expressed protein	**1.12**	up	**1.57**	down	**3.23**	down	**1.29**	down	**1.18**	down	**1.02**	down	ABA
Os.51262.1.S1_at	LOC_Os03g45760	expressed protein	**1.07**	down	**1.17**	down	**3.61**	down	**1.38**	down	**1.91**	down	**1.22**	down	ABA
Os.5127.1.S1_x_at	LOC_Os07g46220	SNARE associated Golgi protein, putative, expressed	**1.07**	up	**1.01**	down	**2.21**	up	**1.02**	down	**1.04**	up	**1.21**	up	ABA
Os.51270.1.S1_at	LOC_Os02g54180	expressed protein	**4.08**	down	**1.59**	down	**18.20**	down	**1.37**	up	**1.08**	up	**4.44**	down	3
Os.51285.1.S1_at	LOC_Os01g04390	expressed protein	**1.22**	up	**2.17**	up	**3.11**	down	**1.29**	down	**1.54**	down	**2.06**	down	3
Os.51291.1.S1_at	NM_001052917	Oryza sativa (japonica cultivar-group) Os02g0234700 (Os02g0234700) mRNA, comple	**1.54**	down	**1.08**	down	**4.32**	down	**1.80**	down	**1.60**	down	**1.40**	down	ABA
Os.51295.1.S1_at	AK062450	Oryza sativa Japonica Group cDNA clone:001-103-C02, full insert sequence.	**1.61**	up	**1.37**	up	**2.39**	up	**1.15**	down	**1.02**	down	**1.43**	down	ABA
Os.51299.1.S1_at	LOC_Os05g38880	expressed protein	**5.18**	up	**1.41**	down	**3.10**	down	**1.52**	down	**1.18**	up	**1.03**	down	2
Os.5130.1.S1_at	LOC_Os04g34630	peroxidase precursor, putative, expressed	**1.07**	down	**1.15**	down	**3.21**	up	**1.14**	up	**1.02**	down	**1.03**	up	ABA
Os.51300.1.S1_x_at	LOC_Os02g10500	expressed protein	**1.18**	down	**1.08**	down	**2.11**	down	**1.40**	down	**1.01**	down	**1.08**	down	ABA
Os.51337.1.S1_at	LOC_Os06g39330	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.42**	up	**1.82**	up	**1.01**	up	**1.20**	down	**2.56**	up	**1.10**	up	SA
Os.51349.1.S1_at	LOC_Os02g53870	expressed protein	**2.02**	up	**1.11**	up	**3.58**	up	**1.42**	up	**2.99**	up	**3.89**	up	4
Os.51369.1.S1_at	LOC_Os02g51740	VQ domain containing protein, putative, expressed	**1.09**	down	**1.15**	down	**2.36**	up	**1.05**	up	**1.32**	up	**1.19**	down	ABA
Os.51382.1.S1_at	LOC_Os01g72470	expressed protein	**1.01**	up	**1.32**	down	**1.20**	down	**1.07**	down	**1.00**	down	**5.05**	up	JA
Os.51389.1.S1_at	LOC_Os11g02670	zinc finger, C3HC4 type domain containing protein, expressed	**1.77**	down	**1.33**	down	**6.18**	down	**1.55**	down	**3.92**	down	**1.67**	up	2
Os.51392.1.S1_at	LOC_Os12g32970	membrane associated DUF588 domain containing protein, putative, expressed	**1.06**	up	**1.09**	up	**3.04**	up	**1.12**	down	**1.20**	up	**1.03**	down	ABA
Os.51394.1.S1_at	LOC_Os05g07890	embryo-specific 3, putative, expressed	**1.05**	up	**1.20**	up	**16.42**	up	**1.07**	down	**1.17**	up	**1.06**	up	ABA
Os.51401.1.S1_at	NM_001068260	Oryza sativa (japonica cultivar-group) Os08g0390700 (Os08g0390700) mRNA, partial	**1.52**	down	**1.12**	down	**3.75**	down	**1.42**	up	**1.55**	up	**1.04**	down	ABA
Os.51413.1.S1_at	NM_001072597	Oryza sativa (japonica cultivar-group) Os12g0129300 (Os12g0129300) mRNA, comple	**1.10**	up	**1.03**	up	**3.35**	up	**1.09**	up	**1.10**	down	**1.03**	down	ABA
Os.51427.1.S1_at	NM_001060644	Oryza sativa (japonica cultivar-group) Os04g0653700 (Os04g0653700) mRNA, comple	**1.48**	down	**1.16**	up	**1.82**	up	**3.79**	up	**7.71**	up	**1.26**	up	2
Os.51432.1.S1_at	NM_001054893	Oryza sativa (japonica cultivar-group) Os02g0791400 (Os02g0791400) mRNA, comple	**2.44**	down	**1.08**	down	**27.91**	down	**1.17**	up	**4.47**	down	**6.69**	down	4
Os.51441.1.S1_at	AK062818	Oryza sativa Japonica Group cDNA clone:001-107-E10, full insert sequence.	**1.02**	down	**1.01**	down	**2.16**	up	**1.04**	down	**1.09**	up	**1.01**	up	ABA
Os.51451.1.S1_at	LOC_Os07g41340	B12D protein, putative, expressed	**5.43**	down	**1.01**	up	**1.59**	up	**1.72**	up	**1.08**	up	**1.24**	up	IAA
Os.51460.1.S1_at	LOC_Os02g33380	pectinesterase inhibitor domain containing protein, putative, expressed	**2.09**	up	**1.18**	down	**22.89**	up	**4.36**	down	**1.65**	up	**1.14**	down	3
Os.51473.2.S1_x_at	LOC_Os05g48160	2Fe-2S iron-sulfur cluster binding domain containing protein, expressed	**2.10**	up	**1.22**	up	**1.88**	up	**1.13**	down	**1.41**	up	**1.01**	down	IAA
Os.51479.1.S1_at	LOC_Os09g25720	glycine-rich cell wall structural protein 2 precursor, putative, expressed	**1.97**	down	**1.01**	up	**5.53**	down	**1.76**	up	**1.17**	down	**1.13**	down	ABA
Os.51480.1.S1_at	LOC_Os01g62980	LTPL101 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.12**	down	**1.04**	up	**13.78**	up	**1.96**	down	**1.29**	down	**1.77**	down	ABA
Os.51480.1.S1_x_at	LOC_Os01g62980	LTPL101 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.08**	down	**1.06**	up	**17.93**	up	**1.75**	down	**1.24**	up	**2.19**	down	2
Os.5152.1.S1_at	LOC_Os11g05400	Ser/Thr protein phosphatase family protein, putative, expressed	**1.01**	up	**1.01**	down	**6.40**	up	**1.13**	up	**1.45**	up	**1.03**	up	ABA
Os.51521.1.S1_at	AK063001	Oryza sativa Japonica Group cDNA clone:001-109-H04, full insert sequence.	**1.05**	up	**1.12**	down	**3.66**	up	**1.06**	down	**1.02**	up	**1.01**	down	ABA
Os.51521.1.S2_at	AK106303	Oryza sativa Japonica Group cDNA clone:002-101-C07, full insert sequence.	**1.06**	down	**1.03**	down	**3.01**	up	**1.61**	down	**1.02**	down	**1.49**	down	ABA
Os.51525.1.S1_at	LOC_Os03g20900	Myb transcription factor, putative, expressed	**1.17**	up	**1.18**	down	**2.83**	down	**1.01**	up	**1.02**	up	**1.46**	down	ABA
Os.5154.1.S1_at	LOC_Os07g49080	COBRA-like protein 7 precursor, putative, expressed	**1.08**	up	**1.25**	up	**3.19**	down	**1.32**	up	**1.10**	up	**1.53**	down	ABA
Os.51546.1.S1_at	LOC_Os03g08520	DUF581 domain containing protein, expressed	**2.09**	down	**1.05**	up	**25.71**	down	**1.13**	down	**1.56**	down	**14.21**	up	3

Os.51550.1.S1_at	LOC_Os05g25784	expressed protein	**2.59**	up	**1.34**	down	**5.75**	up	**1.25**	down	**1.88**	up	**1.10**	down	2
Os.51558.2.S1_at	LOC_Os01g59840	Os1bglu3 - beta-glucosidase homologue, similar to G. max isohydroxyurate hydrolase,	**1.24**	up	**1.16**	up	**3.01**	down	**1.24**	up	**1.67**	down	**1.17**	down	ABA
Os.5156.1.S1_s_at	LOC_Os03g53080	zinc finger, C3HC4 type domain containing protein, expressed	**1.34**	up	**1.16**	up	**2.34**	up	**1.00**	up	**1.39**	up	**1.02**	up	ABA
Os.51562.1.S1_at	LOC_Os04g36770	PME/invertase inhibitor, putative, expressed	**1.17**	down	**2.05**	up	**1.91**	down	**1.24**	up	**2.09**	down	**1.30**	down	2
Os.51564.1.S1_s_at	LOC_Os04g35070	expressed protein	**1.28**	down	**1.27**	down	**2.34**	up	**1.27**	up	**1.03**	down	**1.10**	down	ABA
Os.51574.1.S1_at	LOC_Os04g56390	expressed protein	**16.82**	up	**1.39**	down	**2.80**	down	**1.82**	down	**1.03**	up	**1.68**	down	2
Os.51578.1.S1_x_at	LOC_Os06g37020	expressed protein	**1.34**	down	**1.10**	down	**3.30**	down	**1.06**	down	**1.79**	up	**1.06**	up	ABA
Os.51586.1.S1_at	LOC_Os06g12660	NHL repeat-containing protein, putative, expressed	**1.10**	up	**1.51**	up	**3.92**	down	**1.13**	up	**1.12**	down	**1.15**	down	ABA
Os.51595.1.S1_at	LOC_Os01g46370	lipase class 3 family protein, putative, expressed	**1.02**	down	**1.14**	up	**3.56**	up	**1.13**	down	**1.11**	up	**1.89**	down	ABA
Os.51597.1.S1_at	LOC_Os01g68598	expressed protein	**1.03**	down	**1.05**	up	**3.68**	down	**1.37**	down	**1.60**	down	**1.51**	down	ABA
Os.51599.1.S1_at	LOC_Os09g19820	aminopeptidase, putative, expressed	**3.64**	up	**2.28**	up	**7.33**	up	**2.60**	up	**44.24**	up	**9.66**	up	6
Os.5160.1.S1_at	LOC_Os07g46330	uncharacterized UPF0114 domain containing protein, expressed	**1.17**	down	**1.03**	up	**3.44**	down	**1.03**	up	**1.75**	down	**1.09**	up	ABA
Os.51601.1.S1_at	LOC_Os07g40300	ZOS7-10 - C2H2 zinc finger protein, expressed	**1.25**	up	**2.55**	down	**2.23**	up	**1.05**	down	**1.03**	up	**1.68**	down	2
Os.51606.1.S1_at	AK063156	Oryza sativa Japonica Group cDNA clone:001-111-H12, full insert sequence.	**1.01**	down	**1.16**	up	**9.51**	up	**1.57**	up	**2.18**	up	**1.30**	up	2
Os.51638.1.S1_s_at	LOC_Os09g26310	hypro1, putative, expressed	**1.02**	down	**1.25**	down	**5.93**	up	**1.06**	up	**1.53**	up	**1.74**	up	ABA
Os.51639.1.S1_x_at	LOC_Os10g38040	lysM domain containing protein, putative, expressed	**1.02**	up	**1.41**	up	**3.02**	up	**1.38**	up	**3.05**	up	**2.53**	up	3
Os.5164.1.S1_at	LOC_Os10g25030	red chlorophyll catabolite reductase, putative, expressed	**1.06**	down	**1.08**	down	**3.34**	up	**1.01**	up	**1.22**	up	**1.03**	down	ABA
Os.51648.1.S1_at	LOC_Os03g20910	homeobox domain containing protein, expressed	**12.75**	up	**2.17**	down	**1.49**	up	**2.04**	up	**1.93**	up	**1.99**	up	4
Os.51652.1.S1_at	LOC_Os05g49040	expressed protein	**1.27**	down	**1.36**	up	**2.43**	down	**1.15**	down	**1.35**	down	**1.51**	down	ABA
Os.51655.1.S1_at	LOC_Os08g40720	FAD-binding and arabino-lactone oxidase domains containing protein, putative, express	**1.02**	down	**1.10**	up	**1.03**	down	**2.67**	down	**3.53**	down	**1.37**	down	2
Os.51655.2.S1_x_at	LOC_Os08g40720	FAD-binding and arabino-lactone oxidase domains containing protein, putative, expres	**1.07**	up	**1.21**	up	**1.02**	up	**2.42**	down	**2.95**	down	**1.41**	down	2
Os.51658.1.S1_at	LOC_Os06g49340	OsFBDUF35 - F-box and DUF domain containing protein, expressed	**1.56**	up	**3.89**	up	**3.62**	up	**2.37**	up	**2.07**	up	**1.24**	up	4
Os.51663.1.S1_at	LOC_Os04g50760	ara54-like RING finger protein, putative, expressed	**1.06**	down	**1.07**	down	**2.68**	up	**1.02**	down	**1.34**	up	**1.10**	down	ABA
Os.51664.1.S1_at	LOC_Os06g11720	cytokinin-O-glucosyltransferase 2, putative, expressed	**1.06**	up	**4.91**	up	**4.22**	down	**1.52**	up	**2.01**	up	**1.88**	up	3
Os.51665.1.A1_at	AK063327	Oryza sativa Japonica Group cDNA clone:001-113-H08, full insert sequence.	**1.11**	up	**1.02**	down	**3.21**	up	**1.01**	up	**1.01**	down	**1.00**	down	ABA
Os.51696.1.S1_at	LOC_Os02g43620	transporter, major facilitator family, putative, expressed	**1.03**	up	**1.05**	up	**25.73**	up	**1.00**	up	**1.01**	up	**1.00**	up	ABA
Os.51706.1.S1_at	LOC_Os03g58910	expressed protein	**1.00**	down	**1.03**	down	**3.99**	up	**1.01**	up	**1.06**	up	**1.02**	up	ABA
Os.51709.2.S1_at	LOC_Os04g49700	zinc finger, C3HC4 type domain containing protein, expressed	**1.16**	down	**1.04**	up	**2.66**	up	**1.05**	up	**1.25**	up	**1.24**	down	ABA
Os.51711.1.S1_at	AK063499	Oryza sativa Japonica Group cDNA clone:001-116-E02, full insert sequence.	**1.00**	down	**1.01**	up	**4.87**	up	**1.02**	down	**1.02**	down	**1.02**	up	ABA
Os.51714.1.S1_at	LOC_Os07g48560	homeobox domain containing protein, expressed	**3.39**	up	**2.93**	down	**1.01**	up	**1.86**	up	**3.92**	up	**3.44**	up	4
Os.51718.1.S1_at	LOC_Os11g26780	dehydrin, putative, expressed	**1.01**	up	**1.85**	up	**86.95**	up	**1.29**	down	**1.32**	up	**1.47**	up	ABA
Os.51731.1.S1_at	LOC_Os12g40780	ankyrin repeat domain-containing protein 44, putative, expressed	**1.19**	down	**1.18**	down	**6.24**	up	**1.06**	up	**1.01**	down	**1.03**	up	ABA
Os.51736.1.S1_at	AK063566	Oryza sativa Japonica Group cDNA clone:001-117-F09, full insert sequence.	**2.83**	up	**1.09**	down	**1.01**	up	**1.00**	down	**1.02**	down	**1.01**	down	IAA
Os.51737.1.S1_x_at	LOC_Os12g32970	membrane associated DUF588 domain containing protein, putative, expressed	**1.28**	down	**1.17**	down	**4.56**	up	**1.23**	down	**2.05**	up	**1.21**	down	2
Os.5174.1.S1_at	LOC_Os01g67530	AMP-binding enzyme, putative, expressed	**1.22**	down	**1.27**	down	**3.09**	down	**1.04**	down	**1.15**	down	**1.16**	up	ABA
Os.51741.1.S1_at	LOC_Os05g25920	expressed protein	**2.19**	up	**2.10**	up	**1.98**	up	**1.13**	up	**1.11**	down	**1.04**	down	2
Os.51746.1.S1_s_at	LOC_Os05g50110	oleosin, putative, expressed	**1.04**	up	**1.25**	down	**47.38**	up	**1.00**	up	**1.08**	down	**1.06**	down	ABA
Os.51753.1.A1_at	LOC_Os12g35340	OsGrx_C11 - glutaredoxin subgroup III, expressed	**1.71**	down	**1.86**	up	**11.93**	down	**1.15**	up	**7.61**	down	**1.62**	down	2
Os.51758.2.S1_at	LOC_Os07g47840	expressed protein	**1.01**	down	**1.00**	up	**10.20**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
Os.51763.1.S1_x_at	LOC_Os01g12690	plant-specific domain TIGR01568 family protein, expressed	**1.38**	up	**1.16**	up	**14.79**	up	**1.36**	up	**1.30**	up	**1.20**	up	ABA
Os.51774.1.S1_at	AK063676	Oryza sativa Japonica Group cDNA clone:001-119-E01, full insert sequence.	**1.85**	up	**1.07**	up	**1.07**	up	**1.04**	up	**1.28**	down	**2.49**	down	JA
Os.51775.1.S1_at	LOC_Os12g05210	expressed protein	**1.13**	up	**1.03**	up	**46.95**	up	**1.07**	down	**4.44**	up	**1.02**	up	2
Os.51775.1.S1_x_at	LOC_Os12g05210	expressed protein	**1.29**	up	**1.01**	down	**81.22**	up	**1.02**	up	**4.05**	up	**1.17**	up	2
Os.5178.1.A1_s_at	LOC_Os03g56950	phytochrome-interacting factor 4, putative, expressed	**1.03**	up	**1.98**	up	**12.55**	down	**1.73**	down	**2.35**	down	**2.19**	down	4
Os.51787.1.S1_at	LOC_Os12g24320	ATPase 3, putative, expressed	**2.36**	down	**1.12**	up	**2.76**	down	**1.29**	down	**1.43**	down	**1.81**	down	2
Os.51789.1.S1_at	LOC_Os03g42520	expressed protein	**1.11**	down	**1.33**	down	**49.12**	up	**1.04**	down	**1.08**	down	**1.02**	down	ABA
Os.5179.1.A1_at	LOC_Os08g36310	cytochrome P450, putative, expressed	**1.33**	down	**1.22**	down	**2.03**	down	**1.34**	up	**1.45**	down	**2.03**	down	2
Os.51794.1.S1_at	LOC_Os06g12370	OsFtsH6 FtsH protease, homologue of AtFtsH6, expressed	**1.05**	up	**1.14**	down	**4.51**	up	**1.06**	down	**1.06**	down	**1.05**	down	ABA
Os.51807.1.S1_at	AK063793	Oryza sativa Japonica Group cDNA clone:001-121-E12, full insert sequence.	**1.32**	up	**1.18**	down	**19.78**	up	**1.58**	down	**1.30**	up	**1.58**	down	ABA
Os.51831.1.S1_at	LOC_Os02g15340	no apical meristem protein, putative, expressed	**2.50**	up	**1.21**	down	**2.81**	down	**1.07**	down	**1.05**	up	**1.13**	down	2
Os.51833.1.S1_x_at	LOC_Os07g09050	exostosin family protein, putative, expressed	**1.02**	down	**1.00**	up	**21.93**	up	**1.01**	down	**1.09**	up	**1.01**	up	ABA
Os.51835.1.S1_a_at	LOC_Os05g48700	gibberellin 2-beta-dioxygenase, putative, expressed	**1.91**	up	**2.58**	down	**36.59**	up	**1.22**	up	**3.49**	up	**1.90**	up	3
Os.51847.1.S1_x_at	LOC_Os03g55220	bHelix-loop-helix transcription factor, putative, expressed	**1.18**	up	**1.10**	up	**3.05**	down	**1.48**	up	**1.77**	up	**1.72**	up	ABA
Os.51847.2.S1_at	LOC_Os03g55220	bHelix-loop-helix transcription factor, putative, expressed	**1.75**	up	**1.23**	up	**14.60**	down	**1.19**	up	**1.81**	up	**1.53**	up	ABA
Os.5185.1.S1_at	LOC_Os07g48390	proline-rich protein, putative, expressed	**1.50**	down	**1.41**	down	**3.58**	down	**2.22**	up	**1.02**	up	**1.24**	up	2

Os.51853.1.S1_at	LOC_Os06g28480	polygalacturonase inhibitor 1 precursor, putative, expressed	1.04	down	1.13	down	2.46	down	1.27	down	1.46	down	1.48	down	ABA
Os.5186.1.S1_at	LOC_Os04g33390	prephenate dehydratase domain containing protein, expressed	1.21	down	1.43	up	2.65	down	1.19	up	1.26	down	1.84	up	ABA
Os.519.1.S1_at	LOC_Os01g08860	hsp20/alpha crystallin family protein, putative, expressed	1.46	down	1.44	down	3.04	up	1.05	up	9.19	up	1.21	down	2
Os.51916.1.S1_at	LOC_Os01g39020	HSF-type DNA-binding domain containing protein, expressed	1.55	up	1.01	down	120.32	up	1.07	down	5.30	up	2.19	up	3
Os.51923.1.S1_at	CT831749	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRA123F16, full insert sequence	1.27	down	2.79	up	7.61	up	1.25	up	2.20	up	61.74	up	4
Os.51924.1.S1_at	AK064290	Oryza sativa Japonica Group cDNA clone:002-105-H05, full insert sequence.	1.19	up	1.01	up	3.13	up	1.14	down	1.06	up	1.27	up	ABA
Os.51926.1.S1_at	AK064292	no apical meristem (NAM) family protein	2.25	up	1.33	down	2.65	up	1.19	down	1.49	up	1.13	up	2
Os.51926.1.S1_x_at	AK064292	no apical meristem (NAM) family protein	1.61	up	1.54	down	2.97	up	1.13	down	1.63	up	1.32	up	ABA
Os.51934.1.S1_at	LOC_Os02g03600	dnaJ domain containing protein, expressed	1.12	up	1.00	up	2.26	up	1.27	down	1.39	up	1.01	up	ABA
Os.51935.1.S1_at	LOC_Os11g01830	staphylococcal nuclease homologue, putative, expressed	1.84	down	1.43	down	5.86	down	1.04	up	1.60	down	2.20	down	2
Os.51937.1.S1_a_at	LOC_Os07g09670	galactosyltransferase family protein, putative, expressed	1.19	down	1.09	down	2.76	up	1.14	up	1.06	up	1.28	up	ABA
Os.5194.1.S1_x_at	LOC_Os01g66110	methyltransferase, putative, expressed	1.41	up	1.05	down	2.31	down	1.04	up	1.08	down	1.16	up	ABA
Os.5194.2.S1_at	LOC_Os01g66110	methyltransferase, putative, expressed	1.00	up	1.09	down	2.20	down	1.11	up	1.01	down	1.10	up	ABA
Os.5195.1.S1_at	LOC_Os01g66240	mitochondrion protein, putative, expressed	1.20	up	1.03	up	3.02	up	1.24	up	1.56	up	1.61	up	ABA
Os.51950.1.S1_at	LOC_Os05g38830	HECT-domain domain containing protein, expressed	1.10	up	1.09	down	3.09	up	1.11	up	1.77	up	1.16	down	ABA
Os.51956.1.S1_at	LOC_Os02g52830	lipase, putative, expressed	1.54	down	1.40	down	5.41	up	1.87	up	1.31	up	1.04	up	ABA
Os.51968.1.S1_a_at	LOC_Os05g15040	NB-ARC domain containing protein, expressed	1.17	down	1.18	down	2.11	down	1.03	down	1.83	down	1.40	down	ABA
Os.51975.1.S1_x_at	LOC_Os05g31056	tetratricopeptide repeat containing protein, putative, expressed	1.04	down	1.13	down	2.03	up	1.18	up	1.16	up	1.01	down	ABA
Os.51983.1.A1_x_at	LOC_Os01g12470	mitochondrial carrier protein, putative, expressed	1.07	up	1.08	down	6.31	up	1.05	up	1.64	up	1.29	up	ABA
Os.52000.1.S1_at	LOC_Os12g13950	POLA2 - Putative DNA polymerase alpha complex subunit, expressed	1.35	down	1.05	up	4.97	down	1.18	down	1.66	down	1.64	down	ABA
Os.52001.1.S2_at	LOC_Os05g01040	serine/threonine-protein kinase, putative, expressed	1.21	up	1.03	down	1.37	up	1.53	up	1.68	up	2.50	up	JA
Os.52005.1.S1_at	LOC_Os02g54254	saccharopine dehydrogenase, putative, expressed	1.15	down	1.13	down	4.10	up	1.12	up	1.83	up	1.32	up	ABA
Os.52036.1.S1_at	LOC_Os05g31020	eukaryotic peptide chain release factor subunit 1-1, putative, expressed	1.58	up	1.11	down	99.59	up	1.11	down	1.12	down	1.31	up	ABA
Os.52056.1.S1_at	LOC_Os01g43080	exonuclease, putative, expressed	1.21	down	1.26	down	4.75	up	1.20	up	1.47	up	1.45	up	ABA
Os.5208.1.S1_at	LOC_Os06g36050	expressed protein	1.06	up	1.10	down	3.28	down	1.01	down	1.45	down	1.04	up	ABA
Os.5209.2.S1_at	LOC_Os09g34320	expressed protein	1.23	down	2.30	up	2.68	down	1.73	down	1.87	down	1.55	down	2
Os.52091.1.S1_at	LOC_Os10g40290	pectinacetylesterase domain containing protein, expressed	1.17	up	1.15	down	5.22	down	1.66	down	1.71	down	1.51	down	ABA
Os.52095.2.S1_at	LOC_Os09g32988	POEI18 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.14	down	1.32	down	4.67	down	1.07	up	2.15	down	1.47	down	2
Os.52099.1.S1_at	LOC_Os06g03059	hypothetical protein	1.17	down	1.50	down	2.36	down	1.93	down	1.70	up	4.11	up	2
Os.5210.1.S1_at	LOC_Os08g39370	citrate transporter, putative, expressed	1.35	up	1.04	down	9.91	up	1.23	up	1.89	up	1.30	down	ABA
Os.52112.1.S1_at	LOC_Os07g48320	HAD superfamily phosphatase, putative, expressed	41.26	up	2.71	up	2.31	down	1.54	up	1.19	up	1.13	down	3
Os.5213.1.S1_at	LOC_Os02g44720	expressed protein	1.17	up	1.02	down	1.46	up	1.15	down	1.03	down	2.71	down	JA
Os.52132.1.S2_at	AK068321	Oryza sativa Japonica Group cDNA clone:J013148K15, full insert sequence.	2.20	down	1.13	down	1.01	up	1.01	up	1.29	up	1.00	up	IAA
Os.52136.1.S1_at	LOC_Os03g59430	uncharacterized glycosyltransferase, putative, expressed	1.59	down	1.05	down	5.33	up	1.43	down	1.10	down	1.15	down	ABA
Os.52151.1.S1_at	LOC_Os08g38460	zinc finger, C3HC4 type domain containing protein, expressed	1.23	up	1.73	up	4.44	up	1.17	down	1.06	down	1.16	down	ABA
Os.52154.1.S1_at	LOC_Os05g25400	RNA binding protein, putative, expressed	1.16	up	1.08	up	8.51	down	1.05	down	2.18	down	29.72	down	3
Os.52156.1.S1_at	LOC_Os11g20360	expressed protein	1.45	down	1.37	down	2.38	down	1.06	down	1.06	down	1.14	down	ABA
Os.52181.1.S1_at	AK065487	Oryza sativa Japonica Group cDNA clone:J013003I22, full insert sequence.	2.47	down	1.51	up	1.23	down	1.22	up	1.09	up	1.16	down	IAA
Os.52189.1.S1_at	LOC_Os06g19260	cadmium tolerance factor, putative, expressed	1.12	down	1.54	down	4.05	down	1.46	up	1.83	up	1.07	down	ABA
Os.52193.1.S1_at	LOC_Os12g24170	beta-galactosidase precursor, putative, expressed	1.17	up	1.04	down	2.61	up	1.24	up	1.30	up	1.16	up	ABA
Os.52211.1.S1_at	LOC_Os07g40870	igA FC receptor precursor, putative, expressed	1.06	up	1.10	up	2.26	up	1.21	down	1.01	down	1.24	down	ABA
Os.52234.1.S1_at	LOC_Os02g02910	expressed protein	1.16	up	1.05	up	7.56	down	1.55	down	1.58	down	1.37	down	ABA
Os.52244.2.S1_x_at	LOC_Os05g44570	histidine-containing phosphotransfer protein, putative, expressed	1.17	up	1.14	up	4.12	up	1.01	up	1.41	up	1.13	up	ABA
Os.5225.1.S1_at	LOC_Os01g53420	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	2.27	down	1.42	up	4.25	down	1.07	up	1.09	down	2.29	up	3
Os.52261.1.S1_at	LOC_Os04g47360	OsPOP9 - Putative Prolyl Oligopeptidase homologue, expressed	1.03	up	1.88	up	2.05	down	1.39	down	1.22	down	1.42	down	ABA
Os.52263.1.S1_at	LOC_Os02g50730	metalloendoproteinase 1 precursor, putative, expressed	1.28	up	1.30	up	4.83	up	1.31	down	3.46	up	1.06	down	2
Os.52282.1.S1_at	LOC_Os04g28780	serine/threonine-protein kinase receptor precursor, putative, expressed	1.55	down	1.62	down	3.91	down	1.03	up	1.43	down	1.20	down	ABA
Os.52284.2.S1_x_at	LOC_Os02g35820	retrotransposon protein, putative, unclassified, expressed	1.06	up	1.02	up	2.22	up	1.22	up	1.10	up	1.06	down	ABA
Os.52286.1.S1_at	LOC_Os01g60780	solute carrier family 35 member E3, putative, expressed	1.32	down	1.97	up	2.48	down	1.28	down	1.30	down	1.24	down	ABA
Os.5230.1.S1_at	LOC_Os11g30810	sulfotransferase domain containing protein, expressed	1.46	down	1.01	up	1.20	down	1.38	down	2.03	down	2.81	up	2
Os.52303.1.S1_x_at	LOC_Os11g45820	expressed protein	1.07	up	1.02	up	2.10	up	1.16	up	1.10	up	1.02	up	ABA
Os.52307.1.S1_at	LOC_Os04g35760	expressed protein	1.24	up	1.10	up	4.23	down	1.61	down	1.81	down	1.35	down	ABA
Os.52314.1.S2_at	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed	1.02	up	1.39	down	2.83	down	1.15	down	1.47	down	1.22	down	ABA
Os.52327.1.S1_at	LOC_Os03g04120	AMP-binding enzyme, putative, expressed	1.36	down	1.65	down	4.35	up	1.32	up	1.94	up	2.28	up	2
Os.52329.1.S1_at	LOC_Os02g07044	rhodanese-like domain containing protein, putative, expressed	1.53	up	1.08	down	2.82	down	1.19	down	1.86	up	1.38	up	ABA

Os.52344.1.S1_at	LOC_Os08g26840	plant protein of unknown function domain containing protein, expressed	1.45	down	1.07	down	9.98	down	1.70	up	1.49	down	1.66	up	ABA
Os.52381.1.S1_at	AK066750	Oryza sativa Japonica Group cDNA clone:J013074O22, full insert sequence.	1.15	up	1.45	up	6.30	up	1.49	down	1.16	up	1.66	down	ABA
Os.52391.1.S1_x_at	LOC_Os08g01920	SGR2, putative, expressed	1.03	down	1.05	down	2.56	up	1.07	up	1.39	up	1.08	up	ABA
Os.52393.1.S1_at	AK066822	expressed protein	1.06	down	1.03	down	2.03	down	1.09	down	1.25	down	1.15	down	ABA
Os.52409.1.S1_s_at	LOC_Os10g04620	OsPOP20 - Putative Prolyl Oligopeptidase homologue, expressed	1.27	up	1.25	down	2.30	up	1.02	up	1.74	up	1.16	up	ABA
Os.52416.1.S1_at	LOC_Os02g49820	RNA recognition motif family protein, expressed	1.03	up	1.22	up	2.44	down	1.33	down	1.44	down	1.54	down	ABA
Os.52419.1.S1_at	LOC_Os06g02000	adenylate kinase, putative, expressed	1.02	down	1.05	down	2.66	up	1.47	down	2.12	down	2.09	down	3
Os.5243.1.S1_at	LOC_Os02g55320	two-component response regulator, putative, expressed	1.12	down	1.05	up	2.17	up	1.03	down	1.14	up	1.01	down	ABA
Os.52438.1.S1_at	LOC_Os05g36010	OsSub47 - Putative Subtilisin homologue, expressed	1.12	up	1.21	down	6.10	down	1.22	down	1.37	down	1.04	up	ABA
Os.52445.1.S1_at	LOC_Os04g46740	pectinesterase, putative, expressed	1.19	down	1.31	down	3.05	down	1.46	down	1.49	down	1.26	down	ABA
Os.52460.1.S1_at	LOC_Os06g23114	copper methylamine oxidase precursor, putative, expressed	1.16	up	1.22	up	1.48	down	3.12	down	1.30	up	1.15	up	ACC
Os.52465.1.S1_at	LOC_Os07g36210	expressed protein	1.22	down	1.64	up	4.89	down	1.35	up	1.44	down	1.24	down	ABA
Os.52469.1.S1_at	AK067317	Oryza sativa Japonica Group cDNA clone:J013105D21, full insert sequence.	1.44	up	1.50	up	6.77	down	1.21	down	1.85	down	1.62	up	ABA
Os.52482.1.S1_at	LOC_Os07g36630	CSLF8 - cellulose synthase-like family F; beta1,3;1,4 glucan synthase, expressed	1.91	down	1.35	down	13.09	down	1.67	down	2.09	down	1.47	up	2
Os.52483.1.S1_at	LOC_Os06g19380	expressed protein	1.06	down	1.33	up	2.49	down	1.35	down	1.67	down	1.34	down	ABA
Os.52486.1.S1_at	LOC_Os05g16824	SHR5-receptor-like kinase, putative, expressed	1.00	down	1.22	down	1.22	up	1.03	up	1.01	up	6.07	up	JA
Os.52491.1.A1_at	LOC_Os05g44420	expressed protein	1.12	up	2.57	down	1.27	down	1.03	down	1.13	up	1.27	up	BAP
Os.52500.1.S1_at	LOC_Os05g25890	expressed protein	1.01	down	1.00	up	1.12	down	1.10	down	1.17	up	2.65	up	JA
Os.52522.1.S1_at	LOC_Os08g45130	histone-lysine N-methyltransferase, putative, expressed	1.02	down	1.06	up	2.25	down	1.13	up	1.14	down	1.12	down	ABA
Os.52527.1.S1_s_at	LOC_Os06g03560	oligopeptide transporter, putative, expressed	1.59	down	1.16	up	4.67	down	1.70	up	2.21	down	1.28	down	2
Os.52534.1.S1_x_at	NM_001067852	Oryza sativa (japonica cultivar-group) Os08g0236800 (Os08g0236800) mRNA, partial	1.06	down	1.08	down	2.73	up	1.01	down	1.22	up	1.11	up	ABA
Os.52542.1.S1_at	LOC_Os03g60520	expressed protein	1.01	up	1.53	down	2.13	up	1.14	up	1.52	up	1.32	up	ABA
Os.52543.1.S1_at	LOC_Os04g53580	P21-Rho-binding domain containing protein, putative, expressed	1.07	down	1.37	up	2.65	down	1.03	down	1.18	down	1.07	down	ABA
Os.52552.1.S1_at	LOC_Os06g22390	expressed protein	1.08	down	1.11	down	2.56	up	1.10	down	1.14	down	2.06	down	2
Os.52555.1.S1_at	LOC_Os06g46910	ZOS6-07 - C2H2 zinc finger protein, expressed	1.25	up	1.92	up	17.05	up	1.24	up	1.96	up	1.28	up	ABA
Os.52568.1.S1_at	LOC_Os12g02800	CRP11 - Cysteine-rich family protein precursor, expressed	1.29	down	1.28	down	5.77	up	1.14	down	1.05	up	1.01	down	ABA
Os.52568.1.S1_s_at	LOC_Os11g02820	CRP10 - Cysteine-rich family protein precursor, expressed	1.08	down	1.10	down	4.23	up	1.01	up	1.01	down	1.10	down	ABA
Os.52569.1.S1_at	LOC_Os02g47210	amino acid permease family protein, putative, expressed	1.19	down	2.29	up	3.64	down	1.42	down	1.30	down	1.05	up	2
Os.52574.1.S1_at	LOC_Os04g41450	TGF-beta receptor, type I/II extracellular region, putative, expressed	1.14	down	2.29	up	6.06	down	1.47	down	1.72	down	1.80	down	2
Os.52574.2.S1_x_at	LOC_Os04g41450	TGF-beta receptor, type I/II extracellular region, putative, expressed	1.35	up	2.75	up	2.36	down	1.26	down	1.51	down	1.64	down	2
Os.52579.1.S1_at	LOC_Os06g22070	mitochondrial glycoprotein, putative, expressed	1.05	down	1.05	up	2.29	down	1.10	up	1.44	down	1.42	down	ABA
Os.52590.1.S1_at	LOC_Os04g59540	phosphatidylinositol-4-phosphate 5-Kinase, putative, expressed	1.00	down	1.00	down	8.65	up	1.00	up	1.01	up	1.02	up	ABA
Os.52597.1.S1_at	LOC_Os06g42850	extracellular ligand-gated ion channel, putative, expressed	1.22	up	1.16	up	584.65	up	1.92	down	2.53	up	1.83	down	2
Os.52613.1.S1_at	LOC_Os06g42850	extracellular ligand-gated ion channel, putative, expressed	1.13	down	1.18	up	6.86	up	1.01	down	1.06	up	1.08	down	ABA
Os.52621.1.S1_at	LOC_Os12g44100	peptide transporter PTR2, putative, expressed	1.06	up	1.16	down	2.65	up	1.20	down	1.24	up	1.25	up	ABA
Os.52627.1.S1_at	LOC_Os08g26230	expressed protein	1.08	up	1.00	up	2.71	down	1.34	down	1.32	up	1.27	up	ABA
Os.52638.1.S1_at	LOC_Os02g58120	oxidoreductase/ transition metal ion binding protein, putative, expressed	1.09	up	1.03	up	3.01	down	1.24	down	1.58	down	1.27	down	ABA
Os.52641.1.S1_at	LOC_Os09g30486	fasciclin domain containing protein, expressed	1.35	down	1.04	down	4.73	down	1.55	down	2.59	down	1.30	down	2
Os.52645.1.S1_at	LOC_Os06g17390	auxin-independent growth promoter protein, putative, expressed	1.10	down	1.19	down	2.24	down	1.08	down	1.42	down	1.61	up	ABA
Os.52646.1.S1_at	LOC_Os05g03640	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	3.23	down	2.33	up	11.51	down	1.02	down	2.28	down	4.80	up	5
Os.52648.1.S1_at	LOC_Os04g35540	amino acid permease family protein, putative, expressed	1.18	down	1.31	down	1.30	up	1.15	up	2.43	up	1.60	up	SA
Os.52664.1.S1_at	LOC_Os02g47400	pectinacetylesterase domain containing protein, expressed	1.00	up	1.08	up	3.49	down	1.35	down	1.92	down	1.34	down	ABA
Os.52672.1.S1_at	LOC_Os08g16130	fiber protein Fb34, putative, expressed	1.02	down	1.03	down	2.28	down	1.03	down	1.38	down	1.06	down	ABA
Os.52678.1.S1_at	LOC_Os04g41130	osFTL6 FT-Like6 homologous to Flowering Locus T gene; contains Pfam profile PF01	1.93	down	3.09	up	2.50	down	1.95	up	1.76	down	4.47	down	3
Os.52681.1.S1_at	LOC_Os06g08390	Ser/Thr protein phosphatase family protein, putative, expressed	1.25	up	1.14	up	2.45	up	1.07	down	1.07	up	1.00	up	ABA
Os.52682.1.S1_at	LOC_Os06g22440	SAM dependent carboxyl methyltransferase, putative, expressed	1.14	down	1.14	down	3.10	down	1.09	up	1.57	down	1.11	up	ABA
Os.52689.1.S1_at	LOC_Os03g48310	plasma membrane ATPase, putative, expressed	1.16	up	1.11	up	21.49	up	1.17	down	1.03	up	1.07	up	ABA
Os.52689.1.S2_at	LOC_Os03g48310	plasma membrane ATPase, putative, expressed	1.01	up	1.05	down	33.91	up	1.45	down	1.52	up	1.24	up	ABA
Os.5270.1.S1_at	LOC_Os05g44200	GDSL-like lipase/acylhydrolase, putative, expressed	1.10	up	1.00	up	7.26	down	1.24	down	1.23	down	1.08	up	ABA
Os.52709.1.S1_at	AK068854	Oryza sativa Japonica Group cDNA clone:J013170J18, full insert sequence.	1.01	down	1.00	up	2.67	up	1.00	up	1.00	down	1.02	up	ABA
Os.52712.1.S1_at	LOC_Os09g26840	expressed protein	1.44	up	2.02	down	3.63	up	6.09	up	1.90	up	1.48	down	3
Os.52715.1.S1_at	LOC_Os09g17810	leucine zipper protein-like, expressed	1.12	up	1.14	down	2.88	up	1.14	up	1.01	down	1.21	up	ABA
Os.52742.1.S1_at	LOC_Os05g11010	harpin-induced protein 1 domain containing protein, expressed	1.47	down	1.09	down	2.24	down	1.02	up	1.36	down	1.79	up	ABA
Os.52750.1.S1_x_at	LOC_Os09g03190	expressed protein	1.09	down	1.23	down	2.26	up	1.14	up	3.44	up	1.13	up	2
Os.52754.1.S1_x_at	LOC_Os03g50220	homologous-pairing protein meu13, putative, expressed	1.04	down	1.09	down	3.06	down	1.03	down	1.58	down	1.58	down	ABA

Os.52760.1.S1_at	LOC_Os12g16650	Cyclopropane-fatty-acyl-phospholipid synthase, putative, expressed	**1.12**	down	**1.63**	up	**2.08**	down	**1.12**	down	**1.54**	down	**4.49**	up	2
Os.52767.1.A1_at	LOC_Os08g35160	heat shock protein DnaJ, putative, expressed	**1.21**	up	**1.44**	up	**7.67**	down	**1.85**	up	**1.80**	down	**2.19**	down	2
Os.5277.1.S1_at	AK063889	Oryza sativa Japonica Group cDNA clone:001-122-G04, full insert sequence.	**1.24**	up	**1.36**	down	**20.34**	up	**1.53**	up	**1.02**	up	**1.23**	down	ABA
Os.52778.1.S1_at	LOC_Os02g50810	expressed protein	**1.10**	down	**1.09**	up	**3.62**	down	**1.02**	down	**1.34**	down	**1.24**	down	ABA
Os.52780.1.S1_at	LOC_Os05g07710	WD40-like domain containing protein, putative, expressed	**1.15**	up	**1.31**	down	**6.20**	up	**1.32**	up	**1.59**	up	**1.74**	up	ABA
Os.52791.1.S1_at	LOC_Os09g39960	dynamin family protein, putative, expressed	**1.08**	up	**1.18**	down	**1.90**	up	**1.31**	up	**2.10**	up	**1.27**	up	SA
Os.52793.1.S1_at	LOC_Os04g43840	possible lysine decarboxylase domain containing protein, expressed	**1.31**	down	**5.30**	up	**2.18**	down	**1.72**	down	**1.77**	down	**1.86**	down	2
Os.52803.1.S1_at	LOC_Os06g44500	OsFBK17 - F-box domain and kelch repeat containing protein, expressed	**1.02**	up	**1.14**	down	**3.15**	down	**1.21**	up	**1.25**	down	**1.41**	down	ABA
Os.52814.1.S1_at	LOC_Os05g49480	transcription factor-related, putative, expressed	**1.02**	down	**1.01**	down	**3.67**	up	**1.02**	up	**1.06**	up	**1.01**	up	ABA
Os.52824.1.S1_at	LOC_Os03g40070	transposon protein, putative, unclassified, expressed	**1.31**	down	**1.04**	up	**7.52**	down	**1.04**	down	**1.06**	up	**1.92**	down	ABA
Os.52831.1.S1_at	LOC_Os03g28090	pectinesterase, putative, expressed	**1.20**	down	**1.27**	down	**7.93**	up	**1.01**	up	**1.02**	up	**1.05**	up	ABA
Os.52833.1.S1_at	LOC_Os08g02110	peroxidase precursor, putative, expressed	**2.28**	down	**1.35**	up	**4.16**	down	**1.33**	up	**1.95**	down	**1.40**	down	3
Os.52835.1.S1_at	LOC_Os08g30900	YDG/SRA domain containing protein, expressed	**1.01**	down	**1.00**	up	**2.12**	up	**1.01**	up	**1.01**	up	**1.02**	up	ABA
Os.52843.1.S1_at	LOC_Os07g04210	Ser/Thr protein phosphatase family protein, putative	**1.17**	up	**1.09**	down	**2.50**	up	**1.05**	down	**1.49**	up	**1.26**	up	ABA
Os.52845.1.S1_at	AK069569	expressed protein	**5.05**	down	**2.23**	down	**15.87**	down	**1.82**	down	**3.30**	down	**1.51**	down	4
Os.52863.1.S1_at	LOC_Os09g22000	hydrolase, HAD superfamily, Cof family, putative, expressed	**1.12**	down	**1.11**	down	**1.01**	up	**1.11**	up	**1.02**	down	**4.48**	up	JA
Os.52870.1.S1_at	LOC_Os11g34710	Ser/Thr protein phosphatase family protein, putative, expressed	**1.37**	down	**1.20**	down	**1.27**	down	**1.08**	down	**1.03**	down	**2.65**	up	JA
Os.52910.1.S1_at	LOC_Os04g55700	exonuclease, putative, expressed	**1.73**	up	**1.19**	up	**2.05**	up	**1.82**	up	**4.50**	up	**2.09**	up	3
Os.52913.1.A1_at	LOC_Os08g43450	MYB-like protein 1, putative, expressed	**1.36**	up	**1.40**	up	**2.71**	down	**1.54**	down	**1.80**	down	**1.58**	down	ABA
Os.52921.1.S1_at	LOC_Os08g14760	AMP-binding domain containing protein, expressed	**1.54**	down	**1.20**	up	**5.21**	down	**1.02**	down	**2.26**	down	**1.33**	down	2
Os.52940.1.S1_at	LOC_Os12g05600	hydrolase, alpha/beta fold family protein, putative, expressed	**1.06**	down	**1.53**	up	**3.23**	down	**2.48**	down	**1.46**	down	**1.41**	down	2
Os.52955.1.A1_at	LOC_Os12g42220	expressed protein	**1.24**	up	**1.26**	up	**37.10**	up	**1.47**	up	**1.32**	up	**1.12**	down	ABA
Os.52956.1.S1_at	LOC_Os04g20330	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed	**2.77**	up	**1.06**	up	**1.03**	up	**1.32**	down	**1.58**	down	**1.53**	down	IAA
Os.52974.1.S1_at	LOC_Os04g50940	peptide transporter PTR2, putative, expressed	**1.59**	down	**5.31**	up	**1.13**	up	**1.13**	up	**1.16**	up	**3.31**	up	2
Os.5299.2.S1_a_at	LOC_Os05g37970	universal stress protein domain containing protein, putative, expressed	**1.00**	up	**1.07**	up	**3.16**	up	**1.05**	up	**2.59**	up	**1.02**	down	2
Os.52999.1.S1_at	LOC_Os12g43810	expressed protein	**1.07**	down	**1.88**	up	**2.15**	down	**1.35**	down	**1.47**	down	**1.46**	down	ABA
Os.53007.1.S1_at	LOC_Os02g52360	peptidyl-prolyl cis-trans isomerase CYP40, putative, expressed	**1.47**	down	**1.07**	down	**3.08**	down	**1.14**	down	**1.03**	down	**1.26**	down	ABA
Os.53019.1.S1_at	LOC_Os11g05740	B3 DNA binding domain containing protein, expressed	**12.74**	up	**2.42**	up	**2.20**	down	**1.55**	down	**1.37**	down	**1.68**	down	3
Os.53054.1.S1_at	LOC_Os02g45870	tobamovirus multiplication protein, putative, expressed	**1.16**	down	**1.40**	up	**2.50**	down	**1.20**	down	**1.15**	down	**1.66**	up	ABA
Os.53108.1.S1_at	LOC_Os02g58160	expressed protein	**1.20**	up	**1.23**	up	**9.29**	up	**1.42**	down	**1.05**	down	**1.14**	down	ABA
Os.53114.1.S1_at	LOC_Os07g48610	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.09**	up	**1.15**	up	**2.48**	down	**1.07**	down	**1.05**	down	**1.07**	down	ABA
Os.53115.1.S2_at	AK072949	Oryza sativa Japonica Group cDNA clone:J023147J15, full insert sequence.	**1.11**	up	**1.14**	down	**3.73**	up	**1.05**	down	**1.50**	up	**1.02**	down	ABA
Os.53117.1.S1_x_at	AK070901	Oryza sativa Japonica Group cDNA clone:J023073O19, full insert sequence.	**1.15**	down	**1.14**	down	**24.33**	up	**1.40**	down	**3.95**	up	**1.12**	down	2
Os.5313.1.S1_at	LOC_Os08g09350	gar2, putative, expressed	**1.02**	down	**1.03**	up	**2.12**	down	**1.14**	up	**1.32**	down	**1.25**	down	ABA
Os.53130.1.S1_at	LOC_Os06g48860	OsSAUR28 - Auxin-responsive SAUR gene family member	**1.66**	down	**1.02**	down	**3.26**	down	**1.06**	up	**1.16**	up	**1.10**	up	ABA
Os.53162.1.S1_s_at	LOC_Os04g47780	transmembrane amino acid transporter protein, putative, expressed	**1.53**	up	**1.60**	up	**2.70**	down	**2.76**	up	**1.42**	down	**1.25**	down	2
Os.53172.1.S1_at	LOC_Os03g20410	aquaporin SIP2-1, putative, expressed	**1.05**	down	**1.22**	up	**2.42**	down	**1.30**	down	**1.22**	down	**1.66**	up	ABA
Os.53173.1.S1_at	LOC_Os05g37780	expressed protein	**3.48**	down	**1.13**	down	**2.34**	down	**1.48**	up	**1.17**	down	**2.30**	down	3
Os.53176.1.S1_at	LOC_Os02g26720	Inositol 1, 3, 4-trisphosphate 5/6-kinase, putative, expressed	**1.04**	down	**1.35**	up	**48.04**	up	**1.00**	up	**1.05**	up	**2.62**	up	2
Os.53178.1.S1_s_at	LOC_Os05g47840	IPP transferase, putative, expressed	**1.11**	down	**1.46**	up	**11.12**	down	**1.79**	up	**9.06**	down	**8.36**	down	3
Os.5318.1.S1_a_at	LOC_Os10g42610	expressed protein	**1.47**	down	**1.13**	down	**3.13**	up	**1.99**	up	**1.32**	up	**1.01**	down	ABA
Os.53197.1.S1_at	LOC_Os08g03370	Divergent PAP2 family domain containing protein, expressed	**1.15**	up	**1.03**	down	**2.11**	down	**1.30**	down	**1.28**	down	**1.35**	down	ABA
Os.53206.1.S1_at	LOC_Os06g05424	expressed protein	**1.36**	up	**1.17**	down	**2.30**	up	**1.10**	down	**3.88**	up	**1.92**	up	2
Os.53210.1.S1_at	LOC_Os11g26760	dehydrin, putative, expressed	**1.18**	down	**2.28**	up	**53.10**	up	**1.05**	down	**1.12**	up	**1.13**	down	2
Os.53236.1.S1_at	LOC_Os02g43170	B-box zinc finger family protein, putative, expressed	**1.90**	down	**2.01**	up	**6.21**	down	**1.01**	down	**1.48**	down	**1.48**	up	2
Os.53237.1.S1_at	LOC_Os07g34070	auxin-induced protein 5NG4, putative, expressed	**1.32**	down	**1.79**	down	**2.54**	down	**1.49**	down	**1.72**	up	**1.16**	up	ABA
Os.53242.1.S1_at	LOC_Os02g52180	plastocyanin-like domain containing protein, putative, expressed	**1.44**	down	**1.89**	up	**2.74**	down	**1.31**	down	**1.59**	down	**1.30**	down	ABA
Os.53244.1.A1_at	LOC_Os07g41230	esterase, putative, expressed	**1.17**	down	**2.14**	up	**1.66**	up	**1.30**	up	**1.38**	up	**1.59**	up	BAP
Os.5325.1.S1_at	LOC_Os08g23870	late embryogenesis abundant group 1, putative, expressed	**1.02**	down	**1.17**	down	**178.11**	up	**1.45**	down	**1.08**	up	**1.21**	down	ABA
Os.53254.1.S1_at	AK071601	expressed protein	**18.91**	up	**2.29**	up	**3.08**	down	**1.81**	up	**1.30**	up	**2.35**	down	4
Os.53266.1.S1_at	LOC_Os03g52010	lecithin cholesterol acyltransferase, putative, expressed	**1.27**	down	**1.27**	down	**7.44**	down	**1.12**	down	**1.73**	down	**1.02**	up	ABA
Os.53268.1.S1_at	LOC_Os09g17152	OsFBX319 - F-box domain containing protein, expressed	**1.01**	up	**1.27**	up	**1.05**	down	**1.02**	up	**1.04**	down	**2.47**	up	JA
Os.53277.1.S1_at	LOC_Os06g24490	expressed protein	**1.33**	up	**1.30**	up	**3.42**	up	**1.14**	up	**1.06**	down	**1.07**	down	ABA
Os.53285.1.S1_x_at	LOC_Os08g29770	endoglucanase, putative, expressed	**1.38**	down	**1.57**	up	**1.01**	down	**1.01**	down	**2.93**	up	**1.04**	down	SA
Os.53306.1.S1_at	LOC_Os02g39560	non-receptor tyrosine kinase spore lysis A, putative, expressed	**1.07**	down	**1.00**	up	**3.10**	down	**1.02**	up	**1.12**	down	**1.07**	up	ABA

Os.53328.1.S1_at	LOC_Os09g37180	transferase family protein, putative, expressed	1.02	up	1.21	up	2.05	down	1.24	up	1.59	up	2.90	up	2
Os.53340.1.S1_at	LOC_Os04g52390	potassium transporter, putative, expressed	1.07	up	1.07	down	3.40	up	1.54	down	1.53	up	1.15	up	ABA
Os.53358.1.S1_at	LOC_Os11g37560	expressed protein	1.22	up	1.09	down	6.71	up	1.03	down	1.06	up	1.27	down	ABA
Os.53368.1.S1_at	LOC_Os07g49470	protein kinase APK1B, chloroplast precursor, putative, expressed	1.05	down	1.02	down	3.66	up	1.04	up	1.11	up	1.11	down	ABA
Os.53369.1.S1_at	LOC_Os02g52850	receptor-like protein kinase like protein, putative, expressed	1.33	up	1.10	up	2.08	down	1.08	down	2.34	up	1.41	down	2
Os.53377.1.S1_at	LOC_Os08g28870	receptor-like protein kinase 5 precursor, putative, expressed	1.55	up	1.26	down	2.80	down	1.66	down	1.19	up	1.42	down	ABA
Os.53380.1.S1_at	LOC_Os05g38980	respiratory burst oxidase, putative, expressed	4.84	up	1.08	down	13.75	up	1.00	up	1.00	down	1.02	up	2
Os.53400.1.S1_at	AK072443	14-3-3 protein GF14 epsilon (GRF10)	1.02	down	1.04	up	11.06	up	1.09	down	1.05	down	1.04	down	ABA
Os.53407.1.S1_at	LOC_Os08g06210	expressed protein	1.58	down	1.14	down	1.16	down	1.53	up	3.59	up	1.51	up	SA
Os.53407.1.S1_x_at	LOC_Os08g06210	expressed protein	1.49	down	1.36	down	1.18	down	1.51	up	3.90	up	1.57	up	SA
Os.53410.1.S1_at	LOC_Os05g39000	KIP1, putative, expressed	1.02	up	1.01	down	2.88	up	1.12	up	1.07	up	1.05	up	ABA
Os.53422.1.S1_at	LOC_Os02g15460	expressed protein	1.01	down	1.01	up	5.14	up	1.17	down	1.96	up	1.27	down	ABA
Os.53428.1.S1_at	LOC_Os09g26370	DUF581 domain containing protein, expressed	1.08	down	1.30	down	2.95	up	1.23	down	1.66	down	1.59	down	ABA
Os.53438.1.S1_at	AK072622	Oryza sativa Japonica Group cDNA clone:J023125G21, full insert sequence.	1.03	down	1.23	down	13.34	down	1.73	down	4.84	down	6.87	down	3
Os.53456.1.S1_at	LOC_Os01g32120	OsCML11 - Calmodulin-related calcium sensor protein, expressed	1.02	down	1.01	down	5.61	up	1.34	up	1.15	up	1.56	down	ABA
Os.53459.1.S1_at	AK072753	harpin-induced protein-related	1.65	up	1.65	up	4.10	up	1.55	down	1.08	up	1.22	down	ABA
Os.53489.1.S1_at	LOC_Os11g27329	OsSCP62 - Putative Serine Carboxypeptidase homologue, expressed	1.20	up	1.02	down	3.92	up	1.16	down	1.26	up	1.10	up	ABA
Os.53524.1.S1_at	LOC_Os02g47060	OsWRKY66 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.46	down	1.04	up	2.52	down	1.17	up	2.39	down	1.15	up	2
Os.53526.1.S1_at	LOC_Os04g52110	late embryogenesis abundant protein, group 3, putative, expressed	1.04	down	1.01	up	1285.65	up	1.26	up	1.05	up	1.07	up	ABA
Os.5354.1.S1_at	LOC_Os12g06220	harpin-induced protein 1 domain containing protein, expressed	1.13	up	1.14	up	5.15	down	1.11	up	1.02	up	1.58	down	ABA
Os.53541.1.S1_at	LOC_Os06g48020	peroxidase precursor, putative, expressed	1.01	down	1.01	up	5.12	up	1.58	up	1.13	up	1.02	up	ABA
Os.53549.1.S1_at	LOC_Os05g06840	POLE2A - Putative DNA polymerase epsilon complex subunit, expressed	1.02	down	1.08	down	5.04	down	1.15	down	2.56	down	2.74	down	3
Os.53553.1.S1_at	LOC_Os06g27650	expressed protein	1.29	up	1.12	up	2.10	up	1.29	down	1.03	down	1.22	down	ABA
Os.53561.1.S1_at	LOC_Os07g26110	membrane associated DUF588 domain containing protein, putative, expressed	1.11	down	1.17	up	2.56	down	1.05	up	1.27	up	1.32	down	ABA
Os.53568.1.S1_at	LOC_Os08g39560	OTU-like cysteine protease family protein, putative, expressed	1.08	down	1.20	down	3.80	up	1.02	up	1.42	up	1.07	down	ABA
Os.53574.1.S1_at	LOC_Os06g08280	protein kinase domain containing protein, expressed	1.85	up	1.31	down	6.21	up	1.19	up	1.61	up	1.02	up	ABA
Os.53587.1.S1_at	LOC_Os12g02720	DUF567 domain containing protein, putative, expressed	2.65	up	1.17	up	7.50	down	1.21	up	1.14	down	1.27	down	2
Os.53589.1.S1_at	LOC_Os01g72710	expressed protein	1.03	up	1.14	down	2.24	down	1.26	up	1.18	down	1.12	up	ABA
Os.5361.1.S1_at	LOC_Os12g39380	BTBN24 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hy	1.19	up	1.30	up	2.52	down	1.12	down	1.39	down	1.37	down	ABA
Os.53616.1.S1_at	LOC_Os01g71060	xylanase inhibitor, putative, expressed	1.17	down	1.49	down	2.71	down	1.90	down	1.94	down	2.39	up	2
Os.53619.1.S1_at	LOC_Os01g73300	VAMP-like protein YKT62, putative, expressed	1.13	down	1.08	up	3.53	up	1.02	up	1.31	up	1.06	down	ABA
Os.53627.1.S1_at	AK073654	Oryza sativa Japonica Group cDNA clone:J033050E11, full insert sequence.	1.05	down	1.32	down	5.37	up	1.39	down	1.02	down	1.57	down	ABA
Os.53628.1.S1_x_at	LOC_Os03g61810	tRNA-specific adenosine deaminase, putative, expressed	1.04	down	1.17	down	1.41	down	1.27	down	1.15	down	2.04	up	JA
Os.53632.1.S1_at	LOC_Os05g13370	OsRhmbd12 - Putative Rhomboid homologue, expressed	1.02	up	1.06	up	2.38	up	1.12	down	1.11	down	1.20	down	ABA
Os.53636.1.S1_at	AK073680	zinc finger (C3HC4-type RING finger) family protein	1.10	down	1.03	up	5.03	up	1.19	up	1.11	up	1.03	up	ABA
Os.5365.1.S1_at	LOC_Os02g21040	aspartic proteinase nepenthesin precursor, putative, expressed	2.14	up	1.39	up	2.00	up	1.36	up	1.47	up	2.99	up	3
Os.53651.1.S1_at	LOC_Os06g43960	expressed protein	1.15	up	1.06	up	2.62	up	1.03	down	1.12	up	1.05	up	ABA
Os.53660.1.S1_at	LOC_Os02g43790	ethylene-responsive transcription factor, putative, expressed	1.57	up	2.21	up	2.37	down	1.22	up	1.30	up	2.62	up	3
Os.53665.1.S1_at	LOC_Os02g52370	armadillo/beta-catenin repeat family protein, putative, expressed	1.09	up	1.17	up	2.18	down	1.21	down	1.44	down	1.10	down	ABA
Os.53667.1.S1_at	LOC_Os06g35480	peroxidase precursor, putative, expressed	1.45	down	1.01	down	5.19	down	2.02	up	2.69	down	1.46	up	3
Os.53669.1.S1_at	LOC_Os04g36630	expressed protein	1.02	up	1.03	down	2.44	up	1.18	up	1.32	up	1.02	up	ABA
Os.5367.1.S1_at	LOC_Os01g40094	protein phosphatase 2C, putative, expressed	1.29	up	1.33	down	23.06	up	1.70	down	2.61	up	1.37	up	2
Os.53681.1.S1_at	LOC_Os04g41750	expressed protein	1.17	down	1.91	down	3.25	up	1.75	down	1.30	down	2.43	down	2
Os.5369.1.S1_at	LOC_Os08g43440	cytochrome P450, putative, expressed	1.35	down	1.23	up	2.83	down	1.09	down	1.25	down	1.19	down	ABA
Os.53691.1.S1_at	LOC_Os03g05060	exostosin family domain containing protein, expressed	3.38	down	1.47	down	4.56	down	1.10	down	2.47	down	1.97	down	4
Os.53704.1.S1_x_at	LOC_Os05g48900	fasciclin domain containing protein, expressed	1.13	down	1.02	up	2.25	down	1.21	down	1.51	down	1.03	down	ABA
Os.53705.1.S1_at	LOC_Os06g45060	expressed protein	1.13	up	1.08	up	2.51	up	1.09	up	1.50	up	1.23	up	ABA
Os.53706.1.S1_at	LOC_Os02g12420	receptor-like protein kinase precursor, putative, expressed	1.01	down	1.00	up	2.88	up	1.02	up	1.04	up	1.03	up	ABA
Os.53710.1.S1_at	LOC_Os01g25500	sterol carrier protein-2, putative, expressed	1.14	down	1.30	up	3.36	down	1.07	down	1.35	down	1.34	up	ABA
Os.53716.1.S1_at	LOC_Os03g11230	expressed protein	1.29	up	1.15	up	2.04	down	1.18	down	1.36	down	1.27	down	ABA
Os.53721.1.S1_at	LOC_Os03g30830	X8 domain containing protein, expressed	1.34	down	1.04	down	2.59	down	1.03	down	1.16	down	1.01	down	ABA
Os.53726.1.S1_at	LOC_Os07g05370	TKL_IRAK_CrRLK1L-1.15 - The CrRLK1L-1 subfamily has homology to the CrRLK1L h	1.56	up	1.97	up	11.53	up	1.58	up	1.72	up	2.39	down	3
Os.53744.2.S1_x_at	LOC_Os12g40419	protein kinase domain containing protein, expressed	1.21	down	1.17	down	2.99	up	1.05	up	1.15	up	1.13	down	ABA
Os.53748.1.S1_at	LOC_Os02g37950	transposon protein, putative, unclassified, expressed	2.57	up	1.19	up	1.03	up	1.16	down	1.01	down	1.03	down	IAA
Os.53766.1.S1_at	LOC_Os08g37690	expressed protein	1.23	up	1.08	down	4.95	up	1.24	down	1.22	up	1.09	down	ABA

Os.53771.1.A1_at	LOC_Os09g06560	WD domain, G-beta repeat domain containing protein, expressed	1.15	down	1.08	up	7.58	down	1.18	down	2.83	down	1.84	down	2
Os.53771.1.A2_at	LOC_Os09g06560	WD domain, G-beta repeat domain containing protein, expressed	1.70	down	1.12	down	7.16	down	1.09	down	2.44	down	1.77	down	2
Os.53775.1.S1_at	LOC_Os02g01890	cytochrome P450, putative, expressed	1.42	down	1.64	down	2.76	down	1.25	up	1.11	down	1.67	up	ABA
Os.53788.1.S1_at	LOC_Os04g10434	amidase family protein, putative, expressed	1.60	down	1.62	down	3.27	down	1.25	down	1.71	down	1.65	down	ABA
Os.53796.1.S1_at	LOC_Os04g33760	DUF584 domain containing protein, putative, expressed	1.55	up	1.42	up	1.02	up	1.35	down	1.49	down	2.50	down	JA
Os.53801.1.S1_at	LOC_Os03g17800	phosphatidylinositol transfer protein alpha isoform, putative, expressed	1.30	up	1.16	down	7.25	up	1.10	down	1.52	up	1.07	up	ABA
Os.53814.1.S1_at	LOC_Os09g04050	dehydrogenase, putative, expressed	1.01	up	1.65	up	2.94	down	1.34	up	1.62	down	2.60	up	2
Os.53815.1.S1_at	LOC_Os03g04890	zinc finger family protein, putative, expressed	2.83	up	1.20	down	5.56	up	3.18	up	6.51	up	2.93	up	5
Os.53830.1.S1_at	LOC_Os02g40840	alcohol oxidase, putative, expressed	1.64	down	2.00	up	1.40	up	1.21	up	1.20	down	5.45	up	2
Os.53852.1.S1_at	LOC_Os04g13210	multidrug resistance-associated protein, putative, expressed	1.20	down	1.23	up	1.51	up	1.06	down	3.77	up	1.51	up	SA
Os.53853.1.S1_at	LOC_Os03g11490	expressed protein	1.00	up	1.00	down	7.18	up	1.15	down	1.20	down	1.16	down	ABA
Os.53856.1.S1_at	LOC_Os01g34860	expressed protein	1.17	down	1.00	down	7.83	up	1.15	down	1.08	up	1.00	up	ABA
Os.53867.1.S1_s_at	LOC_Os12g38910	expressed protein	1.05	down	1.01	down	4.10	up	1.11	down	1.28	up	1.52	down	ABA
Os.53873.1.S1_x_at	LOC_Os02g57140	expressed protein	1.22	down	1.13	down	2.89	down	1.07	up	1.14	down	1.19	down	ABA
Os.5388.1.S1_at	LOC_Os02g42940	MSP domain containing protein, expressed	1.12	up	1.17	up	2.39	up	1.16	down	1.13	up	1.16	down	ABA
Os.53880.1.S1_at	LOC_Os08g26880	bZIP transcription factor domain containing protein, expressed	1.30	up	1.16	up	6.22	down	1.15	down	1.51	down	1.02	down	ABA
Os.53886.1.S1_at	LOC_Os04g49000	zinc finger, C3HC4 type domain containing protein, expressed	2.02	up	2.02	up	11.68	up	1.04	down	1.13	down	1.14	down	3
Os.53919.1.S1_at	LOC_Os02g09220	cytochrome P450, putative, expressed	2.35	down	2.39	down	7.40	down	1.09	down	2.75	down	15.42	down	5
Os.5395.1.S1_at	LOC_Os05g12260	CAPIP1, putative, expressed	1.19	up	1.27	down	2.15	down	1.14	down	1.02	down	1.18	down	ABA
Os.53968.1.S1_at	LOC_Os02g56310	calcium-dependent protein kinase isoform AK1, putative, expressed	1.55	up	3.70	down	4.11	up	1.43	up	3.59	up	1.36	down	3
Os.53973.1.S1_at	LOC_Os02g50040	endoglucanase, putative, expressed	1.04	down	1.24	down	2.06	down	1.01	up	1.10	down	1.08	up	ABA
Os.53978.1.S1_at	LOC_Os09g14880	transposon protein, putative, Pong sub-class, expressed	2.23	down	1.38	down	1.33	down	1.54	up	1.33	up	1.08	down	IAA
Os.53987.1.S1_at	LOC_Os06g08110	nodulin, putative, expressed	1.64	up	1.12	down	3.15	up	1.21	down	1.69	up	1.04	down	ABA
Os.53993.1.S1_x_at	LOC_Os02g27360	aspartic proteinase-like protein 2 precursor, putative, expressed	1.38	up	1.26	up	5.56	up	1.35	up	4.09	up	1.41	up	2
Os.53996.1.S1_at	AK101198	Oryza sativa Japonica Group cDNA clone:J033030L06, full insert sequence.	1.01	down	1.01	up	11.14	up	1.00	down	1.00	up	1.03	up	ABA
Os.5402.1.S1_at	LOC_Os08g08110	diacylglycerol kinase, putative, expressed	1.04	down	1.13	down	3.54	down	1.14	down	1.72	down	1.57	down	ABA
Os.5403.1.S1_at	AK062758	Oryza sativa Japonica Group cDNA clone:001-106-G10, full insert sequence.	1.33	up	1.00	up	5.71	up	1.31	down	1.01	down	1.17	up	ABA
Os.54033.1.S1_at	LOC_Os08g37180	patatin, putative, expressed	1.06	up	1.02	down	13.97	up	1.01	down	1.77	up	1.41	down	ABA
Os.5406.1.S1_at	LOC_Os03g58040	glutamate dehydrogenase protein, putative, expressed	1.20	down	1.02	up	2.36	down	1.06	up	1.46	down	1.94	up	ABA
Os.54066.1.S1_at	LOC_Os02g33670	expressed protein	5.61	up	1.01	down	1.51	up	1.14	down	1.06	down	1.30	up	IAA
Os.54079.1.S1_x_at	LOC_Os04g35880	retrotransposon protein, putative, unclassified, expressed	1.19	up	1.01	up	3.96	up	1.13	down	1.01	up	1.04	down	ABA
Os.54080.1.S1_at	LOC_Os05g37450	starch binding domain containing protein, putative, expressed	1.37	down	1.41	down	8.83	up	1.25	down	1.18	up	3.27	up	2
Os.54115.1.S1_at	AK102037	phosphoethanolamine N-methyltransferase 1	1.08	down	2.73	up	10.19	up	1.04	up	1.01	down	1.03	down	2
Os.54129.2.S1_x_at	LOC_Os03g06180	expressed protein	1.01	down	1.01	down	19.03	up	1.02	up	1.00	up	1.03	up	ABA
Os.54132.1.S1_at	AK102094	SNF2 domain-containing protein	2.74	down	1.17	down	5.18	down	1.40	down	2.61	down	2.99	down	4
Os.54145.2.S1_at	LOC_Os04g57739	expressed protein	1.70	down	1.18	up	6.62	up	1.18	down	1.19	up	1.01	down	ABA
Os.54156.1.S1_x_at	LOC_Os01g64750	sterol 3-beta-glucosyltransferase, putative, expressed	1.00	down	1.06	up	4.31	up	1.01	up	1.32	up	1.01	up	ABA
Os.54163.1.S1_at	NM_001058191	Oryza sativa (japonica cultivar-group) Os03g0809200 (Os03g0809200) mRNA, partial	1.13	up	1.38	down	10.20	up	1.00	up	1.00	up	1.02	up	ABA
Os.54165.1.S1_at	LOC_Os04g56420	retrotransposon protein, putative, unclassified, expressed	6.73	down	1.32	down	14.53	down	1.00	up	4.70	down	3.21	down	4
Os.54171.1.S1_at	LOC_Os11g03430	CDC45B - Putative DNA replication initiation protein, expressed	1.71	down	1.11	down	3.44	down	1.32	down	1.62	down	1.47	down	ABA
Os.54184.1.S1_at	LOC_Os09g30200	ATP binding protein, putative, expressed	1.00	down	1.01	up	8.06	up	1.04	up	1.03	up	1.01	up	ABA
Os.54219.1.S1_at	LOC_Os05g08970	SSRP1-like FACT complex subunit, putative, expressed	1.44	up	1.02	down	3.69	up	1.09	down	1.10	up	1.46	down	ABA
Os.54229.1.S1_at	LOC_Os04g36670	expressed protein	1.49	up	1.05	down	1.59	up	3.77	up	2.14	up	1.16	up	2
Os.54231.1.S1_at	LOC_Os12g04010	M-phase phosphoprotein 10, putative, expressed	1.18	up	1.26	up	2.12	down	1.06	up	1.26	down	1.13	down	ABA
Os.54251.1.S1_at	LOC_Os07g39530	BTBN16 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hy	1.05	down	1.07	down	2.48	up	1.07	down	1.09	up	1.02	up	ABA
Os.54256.1.S1_at	LOC_Os04g56580	inositol 1,3,4,5,6-pentakisphosphate 2-kinase, putative, expressed	1.29	up	1.23	up	3.19	up	1.12	up	1.15	up	1.26	down	ABA
Os.54267.1.S1_at	LOC_Os05g14590	MCM6 - Putative minichromosome maintenance MCM complex subunit 6, expressed	1.40	down	1.10	down	8.28	down	1.05	down	1.97	down	1.44	down	ABA
Os.54269.1.S1_s_at	LOC_Os05g48060	phosphatidylserine synthase, putative, expressed	1.27	down	1.11	down	2.84	up	1.43	up	1.24	up	1.63	up	ABA
Os.54274.1.S1_at	AK102976	protein kinase family protein	1.01	up	2.65	up	2.06	up	1.35	down	1.52	down	1.24	down	2
Os.54283.1.S1_at	LOC_Os02g36990	dynein light chain type 1 family protein, putative, expressed	1.07	down	1.15	down	2.27	down	1.18	up	1.04	down	1.10	down	ABA
Os.54289.1.S1_x_at	LOC_Os06g10930	xyloglucan fucosyltransferase, putative, expressed	1.22	down	1.21	down	3.62	down	1.28	up	1.52	down	1.66	down	ABA
Os.54299.1.S1_at	LOC_Os06g10880	bZIP transcription factor, putative, expressed	1.05	down	1.06	down	5.03	up	1.36	down	1.16	up	1.22	down	ABA
Os.54303.1.S1_at	LOC_Os04g43300	BRCA1 C Terminus domain containing protein, expressed	1.49	down	1.12	down	4.96	down	1.16	down	1.99	down	1.97	down	ABA
Os.54305.1.S1_at	LOC_Os06g12610	auxin efflux carrier component, putative, expressed	3.26	up	1.17	down	2.53	down	1.26	up	1.34	up	1.09	up	2
Os.54307.1.S1_at	AK103229	Oryza sativa Japonica Group cDNA clone:J033123D06, full insert sequence.	1.12	down	1.13	down	2.53	down	1.09	up	1.02	up	1.86	down	ABA

Os.54324.1.S1_at	LOC_Os08g33479	expressed protein	**1.27**	down	**1.25**	down	**7.82**	down	**1.21**	up	**1.59**	up	**1.14**	up	ABA
Os.54328.1.S1_at	LOC_Os12g02750	expressed protein	**1.03**	down	**2.49**	up	**2.63**	down	**1.05**	down	**1.17**	up	**1.21**	down	2
Os.5434.1.S1_at	LOC_Os08g26850	plant protein of unknown function domain containing protein, expressed	**1.07**	up	**1.83**	up	**6.94**	down	**1.17**	up	**1.87**	down	**1.19**	down	ABA
Os.54341.1.S1_at	LOC_Os12g43720	early-responsive to dehydration protein-related, putative, expressed	**1.02**	down	**1.83**	down	**13.47**	up	**1.17**	down	**1.36**	up	**1.08**	up	ABA
Os.54349.1.S1_at	LOC_Os04g48010	WD-40 repeat family protein, putative, expressed	**1.09**	down	**1.06**	up	**2.74**	up	**1.00**	down	**1.21**	up	**1.30**	down	ABA
Os.54362.1.S1_at	AK103663	Oryza sativa Japonica Group cDNA clone:J033135I20, full insert sequence.	**5.50**	down	**1.35**	up	**1.62**	down	**4.74**	up	**1.04**	up	**1.51**	down	2
Os.54370.1.S1_at	LOC_Os03g48750	Cupin domain containing protein, expressed	**1.00**	down	**1.68**	up	**3.68**	up	**1.61**	up	**2.45**	up	**1.46**	up	2
Os.5438.1.S1_at	LOC_Os10g14870	heavy metal-associated domain containing protein, expressed	**1.32**	up	**1.77**	down	**2.29**	up	**1.63**	down	**1.45**	up	**1.31**	down	ABA
Os.54394.1.S1_at	LOC_Os02g52460	zinc knuckle domain containing protein, expressed	**1.23**	down	**1.14**	down	**2.83**	down	**1.13**	down	**1.30**	down	**1.10**	down	ABA
Os.54410.1.S1_at	LOC_Os06g13720	dehydrogenase E1 component domain containing protein, expressed	**1.31**	up	**1.57**	down	**119.33**	up	**1.17**	up	**1.27**	up	**1.06**	up	ABA
Os.54415.1.S1_at	LOC_Os04g50176	expressed protein	**1.02**	up	**1.17**	up	**2.64**	up	**1.00**	down	**1.01**	down	**1.01**	up	ABA
Os.54416.1.S1_at	LOC_Os02g41450	no apical meristem protein, putative	**1.05**	down	**2.79**	up	**4.32**	up	**1.00**	up	**1.30**	down	**1.17**	down	2
Os.54420.1.S1_x_at	LOC_Os01g16980	expressed protein	**1.37**	down	**3.00**	up	**1.01**	down	**1.09**	up	**1.81**	down	**1.12**	down	BAP
Os.54425.1.S1_at	LOC_Os05g46000	ras-related protein, putative, expressed	**1.14**	up	**1.19**	down	**3.58**	up	**1.28**	down	**1.16**	up	**1.04**	up	ABA
Os.54430.1.S1_at	AK105148	Oryza sativa Japonica Group cDNA clone:001-103-C06, full insert sequence.	**1.07**	up	**1.60**	up	**2.58**	down	**1.21**	down	**1.33**	down	**1.15**	down	ABA
Os.54434.1.S1_at	AK105158	Oryza sativa Japonica Group cDNA clone:001-104-A05, full insert sequence.	**1.25**	down	**1.73**	up	**3.35**	down	**1.47**	down	**1.40**	down	**1.46**	down	ABA
Os.54438.1.S1_x_at	AK105163	Oryza sativa (japonica cultivar-group) Os02g0828500 (Os02g0828500) mRNA, comple	**1.89**	down	**3.64**	up	**2.38**	down	**1.09**	down	**1.31**	down	**1.31**	down	2
Os.54440.1.S1_at	LOC_Os04g53180	expressed protein	**1.30**	up	**1.01**	down	**2.95**	down	**1.38**	down	**1.19**	down	**1.18**	down	ABA
Os.54445.1.S1_at	LOC_Os03g32314	allene oxide cyclase 4, chloroplast precursor, putative, expressed	**2.34**	down	**1.02**	down	**1.25**	down	**1.23**	up	**1.15**	down	**2.45**	up	2
Os.54449.1.S1_at	LOC_Os02g42880	remorin C-terminal domain containing protein, putative, expressed	**1.67**	down	**1.54**	down	**1.69**	down	**1.26**	down	**1.11**	down	**2.27**	up	JA
Os.54453.1.S1_at	LOC_Os08g44220	GLTP domain containing protein, putative, expressed	**1.18**	down	**1.12**	up	**6.12**	down	**1.54**	up	**1.02**	up	**2.75**	down	2
Os.54462.1.S1_at	LOC_Os05g41200	OsCML9 - Calmodulin-related calcium sensor protein, expressed	**1.38**	down	**1.22**	down	**3.44**	up	**1.18**	up	**1.56**	up	**1.03**	up	ABA
Os.54467.1.S1_at	LOC_Os03g21710	WRKY45 transcription factor, putative, expressed	**2.14**	down	**1.04**	down	**2.19**	down	**1.50**	down	**2.27**	up	**1.68**	down	3
Os.54469.1.S1_at	LOC_Os01g62610	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed	**1.12**	up	**1.08**	up	**22.62**	up	**1.22**	down	**1.98**	up	**1.23**	down	ABA
Os.54471.1.S1_at	LOC_Os08g10630	metal cation transporter, putative, expressed	**1.62**	down	**1.40**	up	**1.46**	up	**2.10**	down	**1.28**	down	**1.47**	down	ACC
Os.54472.1.S1_at	LOC_Os07g32060	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed	**1.19**	up	**1.58**	up	**2.89**	down	**1.40**	up	**2.39**	down	**1.32**	down	2
Os.54481.2.S1_at	LOC_Os04g49460	protein kinase domain containing protein, expressed	**1.30**	down	**1.12**	down	**5.37**	up	**1.14**	up	**3.01**	up	**1.10**	up	2
Os.54499.1.S1_at	LOC_Os07g36110	expressed protein	**1.20**	down	**1.34**	down	**4.97**	up	**1.01**	up	**1.03**	down	**1.08**	down	ABA
Os.54509.1.S1_at	LOC_Os09g19650	3-ketoacyl-CoA synthase precursor, putative, expressed	**1.18**	up	**1.31**	up	**4.79**	up	**1.50**	down	**1.46**	up	**2.94**	down	2
Os.5451.1.S1_at	LOC_Os07g41360	alpha-1,4-glucan-protein synthase, putative, expressed	**1.12**	down	**1.08**	down	**2.45**	down	**1.22**	down	**1.39**	down	**1.08**	down	ABA
Os.54510.1.S1_at	LOC_Os07g44640	ZOS7-13 - C2H2 zinc finger protein, expressed	**1.48**	up	**1.37**	up	**2.81**	down	**1.24**	up	**1.15**	down	**1.31**	down	ABA
Os.54511.1.S1_at	LOC_Os11g08380	1-aminocyclopropane-1-carboxylate oxidase, putative, expressed	**1.53**	up	**1.26**	down	**1.78**	up	**1.21**	down	**1.79**	up	**6.48**	down	JA
Os.54531.1.S1_at	LOC_Os06g29460	expressed protein	**1.07**	up	**1.00**	up	**4.05**	up	**1.03**	up	**1.10**	up	**1.03**	up	ABA
Os.54535.1.S1_at	AK105541	Putative clathrin assembly protein	**1.09**	down	**1.63**	up	**7.80**	up	**1.13**	up	**1.02**	down	**1.58**	down	ABA
Os.54545.1.S1_at	LOC_Os07g41060	dihydroflavonol-4-reductase, putative, expressed	**1.90**	down	**1.16**	up	**2.49**	down	**3.47**	down	**1.21**	up	**2.91**	up	3
Os.54548.1.S1_at	LOC_Os02g54560	SCP-like extracellular protein, expressed	**1.30**	down	**1.15**	up	**7.76**	down	**1.11**	up	**2.99**	down	**3.32**	down	3
Os.54548.1.S1_x_at	LOC_Os02g54560	SCP-like extracellular protein, expressed	**1.36**	down	**1.11**	up	**7.79**	down	**1.01**	down	**3.16**	down	**3.07**	down	3
Os.54566.1.S1_at	LOC_Os02g35940	gibberellin receptor GID1L2, putative, expressed	**1.16**	down	**1.02**	up	**2.35**	up	**1.49**	up	**2.98**	up	**2.09**	up	3
Os.54569.1.S1_x_at	LOC_Os06g43090	MYB transcription factor TaMYB1, putative, expressed	**1.26**	up	**1.07**	down	**2.80**	up	**1.18**	up	**1.24**	up	**1.26**	up	ABA
Os.54579.1.S1_s_at	LOC_Os07g23640	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	**1.23**	down	**1.12**	down	**2.90**	up	**1.10**	down	**1.30**	up	**1.55**	up	ABA
Os.54579.1.S1_x_at	LOC_Os07g23660	retrotransposon protein, putative, unclassified, expressed	**1.08**	down	**1.15**	down	**2.46**	up	**1.04**	down	**1.23**	up	**1.95**	up	ABA
Os.54597.1.S1_x_at	LOC_Os12g15520	expressed protein	**1.37**	up	**1.11**	up	**2.11**	up	**1.00**	up	**1.28**	up	**1.10**	down	ABA
Os.54614.1.S1_at	LOC_Os06g05320	transferase family protein, putative, expressed	**1.34**	down	**1.42**	down	**3.40**	up	**1.29**	down	**1.31**	up	**1.03**	up	ABA
Os.54615.1.S1_at	LOC_Os06g18140	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**2.71**	up	**1.14**	up	**15.67**	up	**1.64**	down	**5.84**	up	**1.76**	up	3
Os.54617.1.S1_at	LOC_Os03g20460	guanylate kinase, putative, expressed	**1.11**	down	**1.10**	up	**2.65**	down	**1.24**	up	**1.66**	down	**1.16**	down	ABA
Os.54625.1.S1_at	LOC_Os12g42020	AGC_PVPK_like_kin82y.20 - ACG kinases include homologs to PKA, PKG and PKC, e	**3.30**	up	**1.29**	down	**2.28**	down	**1.25**	up	**1.12**	up	**1.02**	up	2
Os.54630.1.S1_at	LOC_Os03g08700	expressed protein	**1.29**	up	**1.10**	up	**2.23**	up	**1.24**	up	**1.44**	up	**1.38**	up	ABA
Os.54665.1.S1_at	LOC_Os03g47190	expressed protein	**1.03**	down	**1.11**	down	**2.26**	down	**1.10**	down	**1.22**	down	**1.16**	down	ABA
Os.54667.1.S1_at	LOC_Os04g44280	OsRR5 type-A response regulator, expressed	**1.01**	down	**12.77**	up	**1.02**	down	**1.00**	up	**1.00**	down	**1.01**	up	BAP
Os.5467.1.S1_at	LOC_Os04g43990	DUF584 domain containing protein, putative, expressed	**1.29**	up	**1.55**	down	**4.58**	up	**1.03**	up	**1.47**	up	**1.53**	down	ABA
Os.5469.1.S1_at	LOC_Os05g38264	expressed protein	**1.29**	down	**1.08**	up	**6.08**	up	**1.21**	down	**2.69**	up	**1.68**	down	2
Os.54734.1.S1_at	LOC_Os06g09220	cytochrome P450 72A1, putative, expressed	**1.12**	down	**1.83**	down	**2.30**	down	**1.18**	down	**1.82**	up	**2.65**	up	2
Os.54736.1.S1_at	LOC_Os02g52910	zinc finger protein, putative, expressed	**1.13**	down	**1.20**	down	**22.38**	up	**1.01**	up	**2.25**	up	**1.06**	down	2
Os.5476.1.S1_at	LOC_Os05g32630	mitochondrial carrier protein, putative, expressed	**1.06**	up	**1.03**	down	**2.54**	up	**1.24**	up	**1.81**	up	**1.56**	up	ABA
Os.54760.1.S1_at	LOC_Os05g49840	phospholipase, putative, expressed	**1.02**	down	**1.24**	down	**2.39**	up	**1.18**	up	**1.03**	down	**1.97**	down	ABA

Os.54769.1.S1_at	AK106724	Oryza sativa Japonica Group cDNA clone:002-114-G11, full insert sequence.	**3.14**	up	**1.40**	down	**5.49**	up	**1.05**	up	**2.51**	up	**1.72**	up	3
Os.5477.1.S1_at	LOC_Os03g11320	heparanase-like protein precursor, putative, expressed	**1.11**	up	**1.08**	down	**2.04**	up	**1.20**	down	**1.11**	down	**1.21**	up	ABA
Os.54770.1.S1_at	LOC_Os02g03120	endoglucanase, putative, expressed	**1.48**	up	**1.63**	down	**18.52**	down	**1.24**	up	**1.31**	down	**1.29**	up	ABA
Os.54781.1.S1_at	LOC_Os07g39220	BES1/BZR1 homolog protein, putative, expressed	**1.10**	up	**1.03**	up	**2.48**	down	**1.24**	up	**1.20**	down	**1.04**	down	ABA
Os.54786.1.S1_at	LOC_Os08g34360	AP2 domain containing protein, expressed	**1.17**	down	**1.03**	down	**2.98**	up	**1.01**	up	**1.01**	down	**1.01**	down	ABA
Os.54791.1.S1_at	LOC_Os02g53000	lysM domain-containing GPI-anchored protein precursor, putative, expressed	**1.08**	up	**1.16**	down	**1.92**	down	**1.43**	down	**2.00**	down	**1.23**	down	SA
Os.54801.1.A1_at	LOC_Os12g06464	expressed protein	**1.07**	up	**1.21**	up	**2.24**	up	**1.43**	down	**1.04**	down	**1.57**	down	ABA
Os.54806.1.S1_at	LOC_Os01g03230	retrotransposon protein, putative, unclassified, expressed	**1.35**	down	**1.18**	down	**2.06**	down	**1.09**	up	**1.17**	down	**1.22**	down	ABA
Os.54825.1.S1_at	LOC_Os05g33080	serine/threonine-protein kinase, putative, expressed	**1.03**	down	**1.17**	down	**2.47**	down	**1.50**	up	**1.06**	down	**1.01**	down	ABA
Os.54829.1.S1_at	LOC_Os08g02220	endoglucanase, putative, expressed	**1.44**	up	**1.22**	down	**3.10**	down	**1.00**	up	**1.03**	up	**1.07**	up	ABA
Os.54841.1.S1_at	LOC_Os05g50920	transmembrane amino acid transporter protein, putative, expressed	**1.26**	up	**1.24**	down	**3.28**	up	**1.04**	down	**1.08**	up	**1.52**	down	ABA
Os.54853.1.S1_at	AK106908	Oryza sativa Japonica Group cDNA clone:002-119-A04, full insert sequence.	**1.74**	down	**1.08**	up	**4.99**	down	**1.35**	down	**1.57**	down	**1.27**	up	ABA
Os.54859.1.S1_at	LOC_Os04g49550	RING-H2 finger protein ATL2A, putative, expressed	**1.06**	up	**1.68**	up	**1.38**	up	**1.17**	up	**1.31**	down	**3.04**	up	JA
Os.5486.1.S1_at	LOC_Os08g16050	tetraspanin family protein, putative, expressed	**1.60**	down	**1.21**	down	**13.01**	down	**1.24**	up	**1.48**	down	**1.12**	down	ABA
Os.54869.1.S1_at	LOC_Os06g47910	GDSL-like lipase/acylhydrolase, putative, expressed	**2.10**	down	**9.26**	up	**7.36**	down	**1.25**	down	**3.09**	down	**2.82**	down	5
Os.54904.1.S1_at	LOC_Os02g45010	ethylene-responsive protein related, putative, expressed	**1.10**	up	**2.70**	down	**2.04**	down	**1.37**	down	**1.14**	down	**1.45**	down	2
Os.54927.1.S1_at	LOC_Os08g44590	gibberellin 20 oxidase 2, putative, expressed	**1.01**	down	**1.15**	up	**2.87**	up	**1.83**	up	**1.30**	up	**1.29**	up	ABA
Os.54928.1.S1_at	LOC_Os01g59680	NHL25, putative, expressed	**1.34**	down	**2.16**	up	**1.09**	down	**1.18**	down	**1.13**	up	**1.38**	up	BAP
Os.54932.1.S1_at	LOC_Os12g07030	expressed protein	**1.87**	up	**1.90**	down	**11.68**	up	**1.74**	up	**6.97**	up	**12.51**	up	3
Os.54934.1.S1_at	LOC_Os05g37060	MYB family transcription factor, putative, expressed	**1.73**	down	**1.97**	up	**1.98**	down	**3.30**	up	**1.35**	up	**7.43**	up	2
Os.5495.1.S1_at	LOC_Os04g37710	serine hydrolase domain containing protein, expressed	**1.69**	up	**1.12**	down	**1.79**	up	**1.11**	up	**3.25**	up	**1.92**	up	SA
Os.54950.1.S1_at	LOC_Os03g11950	SEC14 cytosolic factor family protein, putative, expressed	**1.45**	up	**1.46**	down	**4.81**	down	**1.16**	down	**1.45**	down	**2.56**	down	2
Os.54959.1.S1_at	LOC_Os03g46860	helix-loop-helix DNA-binding protein, putative, expressed	**1.52**	down	**4.76**	up	**1.81**	down	**1.56**	down	**1.23**	down	**4.56**	up	2
Os.54967.1.S1_at	NM_001062571	Oryza sativa (japonica cultivar-group) Os05g0514600 (Os05g0514600) mRNA, comple	**3.03**	down	**2.17**	up	**2.72**	up	**3.88**	up	**2.08**	down	**10.46**	up	6
Os.54977.1.S1_at	LOC_Os02g37960	expressed protein	**1.21**	up	**1.06**	down	**2.44**	up	**1.01**	up	**1.01**	up	**1.10**	down	ABA
Os.5499.2.S1_at	LOC_Os08g02640	succinate dehydrogenase iron-sulfur subunit 2,mitochondrial precursor, putative, expres	**1.27**	up	**1.11**	down	**1.16**	up	**1.17**	up	**2.03**	up	**1.12**	up	SA
Os.54991.1.S1_at	LOC_Os04g32070	dehydrogenase/reductase, putative, expressed	**1.00**	down	**1.00**	up	**13.02**	up	**1.01**	up	**1.01**	up	**1.01**	up	ABA
Os.54997.1.S1_at	LOC_Os03g51350	expressed protein	**1.12**	up	**1.08**	up	**209.00**	up	**1.19**	down	**1.09**	up	**1.21**	down	ABA
Os.55010.1.S1_at	LOC_Os08g14400	homeobox domain containing protein, expressed	**26.82**	up	**1.07**	down	**1.13**	up	**1.00**	up	**1.00**	down	**1.02**	up	IAA
Os.55040.1.S1_at	LOC_Os04g59120	auxin-induced protein 5NG4, putative, expressed	**1.22**	down	**1.12**	up	**4.97**	down	**1.15**	up	**2.66**	down	**5.46**	up	3
Os.55059.1.S1_at	LOC_Os03g53540	expressed protein	**4.77**	up	**4.17**	up	**1.06**	up	**1.03**	up	**1.13**	up	**1.30**	up	2
Os.55065.1.S1_at	LOC_Os06g04540	DNA binding protein, putative, expressed	**1.10**	up	**1.12**	down	**2.75**	up	**1.03**	down	**1.29**	up	**1.94**	down	ABA
Os.55079.1.S1_at	NM_001049605	Oryza sativa (japonica cultivar-group) Os01g0373800 (Os01g0373800) mRNA, comple	**3.94**	up	**5.99**	up	**1.29**	up	**1.08**	down	**1.44**	up	**1.20**	up	2
Os.55088.1.S1_at	LOC_Os01g16810	MYB family transcription factor, putative, expressed	**1.84**	up	**1.07**	up	**1.49**	up	**1.36**	up	**2.91**	up	**2.11**	up	2
Os.55090.1.S1_at	AK107467	allergen V5/Tpx-1-related family protein	**1.62**	down	**1.53**	down	**7.44**	down	**1.28**	down	**1.12**	down	**1.28**	down	ABA
Os.55093.1.S1_at	LOC_Os03g04370	protein-methionine-S-oxide reductase, putative, expressed	**1.02**	up	**1.05**	up	**2.57**	up	**1.08**	up	**1.36**	up	**1.04**	up	ABA
Os.55096.1.S1_at	LOC_Os06g14670	ODORANT1, putative, expressed	**1.27**	down	**1.32**	down	**14.68**	up	**1.00**	down	**1.00**	down	**1.02**	up	ABA
Os.551.1.S1_at	LOC_Os01g08110	flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed	**1.14**	up	**1.19**	up	**2.10**	up	**1.22**	up	**2.02**	up	**1.60**	up	2
Os.55100.1.S1_at	LOC_Os07g40830	app1, putative, expressed	**1.84**	up	**1.00**	up	**38.62**	up	**1.05**	down	**1.57**	up	**1.08**	up	ABA
Os.55109.1.S1_at	LOC_Os04g57490	cysteine protease, putative, expressed	**1.01**	up	**1.11**	up	**2.18**	up	**1.04**	up	**1.02**	up	**1.03**	up	ABA
Os.55120.1.S1_at	LOC_Os04g52550	PAZ domain-containing protein, putative, expressed	**1.02**	up	**1.02**	up	**2.90**	up	**1.02**	up	**1.06**	up	**1.01**	up	ABA
Os.55132.1.S1_at	LOC_Os03g26990	VQ domain containing protein, putative, expressed	**1.10**	up	**1.01**	up	**2.99**	up	**1.00**	up	**1.01**	down	**1.02**	up	ABA
Os.55139.1.S1_at	LOC_Os11g04380	domain of unknown function, DUF250 domain containing protein, expressed	**2.30**	down	**1.47**	down	**9.14**	down	**1.21**	down	**2.30**	down	**1.86**	down	3
Os.55146.1.S1_at	LOC_Os09g26940	cytochrome P450, putative, expressed	**1.01**	down	**1.40**	up	**1.09**	down	**1.00**	up	**1.04**	down	**5.41**	up	JA
Os.55197.1.S1_at	LOC_Os06g23350	late embryogenesis abundant protein D-34, putative, expressed	**1.26**	down	**1.04**	up	**304.85**	up	**1.37**	up	**1.00**	up	**1.26**	up	ABA
Os.55208.1.S1_at	LOC_Os11g04860	anthocyanin 5-O-glucosyltransferase, putative, expressed	**1.05**	down	**1.25**	up	**2.27**	down	**1.33**	up	**2.56**	up	**1.44**	up	2
Os.55213.1.S1_at	LOC_Os09g24350	THION32 - Plant thionin family protein precursor, expressed	**1.26**	up	**1.35**	up	**3.93**	up	**1.17**	down	**1.32**	down	**1.07**	down	ABA
Os.55224.1.S1_at	LOC_Os12g14220	expressed protein	**1.97**	up	**1.30**	up	**2.59**	down	**1.57**	down	**1.05**	down	**3.28**	down	3
Os.55227.1.S1_at	AK107694	Oryza sativa Japonica Group cDNA clone:002-132-C03, full insert sequence.	**1.01**	down	**1.00**	up	**67.52**	up	**1.00**	up	**1.00**	up	**1.01**	up	ABA
Os.55236.1.S1_at	LOC_Os02g37970	DUF581 domain containing protein, expressed	**2.16**	up	**1.54**	down	**7.48**	up	**1.18**	down	**1.65**	up	**4.28**	down	3
Os.55249.1.S1_at	AK107736	Oryza sativa Japonica Group cDNA clone:002-132-G03, full insert sequence.	**1.26**	down	**1.98**	up	**2.48**	up	**1.10**	up	**1.03**	down	**1.44**	down	ABA
Os.55252.1.S1_at	LOC_Os04g49260	heavy metal-associated domain containing protein, expressed	**7.48**	up	**3.07**	up	**2.46**	up	**1.24**	down	**1.31**	down	**2.77**	down	4
Os.55256.1.S1_at	NM_001071343	Oryza sativa (japonica cultivar-group) Os10g0467000 (Os10g0467000) mRNA, comple	**1.98**	up	**2.24**	up	**1.04**	up	**1.25**	down	**1.60**	down	**1.62**	down	BAP
Os.55259.1.S1_at	LOC_Os04g32480	zinc-finger protein, putative, expressed	**1.15**	down	**3.51**	up	**1.72**	down	**1.24**	up	**1.51**	up	**68.18**	up	2
Os.55263.1.S1_at	LOC_Os08g29600	seed maturation protein PM41, putative, expressed	**1.12**	up	**1.22**	down	**162.31**	up	**1.07**	up	**1.80**	up	**1.17**	up	ABA

Os.55272.1.S1_at	LOC_Os01g03130	expressed protein	**1.01**	down	**1.80**	up	**4.51**	up	**1.23**	down	**2.94**	up	**5.18**	down	3
Os.55273.1.S1_at	NM_001059309	Oryza sativa (japonica cultivar-group) Os04g0419100 (Os04g0419100) mRNA, partial	**1.20**	down	**1.93**	up	**4.55**	down	**2.56**	up	**4.46**	up	**2.09**	up	4
Os.55281.1.S1_at	NM_001068759	Oryza sativa (japonica cultivar-group) Os08g0513100 (Os08g0513100) mRNA, partial	**1.20**	down	**1.04**	up	**2.70**	up	**1.05**	up	**1.20**	up	**1.00**	up	ABA
Os.55283.1.S1_at	LOC_Os05g38660	expressed protein	**1.08**	up	**1.22**	up	**5.29**	up	**1.18**	down	**1.19**	up	**1.05**	up	ABA
Os.55285.1.S1_at	LOC_Os06g40870	expressed protein	**1.05**	up	**1.02**	down	**1.06**	up	**1.16**	down	**2.46**	down	**1.67**	down	SA
Os.55286.1.S1_at	LOC_Os07g47760	POEI50 - Pollen Ole e I allergen and extensin family protein precursor, expressed	**1.11**	down	**1.89**	down	**14.11**	down	**1.03**	up	**1.07**	up	**1.01**	down	ABA
Os.55293.1.S1_at	LOC_Os06g05510	expressed protein	**1.20**	up	**1.14**	down	**1.65**	down	**1.04**	up	**5.07**	up	**1.02**	down	SA
Os.55297.1.S1_at	AK107821	Oryza sativa Japonica Group cDNA clone:002-133-G01, full insert sequence.	**1.08**	up	**1.10**	down	**1.24**	down	**1.02**	up	**2.77**	up	**1.21**	down	SA
Os.55299.1.S1_at	LOC_Os04g43310	expressed protein	**1.34**	down	**1.22**	down	**2.87**	up	**1.04**	up	**1.02**	down	**1.11**	up	ABA
Os.55303.1.S1_at	NM_001052163	Oryza sativa (japonica cultivar-group) Os02g0106600 (Os02g0106600) mRNA, comple	**1.11**	down	**1.19**	up	**3.37**	up	**1.20**	up	**1.18**	up	**1.34**	down	ABA
Os.55306.1.S1_at	LOC_Os09g27330	oxidoreductase/ transition metal ion binding protein, putative, expressed	**1.18**	up	**1.94**	down	**14.88**	up	**1.13**	up	**1.92**	up	**1.47**	down	ABA
Os.55321.1.S1_at	LOC_Os08g08090	wound induced protein, putative, expressed	**3.20**	down	**1.67**	up	**1.06**	down	**1.06**	down	**1.01**	down	**1.03**	up	IAA
Os.55332.1.S1_at	LOC_Os09g04100	expressed protein	**1.02**	down	**1.01**	down	**334.11**	up	**1.00**	up	**1.18**	up	**1.08**	up	ABA
Os.55338.1.S1_at	NM_001054714	Oryza sativa (japonica cultivar-group) Os02g0759000 (Os02g0759000) mRNA, comple	**1.79**	down	**3.37**	up	**1.87**	up	**1.59**	up	**1.21**	up	**1.29**	down	BAP
Os.55358.1.S1_at	LOC_Os04g56680	OsSAUR22 - Auxin-responsive SAUR gene family member, expressed	**1.07**	down	**1.34**	up	**2.39**	down	**1.09**	up	**1.07**	down	**1.27**	down	ABA
Os.55360.1.S1_at	LOC_Os02g50710	expressed protein	**1.38**	down	**1.35**	up	**3.00**	up	**1.22**	down	**2.40**	up	**1.31**	down	2
Os.55363.1.S1_at	LOC_Os07g40250	sex determination protein tasselseed-2, putative, expressed	**1.78**	down	**2.31**	down	**4.06**	up	**1.25**	down	**1.10**	up	**3.76**	up	3
Os.55364.1.S1_at	LOC_Os12g13940	DNA-binding storekeeper protein-related, putative, expressed	**1.38**	up	**1.02**	down	**5.41**	up	**1.37**	down	**1.33**	up	**1.62**	down	ABA
Os.55368.1.S1_at	LOC_Os05g05290	expressed protein	**1.30**	down	**1.27**	up	**1.18**	down	**1.03**	down	**1.10**	up	**3.44**	up	JA
Os.55372.1.S1_at	AK107964	Oryza sativa Japonica Group cDNA clone:002-135-C12, full insert sequence.	**1.46**	down	**1.18**	down	**2.39**	up	**1.42**	up	**1.70**	up	**2.06**	up	2
Os.55372.1.S1_x_at	AK107964	Oryza sativa Japonica Group cDNA clone:002-135-C12, full insert sequence.	**1.16**	down	**1.04**	down	**2.40**	up	**1.27**	up	**1.46**	up	**1.79**	up	ABA
Os.55378.1.S1_at	LOC_Os09g34890	expressed protein	**1.11**	up	**1.72**	down	**2.61**	up	**1.11**	up	**1.33**	up	**1.06**	up	ABA
Os.55380.1.S1_at	LOC_Os06g46740	early nodulin 20 precursor, putative, expressed	**1.14**	up	**1.21**	up	**36.14**	up	**1.18**	down	**1.13**	up	**1.10**	up	ABA
Os.55385.1.S1_at	LOC_Os01g15970	expressed protein	**1.33**	down	**1.27**	down	**2.55**	down	**1.15**	down	**1.31**	down	**1.82**	down	ABA
Os.55388.1.S1_at	LOC_Os04g36600	DUF538 domain containing protein, putative, expressed	**1.00**	up	**1.32**	up	**3.31**	up	**1.02**	up	**1.26**	up	**1.06**	down	ABA
Os.55402.1.S1_at	LOC_Os11g43520	OsGrx_C17 - glutaredoxin subgroup III, expressed	**2.09**	down	**2.35**	up	**5.97**	down	**1.81**	up	**6.30**	down	**3.65**	down	5
Os.55417.1.S1_at	LOC_Os08g15420	CSLC3 - cellulose synthase-like family C, expressed	**2.18**	down	**1.60**	down	**2.23**	down	**1.29**	down	**1.24**	down	**1.43**	down	2
Os.55437.1.S1_at	LOC_Os03g43770	OsFBX97 - F-box domain containing protein, expressed	**1.42**	up	**1.30**	up	**1.43**	down	**1.02**	up	**1.51**	up	**2.70**	up	JA
Os.55438.1.S1_at	AK108095	Oryza sativa Japonica Group cDNA clone:002-139-A07, full insert sequence.	**1.17**	up	**1.19**	up	**4.53**	up	**1.23**	down	**1.03**	up	**1.25**	down	ABA
Os.55447.1.S1_at	LOC_Os02g40440	GDSL-like lipase/acylhydrolase, putative, expressed	**1.06**	down	**1.05**	down	**3.69**	down	**1.53**	up	**1.11**	up	**1.05**	down	ABA
Os.55448.1.S1_at	LOC_Os02g11870	expressed protein	**1.04**	down	**1.04**	down	**6.08**	up	**1.01**	up	**1.01**	up	**1.12**	up	ABA
Os.55453.1.S1_at	LOC_Os04g44570	aquaporin protein, putative, expressed	**1.30**	down	**1.13**	down	**62.87**	up	**1.04**	up	**1.05**	up	**1.02**	down	ABA
Os.55455.1.S1_at	LOC_Os04g45370	OsSAUR19 - Auxin-responsive SAUR gene family member, expressed	**2.53**	up	**1.08**	down	**1.09**	up	**1.56**	down	**1.01**	up	**1.42**	down	IAA
Os.55459.1.S1_at	LOC_Os03g57990	LTPL74 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.03**	down	**1.15**	up	**5.86**	up	**1.19**	down	**1.45**	up	**1.10**	up	ABA
Os.55461.1.S1_at	LOC_Os03g26490	expressed protein	**1.03**	up	**1.01**	up	**75.27**	up	**1.00**	up	**1.19**	up	**1.03**	up	ABA
Os.55469.1.S1_s_at	LOC_Os08g06090	zinc finger, C3HC4 type domain containing protein, expressed	**1.32**	up	**1.34**	down	**2.74**	down	**1.11**	down	**1.06**	up	**1.39**	up	ABA
Os.55479.1.S1_at	LOC_Os05g41490	circadian clock coupling factor ZGT, putative, expressed	**4.98**	up	**1.50**	down	**159.64**	up	**1.94**	down	**2.38**	up	**1.02**	down	3
Os.5549.1.S1_at	LOC_Os07g12340	NAC domain-containing protein 67, putative, expressed	**4.20**	up	**1.36**	up	**1.02**	down	**1.38**	up	**2.61**	up	**2.06**	up	3
Os.55509.1.S1_at	LOC_Os08g34240	CAMK_KIN1/SNF1/Nim1_like.33 - CAMK includes calcium/calmodulin depedent protei	**1.04**	up	**1.10**	down	**3.54**	up	**1.12**	up	**1.56**	up	**1.33**	up	ABA
Os.5551.1.S1_at	LOC_Os04g55720	D-3-phosphoglycerate dehydrogenase, chloroplast precursor, putative, expressed	**1.35**	up	**1.08**	up	**1.41**	down	**1.63**	up	**2.39**	up	**1.84**	up	SA
Os.55512.1.S1_at	LOC_Os11g25700	tropinone reductase, putative, expressed	**1.33**	down	**1.30**	down	**1.09**	up	**2.30**	up	**1.54**	down	**28.93**	up	2
Os.55519.1.S1_at	LOC_Os02g09990	expressed protein	**1.89**	up	**1.44**	up	**1.06**	down	**1.26**	down	**1.40**	up	**2.47**	down	JA
Os.55527.1.S1_at	LOC_Os08g31340	heavy metal-associated domain containing protein, expressed	**1.65**	down	**1.19**	up	**5.30**	up	**1.08**	down	**1.39**	down	**1.47**	down	ABA
Os.55531.1.S1_at	LOC_Os03g32420	expressed protein	**1.21**	up	**1.01**	down	**4.69**	up	**1.11**	up	**1.94**	up	**2.02**	up	2
Os.55539.1.S1_at	LOC_Os03g53690	oxidoreductase, short chain dehydrogenase/reductase family domain containing protei	**1.11**	down	**1.35**	up	**6.32**	down	**1.13**	up	**1.42**	down	**1.47**	up	ABA
Os.55561.1.S1_at	LOC_Os07g39960	ZOS7-07 - C2H2 zinc finger protein	**1.05**	down	**1.07**	down	**19.11**	up	**1.00**	down	**1.00**	up	**1.01**	up	ABA
Os.55564.1.S1_at	LOC_Os02g06410	CBS domain containing membrane protein, putative, expressed	**1.01**	up	**1.00**	down	**880.48**	up	**1.00**	up	**1.23**	up	**1.03**	up	ABA
Os.55575.1.S1_at	LOC_Os05g02200	cysteine-rich repeat secretory protein 55 precursor, putative, expressed	**1.75**	down	**1.08**	down	**2.65**	up	**1.02**	up	**1.27**	up	**1.22**	up	ABA
Os.55579.1.S1_at	NM_001063516	Oryza sativa (japonica cultivar-group) Os06g0181700 (Os06g0181700) mRNA, comple	**2.31**	up	**11.69**	up	**1.14**	down	**1.32**	up	**1.08**	down	**1.03**	up	2
Os.55583.1.S1_at	LOC_Os09g38110	RING-H2 finger protein, putative, expressed	**1.09**	up	**1.01**	down	**2.21**	up	**1.09**	up	**1.02**	down	**1.01**	down	ABA
Os.55583.1.S1_x_at	LOC_Os09g38110	RING-H2 finger protein, putative, expressed	**1.04**	up	**1.01**	up	**2.32**	up	**1.11**	up	**1.00**	down	**1.01**	up	ABA
Os.55585.1.S1_at	AK108363	DNA-binding family protein / AT-hook protein 1 (AHP1)	**1.07**	down	**1.05**	down	**3.65**	up	**1.10**	up	**1.15**	up	**1.19**	up	ABA
Os.55595.1.S1_at	LOC_Os11g02100	peroxidase precursor, putative, expressed	**2.00**	down	**7.61**	up	**7.21**	down	**1.17**	down	**4.83**	up	**1.38**	down	4
Os.5560.1.S1_at	LOC_Os01g62870	oxidoreductase, aldo/keto reductase family protein, putative, expressed	**2.22**	up	**1.19**	down	**1.51**	up	**1.10**	up	**1.51**	up	**2.20**	up	2
Os.55612.1.S1_at	LOC_Os03g18600	cyclase/dehydrase family protein, putative, expressed	**3.50**	down	**1.11**	up	**39.46**	down	**1.54**	up	**1.82**	down	**1.43**	down	2

Os.55624.1.S1_at	LOC_Os06g10160	tyrosine protein kinase domain containing protein, putative, expressed	**1.05**	down	**1.02**	up	**2.17**	down	**1.08**	up	**1.01**	down	**1.80**	up	ABA
Os.55634.1.S1_at	LOC_Os03g19260	expressed protein	**1.61**	up	**1.03**	down	**4.34**	down	**1.44**	up	**1.33**	down	**1.33**	down	ABA
Os.55635.1.S1_at	LOC_Os02g36510	ethylene-insensitive 3, putative, expressed	**1.17**	up	**1.12**	up	**9.09**	up	**1.06**	down	**1.77**	up	**1.30**	up	ABA
Os.55636.1.S1_at	LOC_Os05g48010	MYB family transcription factor, putative, expressed	**1.10**	down	**1.01**	up	**2.67**	down	**1.54**	up	**1.28**	up	**2.04**	up	2
Os.55637.1.S1_at	LOC_Os05g45070	harpin-induced protein 1 domain containing protein, expressed	**1.51**	down	**1.96**	up	**1.07**	up	**1.05**	down	**1.09**	down	**3.52**	up	JA
Os.55638.1.S1_at	LOC_Os09g36750	L-ascorbate peroxidase 4, putative, expressed	**1.17**	up	**1.19**	down	**2.11**	up	**1.24**	up	**1.34**	up	**1.30**	up	ABA
Os.55640.1.S1_at	LOC_Os02g37000	mitochondrial prohibitin complex protein 1, putative, expressed	**1.17**	up	**1.28**	up	**3.06**	up	**1.31**	down	**2.01**	up	**1.18**	up	2
Os.55643.1.S1_at	LOC_Os04g46440	AP2 domain containing protein, expressed	**1.23**	up	**1.43**	up	**5.67**	up	**1.26**	down	**1.09**	down	**1.06**	up	ABA
Os.55651.1.S1_at	LOC_Os06g11450	zinc finger, C3HC4 type domain containing protein, expressed	**1.10**	up	**1.09**	down	**3.01**	up	**1.09**	up	**1.12**	up	**1.63**	up	ABA
Os.55662.1.S1_at	LOC_Os12g38230	expressed protein	**1.07**	up	**6.28**	up	**1.07**	down	**1.17**	up	**1.02**	up	**1.02**	down	BAP
Os.55669.1.S1_at	CT831366	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA011B14, full insert sequence	**1.08**	down	**1.09**	down	**2.69**	down	**1.11**	down	**1.26**	down	**1.03**	down	ABA
Os.55671.1.S1_at	LOC_Os06g44250	haemolysin-III, putative, expressed	**2.06**	up	**1.03**	up	**5.60**	up	**1.06**	up	**1.71**	up	**1.17**	up	2
Os.55682.1.S1_at	LOC_Os03g22820	expressed protein	**1.00**	down	**2.19**	up	**3.71**	up	**1.01**	down	**1.06**	up	**1.97**	up	3
Os.55684.1.S1_at	LOC_Os01g55150	bZIP transcription factor domain containing protein, expressed	**1.05**	down	**1.22**	down	**6.29**	down	**1.25**	down	**1.36**	down	**1.55**	down	ABA
Os.55694.1.S1_at	LOC_Os02g42920	DTA2, putative, expressed	**1.17**	down	**1.01**	down	**2.63**	up	**1.14**	up	**1.20**	up	**1.17**	up	ABA
Os.55696.1.S1_at	LOC_Os12g39100	expressed protein	**1.80**	up	**1.90**	down	**2.79**	down	**1.15**	up	**1.34**	down	**1.02**	down	ABA
Os.55703.1.S1_at	AK108605	basic helix-loop-helix (bHLH) family protein	**1.24**	down	**1.31**	down	**2.01**	down	**1.04**	up	**1.49**	up	**1.00**	up	ABA
Os.55718.1.S1_x_at	LOC_Os12g44320	carbohydrate binding protein, putative, expressed	**1.10**	down	**1.01**	down	**2.55**	down	**1.22**	up	**1.05**	up	**1.03**	down	ABA
Os.55730.1.S1_at	LOC_Os05g01444	polygalacturonase inhibitor precursor, putative, expressed	**2.01**	down	**1.92**	down	**1.20**	up	**1.43**	up	**30.31**	up	**1.98**	up	3
Os.55742.1.S1_at	LOC_Os09g37976	cupin domain containing protein, expressed	**1.12**	down	**1.35**	up	**4.06**	up	**2.64**	down	**3.40**	up	**1.82**	up	3
Os.55750.1.S1_at	LOC_Os05g23398	expressed protein	**1.01**	down	**1.00**	up	**2.17**	up	**1.01**	up	**1.00**	up	**1.02**	up	ABA
Os.55753.1.S1_at	LOC_Os02g10240	ZOS2-05 - C2H2 zinc finger protein, expressed	**1.06**	down	**1.59**	up	**7.69**	up	**1.46**	up	**1.37**	up	**1.14**	up	ABA
Os.55753.1.S1_x_at	LOC_Os02g10240	ZOS2-05 - C2H2 zinc finger protein, expressed	**1.12**	down	**1.30**	up	**5.22**	up	**1.03**	up	**1.24**	up	**1.26**	up	ABA
Os.55764.1.S1_at	LOC_Os02g52590	xyloglucan fucosyltransferase, putative, expressed	**1.02**	up	**1.04**	up	**64.20**	up	**1.00**	up	**1.36**	up	**1.01**	down	ABA
Os.55786.1.S1_at	LOC_Os06g09270	hypro1, putative, expressed	**2.57**	down	**1.31**	down	**1.57**	up	**1.83**	down	**4.12**	down	**1.46**	down	2
Os.55787.1.S1_at	LOC_Os10g28000	glutathione reductase, putative, expressed	**3.87**	up	**1.06**	down	**21.36**	up	**1.30**	down	**17.14**	up	**1.96**	up	4
Os.55800.1.S1_at	LOC_Os04g37980	transporter family protein, putative, expressed	**1.89**	down	**1.27**	up	**5.91**	down	**1.68**	up	**1.75**	down	**1.18**	down	ABA
Os.55820.1.S1_at	AK108847	Oryza sativa Japonica Group cDNA clone:002-152-A03, full insert sequence.	**1.18**	up	**1.01**	down	**10.44**	up	**1.01**	up	**1.00**	down	**1.02**	up	ABA
Os.55827.1.S1_at	LOC_Os11g29870	OsWRKY72 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**1.27**	up	**1.68**	up	**1.83**	up	**1.02**	up	**1.51**	up	**2.39**	up	JA
Os.5583.1.S1_at	LOC_Os03g19270	universal stress protein domain containing protein, putative, expressed	**1.44**	down	**1.16**	up	**31.97**	up	**1.64**	up	**2.44**	up	**1.12**	down	2
Os.5585.1.S1_at	LOC_Os04g54590	expressed protein	**1.66**	down	**2.04**	up	**1.66**	down	**1.04**	down	**1.18**	down	**1.35**	down	BAP
Os.55850.1.S1_at	LOC_Os08g34800	expressed protein	**1.21**	up	**1.41**	up	**2.96**	up	**1.18**	up	**1.85**	up	**1.31**	up	ABA
Os.5587.1.S1_at	CT835794	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN032H02, full insert sequence	**1.06**	up	**1.00**	down	**3.63**	up	**1.03**	up	**1.11**	down	**1.01**	down	ABA
Os.5588.1.S1_s_at	LOC_Os03g09980	sulfate transporter, putative, expressed	**1.45**	down	**1.18**	up	**65.87**	down	**1.48**	up	**5.47**	down	**6.92**	down	3
Os.55886.1.S1_at	LOC_Os01g56030	EF hand family protein, putative, expressed	**1.50**	down	**2.59**	down	**11.57**	down	**1.23**	up	**1.67**	down	**1.79**	up	2
Os.55907.1.S1_at	AK108976	Oryza sativa (japonica cultivar-group) Os01g0754800 (Os01g0754800) mRNA, comple	**1.05**	down	**4.72**	up	**3.59**	down	**2.43**	up	**3.33**	up	**1.79**	up	4
Os.55911.1.S1_at	LOC_Os05g02390	ZOS5-02 - C2H2 zinc finger protein, expressed	**1.26**	up	**1.73**	down	**1.84**	up	**1.23**	down	**2.74**	up	**1.46**	down	SA
Os.5592.1.S1_at	LOC_Os02g48710	expressed protein	**1.14**	up	**1.13**	up	**2.79**	up	**1.24**	down	**1.39**	up	**1.02**	down	ABA
Os.55921.1.S1_at	LOC_Os03g32220	ZOS3-11 - C2H2 zinc finger protein, expressed	**1.01**	down	**1.72**	up	**1.14**	down	**1.33**	up	**1.04**	up	**10.85**	up	JA
Os.5593.1.S1_at	LOC_Os01g32380	expressed protein	**1.05**	up	**1.16**	down	**2.16**	down	**1.41**	up	**8.86**	up	**1.23**	up	2
Os.5594.1.S1_at	LOC_Os05g48340	proteasome-related, putative, expressed	**1.34**	up	**1.14**	up	**5.37**	up	**1.22**	up	**1.42**	up	**1.19**	down	ABA
Os.55956.1.S1_at	LOC_Os03g55380	oxidoreductase, putative, expressed	**1.04**	down	**1.01**	up	**3.90**	up	**1.12**	up	**1.21**	up	**1.05**	down	ABA
Os.5599.1.S1_at	LOC_Os08g31580	ethylene-responsive transcription factor, putative, expressed	**1.23**	up	**1.09**	up	**2.69**	up	**1.04**	up	**1.20**	up	**1.04**	down	ABA
Os.5599.1.S1_x_at	LOC_Os08g31580	ethylene-responsive transcription factor, putative, expressed	**1.15**	up	**1.07**	down	**2.77**	up	**1.03**	up	**1.19**	up	**1.08**	down	ABA
Os.5600.1.S1_s_at	LOC_Os06g03690	RNA recognition motif containing protein, putative, expressed	**1.15**	down	**1.05**	up	**3.51**	up	**1.15**	up	**1.40**	up	**1.08**	up	ABA
Os.56004.1.S1_at	LOC_Os03g22590	nodulin MtN3 family protein, putative, expressed	**1.01**	down	**1.00**	up	**21.24**	up	**1.00**	up	**1.01**	up	**1.02**	up	ABA
Os.56016.1.S1_at	LOC_Os03g63620	tetraspanin family protein, putative, expressed	**3.96**	up	**1.05**	up	**2.07**	down	**3.96**	up	**58.49**	up	**1.64**	down	4
Os.56019.1.S1_at	LOC_Os06g04480	expressed protein	**1.92**	up	**1.14**	down	**3.77**	up	**1.62**	down	**1.24**	down	**1.13**	up	ABA
Os.56048.1.S1_s_at	LOC_Os01g68740	keratin, type I cytoskeletal 9, putative, expressed	**1.82**	down	**1.31**	up	**29.80**	down	**1.32**	down	**3.59**	down	**1.62**	down	2
Os.56072.1.S1_at	LOC_Os11g01550	DUF260 domain containing protein, putative, expressed	**1.36**	up	**1.00**	up	**6.41**	up	**1.21**	up	**1.87**	up	**1.14**	down	ABA
Os.56087.1.S1_at	LOC_Os06g40850	IQ calmodulin-binding motif family protein, putative, expressed	**1.29**	down	**1.43**	down	**2.45**	down	**1.35**	down	**1.06**	down	**1.05**	up	ABA
Os.56093.1.S1_at	LOC_Os07g03170	expressed protein	**2.33**	down	**1.46**	up	**2.57**	down	**1.25**	up	**1.26**	down	**3.02**	up	2
Os.56104.1.A1_at	LOC_Os02g39490	carbonyl reductase 3, putative, expressed	**1.38**	down	**1.33**	down	**2.15**	down	**1.23**	up	**1.42**	down	**1.23**	up	ABA
Os.56129.1.S1_at	NM_001054317	Oryza sativa (japonica cultivar-group) Os02g0689000 (Os02g0689000) mRNA, comple	**1.05**	down	**1.03**	up	**8.79**	up	**1.07**	down	**1.62**	up	**1.02**	up	ABA
Os.56133.1.S1_at	AK109312	Oryza sativa Japonica Group cDNA clone:002-188-F07, full insert sequence.	**1.01**	down	**1.00**	down	**17.92**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA

Os.56134.1.S1_at	AK109313	Oryza sativa Japonica Group cDNA clone:002-188-F12, full insert sequence.	**1.11**	up	**1.13**	up	**2.77**	up	**1.32**	down	**1.15**	up	**1.40**	up	ABA
Os.5614.1.S1_x_at	LOC_Os06g42030	potassium transporter, putative, expressed	**1.33**	down	**1.01**	up	**2.35**	up	**1.01**	up	**1.26**	up	**1.04**	down	ABA
Os.5616.1.S1_at	LOC_Os03g18740	oxidoreductase, short chain dehydrogenase/reductase family, putative, expressed	**1.51**	up	**1.53**	up	**2.98**	down	**1.02**	up	**1.22**	down	**1.45**	down	ABA
Os.56173.1.S1_at	LOC_Os04g45340	expressed protein	**1.06**	up	**1.07**	up	**2.62**	down	**1.07**	down	**1.05**	up	**1.07**	up	ABA
Os.56193.1.S1_at	LOC_Os09g30240	phosphofructokinase, putative, expressed	**1.00**	down	**1.01**	up	**53.93**	up	**1.02**	down	**1.04**	down	**1.01**	up	ABA
Os.56210.1.S1_at	LOC_Os04g42950	MYB family transcription factor, putative, expressed	**1.34**	up	**3.39**	down	**487.23**	up	**1.34**	up	**1.53**	up	**1.24**	up	2
Os.5622.2.S1_x_at	LOC_Os10g33140	hcrVf2 protein, putative, expressed	**1.13**	down	**1.06**	down	**4.76**	down	**1.04**	down	**1.19**	down	**1.54**	up	ABA
Os.56224.1.S1_at	LOC_Os01g02010	expressed protein	**1.14**	down	**1.72**	up	**2.33**	down	**1.36**	down	**2.08**	down	**1.01**	down	2
Os.56229.1.S1_at	LOC_Os11g04330	OsFBK24 - F-box domain and kelch repeat containing protein, expressed	**1.05**	down	**1.09**	up	**3.03**	down	**1.08**	down	**1.42**	down	**1.02**	up	ABA
Os.56257.1.S1_at	LOC_Os05g46750	STE_MEKK_ste11_MAP3K.18 - STE kinases include homologs to sterile 7, sterile 11 a	**1.31**	up	**1.65**	up	**21.95**	up	**1.07**	down	**1.79**	up	**3.33**	up	2
Os.56356.1.S1_at	LOC_Os11g32100	inducer of CBF expression 1, putative, expressed	**1.07**	down	**1.38**	down	**2.78**	down	**1.10**	down	**1.18**	down	**1.00**	down	ABA
Os.56365.1.S1_at	LOC_Os03g19370	CPuORF4 - conserved peptide uORF-containing transcript, expressed	**1.64**	up	**5.24**	down	**1.94**	up	**2.39**	down	**3.56**	up	**2.49**	down	4
Os.56370.1.S1_at	LOC_Os06g05940	DTA2, putative, expressed	**1.11**	down	**1.15**	up	**4.94**	up	**1.23**	down	**1.10**	up	**1.09**	down	ABA
Os.56382.1.S1_at	LOC_Os08g01830	TKL_IRAK_CR4L.6 - The CR4L subfamily has homology with Crinkly4, expressed	**1.20**	up	**1.10**	up	**2.04**	up	**1.01**	up	**1.46**	up	**1.05**	up	ABA
Os.5649.1.S1_at	LOC_Os05g08480	cytokinin-O-glucosyltransferase 1, putative, expressed	**1.12**	up	**1.00**	up	**4.81**	up	**1.27**	down	**1.22**	down	**1.14**	down	ABA
Os.5656.1.S1_at	LOC_Os02g36520	OsFBK9 - F-box domain and kelch repeat containing protein, expressed	**1.43**	up	**1.01**	down	**2.07**	up	**1.10**	up	**1.22**	up	**1.07**	down	ABA
Os.5657.1.S1_at	LOC_Os03g06290	OsSub27 - Putative Subtilisin homologue, expressed	**1.01**	up	**1.04**	up	**9.22**	up	**1.00**	up	**1.02**	up	**1.02**	up	ABA
Os.5661.1.S1_s_at	LOC_Os08g39694	cytochrome P450, putative, expressed	**1.19**	up	**1.53**	down	**6.13**	up	**1.27**	down	**1.64**	up	**1.19**	up	ABA
Os.56612.1.A1_x_at	LOC_Os05g11980	timeless protein, expressed	**2.30**	down	**2.01**	down	**7.33**	down	**1.49**	down	**1.89**	down	**1.95**	down	4
Os.56682.1.S1_at	LOC_Os06g50940	GDSL-like lipase/acylhydrolase, putative, expressed	**1.28**	up	**1.53**	down	**1.97**	down	**1.80**	up	**2.76**	up	**3.95**	up	3
Os.5673.1.S1_at	LOC_Os05g32330	endonuclease/exonuclease/phosphatase family domain containing protein, expressed	**1.06**	up	**1.01**	down	**2.06**	down	**1.05**	down	**1.21**	down	**1.22**	down	ABA
Os.56873.1.S1_at	LOC_Os03g26044	CSLA5 - cellulose synthase-like family A; mannan synthase, expressed	**1.16**	down	**1.14**	down	**13.35**	up	**1.07**	up	**1.04**	down	**1.22**	up	ABA
Os.56873.1.S1_x_at	LOC_Os03g26044	CSLA5 - cellulose synthase-like family A; mannan synthase, expressed	**1.12**	up	**1.00**	up	**8.63**	up	**1.02**	up	**1.01**	up	**1.04**	up	ABA
Os.56875.1.S1_at	LOC_Os08g34390	retrotransposon protein, putative, unclassified, expressed	**1.02**	up	**1.07**	up	**498.65**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
Os.56892.1.S1_at	LOC_Os09g35850	RNA recognition motif containing protein, putative, expressed	**1.12**	up	**1.17**	up	**2.03**	down	**1.19**	down	**1.76**	down	**2.45**	down	2
Os.5690.1.S1_at	LOC_Os01g46760	protein phosphatase 2C, putative, expressed	**1.28**	up	**1.08**	down	**34.60**	up	**1.49**	down	**1.13**	down	**1.02**	up	ABA
Os.56907.1.S1_at	LOC_Os09g27510	cytochrome P450, putative, expressed	**1.56**	down	**1.16**	down	**41.05**	down	**2.05**	up	**2.30**	down	**5.31**	down	4
Os.56918.1.S1_at	LOC_Os03g62330	expressed protein	**1.23**	up	**1.12**	down	**3.08**	up	**1.46**	down	**3.56**	up	**1.50**	down	2
Os.5693.1.S1_at	LOC_Os01g64300	DUF584 domain containing protein, putative, expressed	**1.15**	down	**1.14**	up	**2.42**	up	**1.21**	up	**1.22**	up	**1.05**	up	ABA
Os.56930.1.S1_at	LOC_Os03g17220	dirigent, putative, expressed	**1.09**	up	**1.09**	down	**1.54**	up	**1.14**	up	**2.63**	down	**1.09**	up	SA
Os.56944.1.S1_at	LOC_Os05g25260	AP2 domain containing protein, expressed	**1.09**	up	**1.39**	up	**4.01**	up	**1.15**	up	**1.06**	down	**1.42**	up	ABA
Os.56946.1.S1_at	LOC_Os11g14910	NADP-dependent oxidoreductase, putative, expressed	**6.14**	up	**2.69**	down	**3.06**	up	**1.03**	down	**13.26**	up	**1.35**	up	4
Os.56959.1.S1_at	LOC_Os04g47140	expressed protein	**1.12**	up	**1.92**	down	**15.98**	up	**1.12**	down	**2.17**	up	**1.35**	up	2
Os.56999.1.S1_at	LOC_Os03g17940	phosphatase, putative, expressed	**1.16**	up	**1.00**	down	**2.75**	up	**1.18**	down	**1.09**	down	**1.17**	down	ABA
Os.57028.1.S1_at	LOC_Os04g57380	acyl-protein thioesterase, putative, expressed	**1.18**	up	**1.00**	up	**3.91**	up	**1.03**	down	**1.09**	up	**1.02**	down	ABA
Os.57033.1.S1_at	LOC_Os11g37980	GAUT2/LGT2, putative, expressed	**1.19**	up	**1.18**	down	**4.71**	up	**1.35**	down	**1.64**	up	**1.04**	up	ABA
Os.57036.1.S1_at	LOC_Os08g38580	harpin-induced protein 1 domain containing protein, expressed	**1.68**	up	**1.34**	down	**3.51**	up	**1.33**	down	**1.24**	up	**1.26**	up	ABA
Os.57091.1.S1_at	LOC_Os08g01950	transferase family protein, putative, expressed	**1.84**	down	**1.10**	down	**3.68**	down	**1.17**	up	**1.78**	up	**1.62**	down	ABA
Os.57101.1.S1_at	NM_001071157	Oryza sativa (japonica cultivar-group) Os10g0420200 (Os10g0420200) mRNA, comple	**1.01**	up	**1.26**	up	**2.07**	down	**1.01**	up	**1.25**	down	**1.85**	down	ABA
Os.57108.1.S1_at	LOC_Os12g24330	expressed protein	**2.63**	down	**2.13**	down	**5.73**	down	**2.27**	up	**4.06**	up	**2.81**	down	6
Os.57155.1.S1_at	LOC_Os08g41080	expressed protein	**1.02**	up	**1.00**	down	**3.44**	up	**1.01**	up	**1.02**	down	**1.00**	up	ABA
Os.5717.1.S1_at	LOC_Os04g43170	caleosin related protein, putative, expressed	**1.01**	down	**1.05**	up	**480.45**	up	**1.01**	down	**1.00**	up	**1.02**	up	ABA
Os.57188.1.S1_at	NM_001064804	Oryza sativa (japonica cultivar-group) Os06g0660400 (Os06g0660400) mRNA, comple	**1.18**	up	**1.06**	up	**2.21**	down	**1.34**	down	**1.39**	down	**1.40**	down	ABA
Os.57191.1.S1_at	LOC_Os06g05470	expressed protein	**1.65**	up	**1.07**	down	**2.08**	up	**1.01**	down	**4.13**	up	**1.08**	down	2
Os.57197.1.S1_at	AK287807	Oryza sativa Japonica Group cDNA, clone: J065178H22, full insert sequence.	**1.04**	down	**1.20**	up	**3.36**	up	**1.25**	up	**1.17**	up	**1.39**	down	ABA
Os.57199.1.S1_at	LOC_Os09g35870	OsIAA26 - Auxin-responsive Aux/IAA gene family member, expressed	**67.68**	up	**1.09**	up	**1.01**	down	**1.00**	up	**1.13**	up	**1.01**	up	IAA
Os.5725.1.S1_at	LOC_Os12g07210	expressed protein	**1.09**	up	**1.09**	up	**5.44**	down	**1.59**	down	**1.30**	down	**1.51**	down	ABA
Os.57309.1.S1_at	LOC_Os04g19960	retrotransposon protein, putative, unclassified, expressed	**1.07**	up	**1.85**	down	**2.50**	down	**1.33**	down	**1.63**	down	**2.45**	down	2
Os.57316.1.S1_at	AK111286	Oryza sativa (japonica cultivar-group) Os05g0465000 (Os05g0465000) mRNA, comple	**76.31**	up	**1.49**	down	**1.67**	down	**1.35**	down	**1.58**	up	**2.13**	up	2
Os.57334.1.S1_at	LOC_Os11g13720	expressed protein	**1.35**	up	**1.21**	down	**3.65**	up	**1.00**	up	**3.01**	down	**1.85**	down	2
Os.57338.1.S1_at	LOC_Os02g53030	mitogen-activated protein kinase kinase kinase 1, putative, expressed	**1.35**	down	**1.02**	down	**12.23**	up	**1.08**	up	**1.11**	up	**1.09**	up	ABA
Os.57343.1.S1_at	CT833201	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI016E11, full insert sequence.	**1.25**	up	**1.18**	up	**51.75**	up	**1.22**	up	**1.85**	up	**1.92**	up	ABA
Os.57354.1.S1_at	LOC_Os04g56490	expressed protein	**1.32**	down	**4.08**	down	**1.64**	up	**1.05**	down	**3.43**	up	**1.04**	down	2
Os.5736.1.S1_s_at	LOC_Os10g26620	dof zinc finger domain containing protein, putative, expressed	**1.11**	down	**1.47**	down	**2.70**	up	**1.05**	down	**1.03**	up	**1.18**	down	ABA
Os.5736.2.S1_x_at	LOC_Os10g26620	dof zinc finger domain containing protein, putative, expressed	**3.01**	up	**1.14**	down	**3.83**	up	**1.11**	up	**1.09**	up	**1.17**	up	2

Os.57373.1.S1_at	LOC_Os06g19630	steroid nuclear receptor, ligand-binding, putative, expressed	**1.06**	up	**1.05**	down	**75.12**	up	**1.02**	up	**1.02**	up	**1.03**	up	ABA
Os.5739.1.S1_at	LOC_Os05g49300	iron-sulfur cluster assembly enzyme ISCU, mitochondrial precursor, putative, expressed	**1.22**	up	**1.00**	down	**3.62**	up	**1.32**	down	**1.06**	up	**1.19**	down	ABA
Os.57401.1.S1_at	LOC_Os07g08500	C-5 cytosine-specific DNA methylase, putative, expressed	**1.48**	down	**1.13**	down	**5.07**	down	**1.22**	down	**2.16**	down	**2.05**	down	3
Os.57406.1.S1_at	LOC_Os05g20100	glycerol-3-phosphate acyltransferase, putative, expressed	**1.28**	up	**1.73**	up	**9.48**	up	**1.17**	up	**1.46**	up	**1.63**	down	ABA
Os.57432.1.S1_a_at	LOC_Os08g07290	HEAT repeat family protein, putative, expressed	**1.01**	up	**1.07**	down	**2.13**	down	**1.40**	up	**1.18**	down	**1.10**	down	ABA
Os.57456.1.S1_x_at	LOC_Os01g24710	jacalin-like lectin domain containing protein, expressed	**1.16**	down	**1.08**	up	**4.90**	up	**1.31**	up	**1.73**	up	**1.85**	up	ABA
Os.57464.1.S1_x_at	LOC_Os11g10480	dehydrogenase, putative, expressed	**1.07**	down	**1.14**	up	**2.68**	up	**1.68**	up	**1.95**	up	**1.20**	up	ABA
Os.57465.1.S1_x_at	LOC_Os03g28330	sucrose synthase, putative, expressed	**1.04**	down	**1.01**	down	**2.48**	down	**1.02**	down	**1.21**	down	**1.11**	up	ABA
Os.57499.1.S1_x_at	LOC_Os11g05640	bZIP transcription factor domain containing protein, expressed	**1.15**	up	**1.05**	down	**16.75**	up	**1.07**	down	**1.03**	up	**1.05**	down	ABA
Os.5753.1.S1_x_at	LOC_Os04g56060	protein kinase domain containing protein, expressed	**1.57**	down	**1.04**	down	**4.08**	down	**1.10**	down	**1.84**	down	**1.83**	down	ABA
Os.57531.1.S1_at	LOC_Os04g48170	cytochrome P450, putative, expressed	**15.03**	up	**1.18**	down	**1.08**	down	**1.00**	down	**1.13**	down	**1.16**	down	IAA
Os.57548.1.S1_at	LOC_Os12g05590	RCN3 Centroradialis-like1 homogous to TFL1 gene; contains Pfam profile PF01161: F	**1.27**	down	**3.77**	up	**3.72**	up	**1.53**	down	**1.19**	down	**2.00**	down	3
Os.57569.2.A1_s_at	LOC_Os08g04500	terpene synthase, putative, expressed	**1.07**	down	**1.03**	down	**14.70**	down	**3.83**	down	**2.46**	down	**1.06**	up	3
Os.5757.1.S1_at	LOC_Os12g38360	RALFL31 - Rapid ALkalinization Factor RALF family protein precursor, expressed	**1.02**	down	**1.02**	down	**7.10**	down	**1.05**	up	**1.66**	down	**1.11**	up	ABA
Os.57573.1.S1_at	LOC_Os11g06130	PHD-finger family protein, expressed	**1.11**	up	**1.04**	up	**8.03**	up	**1.08**	up	**1.86**	up	**1.26**	up	ABA
Os.5767.1.S1_at	LOC_Os08g01100	HMG1/2, putative, expressed	**1.74**	down	**1.02**	up	**15.93**	down	**1.34**	down	**3.14**	down	**2.54**	down	3
Os.5768.1.S1_at	LOC_Os09g15320	ubiquitin-conjugating enzyme, putative, expressed	**1.04**	down	**1.11**	down	**2.94**	up	**1.08**	up	**4.72**	up	**1.58**	up	2
Os.5798.1.S1_at	LOC_Os02g36500	expressed protein	**1.04**	down	**1.30**	down	**3.29**	down	**1.39**	down	**2.06**	down	**1.38**	down	2
Os.5808.1.S1_at	LOC_Os09g16920	cytochrome b5 protein, putative, expressed	**1.06**	down	**1.16**	down	**2.45**	down	**1.28**	down	**1.34**	down	**1.06**	up	ABA
Os.5830.1.S1_at	LOC_Os03g21000	thioredoxin, putative, expressed	**1.20**	up	**1.15**	down	**2.38**	up	**1.07**	down	**1.01**	up	**1.12**	down	ABA
Os.5853.1.S1_at	LOC_Os12g44230	expressed protein	**1.20**	down	**1.10**	up	**3.62**	down	**1.30**	up	**1.86**	down	**1.04**	up	ABA
Os.5853.2.S1_x_at	LOC_Os12g44230	expressed protein	**1.41**	down	**1.25**	up	**5.64**	down	**1.31**	up	**2.04**	down	**1.03**	up	2
Os.5860.1.S1_at	LOC_Os03g04310	BHLH transcription factor, putative, expressed	**1.12**	up	**1.83**	up	**1.53**	down	**1.22**	up	**2.34**	down	**3.13**	down	2
Os.5862.1.S1_at	LOC_Os01g50200	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**3.15**	up	**1.01**	up	**1.07**	up	**1.44**	up	**4.15**	up	**1.66**	up	2
Os.5869.3.S1_x_at	LOC_Os04g38410	chlorophyll A-B binding protein, putative, expressed	**1.22**	up	**1.08**	up	**3.45**	down	**1.16**	down	**1.45**	down	**1.24**	down	ABA
Os.5881.1.S1_at	LOC_Os05g19030	expressed protein	**1.32**	down	**1.22**	up	**2.37**	down	**1.08**	up	**1.65**	down	**1.21**	down	ABA
Os.5890.1.S1_at	LOC_Os04g45690	B-box zinc finger family protein, putative, expressed	**1.36**	up	**2.60**	up	**1.27**	down	**1.03**	up	**1.76**	up	**1.06**	down	BAP
Os.5901.1.S1_at	LOC_Os12g29550	expressed protein	**1.09**	up	**1.08**	up	**2.03**	up	**1.06**	down	**1.02**	down	**1.05**	down	ABA
Os.5905.1.S1_at	LOC_Os06g32990	peroxidase precursor, putative, expressed	**2.67**	down	**1.14**	up	**56.43**	down	**2.28**	up	**2.01**	down	**1.21**	up	4
Os.5919.1.S1_at	LOC_Os03g25040	GDSL-like lipase/acylhydrolase, putative, expressed	**1.27**	down	**2.86**	up	**2.30**	down	**1.00**	up	**2.07**	down	**1.80**	up	3
Os.5920.1.S1_at	LOC_Os01g52660	POEI51 - Pollen Ole e I allergen and extensin family protein precursor, expressed	**2.90**	down	**4.10**	down	**5.94**	down	**2.48**	down	**4.85**	down	**3.30**	down	6
Os.5940.1.S1_at	LOC_Os01g50370	STE_MEKK_ste11_MAP3K.4 - STE kinases include homologs to sterile 7, sterile 11 an	**1.24**	up	**1.58**	down	**5.96**	up	**1.45**	up	**2.69**	up	**1.51**	up	2
Os.5975.1.S1_at	LOC_Os02g58650	expressed protein	**1.15**	up	**1.00**	up	**2.56**	down	**1.03**	down	**1.42**	down	**1.05**	up	ABA
Os.5975.1.S2_at	LOC_Os02g58650	expressed protein	**1.03**	down	**1.01**	down	**2.46**	down	**1.01**	down	**1.53**	down	**1.08**	down	ABA
Os.5983.1.S1_at	LOC_Os09g23530	dehydrogenase, putative, expressed	**1.12**	up	**1.34**	up	**9.09**	down	**1.80**	up	**2.01**	up	**3.32**	up	2
Os.5987.1.S1_at	LOC_Os05g32500	expressed protein	**1.02**	down	**1.01**	up	**2.25**	down	**1.12**	down	**1.68**	down	**1.21**	up	ABA
Os.6003.1.S1_x_at	AK069858	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN011H18, full insert sequence	**1.09**	up	**1.17**	down	**4.69**	up	**1.04**	down	**1.10**	up	**1.47**	up	ABA
Os.6019.1.S1_at	LOC_Os11g01570	PMR5, putative, expressed	**1.30**	down	**1.03**	up	**4.28**	down	**1.10**	up	**1.21**	down	**2.11**	up	2
Os.6023.1.S1_s_at	LOC_Os05g46460	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.19**	up	**1.16**	down	**2.36**	up	**1.03**	up	**1.32**	up	**1.91**	up	ABA
Os.6031.1.S1_at	LOC_Os11g36719	lipoxygenase, putative, expressed	**1.23**	down	**1.36**	down	**6.71**	down	**2.39**	down	**2.96**	down	**1.68**	down	3
Os.6035.1.S1_at	LOC_Os07g46350	OsSCP40 - Putative Serine Carboxypeptidase homologue, expressed	**1.64**	down	**1.08**	up	**3.84**	down	**1.05**	down	**1.02**	up	**1.72**	up	ABA
Os.6037.2.S1_x_at	LOC_Os09g27580	potassium transporter, putative, expressed	**1.13**	down	**1.24**	down	**5.22**	down	**1.65**	down	**1.16**	down	**1.26**	up	ABA
Os.6057.1.A1_at	LOC_Os08g04810	serine esterase family protein, putative, expressed	**1.27**	down	**1.28**	down	**4.07**	up	**1.16**	up	**1.88**	up	**1.35**	up	ABA
Os.606.1.S1_at	LOC_Os06g04220	expressed protein	**8.44**	up	**1.33**	up	**4.96**	up	**1.36**	up	**1.25**	up	**1.19**	down	2
Os.6061.1.S1_at	LOC_Os04g40540	protein-L-isoaspartate O-methyltransferase, putative, expressed	**1.00**	up	**1.01**	up	**2.54**	up	**1.14**	up	**1.03**	down	**1.01**	down	ABA
Os.6075.1.S1_at	LOC_Os04g06520	expressed protein	**1.48**	down	**1.35**	down	**1.85**	up	**1.03**	up	**4.98**	up	**1.16**	down	SA
Os.6075.1.S2_at	LOC_Os04g06520	expressed protein	**1.02**	down	**1.02**	up	**1.77**	up	**1.36**	up	**5.96**	up	**1.10**	down	SA
Os.6080.1.S1_at	LOC_Os06g04380	aminomethyltransferase, putative, expressed	**1.09**	up	**1.05**	up	**6.19**	up	**1.14**	up	**1.05**	up	**1.06**	up	ABA
Os.6085.1.S1_at	LOC_Os05g46760	STE_MEKK_ste11_MAP3K.19 - STE kinases include homologs to sterile 7, sterile 11 a	**1.03**	up	**1.01**	down	**2.52**	up	**1.00**	up	**1.01**	up	**1.02**	up	ABA
Os.609.3.S1_a_at	LOC_Os08g37670	plastocyanin-like domain containing protein, putative, expressed	**1.42**	up	**1.11**	up	**2.21**	down	**1.35**	up	**1.95**	up	**1.67**	up	ABA
Os.6090.2.S1_at	AK101123	expressed protein	**1.01**	down	**1.07**	down	**2.74**	up	**1.35**	up	**1.03**	up	**1.00**	down	ABA
Os.6092.1.S1_at	LOC_Os02g44230	CPuORF22 - conserved peptide uORF-containing transcript, expressed	**1.44**	up	**1.11**	up	**7.39**	down	**1.05**	down	**1.17**	up	**1.11**	up	ABA
Os.6116.1.S1_at	LOC_Os12g38150	osmotin, putative, expressed	**1.22**	up	**2.33**	up	**2.23**	up	**1.07**	up	**1.57**	up	**1.50**	up	2
Os.6116.1.S1_x_at	LOC_Os12g38150	osmotin, putative, expressed	**1.17**	up	**2.48**	up	**2.21**	up	**1.14**	up	**1.59**	up	**1.61**	up	2
Os.6118.1.S1_at	LOC_Os11g05700	ABC transporter family protein, putative, expressed	**1.26**	up	**1.22**	down	**1.25**	up	**1.39**	down	**2.50**	up	**1.38**	up	SA

Os.6125.1.S1_at	LOC_Os03g29190	PDI, putative, expressed	**1.18**	down	**1.32**	down	**3.51**	down	**1.18**	up	**2.11**	up	**1.08**	down	2
Os.6133.1.S1_at	LOC_Os02g51540	eukaryotic aspartyl protease domain containing protein, expressed	**1.13**	up	**1.26**	down	**2.42**	up	**1.03**	down	**1.12**	down	**1.19**	down	ABA
Os.6149.1.S1_at	LOC_Os01g04580	Ser/Thr protein kinase, putative, expressed	**1.18**	down	**1.34**	up	**3.02**	down	**1.25**	up	**1.16**	up	**1.15**	up	ABA
Os.6150.1.S1_s_at	LOC_Os03g29240	PDI, putative, expressed	**1.01**	down	**1.22**	up	**1.43**	down	**1.34**	up	**2.36**	up	**1.12**	down	SA
Os.6170.1.S1_at	LOC_Os02g51060	CSLA6 - cellulose synthase-like family A; mannan synthase, expressed	**1.03**	up	**1.23**	down	**2.45**	down	**1.26**	up	**1.05**	up	**1.48**	up	ABA
Os.6176.1.S1_at	LOC_Os08g43370	6-phosphogluconolactonase, putative, expressed	**1.01**	down	**1.13**	down	**3.08**	up	**1.04**	up	**1.23**	up	**1.01**	down	ABA
Os.6190.1.S1_at	LOC_Os04g57890	oligosaccharyl transferase, putative, expressed	**1.26**	down	**1.21**	down	**2.09**	down	**1.12**	down	**1.26**	down	**1.04**	down	ABA
Os.6203.1.S1_at	LOC_Os09g32250	DNA repair ATPase-related, putative, expressed	**1.13**	down	**1.04**	down	**2.36**	down	**1.05**	up	**1.72**	down	**1.41**	down	ABA
Os.6207.1.S1_s_at	LOC_Os06g41840	reductase, putative, expressed	**1.19**	up	**1.18**	down	**2.05**	up	**1.06**	up	**1.80**	up	**2.14**	up	2
Os.6210.1.S1_at	LOC_Os03g56270	receptor protein kinase CLAVATA1 precursor, putative, expressed	**1.18**	down	**1.25**	up	**2.10**	down	**1.30**	down	**1.32**	down	**1.51**	down	ABA
Os.623.1.S1_at	AK102403	Oryza sativa Japonica Group cDNA clone:J033092K06, full insert sequence.	**1.71**	up	**1.18**	up	**8.10**	up	**1.02**	up	**1.24**	up	**1.03**	up	ABA
Os.623.1.S1_x_at	LOC_Os01g09640	Myb transcription factor, putative, expressed	**1.96**	up	**1.09**	down	**8.31**	up	**1.32**	down	**1.15**	up	**1.05**	down	ABA
Os.623.2.S1_x_at	LOC_Os01g09640	Myb transcription factor, putative, expressed	**1.63**	up	**1.13**	down	**5.71**	up	**1.21**	down	**1.17**	up	**1.05**	up	ABA
Os.623.3.S1_x_at	LOC_Os01g09640	Myb transcription factor, putative, expressed	**1.75**	up	**1.15**	down	**7.56**	up	**1.27**	down	**1.21**	up	**1.11**	up	ABA
Os.625.1.S1_at	LOC_Os01g09670	pollen-specific protein SF21, putative, expressed	**1.24**	down	**1.17**	up	**1.25**	down	**1.49**	down	**1.50**	down	**2.41**	up	JA
Os.6269.1.S1_at	LOC_Os03g19090	expressed protein	**1.13**	down	**1.07**	up	**2.10**	up	**1.01**	up	**1.14**	up	**1.08**	up	ABA
Os.6274.1.S1_at	LOC_Os05g47730	LTPL153 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.83**	up	**1.33**	up	**19.58**	up	**1.40**	down	**1.70**	up	**1.03**	up	ABA
Os.6291.1.S1_at	LOC_Os06g47600	thaumatin family domain containing protein, expressed	**1.17**	down	**1.12**	down	**3.16**	down	**1.18**	up	**1.21**	down	**1.11**	up	ABA
Os.6291.1.S1_x_at	LOC_Os06g47600	thaumatin family domain containing protein, expressed	**1.21**	down	**1.11**	down	**3.89**	down	**1.05**	up	**1.40**	down	**1.01**	down	ABA
Os.6297.1.S1_at	LOC_Os02g45700	fringe-related protein, putative, expressed	**1.35**	up	**1.15**	up	**5.47**	up	**1.66**	down	**1.11**	down	**1.17**	down	ABA
Os.6297.2.S1_at	LOC_Os02g45700	fringe-related protein, putative, expressed	**1.04**	up	**1.05**	down	**5.76**	up	**1.02**	up	**1.04**	up	**1.00**	down	ABA
Os.6310.1.S1_at	LOC_Os05g11140	CK1_CaseinKinase_1a.5 - CK1 includes the casein kinase 1 kinases, expressed	**1.07**	down	**1.06**	down	**2.32**	up	**1.00**	up	**1.22**	up	**1.10**	down	ABA
Os.6313.1.S1_at	LOC_Os04g52370	UTP--glucose-1-phosphate uridylyltransferase, putative, expressed	**1.40**	down	**1.12**	down	**2.64**	down	**1.39**	down	**1.51**	down	**1.29**	down	ABA
Os.6314.1.S1_at	LOC_Os04g33820	OsFBX132 - F-box domain containing protein, expressed	**1.16**	down	**1.49**	down	**17.02**	up	**1.38**	down	**2.38**	up	**1.94**	up	2
Os.6318.1.S1_at	LOC_Os05g45020	zinc finger/CCCH transcription factor, putative, expressed	**1.00**	down	**1.34**	up	**9.94**	up	**2.21**	up	**1.41**	up	**2.11**	down	3
Os.6328.1.S1_at	LOC_Os04g41570	ethylene-responsive protein related, putative, expressed	**1.55**	up	**1.02**	up	**2.71**	up	**1.11**	down	**1.54**	up	**1.03**	down	ABA
Os.6330.1.S1_at	LOC_Os03g07180	embryonic protein DC-8, putative, expressed	**1.30**	down	**1.05**	up	**292.94**	up	**1.02**	up	**1.75**	up	**1.16**	up	ABA
Os.6335.1.S1_at	LOC_Os11g13670	gibberellin receptor GID1L2, putative, expressed	**1.16**	up	**1.15**	down	**3.35**	up	**1.06**	up	**1.13**	up	**1.14**	down	ABA
Os.6345.1.S1_at	LOC_Os06g36560	inositol oxygenase, putative, expressed	**1.30**	down	**1.02**	up	**2.17**	down	**1.05**	up	**1.24**	down	**1.17**	up	ABA
Os.6363.1.S1_at	LOC_Os10g38080	OsSub61 - Putative Subtilisin homologue, expressed	**1.53**	up	**1.09**	down	**10.80**	up	**1.14**	down	**1.22**	up	**1.90**	down	ABA
Os.6364.1.S1_at	LOC_Os10g27170	calmodulin-binding protein, putative, expressed	**4.33**	up	**1.05**	down	**2.26**	up	**1.35**	down	**1.27**	down	**1.31**	down	2
Os.6365.1.S1_at	LOC_Os05g09380	AR791, putative, expressed	**1.17**	up	**1.16**	down	**2.30**	up	**1.02**	down	**1.38**	up	**1.12**	up	ABA
Os.6381.1.S1_at	LOC_Os08g40590	oxysterol-binding protein, putative, expressed	**1.46**	up	**1.30**	up	**3.50**	up	**1.09**	up	**3.58**	up	**1.32**	up	2
Os.6398.1.S1_at	LOC_Os04g56750	zinc finger C-x8-C-x5-C-x3-H type family protein, expressed	**1.06**	up	**1.14**	up	**2.45**	up	**1.14**	up	**1.25**	up	**1.02**	up	ABA
Os.6417.1.S1_at	LOC_Os07g37850	expressed protein	**1.04**	up	**1.00**	up	**2.46**	down	**1.10**	down	**1.08**	down	**1.17**	up	ABA
Os.6418.1.S1_at	LOC_Os01g07530	uncharacterized glycosyltransferase, putative, expressed	**1.16**	down	**1.30**	up	**3.26**	up	**1.05**	down	**1.18**	down	**1.17**	up	ABA
Os.6444.2.S1_x_at	LOC_Os10g23100	ras-related protein, putative, expressed	**1.11**	up	**1.05**	up	**2.44**	down	**1.07**	down	**1.47**	down	**1.03**	up	ABA
Os.6450.1.S1_at	LOC_Os07g09190	transketolase, putative, expressed	**1.24**	down	**1.12**	down	**1.25**	down	**1.06**	up	**1.45**	down	**3.72**	up	JA
Os.6517.1.S1_at	LOC_Os08g37432	MATE efflux family protein, putative, expressed	**1.08**	up	**1.66**	up	**2.24**	down	**1.26**	up	**1.43**	up	**1.85**	up	ABA
Os.6539.1.S1_at	LOC_Os04g44670	AP2 domain containing protein, expressed	**1.15**	down	**4.81**	down	**7.25**	down	**1.00**	up	**1.16**	up	**1.32**	up	2
Os.6561.1.A1_at	AU165189		**1.67**	up	**1.21**	up	**5.33**	up	**1.03**	down	**1.02**	up	**2.46**	up	2
Os.6573.1.S1_at	LOC_Os11g19100	retrotransposon protein, putative, unclassified	**1.09**	down	**1.03**	up	**3.34**	up	**1.22**	up	**1.21**	up	**1.16**	up	ABA
Os.6581.1.S1_at	LOC_Os10g43060	expressed protein	**1.28**	up	**1.14**	up	**1.52**	up	**1.19**	up	**2.70**	up	**2.03**	up	2
Os.6585.1.S1_at	LOC_Os04g53210	hydroxyacid oxidase 1, putative, expressed	**1.01**	up	**1.28**	down	**2.51**	up	**1.24**	up	**2.70**	up	**1.03**	up	2
Os.6617.1.S1_s_at	LOC_Os09g15520	oleosin, putative, expressed	**1.01**	down	**1.00**	down	**54.91**	up	**1.01**	up	**1.01**	up	**1.03**	up	ABA
Os.6618.1.S1_at	LOC_Os04g49980	late embryogenesis abundant group 1, putative, expressed	**1.49**	up	**1.76**	up	**30.51**	up	**1.16**	down	**1.00**	down	**1.47**	down	ABA
Os.6625.1.S1_x_at	LOC_Os09g27830	OsPDIL2-3 protein disulfide isomerase PDIL2-3, expressed	**1.44**	down	**1.05**	down	**2.57**	down	**1.12**	up	**1.32**	down	**1.21**	up	ABA
Os.6633.1.S1_at	LOC_Os07g10530	carboxyl-terminal peptidase, putative, expressed	**1.43**	down	**1.29**	down	**2.69**	down	**1.01**	down	**1.24**	down	**1.13**	down	ABA
Os.6648.1.S1_at	LOC_Os03g45420	armadillo/beta-catenin repeat family protein, putative, expressed	**1.24**	down	**1.12**	down	**2.38**	up	**1.71**	up	**1.18**	up	**1.07**	up	ABA
Os.6649.1.S1_at	LOC_Os01g74110	metal cation transporter, putative, expressed	**1.27**	down	**1.47**	down	**3.31**	down	**1.12**	up	**1.64**	down	**1.65**	down	ABA
Os.6651.1.S1_at	LOC_Os07g43670	ribonuclease T2 family domain containing protein, expressed	**1.60**	down	**1.07**	down	**12.41**	down	**1.17**	up	**1.28**	down	**1.22**	down	ABA
Os.6652.1.S1_x_at	LOC_Os10g39200	expressed protein	**1.05**	up	**1.05**	down	**2.21**	up	**1.18**	up	**1.30**	up	**1.23**	up	ABA
Os.6656.1.S1_at	LOC_Os02g18410	salt stress root protein RS1, putative, expressed	**1.03**	down	**1.38**	down	**1.65**	down	**1.30**	up	**1.40**	down	**3.52**	down	JA
Os.6662.1.S1_at	LOC_Os05g44900	expressed protein	**1.33**	up	**1.20**	up	**13.51**	up	**1.69**	down	**1.05**	down	**1.35**	down	ABA
Os.6669.1.S1_at	LOC_Os07g40890	igA FC receptor precursor, putative, expressed	**1.24**	up	**1.21**	up	**2.56**	up	**1.11**	down	**1.02**	up	**1.04**	down	ABA

Os.6671.1.S1_a_at	LOC_Os05g39930	spotted leaf 11, putative, expressed	**1.06**	down	**1.02**	down	**3.66**	up	**1.12**	up	**1.49**	up	**1.91**	up	ABA
Os.6671.2.S1_x_at	LOC_Os05g39930	spotted leaf 11, putative, expressed	**1.19**	down	**1.00**	down	**3.70**	up	**1.15**	up	**1.64**	up	**1.76**	up	ABA
Os.6763.1.S1_at	LOC_Os01g48710	heavy metal-associated domain containing protein, expressed	**1.65**	down	**1.08**	up	**6.16**	down	**1.02**	up	**1.60**	down	**2.04**	down	2
Os.6763.1.S1_x_at	LOC_Os01g48710	heavy metal-associated domain containing protein, expressed	**1.82**	down	**1.01**	down	**5.92**	down	**1.03**	up	**1.56**	down	**1.98**	down	ABA
Os.6764.1.S1_at	AK241357	Oryza sativa Japonica Group cDNA, clone: J065151B01, full insert sequence.	**5.30**	down	**1.95**	up	**7.28**	down	**1.37**	up	**6.41**	down	**4.46**	down	4
Os.6764.2.S1_at	AK241357	Oryza sativa Japonica Group cDNA, clone: J065151B01, full insert sequence.	**1.17**	down	**1.07**	down	**4.31**	up	**1.51**	up	**1.16**	down	**2.42**	down	2
Os.6766.1.S1_s_at	LOC_Os04g48840	expressed protein	**1.14**	down	**1.26**	down	**2.60**	down	**1.10**	down	**1.63**	down	**1.03**	down	ABA
Os.6767.1.S1_at	LOC_Os08g16830	retrotransposon protein, putative, SINE subclass, expressed	**1.88**	up	**1.86**	up	**4.68**	down	**1.70**	down	**1.49**	down	**1.29**	down	ABA
Os.6776.1.S1_at	LOC_Os07g35480	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	**2.39**	down	**1.06**	up	**10.51**	down	**2.61**	up	**1.44**	down	**2.63**	up	4
Os.6786.1.S1_a_at	LOC_Os10g40720	expansin precursor, putative, expressed	**1.33**	up	**1.54**	up	**10.88**	down	**1.01**	up	**1.87**	down	**1.11**	down	ABA
Os.6801.2.S1_x_at	LOC_Os02g02040	protein kinase, putative, expressed	**1.40**	down	**1.39**	down	**2.01**	down	**1.24**	down	**1.26**	down	**1.05**	down	ABA
Os.6822.1.S1_at	LOC_Os08g02670	ATP binding protein, putative, expressed	**1.28**	down	**1.03**	up	**3.92**	up	**1.18**	up	**1.25**	up	**1.37**	down	ABA
Os.6823.1.S1_at	LOC_Os01g62350	60S ribosomal protein L36-2, putative, expressed	**1.00**	down	**1.08**	up	**2.48**	down	**1.09**	up	**1.22**	down	**1.06**	down	ABA
Os.6832.1.S1_at	LOC_Os01g24700	expressed protein	**1.64**	up	**1.00**	up	**28.46**	up	**1.12**	down	**1.68**	up	**1.12**	down	ABA
Os.6838.1.S1_at	LOC_Os10g40510	LTPL144 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.28**	down	**1.31**	up	**2.40**	down	**1.71**	up	**1.58**	down	**1.19**	down	ABA
Os.6840.1.S1_at	LOC_Os09g31454	MYB family transcription factor, putative, expressed	**1.15**	up	**1.21**	down	**3.29**	up	**1.09**	up	**1.60**	up	**1.23**	up	ABA
Os.6851.1.S1_at	LOC_Os02g35590	glutathione S-transferase, putative, expressed	**1.18**	down	**1.12**	down	**2.74**	up	**1.11**	up	**1.38**	up	**1.57**	up	ABA
Os.6861.1.S1_at	AK062784	Oryza sativa Japonica Group cDNA clone:001-107-B06, full insert sequence.	**1.34**	up	**1.08**	up	**4.31**	up	**1.32**	down	**1.27**	up	**1.09**	up	ABA
Os.6862.2.A1_at	LOC_Os09g23550	dehydrogenase, putative, expressed	**1.06**	up	**1.25**	up	**2.64**	down	**1.01**	up	**1.34**	down	**1.28**	down	ABA
Os.6868.1.S1_at	LOC_Os03g43420	single-stranded DNA-binding protein, putative, expressed	**1.18**	up	**1.31**	up	**3.06**	down	**1.05**	down	**1.79**	down	**1.23**	down	ABA
Os.6960.1.S1_at	LOC_Os06g39880	cytochrome P450 72A1, putative	**5.45**	up	**1.53**	down	**2.18**	up	**1.02**	up	**1.64**	up	**1.69**	up	2
Os.6965.1.S1_at	AK099476	sodium-inducible calcium-binding protein (ACP1)	**2.83**	up	**1.34**	up	**1.84**	down	**1.01**	down	**1.60**	up	**1.24**	down	IAA
Os.6998.1.S1_at	LOC_Os03g37490	MATE efflux family protein, putative, expressed	**2.08**	up	**1.11**	down	**3.42**	up	**1.02**	up	**8.67**	up	**2.95**	up	4
Os.7028.1.S1_at	LOC_Os02g45710	zinc finger, C3HC4 type domain containing protein, expressed	**1.06**	down	**1.63**	up	**7.31**	down	**1.23**	up	**1.84**	down	**1.02**	down	ABA
Os.7052.1.S1_at	LOC_Os02g58220	RPA2A - Putative single-stranded DNA binding complex subunit 2, expressed	**1.25**	down	**1.15**	down	**4.77**	down	**1.26**	down	**2.11**	down	**1.76**	down	2
Os.7053.1.S1_s_at	LOC_Os01g65380	patellin protein, putative, expressed	**1.08**	up	**1.12**	down	**2.55**	up	**1.22**	up	**1.09**	up	**1.06**	up	ABA
Os.7058.1.S1_at	LOC_Os04g50060	GRAS family transcription factor domain containing protein, expressed	**1.15**	down	**1.26**	down	**1.84**	up	**2.07**	up	**1.35**	up	**1.20**	down	ACC
Os.7081.1.S1_at	LOC_Os06g20430	BPI/LBP family protein At3g20270 precursor, putative, expressed	**1.09**	down	**1.12**	down	**2.91**	up	**1.19**	up	**1.32**	up	**1.18**	up	ABA
Os.7087.1.S1_at	LOC_Os02g12690	cytochrome P450, putative, expressed	**1.81**	down	**1.27**	down	**63.34**	down	**1.16**	down	**2.95**	down	**1.76**	up	2
Os.7088.1.S1_at	LOC_Os07g01440	plastocyanin-like domain containing protein, putative, expressed	**3.17**	down	**3.06**	down	**5.54**	down	**1.59**	down	**2.69**	down	**2.33**	down	5
Os.7095.1.S1_at	LOC_Os04g49210	naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed	**1.30**	up	**1.02**	down	**2.37**	down	**1.73**	up	**16.39**	up	**2.88**	up	3
Os.7101.1.S1_at	LOC_Os12g16200	glutathione synthetase, chloroplast precursor, putative, expressed	**1.02**	down	**1.25**	up	**2.43**	down	**1.43**	down	**2.01**	down	**1.09**	up	2
Os.7116.1.S1_at	LOC_Os03g53020	helix-loop-helix DNA-binding domain containing protein, expressed	**1.05**	down	**1.38**	up	**2.40**	down	**1.18**	up	**1.17**	up	**2.91**	up	2
Os.7126.1.S1_at	LOC_Os01g18050	tubulin/FtsZ domain containing protein, putative, expressed	**1.09**	down	**1.05**	down	**2.58**	down	**1.21**	down	**1.59**	down	**1.44**	down	ABA
Os.7132.1.S1_at	LOC_Os09g39560	genetic modifier, putative, expressed	**1.07**	up	**1.35**	down	**2.47**	up	**1.14**	up	**1.28**	up	**1.21**	up	ABA
Os.7136.2.S1_x_at	LOC_Os01g27750	bifunctional 3-dehydroquinate dehydratase	**1.09**	up	**1.03**	up	**1.17**	up	**1.11**	up	**2.17**	up	**1.99**	up	SA
Os.7140.1.S1_at	LOC_Os11g16550	uncharacterized protein ycf53, putative, expressed	**1.05**	down	**1.07**	up	**6.28**	down	**1.31**	down	**1.70**	down	**1.56**	down	ABA
Os.7158.1.S1_a_at	LOC_Os07g14270	calreticulin precursor protein, putative, expressed	**1.15**	down	**1.01**	up	**2.38**	down	**1.07**	up	**1.18**	down	**1.16**	up	ABA
Os.7189.1.S1_at	LOC_Os11g04010	ICE-like protease p20 domain containing protein, putative, expressed	**1.09**	up	**1.16**	up	**6.04**	up	**1.11**	up	**1.36**	down	**1.35**	down	ABA
Os.7192.1.S1_at	LOC_Os03g04410	aconitate hydratase protein, putative, expressed	**1.15**	up	**1.14**	down	**2.26**	up	**1.27**	up	**2.95**	up	**2.03**	up	3
Os.72.1.S1_at	LOC_Os01g16350	hydroxymethylglutaryl-CoA lyase, putative, expressed	**1.27**	down	**1.08**	down	**4.16**	up	**1.33**	up	**1.74**	up	**1.28**	up	ABA
Os.72.1.S1_s_at	LOC_Os01g16350	hydroxymethylglutaryl-CoA lyase, putative, expressed	**1.32**	down	**1.02**	down	**3.48**	up	**1.19**	up	**1.74**	up	**1.20**	up	ABA
Os.72.1.S1_x_at	LOC_Os01g16350	hydroxymethylglutaryl-CoA lyase, putative, expressed	**1.10**	down	**1.13**	down	**5.00**	up	**1.43**	up	**1.77**	up	**1.67**	up	ABA
Os.7203.1.S1_at	LOC_Os01g63230	growth regulator related protein, putative, expressed	**1.56**	up	**1.85**	down	**3.35**	up	**1.48**	down	**1.38**	up	**1.22**	up	ABA
Os.7203.2.S1_x_at	LOC_Os01g63230	growth regulator related protein, putative, expressed	**1.96**	up	**2.11**	down	**4.01**	up	**1.97**	down	**1.39**	up	**1.27**	up	3
Os.7218.2.S1_at	LOC_Os02g01140	GDSL-like lipase/acylhydrolase, putative, expressed	**1.10**	up	**1.20**	down	**3.90**	down	**1.23**	down	**1.10**	down	**1.27**	down	ABA
Os.7225.1.S1_at	LOC_Os06g05740	expressed protein	**1.64**	down	**1.14**	up	**4.07**	down	**1.20**	up	**1.26**	down	**1.33**	up	ABA
Os.7228.1.S1_at	LOC_Os02g51970	phosphate-induced protein 1 conserved region domain containing protein, expressed	**5.93**	up	**2.57**	up	**9.80**	up	**1.07**	down	**1.41**	up	**3.94**	down	4
Os.7229.1.S1_at	LOC_Os02g50210	erwinia induced protein 2, putative, expressed	**1.03**	up	**1.02**	up	**2.75**	up	**1.12**	down	**1.18**	up	**1.07**	down	ABA
Os.7235.1.S1_at	LOC_Os03g21030	no apical meristem protein, putative, expressed	**1.58**	up	**1.03**	up	**2.59**	up	**1.41**	up	**1.10**	up	**1.50**	up	ABA
Os.7242.1.S1_at	LOC_Os07g07930	LTPL78 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.24**	up	**1.14**	down	**3.65**	up	**1.16**	down	**1.73**	up	**1.09**	down	ABA
Os.7243.1.S1_s_at	LOC_Os08g06250	tetraspanin family protein, putative, expressed	**1.01**	up	**1.05**	down	**2.23**	up	**1.01**	down	**1.32**	up	**1.18**	up	ABA
Os.7246.1.S1_s_at	LOC_Os06g27560	glycosyltransferase protein, putative, expressed	**1.47**	up	**1.13**	down	**2.39**	up	**1.49**	up	**1.62**	up	**1.38**	up	ABA
Os.7246.2.S1_s_at	LOC_Os06g27560	glycosyltransferase protein, putative, expressed	**2.00**	up	**1.07**	down	**2.57**	up	**1.40**	up	**1.61**	up	**1.57**	up	ABA
Os.7253.1.S1_at	LOC_Os12g28770	POEI19 - Pollen Ole e I allergen and extensin family protein precursor, expressed	**1.18**	down	**1.09**	up	**3.89**	down	**1.25**	down	**1.42**	down	**1.98**	down	ABA

Os.7258.1.S1_at	LOC_Os03g21850	nucleotidyltransferase, putative, expressed	1.13	up	1.31	down	2.21	up	1.02	down	1.06	up	1.01	down	ABA
Os.7269.1.S1_s_at	LOC_Os01g44960	hydrolase, alpha/beta fold family domain containing protein, expressed	2.01	up	1.04	up	5.18	up	2.50	down	2.48	up	1.06	up	4
Os.7281.1.S1_at	LOC_Os01g68730	RNA-binding protein FUS, putative, expressed	1.20	up	1.12	up	13.07	down	1.87	up	1.22	up	1.83	up	ABA
Os.7285.1.S1_at	LOC_Os05g44210	trehalose-6-phosphate synthase, putative, expressed	1.00	up	2.33	up	1.25	down	1.04	up	1.26	down	1.01	down	BAP
Os.7289.2.S1_at	LOC_Os02g11760	pleiotropic drug resistance protein, putative, expressed	1.13	up	1.24	down	2.41	up	1.01	up	1.17	up	1.09	up	ABA
Os.7299.1.S1_at	LOC_Os05g01460	STIP1 homology and U box-containing protein 1, putative, expressed	1.18	up	1.19	up	3.12	up	1.02	up	1.24	up	1.15	down	ABA
Os.7314.1.S1_at	LOC_Os10g22520	cellulase, putative, expressed	1.08	up	1.03	down	2.48	up	2.47	up	2.39	up	1.52	up	3
Os.7317.2.S1_at	LOC_Os01g68589	LTPL39 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.01	down	1.24	down	3.98	down	1.23	down	1.98	down	1.87	down	ABA
Os.7335.1.S1_at	LOC_Os02g36340	riboflavin biosynthesis protein ribAB, chloroplast precursor, putative, expressed	3.00	up	1.26	up	1.00	down	1.32	up	2.56	up	1.60	up	2
Os.7337.1.S1_at	LOC_Os12g32650	expressed protein	1.01	up	1.04	down	1.66	up	1.03	down	2.06	up	1.06	up	SA
Os.7339.1.S1_at	LOC_Os10g31850	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	1.08	down	1.04	up	2.80	up	1.15	down	1.06	up	1.15	down	ABA
Os.7339.2.S1_at	LOC_Os10g31850	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	1.11	down	1.24	up	2.41	up	1.13	down	1.04	up	1.00	down	ABA
Os.7342.1.S1_at	LOC_Os02g57490	DUF260 domain containing protein, putative, expressed	9.70	up	1.76	down	1.11	up	1.23	up	2.53	up	1.67	up	2
Os.7343.1.S1_at	LOC_Os07g02710	expressed protein	1.11	up	1.04	down	19.39	up	1.16	down	1.04	up	1.36	down	ABA
Os.7344.1.S1_at	LOC_Os02g52000	phosphate-induced protein 1 conserved region domain containing protein, expressed	3.59	up	1.68	up	1.50	up	1.17	down	2.03	down	3.31	down	3
Os.7355.1.S1_at	LOC_Os02g13520	OsIAA7 - Auxin-responsive Aux/IAA gene family member, expressed	1.72	down	1.28	up	2.40	down	1.57	down	1.14	down	1.32	down	ABA
Os.7360.1.S1_a_at	LOC_Os01g68370	B3 DNA binding domain containing protein, expressed	1.30	down	1.27	down	18.22	up	1.00	up	1.01	down	1.02	up	ABA
Os.7362.1.S1_at	LOC_Os07g48550	no apical meristem protein, putative, expressed	1.17	up	1.42	down	7.85	up	1.43	up	1.51	up	1.61	up	ABA
Os.7366.1.S1_at	LOC_Os05g38270	regulator of chromosome condensation, putative, expressed	1.83	down	1.35	down	2.52	up	1.26	down	1.06	up	1.42	down	ABA
Os.7371.1.S1_s_at	LOC_Os03g02380	major facilitator superfamily domain-containing protein 5, putative, expressed	1.07	down	1.05	down	2.20	down	1.09	down	1.01	down	1.30	up	ABA
Os.7381.1.S1_at	LOC_Os05g02770	glycine-rich cell wall structural protein precursor, putative, expressed	1.11	down	1.03	down	4.39	up	1.23	down	2.19	up	1.10	up	2
Os.7393.1.S1_at	LOC_Os07g02200	plastocyanin-like domain containing protein, putative, expressed	1.29	down	1.37	down	4.20	down	1.38	down	1.45	down	1.34	down	ABA
Os.7428.1.S1_at	LOC_Os06g44470	pollen allergen, putative, expressed	16.01	up	2.52	up	1.22	up	1.07	up	1.28	down	1.26	down	2
Os.7439.1.S1_at	LOC_Os05g32230	expressed protein	1.38	down	1.07	down	2.84	down	1.04	down	1.29	down	1.07	down	ABA
Os.7443.1.S1_s_at	LOC_Os03g02020	stress responsive A/B Barrel domain containing protein, expressed	1.37	up	1.28	up	2.42	down	1.25	down	1.41	down	1.39	down	ABA
Os.7445.1.S1_at	LOC_Os04g39489	amino acid transporter, putative, expressed	1.07	down	1.28	up	2.12	up	1.21	down	1.44	down	1.08	up	ABA
Os.7457.1.S1_a_at	LOC_Os04g42520	phosphoribosyl transferase, putative, expressed	1.06	down	2.74	up	3.24	down	1.12	up	1.76	down	2.21	down	3
Os.7459.1.S1_at	LOC_Os08g02690	MA3 domain containing protein, expressed	1.01	down	1.03	up	3.36	up	1.00	down	1.04	down	1.01	down	ABA
Os.7472.1.S1_at	LOC_Os03g10750	CUE domain containing protein, expressed	1.00	down	1.02	up	2.50	up	1.28	up	1.53	up	1.46	up	ABA
Os.7494.1.S1_at	LOC_Os02g32060	hydrolase, NUDIX family, domain containing protein, expressed	1.17	down	1.12	up	11.03	down	1.33	up	1.87	up	2.17	down	2
Os.7499.1.S1_at	LOC_Os07g01660	dirigent, putative, expressed	1.06	down	1.01	down	2.24	down	1.15	down	1.28	down	1.01	up	ABA
Os.7506.1.S1_at	LOC_Os02g47450	expressed protein	1.04	down	1.36	up	2.85	down	1.20	up	1.18	down	1.31	down	ABA
Os.7507.1.S1_at	LOC_Os10g02880	O-methyltransferase, putative, expressed	1.57	up	1.08	up	31.07	up	5.74	down	2.20	up	3.73	up	4
Os.7510.1.S1_at	LOC_Os10g41020	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	1.49	up	2.07	up	1.99	down	1.49	up	1.92	up	1.53	up	BAP
Os.7516.1.S1_at	LOC_Os05g43390	signal recognition particle 54 kDa protein, putative, expressed	1.28	up	1.17	up	9.98	up	1.10	down	1.38	up	3.60	up	2
Os.7531.1.S1_at	LOC_Os03g46260	DUF581 domain containing protein, expressed	1.04	down	1.13	down	2.02	down	1.25	down	1.23	down	1.71	down	ABA
Os.7535.1.S1_at	LOC_Os01g32780	universal stress protein domain containing protein, putative, expressed	1.18	down	1.24	down	10.42	up	1.12	down	3.46	up	1.22	up	2
Os.7537.1.S1_at	LOC_Os04g36750	hsp20/alpha crystallin family protein, putative, expressed	1.31	down	1.46	down	1.00	down	1.11	up	13.86	up	1.03	down	SA
Os.7539.1.S1_at	LOC_Os03g03320	expressed protein	3.83	up	1.04	up	1.68	up	1.66	down	1.02	up	1.53	down	IAA
Os.7583.1.S1_x_at	LOC_Os04g44740	glycosyltransferase sugar-binding region containing DXD motif, putative, expressed	1.05	down	1.05	down	2.23	down	2.17	down	2.04	down	2.14	down	4
Os.7587.1.S1_at	LOC_Os09g36619	expressed protein	2.42	down	1.27	down	4.68	down	1.09	up	1.43	down	1.73	up	2
Os.7602.1.S1_at	LOC_Os02g44108	expansin precursor, putative, expressed	1.76	up	2.23	up	12.59	down	1.06	up	3.18	down	1.02	down	3
Os.7607.1.S1_at	LOC_Os07g47480	heavy metal-associated domain containing protein, expressed	1.23	down	1.15	up	1.94	up	1.35	down	1.48	down	2.21	down	JA
Os.7609.1.S1_at	LOC_Os05g32110	COBRA, putative, expressed	1.10	down	1.05	down	2.15	down	1.01	down	1.38	down	1.48	up	ABA
Os.7611.1.S1_at	LOC_Os03g06670	Core histone H2A/H2B/H3/H4 domain containing protein, putative, expressed	1.14	down	1.21	down	4.24	down	1.34	down	1.83	down	1.51	down	ABA
Os.7614.1.S1_at	LOC_Os06g13600	HEAT repeat family protein, putative, expressed	1.15	up	1.01	up	2.41	down	1.09	down	1.43	down	1.40	down	ABA
Os.7625.1.A1_s_at	LOC_Os06g51360	lysM domain containing protein, putative, expressed	1.23	up	1.11	up	2.04	up	1.06	up	1.05	up	1.65	up	ABA
Os.7631.1.S1_at	LOC_Os08g37130	oxidoreductase, short chain dehydrogenase/reductase family domain containing protei	1.37	up	1.06	down	21.01	up	1.20	up	1.33	up	1.05	down	ABA
Os.7644.1.S1_at	LOC_Os06g09630	3-oxoacyl-synthase, putative, expressed	1.07	down	1.09	down	2.13	down	1.08	up	1.22	down	1.00	up	ABA
Os.7662.1.S1_at	LOC_Os02g10350	MLO domain containing protein, putative, expressed	1.58	up	1.29	up	2.52	down	2.02	down	1.67	down	1.28	down	2
Os.7665.1.S1_at	LOC_Os04g56240	lipase, putative, expressed	1.49	down	1.88	up	4.83	down	1.29	down	1.60	down	1.50	down	ABA
Os.7668.2.S1_x_at	LOC_Os04g17479	expressed protein	1.07	down	1.12	down	2.06	down	1.60	down	1.25	down	1.04	up	ABA
Os.767.1.S1_at	LOC_Os01g43700	cytochrome P450 72A1, putative, expressed	2.72	up	1.13	up	4.56	up	1.08	up	3.41	up	1.76	up	3
Os.7674.1.S1_at	LOC_Os06g19070	cytochrome P450, putative, expressed	1.15	up	1.49	up	4.75	down	1.69	up	1.04	down	1.24	up	ABA
Os.7680.1.S1_at	LOC_Os07g04020	expressed protein	1.51	up	1.04	up	2.07	up	1.05	down	1.10	up	1.31	down	ABA

Os.7692.1.S1_at	LOC_Os04g55230	tetratricopeptide repeat domain containing protein, putative, expressed	1.21	up	1.24	up	2.65	down	1.03	down	1.38	down	1.02	down	ABA
Os.7694.1.S1_at	LOC_Os04g41229	helix-loop-helix DNA-binding domain containing protein, expressed	1.32	down	1.30	up	6.19	down	2.71	up	1.47	up	1.33	down	2
Os.7699.1.S1_at	AK120490	Oryza sativa Japonica Group cDNA clone:J013118H09, full insert sequence.	1.08	down	1.12	down	3.93	up	1.12	down	1.18	down	1.47	down	ABA
Os.7705.1.S1_at	LOC_Os04g54300	wound induced protein, putative, expressed	1.79	down	1.04	down	2.20	up	1.22	up	1.23	down	2.20	down	2
Os.7707.1.S1_at	LOC_Os04g54320	expressed protein	1.02	down	1.13	up	3.41	down	1.15	down	1.69	down	1.61	down	ABA
Os.7710.1.S1_a_at	LOC_Os09g29780	expressed protein	1.01	up	1.12	up	2.09	up	1.09	down	1.07	down	1.16	down	ABA
Os.7727.1.S1_at	LOC_Os05g11910	GDSL-like lipase/acylhydrolase, putative, expressed	1.22	up	1.04	down	3.31	up	1.24	up	1.64	up	1.64	up	ABA
Os.7740.1.S1_at	LOC_Os03g43650	uncharacterized protein At4g06744 precursor, putative, expressed	1.34	up	1.62	up	14.77	down	1.16	down	1.56	down	1.16	up	ABA
Os.7745.1.S1_at	LOC_Os05g37700	periplasmic beta-glucosidase precursor, putative, expressed	1.21	down	1.26	down	2.70	up	1.39	down	1.33	up	1.43	up	ABA
Os.7750.1.S1_at	LOC_Os02g06430	DUF292 domain containing protein, expressed	1.24	up	1.08	down	2.44	up	1.11	up	1.14	up	1.04	down	ABA
Os.7751.1.S1_at	LOC_Os02g47660	basic helix-loop-helix, putative, expressed	1.78	up	1.08	up	1.72	up	1.64	up	1.33	up	2.90	down	JA
Os.7756.1.S1_at	LOC_Os10g36500	invertase/pectin methylesterase inhibitor family protein, putative, expressed	1.29	down	1.21	up	4.03	down	1.05	up	1.84	down	1.04	down	ABA
Os.7756.2.S1_at	LOC_Os10g36500	invertase/pectin methylesterase inhibitor family protein, putative, expressed	1.50	down	1.11	up	5.52	down	1.02	down	1.26	down	1.17	down	ABA
Os.7756.2.S1_x_at	LOC_Os10g36500	invertase/pectin methylesterase inhibitor family protein, putative, expressed	1.32	down	1.20	up	7.50	down	1.09	down	1.52	down	1.24	down	ABA
Os.7758.1.S1_at	LOC_Os02g10480	stromal membrane-associated protein, putative, expressed	1.13	down	1.05	up	2.09	up	1.03	down	1.04	down	1.13	up	ABA
Os.7770.1.S1_at	LOC_Os05g05030	expressed protein	1.01	down	1.39	down	1.52	up	1.35	down	1.00	up	2.32	up	JA
Os.7771.1.S1_at	LOC_Os06g43600	LTPL129 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.19	up	1.34	up	1.13	down	2.12	up	1.03	down	1.29	up	ACC
Os.7773.1.S1_at	LOC_Os09g32960	expressed protein	1.05	down	1.00	up	2.08	up	1.13	down	1.17	up	2.23	up	2
Os.7779.1.S1_x_at	LOC_Os05g01570	auxin-induced protein 5NG4, putative, expressed	1.40	down	1.19	down	11.54	down	1.25	up	1.95	down	2.72	down	2
Os.7793.1.S1_at	LOC_Os11g31570	expressed protein	1.46	down	1.12	up	4.73	down	1.01	up	2.00	down	1.11	up	2
Os.7794.1.S1_at	LOC_Os10g38489	glutathione S-transferase GSTU6, putative, expressed	3.41	up	1.73	up	4.33	up	1.41	up	6.56	up	2.91	up	4
Os.7800.1.S1_at	LOC_Os01g58620	expressed protein	1.10	up	1.02	down	5.28	up	1.06	up	1.74	up	1.37	up	ABA
Os.7801.1.S1_at	LOC_Os12g05050	stem-specific protein TSJT1, putative, expressed	1.14	up	1.15	down	2.04	up	1.04	up	2.73	up	1.30	up	2
Os.7805.1.S1_a_at	LOC_Os10g35110	alpha-galactosidase precursor, putative, expressed	1.08	down	1.03	up	2.87	down	1.35	down	1.52	down	1.57	down	ABA
Os.7806.1.S1_at	LOC_Os04g39980	gibberellin 20 oxidase 2, putative, expressed	4.81	up	1.07	up	2.20	up	1.13	down	2.04	up	1.13	up	3
Os.7809.1.S1_at	LOC_Os09g19890	expressed protein	1.14	up	1.17	down	4.07	up	1.17	up	1.31	up	1.03	down	ABA
Os.7826.2.A1_at	LOC_Os05g10730	ABC transporter, ATP-binding protein, putative, expressed	1.25	down	1.15	down	1.97	up	1.12	down	2.02	up	1.34	up	SA
Os.7830.1.S1_at	LOC_Os04g16970	zinc finger, C3HC4 type domain containing protein, expressed	1.42	up	1.31	up	2.02	down	1.44	down	1.48	down	1.07	down	ABA
Os.7831.1.S1_at	LOC_Os06g11980	DUF581 domain containing protein, expressed	1.30	up	1.51	down	5.30	up	1.35	down	1.57	up	1.25	up	ABA
Os.7838.1.S1_at	LOC_Os09g20930	expressed protein	1.10	down	1.95	down	13.22	up	1.01	up	1.16	up	1.07	up	ABA
Os.7853.1.S1_at	LOC_Os01g58459	expressed protein	1.15	down	1.23	down	2.66	up	1.05	up	1.12	down	1.24	down	ABA
Os.7859.1.S1_at	LOC_Os11g07916	nifU, putative, expressed	1.13	down	1.08	up	2.51	up	1.06	up	1.65	up	1.05	up	ABA
Os.7862.1.S1_at	LOC_Os03g13840	senescence-associated protein, putative, expressed	1.27	up	1.43	down	7.84	up	1.38	down	1.03	down	1.09	down	ABA
Os.7868.1.S1_at	LOC_Os01g17170	magnesium-protoporphyrin IX monomethyl ester cyclase,chloroplast precursor, putative	1.16	down	1.07	up	4.53	down	1.27	down	2.59	down	1.73	down	2
Os.7902.1.S1_at	LOC_Os06g46950	EF hand family protein, putative, expressed	3.15	up	1.73	up	5.16	up	1.09	down	1.27	up	1.66	up	2
Os.7911.1.S1_at	LOC_Os01g27210	glutathione S-transferase, putative, expressed	1.49	up	1.11	down	1.73	up	1.01	down	3.57	up	2.91	up	2
Os.7928.1.S1_at	LOC_Os03g48970	nuclear transcription factor Y subunit, putative, expressed	1.37	up	1.47	down	4.72	up	1.17	down	1.22	up	1.01	down	ABA
Os.7929.1.S1_a_at	LOC_Os02g12480	expressed protein	1.08	down	1.05	up	2.35	down	1.03	down	1.20	down	1.13	down	ABA
Os.7929.4.S1_x_at	LOC_Os02g12480	expressed protein	1.11	down	1.04	down	4.92	down	1.59	down	1.64	down	1.98	down	ABA
Os.7932.1.S1_at	LOC_Os09g26880	aldehyde dehydrogenase, putative, expressed	1.01	up	1.03	down	2.54	up	1.09	up	1.72	up	1.11	up	ABA
Os.7938.1.S1_at	LOC_Os04g59190	peroxidase precursor, putative, expressed	1.09	up	1.38	up	6.53	down	1.32	up	4.93	down	3.54	up	3
Os.7972.1.S1_at	LOC_Os02g39790	CPuORF9 - conserved peptide uORF-containing transcript, expressed	1.11	up	1.12	down	2.49	up	1.02	up	1.14	up	1.04	up	ABA
Os.7979.1.S1_at	LOC_Os03g63480	ankyrin repeat domain containing protein, expressed	1.10	down	1.15	up	2.84	down	1.32	down	1.49	down	1.37	down	ABA
Os.7985.1.S1_at	LOC_Os03g18070	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed	1.09	down	1.10	up	11.17	down	1.25	down	1.89	down	1.14	up	ABA
Os.7994.1.S1_at	LOC_Os04g45490	elongation factor, putative, expressed	1.42	up	1.10	up	3.57	down	1.25	down	1.72	down	1.17	down	ABA
Os.7995.1.S1_x_at	LOC_Os01g12690	plant-specific domain TIGR01568 family protein, expressed	1.03	down	1.41	up	10.63	up	1.20	up	1.03	up	1.21	down	ABA
Os.7999.1.S1_at	LOC_Os07g43380	zinc finger, C3HC4 type domain containing protein, expressed	1.08	up	1.16	down	2.07	up	1.07	up	1.35	up	1.26	up	ABA
Os.8007.1.S1_at	LOC_Os12g17910	T-complex protein, putative, expressed	1.02	up	1.06	down	3.25	down	1.15	down	1.65	down	1.16	down	ABA
Os.8014.1.S1_at	LOC_Os10g10180	methyltransferase domain containing protein, putative, expressed	1.03	up	1.06	up	3.44	down	1.19	down	1.96	down	1.45	down	ABA
Os.8014.2.S1_x_at	LOC_Os10g10180	methyltransferase domain containing protein, putative, expressed	1.21	up	1.06	up	3.30	down	1.07	down	1.72	down	1.21	down	ABA
Os.8017.1.S1_at	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	1.04	up	1.08	down	4.31	up	1.22	down	1.14	up	1.21	up	ABA
Os.802.1.S1_at	LOC_Os01g01430	No apical meristem protein, putative, expressed	1.17	up	1.01	down	4.38	up	1.03	down	1.60	down	1.19	up	ABA
Os.8024.1.S1_at	LOC_Os07g30170	nitrilase, putative, expressed	1.10	up	1.04	down	3.51	up	1.16	up	1.60	up	1.42	up	ABA
Os.8032.1.S1_at	LOC_Os04g57440	oryzain beta chain precursor, putative, expressed	1.09	up	1.06	up	3.21	up	1.34	up	1.14	up	1.46	up	ABA
Os.8039.1.S1_at	LOC_Os03g46640	deoxyuridine 5-triphosphate nucleotidohydrolase, putative, expressed	2.18	up	1.08	down	5.35	down	1.25	down	2.02	down	1.54	down	3

Os.8043.1.S1_at	LOC_Os03g51010	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.46**	up	**1.04**	up	**5.39**	up	**1.22**	up	**1.62**	up	**1.49**	up	ABA
Os.8051.1.S1_at	LOC_Os11g47820	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	**1.39**	down	**1.22**	down	**2.52**	up	**1.09**	up	**1.21**	up	**1.01**	up	ABA
Os.8052.1.S1_at	LOC_Os03g51390	expressed protein	**1.37**	up	**1.79**	up	**2.16**	up	**1.68**	up	**2.56**	up	**1.29**	down	2
Os.8081.1.A1_at	LOC_Os07g36390	PPR repeat containing protein, expressed	**1.14**	down	**1.22**	up	**2.99**	down	**1.15**	down	**1.38**	down	**1.21**	down	ABA
Os.8084.1.S1_x_at	AK065049	expressed protein	**1.04**	down	**1.02**	up	**2.01**	up	**1.09**	down	**1.20**	down	**1.34**	down	ABA
Os.8095.1.S1_at	LOC_Os03g22050	CAMK_KIN1/SNF1/Nim1_like.16 - CAMK includes calcium/calmodulin depedent protein	**1.10**	up	**1.32**	up	**3.97**	down	**1.20**	down	**1.61**	down	**1.79**	down	ABA
Os.8095.1.S2_at	LOC_Os03g22050	CAMK_KIN1/SNF1/Nim1_like.16 - CAMK includes calcium/calmodulin depedent protein	**1.16**	up	**1.37**	up	**4.70**	down	**1.26**	down	**1.73**	down	**1.66**	down	ABA
Os.8095.1.S3_at	LOC_Os03g22050	CAMK_KIN1/SNF1/Nim1_like.16 - CAMK includes calcium/calmodulin depedent protein	**1.14**	down	**1.18**	up	**4.31**	down	**1.33**	down	**1.68**	down	**1.53**	down	ABA
Os.8095.1.S4_at	LOC_Os03g22050	CAMK_KIN1/SNF1/Nim1_like.16 - CAMK includes calcium/calmodulin depedent protein	**1.17**	down	**1.36**	up	**5.56**	down	**1.57**	down	**2.47**	down	**2.51**	down	3
Os.8097.1.A1_at	LOC_Os02g28040	lipase, putative, expressed	**1.04**	down	**1.07**	down	**4.05**	up	**1.17**	up	**1.24**	up	**1.12**	up	ABA
Os.8098.1.S1_at	LOC_Os11g18570	cytochrome P450, putative, expressed	**2.61**	up	**1.10**	down	**9.73**	up	**3.10**	down	**2.13**	up	**2.20**	up	5
Os.8107.1.S1_at	LOC_Os07g49330	phospholipase C, putative, expressed	**1.01**	up	**1.22**	down	**2.06**	up	**1.15**	down	**1.14**	up	**1.13**	down	ABA
Os.8108.1.S1_at	LOC_Os03g11260	RING zinc finger protein-like, putative, expressed	**1.03**	down	**1.16**	down	**2.27**	up	**1.08**	down	**1.19**	up	**1.15**	down	ABA
Os.8110.1.S1_at	LOC_Os03g14400	cytochrome P450, putative, expressed	**1.19**	up	**1.16**	down	**2.46**	up	**1.16**	up	**1.01**	up	**1.24**	up	ABA
Os.8113.1.S1_at	LOC_Os01g08470	retrotransposon protein, putative, unclassified, expressed	**1.09**	up	**1.41**	down	**3.10**	up	**1.24**	up	**1.32**	up	**1.05**	down	ABA
Os.8114.1.A1_x_at	LOC_Os03g51240	glycosyl hydrolases family 17, putative, expressed	**1.39**	up	**1.07**	down	**2.68**	up	**1.34**	down	**1.08**	up	**1.06**	down	ABA
Os.8115.1.S1_at	LOC_Os01g68540	rho GDP-dissociation inhibitor 1, putative, expressed	**1.25**	up	**1.13**	up	**3.04**	up	**1.00**	up	**1.00**	up	**1.03**	down	ABA
Os.8117.1.S1_at	LOC_Os04g36062	expressed protein	**1.13**	up	**18.77**	up	**3.28**	down	**1.60**	down	**3.51**	down	**2.98**	down	4
Os.8139.1.S1_at	LOC_Os09g29490	peroxidase precursor, putative, expressed	**1.84**	up	**1.26**	up	**7.74**	down	**1.75**	up	**1.73**	down	**2.72**	down	2
Os.8141.1.S1_at	LOC_Os02g05710	expressed protein	**1.11**	up	**1.19**	down	**3.46**	up	**1.08**	down	**1.01**	down	**1.24**	up	ABA
Os.8147.1.S1_a_at	LOC_Os04g48750	3-oxo-5-alpha-steroid 4-dehydrogenase, putative, expressed	**1.16**	down	**1.10**	down	**3.71**	up	**1.04**	up	**1.31**	up	**1.04**	up	ABA
Os.8149.1.S1_at	LOC_Os02g46030	MYB family transcription factor, putative, expressed	**1.88**	down	**2.66**	down	**26.22**	up	**1.03**	down	**1.05**	up	**1.06**	down	2
Os.8150.1.S1_a_at	LOC_Os05g42350	ferredoxin--nitrite reductase, putative, expressed	**1.84**	up	**1.47**	up	**2.02**	down	**1.00**	up	**2.26**	up	**1.18**	up	2
Os.8150.1.S1_at	LOC_Os05g42350	ferredoxin--nitrite reductase, putative, expressed	**1.95**	up	**1.52**	up	**1.97**	down	**1.07**	down	**2.01**	up	**1.06**	up	SA
Os.8150.2.S1_x_at	LOC_Os05g42350	ferredoxin--nitrite reductase, putative, expressed	**2.30**	up	**1.64**	up	**1.93**	down	**1.04**	down	**2.20**	up	**1.20**	up	2
Os.8195.1.S1_at	AK241299	Oryza sativa Japonica Group cDNA, clone: J065139L09, full insert sequence.	**1.51**	up	**1.15**	down	**61.59**	up	**1.08**	down	**7.00**	up	**1.19**	up	2
Os.820.1.S1_s_at	LOC_Os01g19020	peroxidase precursor, putative, expressed	**1.52**	down	**1.26**	down	**2.55**	down	**1.08**	down	**1.44**	down	**1.08**	down	ABA
Os.8201.1.S1_x_at	LOC_Os12g01380	proteins of unknown function domain containing protein, expressed	**1.14**	up	**1.15**	down	**1.72**	down	**1.08**	up	**1.06**	down	**2.01**	up	JA
Os.8208.1.S1_at	LOC_Os03g57960	cupin domain containing protein, expressed	**1.02**	down	**1.01**	down	**22.78**	up	**1.01**	up	**1.01**	up	**1.03**	up	ABA
Os.8221.1.S1_a_at	LOC_Os04g35100	phospholipase C, putative, expressed	**1.58**	up	**1.28**	down	**18.96**	up	**1.36**	down	**1.15**	down	**1.11**	down	ABA
Os.8240.1.S1_at	LOC_Os11g26850	erythronate-4-phosphate dehydrogenase, putative, expressed	**1.06**	up	**1.05**	up	**2.42**	down	**1.04**	up	**1.22**	down	**1.39**	up	ABA
Os.8244.1.S1_at	LOC_Os04g43490	CK1_CaseinKinase_1.7 - CK1 includes the casein kinase 1 kinases, expressed	**1.40**	up	**1.02**	up	**2.38**	down	**1.01**	down	**1.52**	down	**1.63**	up	ABA
Os.8250.1.S1_at	AK107488	expressed protein	**1.08**	up	**1.13**	down	**2.53**	down	**1.34**	up	**1.02**	up	**1.00**	down	ABA
Os.8252.1.S1_s_at	LOC_Os01g34690	expressed protein	**1.22**	up	**1.08**	down	**2.23**	down	**1.10**	down	**1.05**	down	**1.03**	down	ABA
Os.8259.1.S1_at	LOC_Os05g31760	annexin, putative, expressed	**1.03**	down	**1.18**	down	**2.04**	down	**1.66**	down	**1.18**	down	**2.67**	up	2
Os.8260.1.S1_at	LOC_Os10g28680	DUF581 domain containing protein, expressed	**1.04**	down	**2.00**	down	**6.05**	up	**1.68**	down	**1.33**	up	**1.76**	down	2
Os.8266.1.A1_at	LOC_Os03g55800	cytochrome P450, putative, expressed	**1.08**	up	**1.06**	down	**2.16**	down	**1.13**	up	**1.17**	down	**5.78**	up	2
Os.8279.1.S1_at	LOC_Os05g42020	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.12**	up	**1.09**	down	**2.32**	up	**1.18**	up	**1.06**	down	**1.12**	down	ABA
Os.8347.1.S1_at	LOC_Os09g35680	OsFBX339 - F-box domain containing protein, expressed	**1.13**	down	**1.22**	down	**2.04**	up	**1.02**	down	**1.11**	up	**1.06**	down	ABA
Os.8360.1.S1_at	LOC_Os01g24550	fruit bromelain precursor, putative, expressed	**3.12**	down	**1.41**	up	**21.55**	down	**1.19**	up	**6.02**	down	**1.99**	down	4
Os.8362.1.S1_at	LOC_Os10g03690	OsFBX346 - F-box domain containing protein, expressed	**1.12**	down	**1.23**	down	**2.09**	up	**1.06**	down	**1.15**	up	**1.11**	down	ABA
Os.8374.1.S1_at	LOC_Os04g43910	auxin response factor, putative, expressed	**3.73**	up	**1.53**	down	**1.84**	down	**1.69**	down	**1.19**	up	**1.18**	down	IAA
Os.8379.1.S1_at	LOC_Os07g29190	expressed protein	**1.31**	down	**1.04**	down	**2.82**	down	**1.08**	down	**1.56**	down	**1.55**	down	ABA
Os.8427.1.S1_s_at	AK122041	DC1 domain-containing protein	**1.96**	up	**1.09**	down	**29.79**	up	**1.31**	up	**1.36**	up	**1.22**	up	ABA
Os.8428.1.S1_at	LOC_Os05g30530	40S ribosomal protein S4, putative, expressed	**1.01**	down	**1.17**	up	**2.18**	down	**1.10**	up	**1.21**	down	**1.08**	down	ABA
Os.8446.1.S1_at	LOC_Os09g31230	expressed protein	**1.04**	up	**1.05**	down	**2.12**	down	**1.27**	down	**1.15**	up	**1.02**	down	ABA
Os.8458.1.S1_s_at	LOC_Os04g05050	pectate lyase precursor, putative, expressed	**1.15**	down	**1.14**	down	**3.15**	down	**1.18**	down	**1.16**	down	**1.28**	up	ABA
Os.8475.2.S1_at	LOC_Os08g38170	methyladenine glycosylase, putative, expressed	**1.13**	up	**1.30**	up	**4.80**	down	**1.18**	down	**1.67**	down	**1.15**	down	ABA
Os.8483.1.S1_at	LOC_Os04g39440	ras-related protein, putative, expressed	**1.20**	up	**1.01**	up	**2.99**	up	**1.03**	down	**1.59**	up	**1.14**	down	ABA
Os.8487.1.S1_at	LOC_Os05g18470	CRAL/TRIO domain containing protein, expressed	**1.04**	up	**1.01**	down	**5.61**	up	**1.94**	down	**1.48**	up	**1.38**	up	ABA
Os.8493.1.A1_at	LOC_Os06g43430	cytochrome P450, putative, expressed	**1.41**	down	**1.45**	up	**4.69**	down	**1.10**	up	**1.57**	down	**1.59**	down	ABA
Os.8503.1.S1_at	LOC_Os06g39110	expressed protein	**1.36**	down	**1.05**	up	**4.24**	down	**1.25**	down	**1.69**	down	**1.09**	down	ABA
Os.8508.1.S1_at	LOC_Os10g38880	DUF623 domain containing protein, expressed	**2.36**	down	**2.38**	down	**11.07**	down	**1.04**	down	**1.34**	down	**1.48**	down	3
Os.8509.1.S1_at	LOC_Os05g50260	polygalacturonase, putative, expressed	**1.71**	down	**1.24**	up	**2.55**	up	**1.71**	up	**1.83**	down	**1.67**	down	ABA
Os.8517.1.S1_at	LOC_Os03g62010	harpin-induced protein 1 domain containing protein, expressed	**1.08**	down	**1.15**	up	**3.42**	down	**1.76**	up	**1.10**	up	**1.59**	down	ABA

Os.8519.1.S1_a_at	LOC_Os05g51830	ZOS5-12 - C2H2 zinc finger protein, expressed	1.06	down	1.01	up	2.26	down	1.12	up	1.39	down	1.05	down	ABA
Os.8522.1.S1_at	LOC_Os06g45980	toprim domain-containing protein, putative, expressed	1.21	up	1.21	up	4.38	down	1.01	down	1.76	down	1.66	down	ABA
Os.8527.2.S1_x_at	LOC_Os10g20240	syntaxin 6, N-terminal domain containing protein, expressed	1.10	up	1.11	down	2.51	up	1.03	up	1.33	up	1.32	up	ABA
Os.8549.1.S1_at	LOC_Os03g50130	microsomal glutathione S-transferase 3, putative, expressed	1.15	up	1.42	up	1.67	down	1.19	up	2.38	up	1.31	down	SA
Os.855.1.S1_at	LOC_Os01g03730	nuclease PA3, putative, expressed	1.25	up	1.46	down	7.16	up	1.01	down	1.51	up	1.40	up	ABA
Os.8551.1.S1_s_at	LOC_Os02g04520	AGG2, putative, expressed	1.03	down	1.09	down	2.02	down	1.08	down	1.23	down	1.09	down	ABA
Os.8554.1.S1_at	LOC_Os01g74190	radical SAM enzyme, putative, expressed	1.21	up	1.09	up	2.69	down	1.33	down	1.62	down	1.34	down	ABA
Os.8554.2.S1_x_at	LOC_Os01g74190	radical SAM enzyme, putative, expressed	1.36	up	1.05	up	2.80	down	1.19	down	1.51	down	1.12	down	ABA
Os.8559.1.S1_at	AK107748	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA020C20, full insert sequence	1.35	up	1.06	up	165.33	up	1.42	down	4.05	up	1.05	down	2
Os.8575.1.S1_at	LOC_Os12g08200	expressed protein	1.08	down	1.02	down	2.81	down	1.72	down	1.68	down	1.99	down	ABA
Os.8578.1.S1_at	LOC_Os06g01350	transferase family protein, putative, expressed	1.53	up	1.17	up	1.25	up	1.90	up	4.27	up	1.80	up	SA
Os.8593.1.S1_at	LOC_Os04g53930	organic cation transporter protein, putative, expressed	1.47	down	1.37	down	2.88	up	1.31	up	2.62	up	6.32	up	3
Os.8600.1.S1_at	LOC_Os04g37480	oxidoreductase, aldo/keto reductase family protein, putative, expressed	1.18	up	1.20	down	2.38	down	1.06	down	1.08	down	1.26	down	ABA
Os.8615.1.S1_at	LOC_Os08g38400	oligopeptide transporter, putative, expressed	1.43	down	1.35	down	4.24	down	1.04	up	1.27	down	1.09	down	ABA
Os.8621.1.S1_a_at	LOC_Os08g37300	expressed protein	1.15	up	1.01	down	2.70	up	1.15	down	1.10	down	1.25	down	ABA
Os.8622.1.S1_at	LOC_Os07g08460	OsIAA24 - Auxin-responsive Aux/IAA gene family member, expressed	3.52	up	1.21	down	2.28	up	1.18	down	1.15	up	1.01	up	2
Os.8633.1.S1_a_at	LOC_Os04g53760	kinesin motor domain containing protein, putative, expressed	1.18	down	1.39	down	2.08	down	1.53	down	1.41	down	1.07	up	ABA
Os.8638.1.S1_at	LOC_Os10g05950	POEI11 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.09	down	1.03	down	3.97	down	1.17	up	1.07	up	1.12	down	ABA
Os.8638.1.S1_s_at	LOC_Os10g05950	POEI11 - Pollen Ole e I allergen and extensin family protein precursor, expressed	1.01	up	1.06	down	4.90	down	1.26	up	1.03	down	1.04	down	ABA
Os.8639.1.S1_at	LOC_Os02g24700	OsSAUR8 - Auxin-responsive SAUR gene family member, expressed	1.15	up	1.09	down	7.87	down	1.28	up	1.05	down	1.50	down	ABA
Os.8648.1.S1_s_at	LOC_Os08g37250	patatin, putative, expressed	1.00	down	1.24	down	1.62	up	1.70	up	1.81	up	3.13	up	JA
Os.8649.1.S1_at	LOC_Os11g43590	kelch repeat protein, putative, expressed	1.01	down	1.11	down	2.76	down	1.45	down	1.03	up	1.21	down	ABA
Os.8653.1.S1_at	LOC_Os02g32610	protein kinase domain containing protein, expressed	1.27	up	1.04	up	1.12	up	2.80	up	1.52	up	1.09	up	ACC
Os.8666.1.S1_at	LOC_Os02g57110	GDSL-like lipase/acylhydrolase, putative, expressed	1.11	up	1.11	down	3.72	down	1.12	down	1.15	down	1.01	down	ABA
Os.8668.1.S1_at	LOC_Os12g36640	universal stress protein domain containing protein, putative, expressed	1.06	down	1.08	down	2.74	up	1.47	up	1.46	up	1.01	down	ABA
Os.8668.1.S1_x_at	LOC_Os12g36640	universal stress protein domain containing protein, putative, expressed	1.09	up	1.05	down	2.33	up	1.40	up	1.37	up	1.07	down	ABA
Os.8681.1.S1_at	CT829869	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA016C17, full insert sequence	1.51	up	1.28	down	2.66	up	1.10	up	1.14	down	1.24	down	ABA
Os.8682.1.S1_a_at	LOC_Os10g08780	expressed protein	1.49	up	1.82	down	4.44	down	1.19	down	1.94	down	2.14	down	2
Os.8682.1.S1_at	LOC_Os10g08780	expressed protein	1.12	up	1.79	down	3.35	down	1.01	up	1.47	down	1.77	down	ABA
Os.8682.2.S1_x_at	LOC_Os10g08780	expressed protein	1.32	up	1.62	down	3.91	down	1.18	down	1.82	down	1.98	down	ABA
Os.8684.1.S1_a_at	LOC_Os02g09490	dehydrogenase, putative, expressed	1.19	down	1.21	up	2.21	down	1.16	down	1.96	down	1.30	down	ABA
Os.8707.2.A1_at	LOC_Os03g62730	transposon protein, putative, unclassified, expressed	1.11	down	1.14	down	3.20	down	1.17	up	1.01	down	1.09	up	ABA
Os.8707.3.S1_x_at	LOC_Os03g62730	transposon protein, putative, unclassified, expressed	1.28	down	1.19	down	3.11	down	1.21	up	1.06	up	1.05	up	ABA
Os.872.2.S1_at	LOC_Os01g14580	dehydrogenase, putative, expressed	1.03	down	1.49	down	3.41	down	1.29	down	1.15	up	4.04	up	2
Os.8732.1.S1_at	LOC_Os02g53340	cyclic nucleotide-gated ion channel, putative, expressed	1.46	up	1.01	down	2.04	up	1.06	down	1.14	up	1.14	down	ABA
Os.8734.1.S1_a_at	LOC_Os09g35810	NC domain-containing protein, putative, expressed	1.29	down	1.08	down	2.23	down	1.04	down	1.22	down	1.04	down	ABA
Os.8742.1.S1_at	LOC_Os03g19250	AMP-binding enzyme, putative, expressed	1.41	up	1.10	down	3.26	up	1.62	up	2.75	up	2.09	up	3
Os.8746.1.S1_at	LOC_Os05g02670	kinesin motor domain containing protein, putative, expressed	1.10	down	1.07	down	2.51	down	1.03	up	1.20	down	1.04	up	ABA
Os.8749.1.S1_at	LOC_Os07g39300	expressed protein	1.03	down	1.02	down	3.63	up	1.24	down	1.02	up	1.18	down	ABA
Os.8760.1.S1_a_at	LOC_Os09g36600	nodulin, putative, expressed	1.39	down	1.08	down	6.07	down	1.18	up	1.16	down	1.16	up	ABA
Os.8760.2.S1_a_at	LOC_Os09g36600	nodulin, putative, expressed	1.06	down	1.13	up	5.37	down	1.02	up	1.17	down	1.02	down	ABA
Os.8762.1.S1_at	LOC_Os12g25630	sulfite oxidase, putative, expressed	2.34	up	1.31	down	1.76	up	1.34	up	11.16	up	4.76	up	3
Os.8765.1.S1_a_at	LOC_Os01g47690	metallo-beta-lactamase family protein, putative, expressed	1.66	up	1.12	down	3.53	up	1.39	up	2.86	up	2.63	up	3
Os.8768.1.S1_a_at	LOC_Os02g48630	expressed protein	1.10	down	1.15	down	4.98	up	1.32	up	1.86	up	1.32	up	ABA
Os.8773.2.S1_a_at	LOC_Os06g09679	chaperonin, putative, expressed	1.23	up	1.06	up	2.16	down	1.15	down	1.32	down	1.22	down	ABA
Os.8776.1.S1_at	LOC_Os03g64219	OTU-like cysteine protease family protein, putative, expressed	1.08	up	1.02	up	2.99	up	1.32	up	1.81	up	1.36	up	ABA
Os.8778.1.S1_a_at	LOC_Os06g11290	12-oxophytodienoate reductase, putative, expressed	4.53	up	1.38	down	1.25	up	1.10	up	8.10	up	2.03	up	3
Os.8779.1.S1_at	LOC_Os07g49270	AMP deaminase, putative, expressed	1.03	up	1.02	up	2.60	up	1.07	up	2.00	up	1.14	up	2
Os.8786.1.S1_a_at	AK067371	leucine-rich repeat transmembrane protein kinase, putative	1.21	up	1.09	up	4.18	down	1.18	up	1.35	down	1.26	down	ABA
Os.8786.3.S1_x_at	LOC_Os05g40270	expressed protein	1.27	up	1.13	up	3.86	down	1.14	up	1.27	down	1.15	down	ABA
Os.8786.4.S1_x_at	AK067371	leucine-rich repeat transmembrane protein kinase, putative	1.29	up	1.06	up	4.39	down	1.15	up	1.47	down	1.17	down	ABA
Os.8793.1.S1_at	LOC_Os06g10520	pantothenate kinase, putative, expressed	1.02	up	1.18	down	1.35	up	1.04	up	2.00	up	1.60	up	SA
Os.8802.1.S1_at	LOC_Os02g22160	DNA binding protein, putative, expressed	1.06	up	1.02	up	3.47	up	1.29	up	1.17	down	1.11	up	ABA
Os.8833.1.S1_at	LOC_Os04g48070	homeobox and START domains containing protein, putative, expressed	1.75	up	1.09	down	9.84	up	1.17	down	1.38	up	1.06	up	ABA
Os.8840.1.S1_at	LOC_Os02g48390	phosphoribosyl transferase, putative, expressed	1.28	down	1.47	down	4.60	down	1.01	down	1.50	down	1.38	down	ABA

Os.8851.1.S1_at	LOC_Os08g35630	MTD1, putative, expressed	**1.12**	down	**1.01**	down	**9.89**	up	**1.13**	up	**2.11**	up	**1.03**	down	2
Os.8865.2.S1_x_at	LOC_Os01g61320	thioredoxin, putative, expressed	**1.05**	down	**1.00**	up	**3.40**	down	**1.13**	down	**1.68**	down	**1.44**	down	ABA
Os.8868.1.S1_at	LOC_Os10g38610	glutathione S-transferase, putative, expressed	**1.01**	up	**1.14**	down	**1.02**	down	**1.53**	down	**3.36**	up	**1.33**	down	SA
Os.8870.1.S1_s_at	LOC_Os12g12370	outer envelope protein, putative, expressed	**1.04**	up	**1.31**	up	**2.34**	up	**1.22**	down	**1.06**	up	**1.05**	down	ABA
Os.8895.1.S1_at	LOC_Os03g25050	chaperonin, putative, expressed	**1.12**	down	**1.09**	up	**2.32**	down	**1.05**	up	**1.17**	down	**1.08**	down	ABA
Os.8897.1.S1_at	AK107786	Oryza sativa Japonica Group cDNA clone:002-133-C12, full insert sequence.	**1.09**	up	**1.40**	up	**81.39**	up	**1.18**	down	**1.62**	up	**1.24**	down	ABA
Os.8900.1.S1_a_at	LOC_Os03g06139	ABC-2 type transporter domain containing protein, expressed	**1.36**	up	**1.28**	down	**2.06**	up	**1.35**	down	**1.02**	down	**1.07**	down	ABA
Os.8906.1.S1_at	LOC_Os04g48480	exostosin family domain containing protein, expressed	**1.70**	down	**1.43**	up	**2.50**	down	**1.11**	down	**1.11**	down	**1.16**	down	ABA
Os.8908.1.S1_at	LOC_Os02g53320	universal stress protein domain containing protein, putative, expressed	**1.04**	up	**1.07**	down	**4.38**	up	**1.75**	down	**1.21**	up	**1.93**	down	ABA
Os.8910.1.S1_at	LOC_Os02g37830	protein kinase domain containing protein, expressed	**1.02**	down	**1.17**	down	**2.12**	down	**1.10**	down	**1.04**	up	**1.44**	up	ABA
Os.8928.1.S1_at	LOC_Os05g48590	OsIAA19 - Auxin-responsive Aux/IAA gene family member, expressed	**2.42**	up	**1.05**	up	**1.42**	up	**1.06**	down	**1.60**	up	**1.09**	up	IAA
Os.8936.1.S1_at	LOC_Os08g07390	mla1, putative, expressed	**1.11**	down	**1.06**	down	**3.21**	up	**1.03**	down	**1.29**	up	**1.01**	up	ABA
Os.8941.1.S1_at	LOC_Os06g47840	ZOS6-08 - C2H2 zinc finger protein, expressed	**1.48**	up	**1.16**	up	**1.44**	up	**1.24**	up	**2.40**	up	**1.05**	up	SA
Os.8942.1.S1_at	LOC_Os02g53700	DENN domain containing protein, expressed	**1.18**	up	**1.13**	up	**8.76**	up	**1.03**	up	**1.35**	up	**1.10**	down	ABA
Os.8942.2.S1_at	LOC_Os02g53700	DENN domain containing protein, expressed	**1.03**	down	**1.11**	down	**4.42**	up	**1.07**	down	**1.15**	up	**1.36**	down	ABA
Os.8945.1.S1_at	LOC_Os06g39370	OsFBK16 - F-box domain and kelch repeat containing protein, expressed	**1.07**	down	**1.36**	up	**2.44**	up	**1.46**	down	**1.33**	down	**2.78**	down	2
Os.8947.1.S1_at	LOC_Os03g05910	expressed protein	**16.34**	up	**1.11**	down	**58.28**	up	**1.97**	up	**70.08**	up	**27.29**	up	4
Os.8957.1.S1_a_at	LOC_Os01g63060	phosphatidic acid phosphatase-related, putative, expressed	**1.03**	down	**1.39**	down	**2.23**	up	**1.06**	up	**1.44**	up	**1.11**	up	ABA
Os.8965.1.S1_at	LOC_Os01g40280	integral membrane protein, putative, expressed	**1.17**	up	**1.02**	up	**6.27**	up	**1.15**	down	**3.30**	up	**1.14**	down	2
Os.8971.1.S1_at	LOC_Os05g44340	heat shock protein 101, putative, expressed	**1.16**	down	**1.14**	down	**11.37**	up	**1.26**	down	**4.97**	up	**1.11**	down	2
Os.8982.1.S1_at	LOC_Os01g58194	protein disulfide isomerase, putative, expressed	**1.01**	down	**1.06**	up	**3.95**	up	**1.02**	up	**1.65**	up	**1.01**	up	ABA
Os.8984.1.S1_at	LOC_Os02g13660	meiosis 5, putative, expressed	**1.09**	up	**1.15**	up	**2.05**	down	**1.70**	up	**1.13**	up	**1.30**	up	ABA
Os.9002.1.S1_at	AK062691	Oryza sativa Japonica Group cDNA clone:001-106-A03, full insert sequence.	**2.23**	up	**1.11**	up	**1.29**	up	**1.10**	down	**1.07**	up	**1.23**	down	IAA
Os.9003.1.S1_at	LOC_Os11g43620	LSM domain containing protein, expressed	**1.04**	down	**1.16**	up	**2.26**	down	**1.12**	down	**1.36**	down	**1.00**	up	ABA
Os.9016.1.S1_x_at	AK287455	Oryza sativa Japonica Group cDNA, clone: J043019E16, full insert sequence.	**1.08**	down	**1.13**	down	**2.02**	up	**1.33**	up	**10.45**	up	**1.52**	up	2
Os.9017.1.S1_x_at	LOC_Os07g23570	cytochrome P450 72A1, putative, expressed	**27.16**	up	**8.66**	up	**3.18**	up	**1.65**	down	**13.58**	up	**2.31**	up	5
Os.9022.1.S1_at	LOC_Os09g15670	protein phosphatase 2C, putative, expressed	**2.33**	up	**1.08**	down	**123.44**	up	**2.14**	down	**2.34**	up	**1.06**	up	4
Os.9039.1.S1_at	AK066796	formamidase, putative / formamide amidohydrolase, putative	**1.62**	up	**1.19**	up	**2.73**	down	**1.38**	down	**1.44**	down	**1.24**	down	ABA
Os.9043.1.S1_at	LOC_Os06g03720	ribonucleoside-diphosphate reductase small chain, putative, expressed	**1.42**	down	**1.02**	down	**6.22**	down	**1.13**	down	**1.95**	down	**1.91**	down	ABA
Os.9065.1.S1_at	LOC_Os04g35130	expressed protein	**1.19**	up	**1.36**	up	**2.67**	up	**1.69**	up	**2.05**	up	**1.18**	up	2
Os.9067.1.S1_at	LOC_Os07g44140	cytochrome P450 72A1, putative, expressed	**3.42**	up	**1.08**	up	**2.32**	up	**1.31**	up	**9.45**	up	**2.25**	up	4
Os.9069.1.S1_at	LOC_Os01g08320	OsIAA1 - Auxin-responsive Aux/IAA gene family member, expressed	**3.67**	up	**1.01**	up	**1.88**	down	**1.11**	down	**1.09**	up	**1.08**	down	IAA
Os.9072.1.S1_at	LOC_Os11g30360	expressed protein	**1.55**	down	**1.31**	down	**2.23**	down	**1.01**	down	**1.44**	up	**2.14**	up	2
Os.9074.1.S1_s_at	LOC_Os03g02960	nascent polypeptide-associated complex subunit alpha, putative, expressed	**1.10**	up	**1.07**	up	**2.83**	down	**1.11**	down	**1.43**	down	**1.09**	down	ABA
Os.9080.1.S1_at	LOC_Os03g08550	STRUBBELIG-RECEPTOR FAMILY 6 precursor, putative, expressed	**1.09**	up	**1.09**	down	**2.54**	up	**1.37**	down	**1.14**	up	**1.42**	down	ABA
Os.9101.1.S1_at	LOC_Os10g38780	glutathione S-transferase, putative, expressed	**1.16**	up	**1.82**	up	**3.25**	down	**1.39**	up	**1.20**	down	**1.47**	down	ABA
Os.9105.1.S1_at	LOC_Os09g33680	Os9bglu31 - beta-glucosidase, dhurrinase, similar to G. max hydroxyisourate hydrolase	**1.58**	up	**1.14**	down	**4.03**	up	**1.26**	down	**6.36**	up	**2.32**	up	3
Os.9108.1.S1_a_at	LOC_Os10g30156	starch synthase, putative, expressed	**1.10**	up	**1.31**	down	**3.43**	up	**1.14**	down	**1.09**	up	**1.00**	up	ABA
Os.9116.1.S1_at	LOC_Os01g28680	WD domain, G-beta repeat domain containing protein, expressed	**3.24**	up	**1.18**	down	**1.15**	down	**1.13**	down	**1.97**	up	**1.20**	up	IAA
Os.9121.1.S1_at	LOC_Os05g29010	POLA4 - Putative DNA polymerase alpha complex subunit, expressed	**1.38**	down	**1.08**	down	**6.53**	down	**1.15**	down	**2.11**	down	**1.82**	down	2
Os.9159.2.S1_x_at	LOC_Os06g02530	expressed protein	**2.03**	down	**1.24**	down	**11.33**	down	**1.09**	down	**1.90**	down	**2.10**	down	3
Os.9169.1.S1_x_at	AK058739	subtilisin/chymotrypsin inhibitor	**1.21**	down	**1.07**	up	**1.13**	down	**1.34**	down	**1.03**	up	**6.16**	up	JA
Os.9174.1.S1_at	LOC_Os06g51480	expressed protein	**1.12**	up	**1.07**	down	**2.11**	up	**1.04**	down	**1.02**	up	**1.10**	down	ABA
Os.9178.1.S1_at	LOC_Os11g07670	dirigent, putative, expressed	**1.38**	down	**1.04**	up	**2.32**	down	**1.03**	down	**1.36**	down	**1.01**	down	ABA
Os.9199.1.S1_at	LOC_Os06g50330	senescence-associated protein, putative, expressed	**1.14**	up	**1.08**	down	**2.27**	up	**1.04**	up	**1.18**	up	**1.30**	down	ABA
Os.9201.2.S1_x_at	LOC_Os02g40010	phosphoribosyl transferase, putative, expressed	**1.45**	down	**5.85**	up	**19.27**	down	**1.25**	down	**2.74**	down	**2.28**	down	4
Os.9207.1.S1_at	LOC_Os11g48020	fatty acid hydroxylase, putative, expressed	**1.00**	up	**1.00**	down	**2.84**	up	**1.13**	up	**1.24**	down	**1.05**	down	ABA
Os.9217.1.S1_at	LOC_Os05g48980	ras-related protein, putative, expressed	**1.09**	up	**1.09**	up	**2.02**	down	**1.07**	down	**1.45**	down	**1.07**	up	ABA
Os.9230.1.S1_x_at	LOC_Os10g35370	oxidoreductase, short chain dehydrogenase/reductase family domain containing family,	**1.11**	down	**1.03**	up	**3.69**	down	**1.13**	down	**1.68**	down	**1.33**	down	ABA
Os.9292.1.S1_at	LOC_Os11g39370	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative	**1.01**	down	**1.18**	up	**2.02**	down	**1.25**	up	**1.03**	down	**1.30**	down	ABA
Os.9300.1.S1_at	LOC_Os05g29710	RING-H2 finger protein, putative, expressed	**1.26**	down	**1.01**	down	**7.17**	down	**1.09**	up	**2.13**	down	**1.02**	down	2
Os.9312.1.S1_at	LOC_Os03g01270	expansin precursor, putative, expressed	**1.96**	down	**2.37**	up	**2.31**	down	**1.34**	up	**3.30**	down	**7.66**	down	4
Os.9332.1.S1_at	LOC_Os06g01934	homeobox domain containing protein, expressed	**1.02**	up	**1.02**	down	**5.07**	down	**1.42**	down	**1.52**	down	**1.01**	up	ABA
Os.9333.1.A1_s_at	LOC_Os06g12410	GDSL-like lipase/acylhydrolase, putative, expressed	**1.17**	up	**1.59**	up	**5.10**	up	**1.53**	down	**1.83**	up	**1.43**	down	ABA
Os.9389.2.S2_a_at	LOC_Os10g38050	HOTHEAD precursor, putative, expressed	**1.26**	down	**1.04**	down	**2.01**	up	**1.21**	up	**1.27**	up	**1.02**	up	ABA

Os.941.1.S1_at	LOC_Os01g52830	DUF1264 domain containing protein, putative, expressed	**1.00**	down	**1.00**	up	**908.45**	up	**1.01**	down	**1.01**	down	**1.03**	up	ABA
Os.9416.1.S1_at	LOC_Os02g33110	glycosyl hydrolases, putative, expressed	**1.52**	down	**2.82**	up	**3.34**	down	**1.03**	down	**1.43**	down	**1.25**	up	2
Os.9420.1.S1_at	LOC_Os07g15370	metal transporter Nramp6, putative, expressed	**1.37**	down	**1.98**	down	**5.96**	down	**1.35**	down	**1.66**	down	**1.29**	up	ABA
Os.9421.1.S1_at	LOC_Os10g11500	SCP-like extracellular protein, expressed	**1.44**	down	**1.20**	up	**2.21**	down	**1.15**	down	**1.91**	down	**1.11**	down	ABA
Os.9423.1.S1_at	LOC_Os02g35190	chloride channel protein, putative, expressed	**1.12**	down	**1.07**	down	**2.18**	up	**1.21**	up	**1.09**	up	**1.73**	up	ABA
Os.9424.1.S1_at	LOC_Os04g38310	expressed protein	**1.03**	up	**1.12**	down	**2.01**	down	**1.28**	down	**1.54**	down	**1.38**	down	ABA
Os.9431.1.A1_a_at	LOC_Os08g16610	Rad21 / Rec8 like protein, putative, expressed	**1.59**	down	**1.22**	up	**3.61**	down	**1.31**	down	**1.69**	down	**1.42**	down	ABA
Os.9442.1.S1_s_at	LOC_Os03g50530	expressed protein	**1.03**	up	**1.04**	down	**2.09**	down	**1.01**	down	**1.47**	down	**1.21**	up	ABA
Os.9456.1.S1_at	LOC_Os02g28170	transferase family protein, putative, expressed	**1.03**	down	**1.02**	down	**4.08**	up	**1.01**	up	**1.07**	down	**1.06**	up	ABA
Os.9461.1.S1_at	LOC_Os08g30810	puromycin-sensitive aminopeptidase, putative, expressed	**1.02**	up	**1.05**	down	**2.08**	up	**1.07**	up	**1.11**	up	**1.03**	down	ABA
Os.9471.1.S1_a_at	LOC_Os08g40790	DNA repair ATPase-related, putative, expressed	**1.12**	up	**1.01**	up	**2.12**	up	**1.11**	down	**1.10**	up	**1.09**	up	ABA
Os.9484.1.S1_at	LOC_Os12g09580	leafbladeless1, putative, expressed	**1.26**	down	**1.11**	down	**2.36**	down	**1.03**	up	**1.39**	down	**1.30**	down	ABA
Os.9484.1.S2_at	LOC_Os12g09580	leafbladeless1, putative, expressed	**1.01**	down	**1.14**	down	**2.82**	down	**1.06**	down	**1.66**	down	**1.56**	down	ABA
Os.9486.1.S1_at	LOC_Os06g28124	glycosyltransferase, putative, expressed	**1.11**	down	**2.20**	down	**1.45**	down	**1.36**	down	**1.03**	down	**1.60**	up	BAP
Os.9487.1.S1_a_at	LOC_Os01g10250	hydrolase, alpha/beta fold family domain containing protein, expressed	**1.14**	up	**1.01**	up	**2.28**	up	**1.08**	down	**1.40**	up	**1.10**	up	ABA
Os.9506.1.S1_a_at	LOC_Os02g38020	inorganic phosphate transporter 2-1, chloroplast precursor, putative, expressed	**1.16**	up	**1.17**	up	**4.84**	down	**1.41**	down	**1.66**	down	**1.65**	down	ABA
Os.9523.1.S1_at	LOC_Os04g32620	ethylene-responsive transcription factor ERF114, putative, expressed	**1.03**	down	**1.11**	down	**4.54**	up	**1.68**	up	**3.03**	up	**2.12**	up	3
Os.9527.1.S1_at	LOC_Os07g41460	sulfotransferase domain containing protein, expressed	**1.44**	up	**1.20**	up	**1.44**	down	**1.47**	up	**3.03**	up	**1.62**	down	SA
Os.9530.2.S1_at	LOC_Os01g40420	CBS domain containing membrane protein, putative, expressed	**1.08**	up	**1.01**	down	**2.02**	up	**1.07**	up	**1.32**	up	**1.05**	up	ABA
Os.9530.2.S1_x_at	LOC_Os01g40420	CBS domain containing membrane protein, putative, expressed	**1.04**	up	**1.01**	up	**2.18**	up	**1.26**	up	**1.35**	up	**1.33**	up	ABA
Os.9534.1.S1_at	LOC_Os01g65830	acyl-desaturase, chloroplast precursor, putative, expressed	**2.15**	down	**1.54**	up	**1.38**	up	**2.12**	up	**1.53**	down	**1.32**	down	2
Os.9538.1.S1_s_at	LOC_Os06g39875	ras-related protein, putative, expressed	**1.47**	up	**1.08**	down	**12.45**	up	**1.13**	up	**2.60**	up	**1.95**	down	3
Os.9544.1.A1_at	LOC_Os07g07920	LTPL100 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.25**	up	**1.18**	up	**7.84**	up	**1.19**	down	**1.83**	up	**1.35**	down	ABA
Os.9554.1.S1_at	LOC_Os04g52504	adhesive/proline-rich protein, putative, expressed	**1.05**	up	**1.00**	up	**1.28**	down	**1.01**	down	**2.07**	up	**1.57**	up	SA
Os.9573.1.A1_at	AK243284	Oryza sativa Japonica Group cDNA, clone: J100051M17, full insert sequence.	**1.16**	down	**1.06**	up	**2.16**	down	**1.03**	up	**1.30**	down	**1.08**	down	ABA
Os.9581.1.S1_a_at	LOC_Os06g22380	expressed protein	**1.11**	up	**1.37**	down	**2.77**	down	**1.41**	down	**1.50**	down	**1.46**	down	ABA
Os.9594.1.S1_at	LOC_Os08g05780	expressed protein	**1.02**	up	**1.30**	up	**10.24**	up	**1.02**	up	**1.54**	up	**1.23**	up	ABA
Os.9624.1.S1_a_at	LOC_Os08g42420	expressed protein	**1.14**	up	**1.28**	down	**3.00**	up	**1.01**	down	**1.16**	up	**1.06**	down	ABA
Os.9626.1.S1_at	LOC_Os08g44870	MATE efflux family protein, putative, expressed	**1.15**	up	**1.10**	down	**6.93**	down	**1.22**	down	**1.39**	down	**1.51**	up	ABA
Os.9638.1.S1_at	LOC_Os08g01410	phosphate/phosphoenolpyruvate translocator-related protein, putative, expressed	**1.03**	down	**1.03**	up	**4.35**	up	**1.17**	up	**1.22**	up	**1.65**	up	ABA
Os.9653.1.S1_at	LOC_Os05g04360	protein phosphatase 2C, putative, expressed	**1.36**	up	**1.02**	up	**3.02**	up	**1.04**	up	**1.06**	down	**1.12**	down	ABA
Os.9653.1.S1_s_at	LOC_Os05g04360	protein phosphatase 2C, putative, expressed	**1.12**	up	**1.13**	down	**2.92**	up	**1.01**	up	**1.08**	up	**1.07**	down	ABA
Os.9654.2.S1_x_at	LOC_Os04g35840	T-complex protein 11, putative, expressed	**1.12**	up	**1.14**	down	**2.33**	up	**1.14**	down	**1.02**	down	**1.06**	up	ABA
Os.9659.1.S1_at	LOC_Os08g17680	stromal cell-derived factor 2-like protein precursor, putative, expressed	**2.26**	down	**1.07**	up	**3.42**	down	**1.23**	up	**1.24**	down	**1.09**	up	2
Os.9661.1.S1_at	LOC_Os03g04620	CCT motif family protein, expressed	**1.01**	up	**4.10**	up	**1.23**	down	**1.37**	up	**1.38**	up	**1.01**	down	BAP
Os.9684.1.S1_at	LOC_Os06g38960	expressed protein	**1.09**	up	**1.05**	down	**2.44**	down	**1.31**	down	**1.46**	down	**1.26**	down	ABA
Os.9690.1.S1_at	LOC_Os06g14390	1-aminocyclopropane-1-carboxylate oxidase homolog 4, putative, expressed	**1.04**	down	**1.06**	up	**2.86**	down	**1.07**	down	**1.33**	down	**1.02**	down	ABA
Os.9704.1.S1_at	LOC_Os01g12820	harpin-induced protein, putative, expressed	**1.05**	down	**1.04**	down	**97.28**	up	**1.00**	up	**2.76**	up	**1.03**	up	2
Os.9713.2.S1_at	LOC_Os05g51690	CCT motif family protein, expressed	**1.27**	down	**1.76**	down	**1.46**	up	**1.47**	up	**2.44**	up	**1.39**	down	SA
Os.9729.1.S1_a_at	LOC_Os02g17390	3-hydroxyacyl-CoA dehydrogenase, putative, expressed	**1.24**	up	**1.08**	down	**1.81**	up	**1.23**	up	**2.06**	up	**1.68**	up	SA
Os.9749.1.S1_at	LOC_Os08g44340	monodehydroascorbate reductase, putative, expressed	**1.39**	up	**1.14**	down	**2.86**	up	**1.26**	up	**3.22**	up	**1.48**	up	2
Os.9751.1.S1_at	LOC_Os11g40090	A49-like RNA polymerase I associated factor family protein, expressed	**1.08**	up	**1.16**	up	**2.59**	down	**1.06**	down	**1.64**	down	**1.38**	down	ABA
Os.9752.1.S1_a_at	LOC_Os12g03899	major facilitator superfamily antiporter, putative, expressed	**1.11**	up	**1.25**	down	**2.03**	up	**1.70**	down	**4.31**	up	**1.25**	up	2
Os.9752.2.S1_x_at	LOC_Os12g03899	major facilitator superfamily antiporter, putative, expressed	**1.47**	up	**1.12**	down	**2.36**	up	**1.60**	down	**3.99**	up	**1.96**	up	3
Os.9752.3.S1_x_at	LOC_Os12g03899	major facilitator superfamily antiporter, putative, expressed	**1.36**	up	**1.09**	down	**2.32**	up	**1.39**	down	**3.74**	up	**1.74**	up	2
Os.9759.1.S1_x_at	LOC_Os05g46510	polygalacturonase, putative, expressed	**1.35**	down	**1.15**	down	**3.24**	up	**1.24**	up	**1.67**	up	**1.35**	up	ABA
Os.9765.2.S1_at	LOC_Os03g03470	expressed protein	**1.02**	up	**1.15**	up	**3.99**	down	**1.35**	down	**2.02**	down	**1.41**	down	2
Os.9767.1.S1_at	LOC_Os03g38950	chloroplast post-illumination chlorophyll fluorescence increase protein, putative, expres	**1.96**	up	**1.11**	up	**2.00**	down	**1.09**	down	**1.23**	down	**1.02**	down	ABA
Os.9782.1.S1_at	LOC_Os09g19930	HOTHEAD precursor, putative, expressed	**1.20**	down	**1.15**	down	**2.58**	down	**1.10**	up	**1.02**	down	**1.06**	down	ABA
Os.9788.1.S1_x_at	LOC_Os01g57740	expressed protein	**1.42**	up	**1.18**	up	**3.22**	up	**1.14**	down	**1.07**	up	**1.03**	down	ABA
Os.9790.2.S1_x_at	LOC_Os01g63880	expressed protein	**1.31**	up	**1.53**	down	**3.11**	down	**1.24**	down	**1.13**	down	**1.23**	up	ABA
Os.9792.1.S1_at	LOC_Os02g05890	EMB1303, putative, expressed	**1.06**	up	**1.07**	up	**2.93**	down	**1.26**	down	**1.53**	down	**1.33**	down	ABA
Os.9795.1.S1_at	LOC_Os05g23924	glycosyl hydrolase family 10 protein, putative, expressed	**1.02**	up	**1.34**	down	**4.55**	up	**1.51**	down	**1.35**	down	**1.04**	up	ABA
Os.9798.1.S1_at	LOC_Os06g39875	ras-related protein, putative, expressed	**1.09**	down	**1.46**	up	**3.37**	down	**1.27**	up	**1.11**	up	**1.17**	down	ABA
Os.9811.1.S1_at	LOC_Os07g44004	expressed protein	**1.03**	down	**1.04**	up	**2.00**	down	**1.06**	down	**1.30**	down	**1.06**	down	ABA

Os.9824.1.S2_at	LOC_Os05g39690	oxidoreductase, aldo/keto reductase family protein, putative, expressed	**1.23**	up	**1.17**	up	**105.18**	up	**1.00**	down	**1.44**	up	**1.14**	down	ABA
Os.9835.1.S1_a_at	LOC_Os01g62020	NAD dependent epimerase/dehydratase family domain containing protein, expressed	**1.13**	up	**1.04**	down	**2.12**	down	**1.34**	up	**1.44**	down	**1.48**	up	ABA
Os.9836.1.S1_at	LOC_Os11g10590	Hypothetical protein	**1.16**	up	**1.28**	up	**4.98**	up	**1.02**	down	**3.41**	up	**1.70**	up	2
Os.9838.1.S1_at	LOC_Os02g07760	aldehyde dehydrogenase, putative, expressed	**1.08**	down	**1.00**	up	**2.50**	up	**1.01**	down	**1.03**	down	**1.17**	up	ABA
Os.9840.1.S1_at	LOC_Os10g17489	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed	**1.07**	up	**1.31**	down	**3.05**	up	**1.45**	up	**2.86**	up	**2.08**	up	3
Os.9842.1.S1_at	LOC_Os07g34020	expressed protein	**1.13**	up	**1.28**	down	**6.12**	down	**2.12**	down	**1.11**	up	**1.84**	down	2
Os.9848.1.S1_at	LOC_Os05g10650	6-phosphofructokinase, putative, expressed	**1.60**	up	**1.34**	up	**4.52**	up	**1.16**	down	**10.27**	up	**2.27**	up	3
Os.9858.1.S1_at	LOC_Os06g35670	expressed protein	**1.09**	down	**1.01**	down	**2.02**	up	**1.14**	up	**1.27**	up	**1.14**	up	ABA
Os.9873.1.S1_at	LOC_Os05g48416	lipase-related, putative, expressed	**1.10**	down	**1.49**	up	**63.63**	up	**1.05**	up	**1.03**	down	**1.09**	down	ABA
Os.9875.1.S1_at	LOC_Os03g11210	DUF538 domain containing protein, putative, expressed	**1.09**	down	**1.05**	up	**4.55**	down	**1.31**	down	**1.22**	up	**1.18**	down	ABA
Os.9880.1.S1_a_at	LOC_Os01g68480	thioredoxin, putative, expressed	**1.24**	up	**1.09**	up	**2.30**	down	**1.16**	down	**1.44**	down	**1.22**	down	ABA
Os.9894.1.S1_at	LOC_Os02g57120	HEAT repeat family protein, putative, expressed	**1.08**	up	**1.23**	down	**6.56**	down	**1.00**	up	**1.33**	down	**1.04**	down	ABA
Os.9923.1.S1_at	LOC_Os03g08330	ZIM domain containing protein, putative, expressed	**2.98**	up	**2.07**	up	**2.11**	down	**1.31**	down	**1.06**	down	**4.76**	up	4
Os.9945.1.S1_at	LOC_Os03g43410	OsIAA12 - Auxin-responsive Aux/IAA gene family member, expressed	**4.59**	up	**1.56**	up	**3.83**	down	**1.10**	down	**1.13**	down	**1.43**	down	2
Os.9946.1.S1_at	LOC_Os01g14830	ribosomal protein L3, putative, expressed	**1.26**	up	**1.32**	up	**2.23**	down	**1.16**	up	**1.41**	down	**1.14**	down	ABA
Os.9948.1.S1_at	LOC_Os08g38880	WD-40 repeat family protein, putative, expressed	**1.02**	down	**1.01**	up	**2.24**	up	**1.02**	down	**1.14**	up	**1.10**	down	ABA
Os.9954.1.S1_at	LOC_Os03g42840	calcineurin B, putative, expressed	**1.29**	up	**1.04**	up	**2.15**	up	**1.04**	up	**1.59**	up	**1.30**	up	ABA
Os.996.1.S1_at	LOC_Os01g01620	kinase, pfkB family, putative, expressed	**1.34**	down	**1.08**	up	**2.37**	up	**1.24**	up	**1.12**	down	**1.04**	down	ABA
Os.9967.1.S1_at	LOC_Os07g34580	glycosyl hydrolases family 16, putative, expressed	**1.53**	down	**1.16**	down	**2.90**	down	**1.15**	down	**1.59**	down	**1.79**	down	ABA
Os.9971.1.S1_s_at	LOC_Os02g42850	MYB family transcription factor, putative, expressed	**2.07**	down	**1.02**	up	**1.20**	up	**1.22**	up	**1.03**	down	**1.56**	up	IAA
Os.9975.1.S1_at	AK063845	Oryza sativa (japonica cultivar-group) Os03g0280400 (Os03g0280400) mRNA, comple	**1.02**	down	**1.08**	down	**10.09**	up	**1.07**	up	**1.41**	up	**1.43**	down	ABA
Os.9978.1.S1_at	AK121200	Oryza sativa Japonica Group cDNA clone:J023087I02, full insert sequence.	**1.05**	down	**1.10**	up	**8.54**	up	**1.06**	up	**1.20**	up	**1.12**	up	ABA
Os.9978.1.S2_at	AK121200	Oryza sativa Japonica Group cDNA clone:J023087I02, full insert sequence.	**1.01**	down	**1.01**	up	**7.23**	up	**1.01**	up	**1.00**	up	**1.02**	up	ABA
Os.9979.1.S1_at	LOC_Os09g22440	expressed protein	**1.00**	up	**1.17**	down	**2.16**	up	**1.01**	down	**1.09**	up	**1.05**	up	ABA
Os.9988.1.S1_at	LOC_Os11g32890	expressed protein	**1.43**	down	**1.64**	up	**182.06**	up	**1.20**	up	**1.48**	up	**1.10**	down	ABA
OsAffx.10060.1.S1_at	LOC_Os03g12660	cytochrome P450, putative, expressed	**1.74**	up	**4.69**	down	**1.56**	down	**1.04**	up	**1.69**	up	**1.62**	down	BAP
OsAffx.10368.1.S1_at	LOC_Os06g02250	MYB family transcription factor, putative	**1.05**	up	**1.04**	down	**10.03**	up	**1.00**	up	**1.09**	up	**1.05**	down	ABA
OsAffx.10756.1.S1_x_a	LOC_Os02g47200	transposon protein, putative, unclassified, expressed	**1.48**	up	**1.02**	down	**13.89**	up	**1.40**	down	**1.34**	up	**1.24**	up	ABA
OsAffx.10905.3.S1_at	LOC_Os01g04360	hsp20/alpha crystallin family protein, putative, expressed	**1.13**	up	**1.12**	up	**2.76**	up	**1.37**	up	**1.13**	down	**1.18**	down	ABA
OsAffx.10948.1.S1_at	LOC_Os01g07030	POEI40 - Pollen Ole e I allergen and extensin family protein precursor, expressed	**1.12**	up	**4.90**	up	**1.11**	down	**1.03**	up	**1.07**	down	**1.03**	down	BAP
OsAffx.10957.1.S1_at	LOC_Os01g07850	glyoxalase family protein, putative, expressed	**5.88**	down	**1.06**	up	**12.90**	down	**1.26**	up	**3.77**	down	**3.83**	up	4
OsAffx.10957.1.S1_x_a	LOC_Os01g07850	glyoxalase family protein, putative, expressed	**3.48**	down	**1.28**	down	**8.13**	down	**1.64**	up	**3.96**	down	**3.40**	up	4
OsAffx.10962.1.S1_x_a	LOC_Os01g08310	serine/threonine protein phosphatase 2A 59 kDa regulatory subunit Bgamma isoform, p	**1.48**	up	**1.11**	down	**2.03**	down	**1.02**	down	**1.22**	down	**1.04**	up	ABA
OsAffx.10973.1.S1_s_a	LOC_Os01g08760	choline/ethanolamine kinase, putative	**1.08**	up	**1.13**	up	**2.90**	up	**1.21**	up	**1.12**	up	**1.93**	up	ABA
OsAffx.10973.1.S1_x_a	LOC_Os01g08760	choline/ethanolamine kinase, putative	**1.05**	up	**1.15**	up	**3.52**	up	**1.32**	up	**1.01**	up	**1.86**	up	ABA
OsAffx.10973.2.S1_at	LOC_Os01g08760	choline/ethanolamine kinase, putative	**1.27**	down	**1.18**	down	**5.24**	up	**1.32**	up	**1.13**	up	**1.97**	up	ABA
OsAffx.10973.2.S1_s_a	LOC_Os01g12160	OsGH3.3 - Probable indole-3-acetic acid-amido synthetase, expressed	**1.03**	up	**1.21**	up	**3.19**	up	**1.27**	up	**1.16**	up	**1.67**	up	ABA
OsAffx.10978.1.S1_at	LOC_Os01g09080	WRKY DNA-binding domain containing protein, expressed	**1.33**	down	**1.09**	down	**2.13**	down	**1.30**	up	**1.44**	up	**1.46**	up	ABA
OsAffx.11003.1.S1_s_a	LOC_Os01g10870	CAMK_KIN1/SNF1/Nim1_like.7 - CAMK includes calcium/calmodulin depedent protein	**1.01**	down	**1.00**	up	**7.17**	up	**1.00**	down	**1.00**	down	**1.01**	up	ABA
OsAffx.11003.2.S1_at	LOC_Os01g10870	CAMK_KIN1/SNF1/Nim1_like.7 - CAMK includes calcium/calmodulin depedent protein	**1.01**	down	**1.04**	up	**130.15**	up	**1.00**	down	**1.01**	down	**1.03**	up	ABA
OsAffx.11075.1.S1_x_a	LOC_Os01g16146	phenazine biosynthesis protein, putative, expressed	**1.80**	up	**1.51**	down	**1.58**	up	**1.26**	down	**2.09**	up	**1.77**	up	SA
OsAffx.11172.1.S1_at	LOC_Os01g23530	terpene synthase, putative	**1.02**	down	**1.00**	up	**1.03**	down	**1.00**	up	**3.53**	up	**1.03**	up	SA
OsAffx.11193.2.S1_at	LOC_Os01g24730	hypothetical protein	**1.01**	up	**1.01**	up	**3.52**	up	**1.02**	up	**1.00**	up	**1.03**	up	ABA
OsAffx.11437.1.S1_at	LOC_Os01g42350	pleiotropic drug resistance protein, putative	**1.61**	down	**2.71**	up	**2.07**	up	**1.03**	down	**1.04**	down	**1.02**	up	2
OsAffx.11499.1.S1_at	LOC_Os01g47190	phosphoglycerate mutase, putative, expressed	**1.49**	up	**1.09**	up	**2.54**	up	**1.05**	up	**1.04**	up	**1.06**	down	ABA
OsAffx.11501.1.S1_x_a	LOC_Os01g47262	AMSH-like protease, putative, expressed	**1.19**	up	**1.16**	down	**3.06**	up	**1.16**	down	**1.08**	up	**1.14**	down	ABA
OsAffx.11516.1.S1_x_a	LOC_Os01g48310	expressed protein	**1.08**	down	**1.07**	down	**2.30**	up	**1.03**	down	**1.18**	up	**1.12**	up	ABA
OsAffx.11535.1.S1_at	LOC_Os01g49720	glutathione S-transferase, putative, expressed	**1.18**	up	**1.21**	up	**55.47**	up	**1.10**	down	**2.98**	up	**1.10**	up	2
OsAffx.11552.1.S1_at	9629	---	**1.51**	down	**1.10**	down	**31.64**	down	**2.79**	down	**5.35**	down	**2.70**	down	4
OsAffx.11559.1.S1_at	LOC_Os01g51420	calcineurin B, putative, expressed	**1.21**	down	**1.19**	down	**3.49**	up	**1.35**	up	**1.25**	up	**2.03**	up	2
OsAffx.11701.1.S1_s_a	LOC_Os01g62610	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed	**1.04**	up	**1.18**	up	**25.91**	up	**1.11**	down	**2.19**	up	**1.04**	down	2
OsAffx.11734.1.S1_at	LOC_Os01g64840	aspartic proteinase nepenthesin-1 precursor, putative, expressed	**1.17**	down	**1.27**	down	**1.28**	down	**5.97**	up	**1.04**	up	**1.09**	down	ACC
OsAffx.11835.1.S1_x_a	LOC_Os01g73000	copine, putative, expressed	**1.10**	up	**1.14**	down	**2.55**	up	**1.07**	up	**1.31**	up	**1.05**	up	ABA
OsAffx.11891.1.S1_at	LOC_Os02g04630	sodium/calcium exchanger protein, putative, expressed	**1.05**	down	**1.05**	up	**5.39**	up	**1.01**	down	**1.10**	up	**1.06**	down	ABA
OsAffx.11915.1.S1_at	LOC_Os02g06205	phytosulfokine receptor precursor, putative, expressed	**1.32**	up	**1.11**	up	**3.30**	up	**1.08**	up	**1.51**	up	**1.08**	up	ABA

OsAffx.11926.1.S1_s_a	LOC_Os02g07210	OTU-like cysteine protease family protein, putative, expressed	**1.04**	up	**1.03**	up	**2.06**	up	**1.03**	up	**1.18**	up	**1.23**	up	ABA
OsAffx.11956.1.S1_at	LOC_Os02g09480	myb-like DNA-binding domain containing protein, putative, expressed	**1.37**	up	**1.18**	down	**7.35**	up	**1.20**	down	**1.46**	up	**1.11**	up	ABA
OsAffx.11963.1.S1_at	LOC_Os02g09830	bZIP transcription factor domain containing protein, expressed	**2.15**	up	**1.45**	down	**22.65**	up	**1.00**	up	**1.18**	up	**1.02**	up	2
OsAffx.12022.1.S1_s_a	LOC_Os02g13600	expressed protein	**1.19**	up	**1.66**	down	**4.20**	up	**1.61**	up	**1.05**	up	**1.77**	up	ABA
OsAffx.12052.1.S1_at	LOC_Os02g15280	VQ domain containing protein, putative, expressed	**1.24**	up	**1.28**	up	**2.55**	down	**1.07**	up	**1.45**	down	**1.46**	down	ABA
OsAffx.12255.1.S1_at	LOC_Os02g28720	spotted leaf 11, putative, expressed	**1.24**	up	**1.40**	down	**4.93**	up	**1.01**	up	**1.58**	up	**1.35**	up	ABA
OsAffx.12451.1.S1_x_a	LOC_Os02g42220	transposon protein, putative, unclassified, expressed	**1.10**	down	**1.18**	down	**2.02**	up	**1.14**	down	**1.24**	down	**1.21**	down	ABA
OsAffx.12459.1.S1_at	LOC_Os02g42650	expansin precursor, putative, expressed	**1.16**	up	**1.86**	down	**2.41**	down	**1.18**	up	**1.01**	down	**1.33**	up	ABA
OsAffx.12561.1.S1_s_a	LOC_Os02g49160	OsIAA8 - Auxin-responsive Aux/IAA gene family member, expressed	**1.09**	up	**1.13**	down	**2.62**	down	**1.09**	up	**1.09**	up	**1.24**	down	ABA
OsAffx.12566.1.S1_at	LOC_Os02g49560	bZIP transcription factor domain containing protein, expressed	**1.06**	up	**3.93**	up	**1.05**	down	**1.04**	down	**1.00**	down	**1.10**	down	BAP
OsAffx.12578.1.S1_at	LOC_Os02g50480	histidine kinase, putative, expressed	**1.09**	up	**1.02**	down	**2.20**	down	**1.20**	down	**1.26**	down	**1.05**	up	ABA
OsAffx.12587.1.S1_s_a	LOC_Os02g51320	helix-loop-helix DNA-binding domain containing protein, expressed	**4.22**	up	**1.01**	down	**1.19**	up	**1.15**	up	**1.41**	up	**1.01**	up	IAA
OsAffx.12613.1.S1_at	9630	---	**1.01**	down	**1.02**	up	**16.74**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
OsAffx.12626.1.S1_at	LOC_Os02g53620	nuclear transcription factor Y subunit, putative, expressed	**1.17**	up	**2.02**	down	**5.24**	down	**1.34**	down	**1.40**	down	**2.44**	down	3
OsAffx.12634.1.S1_at	LOC_Os02g54100	expressed protein	**1.34**	up	**1.11**	up	**4.22**	up	**1.02**	up	**1.13**	up	**1.11**	up	ABA
OsAffx.12645.1.S1_s_a	LOC_Os02g54870	expressed protein	**1.28**	down	**1.74**	up	**4.73**	down	**3.12**	up	**1.56**	down	**1.10**	down	2
OsAffx.12655.1.S1_at	LOC_Os02g55580	hypothetical protein	**14.82**	up	**1.00**	up	**1.05**	down	**1.00**	down	**1.01**	down	**1.03**	up	IAA
OsAffx.12715.1.S1_at	Os03g0121600	---	**1.07**	up	**2.14**	up	**3.10**	up	**1.07**	up	**1.07**	up	**16.53**	up	3
OsAffx.12715.1.S1_x_a	Os03g0121600	---	**1.03**	down	**2.25**	up	**2.77**	up	**1.10**	down	**1.10**	down	**10.52**	up	3
OsAffx.12721.1.S1_at	LOC_Os03g03510	CAMK_KIN1/SNF1/Nim1_like.15 - CAMK includes calcium/calmodulin depedent protein	**1.01**	down	**1.07**	down	**2.35**	up	**1.12**	down	**1.11**	up	**1.13**	up	ABA
OsAffx.12778.1.S1_at	LOC_Os03g08200	DUF567 domain containing protein, putative, expressed	**1.03**	down	**1.01**	down	**16.08**	up	**1.01**	down	**1.00**	up	**1.02**	down	ABA
OsAffx.12783.1.S1_at	LOC_Os03g08530	aminotransferase, classes I and II, domain containing protein, expressed	**1.27**	up	**1.28**	down	**5.17**	up	**1.52**	up	**15.84**	up	**4.54**	up	3
OsAffx.12799.1.S1_s_a	LOC_Os03g09170	ethylene-responsive transcription factor, putative, expressed	**1.47**	up	**1.47**	down	**7.86**	up	**1.09**	down	**1.28**	up	**1.24**	down	ABA
OsAffx.12806.1.S1_x_a	LOC_Os03g10220	methyladenine glycosylase, putative	**1.19**	up	**1.25**	down	**2.34**	up	**1.28**	down	**1.52**	down	**1.47**	down	ABA
OsAffx.12855.1.S1_at	9631	---	**1.05**	down	**1.05**	down	**2.19**	up	**1.04**	down	**1.06**	down	**1.03**	down	ABA
OsAffx.12887.2.S1_at	LOC_Os03g16920	DnaK family protein, putative, expressed	**1.01**	down	**1.01**	down	**72.18**	up	**1.14**	up	**2.33**	up	**1.00**	down	2
OsAffx.12887.2.S1_s_a	LOC_Os03g16920	DnaK family protein, putative, expressed	**1.31**	down	**1.03**	up	**53.27**	up	**1.21**	up	**2.25**	up	**1.01**	down	2
OsAffx.12910.1.S1_at	LOC_Os03g18150	protein phosphatase 2C, putative, expressed	**1.03**	up	**1.11**	down	**2.81**	up	**1.07**	down	**1.06**	up	**1.19**	down	ABA
OsAffx.12915.1.S1_at	LOC_Os03g18300	chloroplast unusual positioning protein, putative, expressed	**1.25**	down	**1.07**	down	**5.47**	down	**1.36**	down	**1.07**	down	**1.90**	up	ABA
OsAffx.12920.1.S1_at	LOC_Os03g18490	RPGR, putative, expressed	**1.18**	up	**1.18**	up	**6.14**	up	**1.02**	down	**1.03**	up	**1.02**	down	ABA
OsAffx.12938.1.S1_at	LOC_Os03g19570	fip1 motif family protein, expressed	**1.18**	up	**1.08**	up	**2.36**	down	**1.00**	down	**1.13**	down	**1.12**	down	ABA
OsAffx.12954.1.S1_at	LOC_Os03g20680	late embryogenesis abundant protein 1, putative, expressed	**1.05**	down	**1.15**	down	**2.94**	up	**1.31**	down	**1.17**	down	**1.12**	down	ABA
OsAffx.12962.1.S1_at	LOC_Os03g21000	thioredoxin, putative, expressed	**1.04**	down	**1.42**	down	**2.70**	up	**1.08**	down	**1.06**	down	**1.07**	down	ABA
OsAffx.12986.1.S1_at	LOC_Os03g22200	nodulin MtN3 family protein, putative, expressed	**1.08**	up	**1.22**	up	**10.58**	up	**1.67**	down	**2.40**	up	**1.59**	up	2
OsAffx.13014.1.S1_s_a	LOC_Os03g25050	chaperonin, putative, expressed	**1.11**	down	**1.05**	down	**2.38**	down	**1.13**	down	**1.20**	down	**1.14**	down	ABA
OsAffx.13016.1.S1_at	LOC_Os03g25150	transposon protein, putative, unclassified, expressed	**1.22**	down	**2.29**	up	**2.54**	down	**1.11**	up	**3.02**	down	**1.39**	down	3
OsAffx.13016.1.S1_x_a	LOC_Os03g25150	transposon protein, putative, unclassified, expressed	**1.14**	down	**2.52**	up	**2.02**	down	**1.07**	up	**2.53**	down	**1.74**	down	3
OsAffx.13360.1.S1_at	LOC_Os03g45280	dehydrin, putative, expressed	**1.03**	up	**1.12**	down	**3.51**	up	**1.68**	down	**1.19**	down	**2.91**	down	2
OsAffx.13377.1.S1_at	LOC_Os03g46180	LTPL71 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.25**	up	**1.48**	up	**3.60**	up	**1.02**	down	**1.26**	up	**1.06**	up	ABA
OsAffx.13380.1.S1_at	LOC_Os03g46300	conserved hypothetical protein	**1.36**	up	**1.46**	up	**7.27**	down	**1.34**	down	**1.85**	down	**1.70**	down	ABA
OsAffx.13399.1.S1_at	LOC_Os03g48010	exostosin, putative, expressed	**1.03**	down	**1.05**	down	**2.93**	up	**1.06**	up	**1.12**	up	**1.01**	up	ABA
OsAffx.13423.1.S1_at	LOC_Os03g49485	expressed protein	**1.05**	up	**1.11**	up	**2.15**	down	**1.07**	down	**1.15**	down	**1.18**	down	ABA
OsAffx.13437.1.S1_at	LOC_Os03g50280	GLTP domain containing protein, putative, expressed	**1.26**	up	**1.32**	down	**1.75**	up	**1.18**	down	**1.10**	up	**2.36**	down	JA
OsAffx.13465.1.S1_at	LOC_Os03g52180	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, putative, expressed	**1.15**	down	**3.88**	up	**1.11**	down	**1.04**	down	**1.08**	down	**1.00**	up	BAP
OsAffx.13491.1.S1_at	LOC_Os03g55180	DUF1336 domain containing protein, expressed	**1.57**	up	**1.69**	up	**3.22**	down	**1.11**	up	**1.09**	down	**1.61**	up	ABA
OsAffx.13543.1.S1_s_a	LOC_Os03g58850	uncharacterized PE-PGRS family protein PE_PGRS3 precursor, putative, expressed	**1.23**	down	**1.15**	up	**6.83**	up	**1.21**	down	**1.73**	up	**1.16**	up	ABA
OsAffx.13553.1.S1_at	LOC_Os03g59670	basic helix-loop-helix, putative, expressed	**1.02**	down	**1.24**	up	**2.42**	down	**1.16**	up	**1.22**	down	**1.42**	up	ABA
OsAffx.13602.1.S1_at	LOC_Os03g60430	AP2 domain containing protein, expressed	**1.26**	up	**1.79**	down	**4.43**	down	**1.30**	down	**1.07**	down	**1.23**	up	ABA
OsAffx.13615.1.S1_at	LOC_Os04g01740	heat shock protein, putative, expressed	**1.03**	down	**1.02**	down	**1.02**	down	**1.00**	down	**2.45**	up	**1.11**	up	SA
OsAffx.13765.1.S1_at	LOC_Os04g11060	expressed protein	**1.83**	down	**2.34**	up	**11.87**	down	**2.15**	down	**11.74**	down	**11.38**	down	5
OsAffx.13902.1.S1_at	LOC_Os04g21130	F-box protein PP2-B1, putative, expressed	**1.16**	up	**1.01**	up	**2.42**	down	**1.72**	down	**1.10**	down	**1.06**	down	ABA
OsAffx.13941.1.S1_at	LOC_Os04g23580	xylosyltransferase, putative, expressed	**1.07**	up	**1.71**	down	**16.88**	up	**1.06**	down	**1.32**	up	**1.71**	up	ABA
OsAffx.13950.2.S1_x_a	LOC_Os04g24170	RNA recognition motif containing protein, putative, expressed	**1.09**	up	**1.09**	up	**2.28**	down	**1.13**	down	**1.38**	down	**1.16**	down	ABA
OsAffx.13951.2.S1_s_a	LOC_Os04g24310	retrotransposon protein, putative, unclassified	**1.14**	down	**2.05**	up	**1.04**	up	**1.06**	up	**1.13**	down	**8.92**	up	2
OsAffx.14027.1.S1_at	LOC_Os04g28850	RALFL36 - Rapid ALkalinization Factor RALF family protein precursor, expressed	**1.23**	down	**1.66**	up	**3.38**	down	**1.13**	up	**2.60**	up	**1.27**	up	2

OsAffx.14113.1.S1_at	LOC_Os04g33490	neutral/alkaline invertase, putative, expressed	**1.31**	up	**1.04**	down	**31.70**	up	**2.27**	up	**2.73**	up	**3.33**	up	4
OsAffx.14113.1.S1_s_a	LOC_Os04g33490	neutral/alkaline invertase, putative, expressed	**1.07**	down	**1.36**	down	**11.56**	up	**1.22**	up	**1.65**	up	**1.33**	up	ABA
OsAffx.14149.1.S1_at	LOC_Os04g35270	alpha-1,4-fucosyltransferase, putative, expressed	**1.12**	down	**1.06**	down	**8.70**	up	**1.06**	down	**1.11**	up	**1.07**	down	ABA
OsAffx.14165.1.S1_x_a	LOC_Os04g35750	expressed protein	**1.42**	down	**1.48**	down	**10.64**	down	**1.04**	down	**9.49**	down	**1.47**	down	2
OsAffx.14196.1.S1_at	LOC_Os04g38860	expressed protein	**1.73**	up	**2.26**	down	**2.43**	down	**1.25**	down	**1.19**	down	**1.67**	up	2
OsAffx.14201.1.S1_at	LOC_Os04g39360	heavy metal transport	**1.13**	down	**1.38**	down	**11.47**	down	**1.71**	up	**4.34**	down	**2.28**	up	3
OsAffx.14202.1.S1_at	LOC_Os04g39380	heavy metal transport/detoxification protein, putative, expressed	**1.20**	down	**1.58**	down	**4.88**	down	**1.84**	up	**1.95**	down	**1.39**	up	ABA
OsAffx.14231.1.S1_at	LOC_Os04g41400	peptide transporter PTR2, putative, expressed	**1.15**	down	**1.72**	up	**3.85**	down	**1.07**	up	**1.56**	down	**1.19**	up	ABA
OsAffx.14278.1.S1_at	LOC_Os04g45590	glyoxalase family protein, putative, expressed	**1.17**	up	**1.10**	down	**3.87**	up	**1.27**	up	**2.41**	up	**1.01**	up	2
OsAffx.14384.1.S1_at	LOC_Os04g52890	ATBAG1, putative, expressed	**1.12**	up	**1.03**	down	**2.20**	up	**1.11**	up	**1.33**	up	**1.11**	up	ABA
OsAffx.14425.1.S1_at	LOC_Os04g55200	coatomer subunit epsilon, putative, expressed	**1.01**	down	**1.00**	up	**8.75**	up	**1.00**	up	**1.03**	up	**1.02**	up	ABA
OsAffx.14430.1.S1_s_a	LOC_Os04g55980	glycine-rich RNA-binding, abscisic acid-inducible protein, putative	**1.17**	up	**1.34**	up	**1.29**	up	**2.86**	up	**4.99**	up	**1.17**	up	2
OsAffx.14448.1.S1_at	LOC_Os04g56930	glycosyl hydrolases, putative, expressed	**1.51**	down	**1.66**	down	**3.28**	down	**1.39**	up	**2.79**	up	**1.79**	down	2
OsAffx.14458.1.S1_x_a	LOC_Os04g57760	expressed protein	**2.19**	up	**1.82**	up	**4.92**	up	**1.10**	up	**1.31**	up	**1.96**	up	3
OsAffx.14464.1.S1_at	LOC_Os04g58070	aspartic proteinase nepenthesin precursor, putative, expressed	**1.00**	down	**1.01**	down	**3.62**	up	**1.01**	down	**1.01**	up	**1.01**	up	ABA
OsAffx.14473.1.S1_at	LOC_Os04g58740	expressed protein	**5.33**	up	**1.04**	up	**1.05**	down	**1.01**	down	**1.01**	down	**1.03**	up	IAA
OsAffx.14474.1.S1_at	LOC_Os04g58890	expressed protein	**1.55**	up	**1.07**	down	**2.94**	up	**1.19**	up	**1.63**	up	**1.62**	up	ABA
OsAffx.14519.1.S1_s_a	LOC_Os05g03070	transporter, putative, expressed	**1.02**	up	**1.18**	down	**3.24**	up	**1.11**	down	**1.06**	up	**1.30**	up	ABA
OsAffx.14523.1.S1_s_a	LOC_Os05g03130	OsRCI2-7 - Putative low temperature and salt responsive protein, expressed	**1.02**	up	**1.03**	up	**796.78**	up	**1.02**	down	**1.10**	down	**1.08**	down	ABA
OsAffx.14631.1.S1_at	LOC_Os05g11130	cytochrome P450, putative, expressed	**2.12**	down	**1.88**	down	**1.74**	down	**1.01**	down	**1.21**	down	**1.30**	down	IAA
OsAffx.14641.1.S1_at	LOC_Os05g11620	expressed protein	**3.32**	up	**1.83**	down	**36.19**	up	**1.00**	up	**1.02**	down	**1.02**	up	2
OsAffx.14656.1.S1_at	LOC_Os05g12320	nodulin MtN3 family protein, putative, expressed	**1.25**	up	**2.39**	down	**1.14**	down	**2.16**	down	**3.46**	down	**1.19**	down	3
OsAffx.14689.1.S1_at	LOC_Os05g14370	WRKY DNA-binding domain containing protein, expressed	**1.09**	up	**1.11**	up	**1.17**	down	**1.04**	up	**34.58**	up	**1.10**	down	SA
OsAffx.14759.1.S1_s_a	LOC_Os05g19270	MSH-like DNA mismatch repair protein, putative, expressed	**1.07**	down	**1.01**	down	**3.12**	down	**1.08**	down	**1.95**	down	**1.14**	down	ABA
OsAffx.14766.1.S1_at	LOC_Os05g20020	polygalacturonase, putative, expressed	**1.66**	down	**2.13**	down	**1.13**	up	**1.15**	down	**1.05**	down	**1.05**	down	BAP
OsAffx.14810.1.S1_at	LOC_Os05g24684	structural constituent of ribosome, putative, expressed	**1.15**	up	**1.21**	down	**2.73**	up	**1.14**	up	**1.62**	up	**1.47**	up	ABA
OsAffx.14929.1.S1_x_a	LOC_Os05g32810	expressed protein	**1.09**	up	**1.13**	up	**2.88**	down	**1.19**	down	**1.37**	down	**1.10**	down	ABA
OsAffx.14937.1.S1_at	LOC_Os05g33320	expressed protein	**1.32**	up	**1.05**	down	**2.98**	up	**1.23**	up	**2.15**	up	**1.07**	up	2
OsAffx.14981.1.S1_at	LOC_Os05g36050	serine/threonine-protein kinase, putative, expressed	**1.11**	down	**1.20**	up	**2.21**	down	**1.20**	down	**1.44**	down	**1.25**	down	ABA
OsAffx.14990.1.S1_at	LOC_Os05g37050	MYB family transcription factor, putative, expressed	**1.40**	down	**2.43**	up	**1.17**	down	**1.16**	up	**1.06**	up	**1.35**	up	BAP
OsAffx.14991.1.S1_at	LOC_Os05g37210	eukaryotic protein of unknown function DUF914 domain containing protein	**1.03**	down	**1.02**	down	**3.48**	up	**1.01**	up	**1.01**	down	**1.02**	up	ABA
OsAffx.15013.1.S1_at	LOC_Os05g38670	cation efflux family protein, putative	**1.04**	down	**1.00**	up	**4.92**	up	**1.09**	up	**1.01**	up	**1.02**	down	ABA
OsAffx.15019.1.S1_s_a	LOC_Os05g39060	expressed protein	**1.32**	up	**1.25**	down	**4.62**	up	**1.16**	down	**1.44**	up	**1.08**	up	ABA
OsAffx.15020.1.S1_at	LOC_Os05g39070	NLI interacting factor-like phosphatase, putative, expressed	**1.04**	up	**1.11**	down	**2.87**	up	**1.04**	up	**1.19**	up	**1.17**	up	ABA
OsAffx.15035.1.S1_at	LOC_Os05g40070	WRKY DNA-binding domain containing protein, expressed	**1.09**	up	**1.14**	down	**1.64**	down	**2.12**	up	**32.01**	up	**1.67**	down	2
OsAffx.15081.1.S1_at	LOC_Os05g43230	oryzain alpha chain precursor, putative, expressed	**1.15**	down	**1.13**	down	**1.14**	up	**1.02**	up	**1.16**	down	**2.05**	up	JA
OsAffx.15116.1.S1_at	LOC_Os05g45740	mitochondrial ATP synthase g subunit family protein, putative, expressed	**1.01**	up	**1.14**	up	**2.33**	down	**1.01**	up	**1.17**	down	**1.07**	down	ABA
OsAffx.15138.1.S1_at	LOC_Os05g47660	lipid phosphatase protein, putative, expressed	**1.04**	down	**1.17**	down	**2.46**	up	**1.13**	up	**1.11**	up	**1.43**	down	ABA
OsAffx.15154.1.S1_at	LOC_Os05g48650	transcription factor HBP-1b, putative, expressed	**1.22**	down	**1.06**	up	**40.14**	up	**1.69**	down	**2.26**	up	**1.46**	up	2
OsAffx.15155.1.S1_at	LOC_Os05g48730	hypothetical protein	**3.28**	up	**1.25**	down	**1.15**	down	**1.05**	up	**1.05**	up	**1.14**	down	IAA
OsAffx.15160.1.S1_at	LOC_Os05g48890	fasciclin domain containing protein, expressed	**2.61**	down	**1.19**	down	**4.86**	down	**1.37**	down	**2.45**	down	**1.50**	down	3
OsAffx.15160.1.S1_s_a	LOC_Os05g48890	fasciclin domain containing protein, expressed	**1.85**	down	**1.04**	up	**3.73**	down	**1.18**	down	**2.23**	down	**1.17**	down	2
OsAffx.15177.1.S1_at	LOC_Os05g50260	polygalacturonase, putative, expressed	**1.71**	down	**1.12**	up	**2.31**	up	**1.80**	up	**1.87**	down	**1.41**	down	ABA
OsAffx.15177.1.S1_x_a	LOC_Os05g50260	polygalacturonase, putative, expressed	**1.69**	down	**1.21**	up	**2.40**	up	**1.77**	up	**1.95**	down	**1.53**	down	ABA
OsAffx.15178.1.S1_s_a	AK241528	myb family transcription factor	**1.23**	up	**3.74**	up	**13.98**	down	**1.88**	down	**5.00**	down	**3.43**	down	4
OsAffx.15193.1.S1_at	LOC_Os05g51390	uncharacterized protein PA4923, putative, expressed	**3.29**	up	**1.06**	up	**1.83**	up	**1.14**	up	**2.29**	up	**1.49**	up	2
OsAffx.15279.1.S1_x_a	LOC_Os06g05860	6-phosphofructokinase, putative, expressed	**1.00**	up	**1.24**	down	**2.58**	down	**1.16**	up	**1.48**	down	**1.10**	down	ABA
OsAffx.15312.1.S1_at	LOC_Os06g08540	formin-like protein 13, putative, expressed	**1.08**	up	**1.16**	down	**3.64**	down	**1.19**	up	**1.01**	down	**1.14**	down	ABA
OsAffx.15319.1.S1_at	LOC_Os06g08830	UDP-glucoronosyl and UDP-glucosyl transferase, putative, expressed	**1.41**	down	**2.67**	up	**9.25**	down	**1.09**	down	**1.57**	down	**1.33**	down	2
OsAffx.15384.1.S1_at	LOC_Os06g12290	glutathione S-transferase GSTU6, putative	**1.07**	up	**1.03**	up	**30.63**	up	**1.01**	down	**1.28**	up	**1.02**	down	ABA
OsAffx.15391.1.S1_at	LOC_Os06g12500	membrane associated DUF588 domain containing protein, putative, expressed	**9.93**	up	**6.01**	up	**1.08**	down	**1.02**	down	**1.02**	down	**1.01**	up	2
OsAffx.15442.1.S1_at	LOC_Os06g15600	plastocyanin-like domain containing protein, putative, expressed	**3.18**	up	**1.12**	down	**1.02**	down	**2.23**	down	**1.23**	up	**1.47**	down	2
OsAffx.15474.1.S1_s_a	LOC_Os06g17450	expressed protein	**1.46**	up	**1.34**	up	**5.41**	up	**1.05**	down	**1.04**	down	**1.06**	down	ABA
OsAffx.15484.1.S1_at	LOC_Os06g18820	serine threonine kinase, putative, expressed	**1.00**	up	**1.02**	up	**3.21**	up	**1.02**	down	**1.03**	up	**1.28**	up	ABA
OsAffx.15485.1.S1_at	LOC_Os06g18900	cadmium tolerance factor, putative, expressed	**1.06**	up	**1.09**	down	**4.80**	down	**1.30**	up	**1.18**	down	**1.22**	up	ABA

OsAffx.15523.1.S1_at	LOC_Os06g20610	seven in absentia protein family domain containing protein, expressed	1.12	up	1.23	down	3.34	up	1.08	up	1.12	up	1.03	up	ABA
OsAffx.15533.1.S1_at	LOC_Os06g21140	glycine-rich cell wall structural protein precursor, putative, expressed	1.08	down	1.47	up	1.79	down	1.70	down	2.32	down	1.77	down	SA
OsAffx.15538.1.S1_at	LOC_Os06g21570	Os6bglu24 - beta-glucosidase homologue, similar to G. max isohydroxyurate hydrolase	1.45	up	1.40	up	25.70	down	1.46	down	24.46	down	23.37	down	3
OsAffx.15562.1.S1_s_a	LOC_Os06g22870	OsIAA21 - Auxin-responsive Aux/IAA gene family member, expressed	1.33	up	1.32	down	2.05	down	1.35	down	1.41	down	1.19	down	ABA
OsAffx.15898.1.S1_s_a	LOC_Os06g42700	zinc finger, C3HC4 type domain containing protein, expressed	1.11	up	1.09	up	2.03	up	1.07	up	1.08	up	1.02	up	ABA
OsAffx.15903.1.S1_s_a	LOC_Os06g43044	GDSL-like lipase/acylhydrolase, putative, expressed	1.14	down	1.41	down	2.57	down	1.38	down	1.80	down	1.06	down	ABA
OsAffx.15908.1.S1_x_a	LOC_Os06g43410	cytochrome P450, putative, expressed	1.01	down	1.00	down	2.36	up	1.00	down	1.02	up	1.00	up	ABA
OsAffx.15951.1.S1_at	LOC_Os06g46350	PLA IIIA/PLP7, putative, expressed	1.25	up	1.40	up	3.73	up	1.78	down	1.04	up	1.47	up	ABA
OsAffx.16008.1.S1_at	LOC_Os06g50420	plastocyanin-like domain containing protein, putative, expressed	2.05	up	1.49	down	4.10	down	1.04	down	2.46	up	1.04	down	3
OsAffx.16059.1.S1_at	LOC_Os07g03120	expressed protein	1.04	up	1.91	down	6.76	up	1.39	down	1.31	up	2.49	up	2
OsAffx.16082.1.S1_at	LOC_Os07g04560	no apical meristem protein, putative	1.76	up	3.79	up	1.65	up	1.60	down	1.96	up	1.07	up	BAP
OsAffx.16108.1.S1_at	LOC_Os07g05740	receptor-like protein kinase 2 precursor, putative, expressed	1.15	down	1.21	down	2.95	down	1.15	down	1.01	down	1.19	up	ABA
OsAffx.16154.1.S1_at	LOC_Os07g08320	RNA recognition motif containing protein, expressed	1.00	down	1.02	down	3.04	up	1.01	up	1.01	up	1.02	up	ABA
OsAffx.16482.1.S1_at	LOC_Os07g29750	glycosyl hydrolases family 16, putative, expressed	1.56	up	1.02	up	5.02	down	1.03	down	1.22	up	1.95	up	ABA
OsAffx.16482.1.S1_x_a	LOC_Os07g29750	glycosyl hydrolases family 16, putative, expressed	1.42	up	1.13	up	5.84	down	1.18	down	1.12	down	1.53	up	ABA
OsAffx.16631.1.S1_at	LOC_Os07g39210	expressed protein	1.50	up	1.11	down	3.80	down	1.16	up	1.45	down	1.49	down	ABA
OsAffx.16669.1.S1_at	LOC_Os07g41160	protein of unknown function DUF1675 domain containing protein, expressed	1.92	up	1.93	up	40.79	up	1.05	up	1.05	up	1.07	down	ABA
OsAffx.16677.1.S1_at	LOC_Os07g41600	proline-rich protein, putative, expressed	1.10	up	1.07	down	3.36	up	1.15	down	1.61	up	2.18	up	2
OsAffx.16682.1.S1_at	LOC_Os07g42220	expressed protein	1.02	down	1.02	down	3.11	up	1.10	up	1.70	up	1.03	up	ABA
OsAffx.16693.1.S1_x_a	LOC_Os07g43322	expressed protein	1.25	up	1.08	up	2.03	up	1.07	up	1.06	up	1.12	up	ABA
OsAffx.16695.1.S1_s_a	LOC_Os07g43440	expressed protein	1.02	down	1.00	down	7.03	up	1.00	up	1.03	down	1.02	down	ABA
OsAffx.16697.1.S1_at	LOC_Os07g43540	ORC6 - Putative origin recognition complex subunit 6, expressed	1.36	down	1.01	up	6.48	down	1.15	down	2.09	down	1.98	down	3
OsAffx.16752.1.S1_at	LOC_Os07g47540	DUF567 domain containing protein, putative, expressed	1.12	down	1.56	down	1.54	down	1.08	up	1.09	up	13.98	up	JA
OsAffx.16767.1.S1_at	LOC_Os07g48890	expressed protein	1.35	down	1.21	down	2.50	up	1.01	up	1.25	up	1.13	down	ABA
OsAffx.16767.2.S1_x_a	LOC_Os07g48890	expressed protein	1.13	down	1.01	up	2.72	up	1.01	down	1.03	up	1.03	up	ABA
OsAffx.16770.1.S1_at	LOC_Os07g49390	P-protein, putative, expressed	1.06	down	1.13	down	1.38	down	1.17	up	1.02	up	2.49	up	JA
OsAffx.16770.1.S1_x_a	LOC_Os07g49390	P-protein, putative, expressed	1.08	up	1.05	down	1.49	down	1.08	up	1.01	up	2.32	up	JA
OsAffx.16772.1.S1_at	LOC_Os08g01190	ATOFP18/OFP18, putative, expressed	1.08	down	3.78	up	1.11	down	1.01	down	1.14	up	1.00	up	BAP
OsAffx.16792.1.S1_at	LOC_Os08g02500	ACT domain containing protein, putative	2.14	up	1.50	down	1.43	up	1.43	down	1.28	up	1.04	down	IAA
OsAffx.16875.1.S1_x_a	LOC_Os08g07390	mla1, putative, expressed	1.08	down	1.13	down	4.62	up	1.01	down	1.18	up	1.01	up	ABA
OsAffx.16911.1.S1_at	LOC_Os08g09240	autophagy-related protein, putative, expressed	1.13	down	1.09	down	2.03	up	1.04	down	1.04	up	1.07	down	ABA
OsAffx.17113.1.S1_at	LOC_Os08g23290	serine/threonine-protein kinase BRI1-like 2 precursor, putative	2.00	up	1.98	down	1.15	down	1.02	up	1.34	up	1.17	up	IAA
OsAffx.17216.1.S1_at	LOC_Os08g28880	patatin, putative, expressed	1.37	up	1.24	up	1.56	down	1.29	up	1.23	up	3.50	up	JA
OsAffx.17267.1.S1_at	LOC_Os08g31280	DC1, putative, expressed	1.00	up	1.02	down	1.02	down	1.17	up	10.71	up	1.03	up	SA
OsAffx.17347.1.S1_at	LOC_Os08g35470	exo70 exocyst complex subunit, putative, expressed	1.06	down	1.18	down	3.14	up	1.19	up	1.06	up	1.08	up	ABA
OsAffx.17364.1.S1_at	LOC_Os08g36820	expressed protein	2.85	up	1.02	down	1.01	down	1.02	down	1.04	down	1.00	up	IAA
OsAffx.17366.1.S1_at	LOC_Os08g36920	AP2 domain containing protein, expressed	1.29	down	1.01	down	39.15	up	1.17	down	3.38	up	1.02	up	2
OsAffx.17389.1.S1_s_a	LOC_Os08g37930	beta-expansin precursor, putative, expressed	1.97	down	1.46	up	4.42	down	1.46	down	1.08	down	1.14	down	ABA
OsAffx.17457.1.S1_at	LOC_Os08g41420	expressed protein	1.00	down	1.46	down	3.97	up	1.08	up	1.34	up	1.01	up	ABA
OsAffx.17463.1.S1_at	LOC_Os08g41750	OsFBX303 - F-box domain containing protein, expressed	1.01	down	1.00	up	3.23	up	1.02	up	1.00	up	1.03	up	ABA
OsAffx.17468.1.S1_s_a	LOC_Os08g42080	ACR5, putative, expressed	2.46	down	3.38	up	4.61	down	1.30	up	1.81	down	1.51	down	3
OsAffx.17505.1.S1_at	LOC_Os08g43770	carrier, putative	5.15	up	1.39	down	1.41	down	1.41	down	1.34	down	1.40	down	IAA
OsAffx.17506.1.S1_at	LOC_Os08g43900	carrier, putative, expressed	2.05	up	1.02	down	1.04	down	1.01	down	1.01	down	1.01	up	IAA
OsAffx.17516.1.S1_at	LOC_Os08g44940	DUF260 domain containing protein, putative, expressed	9.15	up	1.49	down	1.42	down	1.13	down	1.42	down	2.75	down	2
OsAffx.17894.1.S1_at	LOC_Os09g25650	GEX2, putative, expressed	1.01	down	1.00	up	2.21	up	1.01	up	1.03	up	1.02	up	ABA
OsAffx.17906.1.S1_x_a	LOC_Os09g26210	ZOS9-12 - C2H2 zinc finger protein, expressed	1.58	down	1.22	up	1.90	down	2.56	down	1.03	down	2.51	up	2
OsAffx.17922.1.S1_x_a	LOC_Os01g59250	expressed protein	2.10	up	2.73	up	6.59	down	1.04	up	1.32	down	1.21	down	3
OsAffx.17972.1.S1_at	LOC_Os09g31270	polygalacturonase, putative, expressed	1.21	down	1.00	down	6.99	up	1.04	up	1.26	up	1.21	up	ABA
OsAffx.17976.1.S1_at	LOC_Os09g31410	Os9bglu29 - beta-glucosidase homologue, similar to Os4bglu12 exoglucanase, express	1.68	down	1.22	up	5.00	down	1.71	down	2.24	down	1.32	down	2
OsAffx.18005.1.S1_at	LOC_Os09g36070	cytochrome P450, putative	1.20	down	1.04	up	4.34	down	1.04	down	3.31	down	3.20	down	3
OsAffx.18042.1.S1_at	LOC_Os09g38100	phosphate carrier protein, mitochondrial precursor, putative, expressed	2.56	up	1.65	up	2.03	up	1.05	up	2.87	up	1.54	up	3
OsAffx.18050.2.S1_at	LOC_Os02g56370	OsWAK20 - OsWAK receptor-like protein kinase, expressed	1.05	up	1.02	down	6.23	down	1.88	up	1.30	down	1.11	down	ABA
OsAffx.18298.1.S1_at	LOC_Os10g19160	receptor kinase, putative, expressed	1.03	down	1.00	up	34.46	up	1.03	down	1.01	down	1.00	up	ABA
OsAffx.18396.1.S1_at	LOC_Os10g25450	OsSub60 - Putative Subtilisin homologue, expressed	1.11	down	1.45	down	3.46	down	1.07	down	1.46	down	1.01	up	ABA
OsAffx.18575.1.S1_x_a	LOC_Os10g39140	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	1.02	up	1.10	down	3.06	down	1.28	up	1.23	up	1.54	up	ABA

OsAffx.18586.1.S1_at	LOC_Os10g40020	oxidoreductase, short chain dehydrogenase/reductase family domain containing family,	1.17	down	1.09	down	3.78	up	1.28	down	1.30	up	1.12	up	ABA
OsAffx.18589.1.S1_s_a	LOC_Os10g40480	LTPL143 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.17	down	1.59	up	1.12	up	1.15	up	1.78	down	5.08	down	JA
OsAffx.18681.1.S1_s_a	LOC_Os11g05170	expressed protein	1.90	up	2.33	up	13.13	up	1.29	up	3.39	up	1.07	down	3
OsAffx.18737.1.S1_at	LOC_Os11g07911	expressed protein	1.03	down	1.09	down	714.33	up	1.06	down	1.71	up	1.13	down	ABA
OsAffx.18758.1.S1_at	LOC_Os11g09110	receptor-like protein kinase 5 precursor, putative	1.00	up	1.00	up	4.16	up	1.01	up	1.22	up	1.02	up	ABA
OsAffx.18836.1.S1_at	LOC_Os11g13890	chlorophyll A-B binding protein, putative, expressed	1.34	down	1.43	down	11.49	down	2.01	down	1.75	down	2.16	down	3
OsAffx.1887.1.S1_x_at	LOC_Os10g39470	expressed protein	1.54	up	1.53	down	2.14	up	2.05	down	1.50	up	1.34	down	2
OsAffx.19111.1.S1_s_a	LOC_Os11g31900	acyl carrier protein, putative, expressed	1.05	up	1.02	up	3.16	down	1.09	down	1.43	down	1.21	down	ABA
OsAffx.19165.1.S1_at	LOC_Os11g35040	aminotransferase, classes I and II, domain containing protein, expressed	2.25	up	3.62	up	2.51	up	1.37	up	8.64	up	4.31	up	5
OsAffx.19171.1.S1_s_a	LOC_Os11g35274	protein kinase domain containing protein, expressed	1.08	down	1.34	down	4.31	down	1.14	down	1.15	down	1.18	up	ABA
OsAffx.193.1.S1_x_at	LOC_Os10g25020	red chlorophyll catabolite reductase, putative	1.09	up	1.02	down	4.40	up	1.01	up	1.20	up	1.09	up	ABA
OsAffx.19332.1.S1_at	LOC_Os11g42430	transporter family protein, putative, expressed	2.72	down	1.53	down	24.44	down	1.89	down	2.39	down	5.35	up	4
OsAffx.19357.1.S1_at	LOC_Os11g43790	DUF581 domain containing protein, expressed	1.00	down	1.00	down	237.39	up	1.00	up	1.00	up	1.02	up	ABA
OsAffx.19438.1.S1_at	LOC_Os11g01030	conserved hypothetical protein	1.79	down	6.02	down	1.11	down	1.06	down	1.07	down	1.06	down	BAP
OsAffx.19451.3.S1_x_a	LOC_Os02g13190	F-box family protein, putative, expressed	1.05	down	1.06	up	2.39	down	1.06	up	1.40	down	1.03	down	ABA
OsAffx.19478.1.S1_at	LOC_Os11g04150	major facilitator superfamily antiporter, putative, expressed	1.06	down	2.23	up	4.57	up	1.62	down	1.01	down	1.04	down	2
OsAffx.19515.1.S1_s_a	LOC_Os12g06080	hypothetical protein	2.93	up	1.33	up	1.62	up	2.53	down	1.08	down	1.57	up	2
OsAffx.19632.1.S1_at	LOC_Os12g12590	NADP-dependent oxidoreductase, putative, expressed	2.12	up	1.19	down	1.14	down	1.28	down	1.17	up	1.34	up	IAA
OsAffx.19633.1.S1_at	LOC_Os12g12600	dirigent, putative, expressed	4.37	down	1.47	down	33.99	down	10.26	down	18.00	down	3.84	up	5
OsAffx.19635.1.S1_at	LOC_Os12g12720	jasmonate-induced protein, putative, expressed	1.16	down	1.47	down	3.79	down	1.66	down	4.33	down	20.27	up	3
OsAffx.19698.1.S1_at	LOC_Os12g15920	laccase precursor protein, putative, expressed	3.92	down	1.10	up	4.67	down	1.45	down	4.20	down	1.92	down	3
OsAffx.19817.2.S1_at	LOC_Os01g69010	MATE efflux protein, putative	1.15	up	1.01	up	7.52	up	1.00	down	1.00	down	1.01	up	ABA
OsAffx.19841.1.S1_at	LOC_Os12g26880	plastocyanin-like domain containing protein, putative, expressed	1.07	down	1.01	up	2.59	down	1.46	down	2.19	down	1.15	up	2
OsAffx.20067.1.S1_s_a	LOC_Os12g41090	CAMK_KIN1/SNF1/Nim1_like.38 - CAMK includes calcium/calmodulin depedent protein	1.87	down	1.07	down	2.56	down	1.20	down	1.12	down	1.68	down	ABA
OsAffx.20100.1.S1_x_a	LOC_Os03g05410	hypothetical protein	1.01	down	1.02	up	6.04	up	1.03	up	1.02	up	1.01	up	ABA
OsAffx.20100.2.S1_x_a	LOC_Os04g33120	retrotransposon protein, putative, unclassified	1.01	up	1.01	up	4.53	up	1.04	up	1.01	down	1.03	up	ABA
OsAffx.20109.1.S1_at	LOC_Os12g43820	GCRP5 - Glycine and cysteine rich family protein precursor, expressed	1.01	down	1.01	up	2.25	up	1.01	down	1.01	up	1.05	down	ABA
OsAffx.20116.1.S1_at	LOC_Os12g44290	cytochrome P450, putative, expressed	1.09	down	1.07	down	1.02	down	1.01	up	1.50	up	12.76	up	JA
OsAffx.20132.1.S1_at	9638	---	1.20	up	1.18	up	11.96	up	1.03	up	1.00	down	1.12	up	ABA
OsAffx.20242.2.S1_at	LOC_Os10g34040	nodulin, putative, expressed	1.03	down	1.02	down	1.01	down	3.96	up	1.19	up	1.02	up	ACC
OsAffx.20285.2.S1_at	LOC_Os05g43530	CSLC7 - cellulose synthase-like family C, expressed	1.02	up	1.07	down	2.19	down	1.18	down	1.19	down	1.41	up	ABA
OsAffx.20360.1.S1_x_a	LOC_Os10g26410	bHLH family protein, putative, expressed	11.70	up	1.32	up	1.31	down	1.10	down	1.09	down	1.09	down	IAA
OsAffx.2070.2.S1_at	LOC_Os01g23850	transposon protein, putative, CACTA, En/Spm sub-class, expressed	1.34	down	1.19	down	3.01	down	1.00	up	1.17	down	1.47	down	ABA
OsAffx.20724.2.S1_s_a	LOC_Os10g07010	3-ketoacyl-CoA synthase, putative, expressed	1.83	down	1.16	down	3.71	up	1.33	up	1.54	up	5.96	up	2
OsAffx.20736.2.S1_at	LOC_Os01g73100	retrotransposon protein, putative, unclassified	1.03	up	1.00	up	2.21	up	1.02	up	1.02	up	1.05	up	ABA
OsAffx.21062.1.S1_at	NM_001053028	Oryza sativa (japonica cultivar-group) Os02g0263300 (Os02g0263300) mRNA, comple	1.01	down	1.01	down	2.24	up	1.00	up	1.00	down	1.04	up	ABA
OsAffx.21077.1.S1_at	NM_194147	---	1.34	down	2.01	up	4.08	down	1.40	down	3.92	down	3.76	down	4
OsAffx.21102.2.S1_x_a	LOC_Os01g25660	hypothetical protein	1.03	up	1.12	up	1.66	down	1.13	up	1.35	down	2.19	up	JA
OsAffx.21410.1.S1_x_a	LOC_Os01g40560	hypersensitive-induced response protein, putative, expressed	1.71	down	1.59	down	6.54	down	1.74	up	6.43	down	5.86	down	3
OsAffx.21591.1.S1_at	LOC_Os01g56660	expressed protein	3.42	up	1.09	down	1.03	down	1.00	down	1.00	down	1.05	up	IAA
OsAffx.21616.1.S1_s_a	LOC_Os01g54890	ethylene-responsive transcription factor 2, putative, expressed	2.26	up	1.40	down	1.98	up	1.38	up	3.45	up	1.54	up	3
OsAffx.2170.1.S1_s_at	LOC_Os01g36880	hypothetical protein	2.46	up	1.02	down	1.13	down	1.08	up	1.02	down	1.01	down	IAA
OsAffx.2171.1.S1_at	LOC_Os01g36950	N-rich protein, putative, expressed	2.27	up	1.14	down	4.51	up	1.04	down	2.54	up	1.61	up	3
OsAffx.21742.2.S1_at	LOC_Os01g62780	hypothetical protein	1.07	up	1.18	up	2.10	up	1.36	up	1.24	up	1.54	up	ABA
OsAffx.21844.1.S1_at	LOC_Os01g70150	hypothetical protein	1.01	down	1.00	up	1.02	down	1.00	up	1.23	up	16.57	up	JA
OsAffx.21963.1.S1_s_a	LOC_Os01g19770	mitochondrial import inner membrane translocase subunit Tim17, putative, expressed	1.01	down	1.00	up	323.85	up	1.00	down	1.00	up	1.03	up	ABA
OsAffx.21988.1.S1_at	LOC_Os08g06190	berberine and berberine like domain containing protein, expressed	1.08	down	1.27	down	2.60	up	1.05	down	2.31	up	1.41	down	2
OsAffx.22181.1.S1_s_a	LOC_Os01g17050	VQ domain containing protein, putative, expressed	1.04	down	1.05	down	2.96	down	1.25	down	1.30	down	1.66	down	ABA
OsAffx.22225.2.S1_at	LOC_Os01g14990	GCRP6 - Glycine and cysteine rich family protein precursor, putative, expressed	1.01	down	1.00	up	6.38	up	1.00	down	1.00	up	1.00	up	ABA
OsAffx.22225.2.S1_s_a	LOC_Os01g14990	GCRP6 - Glycine and cysteine rich family protein precursor, putative, expressed	1.01	down	1.00	up	9.64	up	1.00	down	1.01	up	1.01	up	ABA
OsAffx.22469.1.S1_x_a	LOC_Os07g07040	erythrocyte binding protein 3, putative, expressed	1.09	down	1.22	down	14.83	up	1.01	down	1.13	up	1.24	up	ABA
OsAffx.22529.1.S1_s_a	LOC_Os07g46830	sex determination protein tasselseed-2, putative, expressed	1.01	down	5.11	up	1.03	down	1.00	up	1.00	down	1.01	up	BAP
OsAffx.22569.1.S1_x_a	LOC_Os06g07914	hydroxylase, putative, expressed	1.01	down	2.21	up	1.01	down	1.00	up	1.00	down	1.01	up	BAP
OsAffx.22569.2.S1_x_a	LOC_Os06g07914	hydroxylase, putative, expressed	1.01	up	3.95	up	1.11	down	1.08	down	1.11	down	1.06	down	BAP
OsAffx.22584.1.S1_at	LOC_Os06g06390	NBS-LRR type disease resistance protein, putative, expressed	1.00	down	1.01	down	2.05	up	1.00	down	1.12	up	1.01	up	ABA

OsAffx.22650.1.S1_x_a	LOC_Os03g61480	uncharacterized Cys-rich domain containing protein, putative	**1.28**	up	**1.23**	up	**2.17**	down	**1.48**	up	**1.10**	down	**1.65**	up	ABA
OsAffx.22650.2.S1_x_a	LOC_Os03g61470	uncharacterized Cys-rich domain containing protein, putative, expressed	**1.28**	up	**1.48**	up	**2.23**	down	**1.71**	up	**1.09**	down	**1.05**	up	ABA
OsAffx.22754.1.S1_s_a	LOC_Os01g07410	growth regulator related protein, putative, expressed	**1.06**	down	**1.58**	up	**2.21**	down	**1.17**	down	**1.43**	down	**1.13**	down	ABA
OsAffx.22754.1.S1_x_a	LOC_Os01g07410	growth regulator related protein, putative, expressed	**1.17**	down	**1.37**	up	**2.33**	down	**1.10**	down	**1.43**	down	**1.00**	up	ABA
OsAffx.2280.1.S1_at	LOC_Os01g49280	zinc finger family protein, putative, expressed	**1.09**	down	**1.30**	down	**4.89**	up	**1.41**	down	**1.10**	down	**1.00**	down	ABA
OsAffx.23005.1.S1_x_a	AK108349	Oryza sativa Japonica Group cDNA clone:002-142-B10, full insert sequence.	**2.19**	up	**1.01**	up	**2.93**	down	**1.12**	up	**1.04**	down	**1.14**	down	2
OsAffx.2304.1.S1_s_at	LOC_Os01g51780	auxin efflux carrier component, putative, expressed	**3.17**	up	**1.07**	down	**1.02**	down	**1.07**	up	**1.00**	down	**1.01**	up	IAA
OsAffx.23051.1.S1_x_a	LOC_Os01g02000	phosphate transporter 1, putative, expressed	**1.03**	down	**1.19**	up	**2.65**	up	**1.39**	down	**1.34**	down	**1.42**	down	ABA
OsAffx.23090.1.S1_x_a	AK243318	receptor serine/threonine kinase, putative	**1.25**	up	**1.10**	up	**2.84**	up	**1.08**	down	**1.71**	up	**1.34**	up	ABA
OsAffx.23090.4.S1_x_a	LOC_Os01g02460	receptor kinase LRK10, putative	**1.10**	up	**1.05**	down	**2.35**	up	**1.02**	down	**1.40**	up	**1.28**	up	ABA
OsAffx.2315.1.S1_at	LOC_Os01g52540	B3 DNA binding domain containing protein, expressed	**1.09**	down	**1.02**	up	**2.28**	up	**1.23**	up	**1.06**	up	**1.02**	up	ABA
OsAffx.23156.1.S1_at	LOC_Os01g07800	thiol-disulphide oxidoreductase DCC, putative, expressed	**1.04**	up	**1.28**	down	**2.09**	up	**1.14**	down	**1.08**	up	**1.00**	down	ABA
OsAffx.23175.1.S1_x_a	LOC_Os01g09880	harpin-induced protein 1 domain containing protein, expressed	**1.05**	up	**1.12**	down	**2.31**	down	**1.23**	down	**1.76**	down	**1.36**	up	ABA
OsAffx.23225.1.S1_at	LOC_Os01g13425	expressed protein	**1.03**	down	**1.09**	down	**9.80**	up	**1.20**	up	**1.40**	up	**1.09**	up	ABA
OsAffx.23248.1.S1_at	LOC_Os01g14710	conserved hypothetical protein	**2.66**	down	**1.51**	down	**8.95**	down	**1.15**	up	**2.22**	down	**4.14**	down	4
OsAffx.2326.1.S1_x_at	LOC_Os01g53800	glutamate carboxypeptidase 2, putative, expressed	**1.48**	down	**1.79**	down	**3.24**	down	**1.24**	down	**1.96**	down	**1.69**	down	ABA
OsAffx.2326.2.S1_at	LOC_Os01g53800	glutamate carboxypeptidase 2, putative, expressed	**1.36**	down	**1.34**	down	**2.06**	down	**1.25**	down	**1.40**	down	**1.24**	down	ABA
OsAffx.23292.1.S1_at	LOC_Os01g18584	OsWRKY9 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**2.32**	down	**1.43**	down	**1.30**	up	**1.07**	up	**1.14**	up	**1.37**	up	IAA
OsAffx.2348.1.S1_at	LOC_Os01g57050	expressed protein	**1.10**	up	**1.84**	up	**1.64**	down	**1.56**	down	**2.22**	down	**1.18**	down	SA
OsAffx.23482.1.S1_x_a	LOC_Os01g32980	mitochondrial carrier protein, putative, expressed	**1.09**	up	**1.00**	down	**2.65**	up	**1.07**	up	**1.06**	down	**1.26**	up	ABA
OsAffx.23482.2.S1_at	LOC_Os01g32980	mitochondrial carrier protein, putative, expressed	**1.21**	up	**1.06**	up	**2.27**	up	**1.03**	down	**1.09**	up	**1.06**	down	ABA
OsAffx.23594.1.S1_at	LOC_Os01g40094	protein phosphatase 2C, putative, expressed	**1.52**	up	**1.60**	down	**31.38**	up	**2.06**	down	**2.69**	up	**1.08**	up	3
OsAffx.23595.1.S1_at	LOC_Os01g40094	protein phosphatase 2C, putative, expressed	**1.04**	up	**1.05**	down	**4.79**	up	**1.02**	up	**1.01**	down	**1.05**	up	ABA
OsAffx.2361.1.S1_x_at	LOC_Os01g58850	circadian clock coupling factor-related, putative, expressed	**1.00**	down	**1.01**	down	**9.80**	up	**1.01**	down	**1.10**	up	**1.05**	up	ABA
OsAffx.2362.1.S1_at	LOC_Os01g59000	cytochrome P450, putative, expressed	**1.07**	down	**1.12**	up	**3.09**	up	**1.32**	down	**2.18**	up	**1.94**	up	2
OsAffx.2362.1.S1_s_at	LOC_Os01g59000	cytochrome P450, putative, expressed	**1.07**	up	**1.77**	up	**2.12**	up	**1.23**	down	**1.41**	up	**1.10**	down	ABA
OsAffx.23652.1.S1_at	LOC_Os01g43890	OsSCP4 - Putative Serine Carboxypeptidase homologue, expressed	**4.29**	up	**1.23**	up	**3.22**	down	**1.02**	up	**3.21**	up	**1.84**	up	3
OsAffx.23673.1.S1_at	LOC_Os01g45670	expressed protein	**1.72**	down	**1.23**	down	**2.49**	up	**1.15**	up	**1.01**	down	**1.38**	up	ABA
OsAffx.23718.2.S1_x_a	LOC_Os05g48330	aspartyl protease family protein, putative, expressed	**1.04**	up	**1.59**	up	**5.91**	up	**1.17**	up	**1.17**	up	**1.41**	down	ABA
OsAffx.23744.1.S1_s_a	LOC_Os01g51310	expressed protein	**1.50**	down	**1.26**	down	**12.80**	up	**1.03**	up	**1.23**	down	**1.22**	down	ABA
OsAffx.23754.1.S1_x_a	LOC_Os01g51870	methyltransferase, putative, expressed	**1.03**	down	**1.01**	down	**2.12**	up	**1.02**	down	**5.22**	up	**1.74**	up	2
OsAffx.23787.2.S1_at	LOC_Os01g54360	hypothetical protein	**1.13**	down	**1.21**	down	**1.05**	down	**1.02**	down	**1.02**	down	**3.04**	up	JA
OsAffx.23810.1.S1_at	LOC_Os01g56560	cyclase/dehydrase family protein, expressed	**1.19**	up	**1.03**	down	**2.99**	up	**1.09**	up	**1.44**	up	**1.44**	up	ABA
OsAffx.23819.1.S1_at	LOC_Os01g57370	cyclic nucleotide-gated ion channel 2, putative, expressed	**1.04**	up	**1.05**	up	**2.24**	up	**1.01**	up	**1.03**	up	**1.16**	up	ABA
OsAffx.23927.2.S1_at	LOC_Os01g65550	RNA recognition motif containing protein, putative, expressed	**1.17**	up	**1.06**	down	**2.07**	down	**1.10**	down	**1.47**	down	**1.13**	up	ABA
OsAffx.23951.1.S1_x_a	LOC_Os01g67100	expressed protein	**1.18**	down	**1.07**	down	**4.08**	down	**1.28**	down	**2.33**	down	**1.50**	down	2
OsAffx.23951.3.S1_x_a	LOC_Os01g67100	expressed protein	**1.24**	down	**1.10**	down	**9.77**	down	**1.06**	up	**2.46**	down	**1.55**	down	2
OsAffx.23978.1.S1_at	LOC_Os01g68960	conserved hypothetical protein	**1.01**	down	**1.00**	up	**2.75**	up	**1.07**	up	**1.10**	up	**1.05**	up	ABA
OsAffx.24050.1.S1_at	LOC_Os02g01700	RNA recognition motif containing protein, putative	**1.13**	down	**1.19**	up	**4.00**	up	**1.07**	up	**1.08**	down	**1.43**	down	ABA
OsAffx.24089.1.S1_x_a	LOC_Os02g03870	periplasmic beta-glucosidase precursor, putative, expressed	**1.82**	down	**1.00**	up	**3.69**	down	**1.31**	down	**2.19**	down	**1.23**	down	2
OsAffx.24138.1.S1_s_a	AK242133	Oryza sativa Japonica Group cDNA, clone: J075149F15, full insert sequence.	**1.43**	up	**2.42**	down	**9.56**	up	**1.03**	down	**1.11**	down	**1.12**	up	2
OsAffx.24153.1.S1_s_a	LOC_Os02g07690	VQ domain containing protein, putative, expressed	**1.81**	up	**1.27**	up	**2.09**	up	**1.16**	up	**1.17**	up	**1.44**	up	ABA
OsAffx.24157.1.S1_s_a	LOC_Os02g07930	B-box zinc finger family protein, putative, expressed	**1.08**	up	**1.05**	down	**3.67**	up	**2.01**	up	**1.13**	down	**1.13**	down	2
OsAffx.24166.1.S1_at	LOC_Os02g08440	OsWRKY71 - Superfamily of TFs having WRKY and zinc finger domains, expressed	**1.40**	up	**1.20**	up	**1.09**	down	**1.15**	up	**1.01**	down	**2.32**	up	JA
OsAffx.24189.1.S1_at	LOC_Os02g10730	expressed protein	**1.47**	up	**1.22**	down	**2.51**	up	**1.27**	up	**1.48**	up	**1.06**	up	ABA
OsAffx.24237.1.S1_x_a	LOC_Os06g35900	BES1/BZR1 homolog protein, putative, expressed	**2.32**	up	**1.16**	down	**1.30**	up	**1.14**	down	**1.18**	up	**1.37**	down	IAA
OsAffx.24317.1.S1_x_a	LOC_Os10g14040	transposon protein, putative, unclassified	**1.03**	down	**1.08**	up	**3.81**	up	**1.10**	down	**1.12**	down	**1.23**	down	ABA
OsAffx.2442.1.S1_x_at	LOC_Os01g69830	OsSPL2 - SBP-box gene family member, expressed	**1.06**	up	**1.74**	down	**3.24**	up	**1.32**	down	**1.07**	up	**1.52**	up	ABA
OsAffx.24484.1.S1_at	LOC_Os02g28850	Kinesin motor domain domain containing protein, expressed	**1.24**	down	**1.24**	down	**4.51**	up	**1.26**	down	**1.55**	down	**1.05**	up	ABA
OsAffx.24492.1.S1_at	LOC_Os02g29210	ankyrin, putative, expressed	**1.17**	down	**1.09**	down	**3.40**	up	**1.18**	up	**1.32**	up	**1.30**	down	ABA
OsAffx.24599.1.S1_s_a	LOC_Os02g36510	ethylene-insensitive 3, putative, expressed	**1.00**	down	**1.00**	up	**3.50**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
OsAffx.24603.1.S1_at	LOC_Os02g36810	cytokinin-O-glucosyltransferase 2, putative	**64.57**	up	**1.30**	up	**2.35**	up	**1.51**	up	**18.75**	up	**4.69**	up	4
OsAffx.24603.1.S1_x_a	LOC_Os02g36810	cytokinin-O-glucosyltransferase 2, putative	**21.77**	up	**1.08**	down	**2.84**	up	**1.08**	up	**12.55**	up	**2.91**	up	4
OsAffx.24612.1.S1_at	LOC_Os02g37300	heavy metal associated domain containing protein, expressed	**1.57**	down	**1.16**	up	**2.74**	down	**1.15**	down	**1.04**	down	**1.70**	down	ABA
OsAffx.24626.1.S1_at	LOC_Os02g38120	BTBN3 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hyp	**3.14**	up	**1.14**	down	**1.98**	up	**1.50**	down	**1.04**	up	**1.71**	down	IAA

OsAffx.24626.1.S1_x_a	LOC_Os02g38120	BTBN3 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hyp	3.05	up	1.10	down	1.39	up	1.34	down	1.08	up	2.03	down	2
OsAffx.24629.1.S1_at	LOC_Os02g38230	high affinity nitrate transporter, putative, expressed	1.23	up	1.37	down	1.46	down	2.46	down	1.72	down	3.38	down	2
OsAffx.24631.1.S1_at	LOC_Os02g38410	ubiquitin family protein, putative, expressed	1.03	up	1.79	up	2.43	down	1.05	down	1.09	down	1.14	up	ABA
OsAffx.24631.1.S1_s_a	LOC_Os02g38410	ubiquitin family protein, putative, expressed	1.07	up	1.75	up	3.07	down	1.17	down	1.18	down	1.15	down	ABA
OsAffx.24657.1.S1_at	LOC_Os02g40110	expressed protein	1.00	up	1.12	down	2.09	down	1.12	up	1.38	up	1.05	down	ABA
OsAffx.24672.1.S1_at	LOC_Os02g41770	uncharacterized protein PA4923, putative	2.46	up	1.21	down	1.00	up	1.01	up	1.01	up	1.02	up	IAA
OsAffx.24682.1.S1_s_a	LOC_Os02g41954	gibberellin 2-beta-dioxygenase 7, putative, expressed	2.29	up	1.89	down	1.01	up	1.02	up	1.02	up	1.00	down	IAA
OsAffx.24694.1.S1_x_a	LOC_Os02g42920	DTA2, putative, expressed	1.08	down	1.44	down	4.55	up	1.57	up	1.54	up	1.50	up	ABA
OsAffx.24732.1.S1_x_a	LOC_Os02g44900	expressed protein	1.15	down	1.14	up	2.09	up	1.05	down	1.02	up	1.22	down	ABA
OsAffx.24733.1.S1_s_a	LOC_Os02g44940	RALFL8 - Rapid ALkalinization Factor RALF family protein precursor, expressed	1.11	down	1.01	up	2.01	down	1.03	down	1.10	down	1.15	up	ABA
OsAffx.24862.1.S1_at	LOC_Os02g54240	OsFBX62 - F-box domain containing protein	1.48	down	1.55	down	22.21	up	1.12	down	1.16	down	1.78	up	ABA
OsAffx.24890.1.S1_at	LOC_Os02g56250	GATA zinc finger domain containing protein, expressed	1.08	up	1.07	down	2.42	down	1.44	down	1.63	down	1.05	up	ABA
OsAffx.24953.1.S1_s_a	LOC_Os03g03370	fatty acid hydroxylase, putative, expressed	1.13	up	1.19	down	16.93	up	1.17	up	1.82	up	1.63	up	ABA
OsAffx.24980.1.S1_at	LOC_Os03g05510	DUF260 domain containing protein, putative, expressed	13.93	up	1.01	down	1.21	down	1.03	up	1.05	down	1.03	down	IAA
OsAffx.24981.1.S1_at	LOC_Os03g05530	nodulin, putative, expressed	1.16	down	1.02	down	15.99	down	1.36	down	2.80	down	1.80	down	2
OsAffx.25002.1.S1_at	LOC_Os03g07120	expressed protein	1.05	up	1.04	down	2.22	down	1.17	down	1.47	down	1.41	down	ABA
OsAffx.25008.1.S1_s_a	LOC_Os03g07510	expressed protein	11.98	down	5.41	down	14.19	down	2.69	down	6.11	down	1.45	down	5
OsAffx.25011.1.S1_at	LOC_Os03g07660	conserved hypothetical protein	1.16	down	1.19	down	2.09	up	1.06	down	1.12	down	1.12	down	ABA
OsAffx.25038.1.S1_at	LOC_Os03g10440	glycosyl hydrolase family 10 protein, putative, expressed	1.15	down	2.81	up	6.28	up	1.05	up	1.14	down	1.34	down	2
OsAffx.25045.1.S1_at	LOC_Os03g10810	HLS, putative, expressed	1.04	up	1.01	up	4.90	up	1.01	up	1.01	up	1.01	up	ABA
OsAffx.25079.1.S1_at	LOC_Os03g12940	OsFBO13 - F-box and other domain containing protein, expressed	1.05	up	1.18	up	2.87	up	1.04	up	1.05	up	1.04	up	ABA
OsAffx.2509.1.S1_at	LOC_Os02g04810	auxin response factor 5, putative, expressed	1.69	up	1.29	down	2.07	up	1.35	up	1.29	up	2.05	down	2
OsAffx.25137.1.S1_at	LOC_Os03g19010	peroxisomal biogenesis factor 11, putative, expressed	1.36	up	1.19	up	4.44	up	1.50	up	1.59	up	1.52	up	ABA
OsAffx.25137.1.S1_s_a	LOC_Os03g19010	peroxisomal biogenesis factor 11, putative, expressed	1.02	up	1.08	down	4.16	up	1.48	up	1.69	up	1.81	up	ABA
OsAffx.25178.1.S1_at	LOC_Os03g21260	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative	1.23	down	1.21	down	248.46	up	1.01	up	1.01	up	1.02	up	ABA
OsAffx.25245.1.S1_at	LOC_Os03g27110	hydrolase protein, putative, expressed	1.01	down	1.01	up	39.95	up	1.01	up	1.04	down	1.01	down	ABA
OsAffx.2528.1.S1_at	LOC_Os02g06950	no apical meristem protein, putative	1.01	down	1.00	up	2.21	up	1.01	up	1.00	up	1.02	up	ABA
OsAffx.25290.1.S1_at	LOC_Os03g29960	DEK C terminal domain containing protein, expressed	1.10	down	1.11	down	3.05	up	1.10	down	1.10	up	1.07	up	ABA
OsAffx.2537.1.S1_at	LOC_Os02g07440	DEFL78 - Defensin and Defensin-like DEFL family	1.17	down	1.22	up	4.42	down	1.70	down	2.20	down	3.50	down	3
OsAffx.25443.1.S1_at	LOC_Os03g39980	expressed protein	32.65	up	1.00	down	1.07	up	1.00	up	1.01	up	1.02	up	IAA
OsAffx.25463.1.S1_at	LOC_Os03g41100	cyclin, putative, expressed	1.27	down	1.24	down	3.10	down	1.05	up	2.13	down	1.02	down	2
OsAffx.25498.1.S1_at	LOC_Os03g42710	WD-40 repeat family protein, putative, expressed	1.01	down	1.00	up	23.58	up	1.01	down	1.06	down	1.19	up	ABA
OsAffx.25512.1.S1_s_a	LOC_Os03g43400	OsIAA11 - Auxin-responsive Aux/IAA gene family member, expressed	3.61	up	1.52	up	6.62	down	1.54	down	2.32	down	1.97	down	4
OsAffx.25512.1.S1_x_a	LOC_Os03g43400	OsIAA11 - Auxin-responsive Aux/IAA gene family member, expressed	2.94	up	1.48	up	2.64	down	1.23	down	1.40	down	1.29	down	2
OsAffx.25668.1.S1_at	LOC_Os03g50780	PHD-finger domain containing protein, putative, expressed	1.01	down	1.11	down	2.22	up	1.19	up	1.06	up	1.00	up	ABA
OsAffx.25749.1.S1_at	LOC_Os03g57880	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	1.06	up	1.12	up	5.07	up	1.14	down	1.06	up	1.09	up	ABA
OsAffx.25749.1.S1_s_a	LOC_Os03g57880	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	1.02	up	1.07	up	5.25	up	1.41	down	1.25	up	1.21	down	ABA
OsAffx.25751.1.S1_at	LOC_Os03g57980	LTPL99 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.36	up	1.98	up	10.53	up	1.99	down	1.38	up	2.19	down	4
OsAffx.25751.1.S1_s_a	LOC_Os03g57980	LTPL99 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.16	up	1.53	up	10.09	up	1.38	down	1.64	up	1.43	down	ABA
OsAffx.25760.1.S1_at	LOC_Os03g58800	ATPase, putative, expressed	1.94	up	1.03	down	2.23	down	1.13	down	2.18	up	1.58	up	2
OsAffx.25760.1.S1_x_a	LOC_Os03g58800	ATPase, putative, expressed	1.63	up	1.02	down	2.26	down	1.09	down	2.14	up	1.80	up	2
OsAffx.25764.1.S1_at	LOC_Os03g59110	pheophorbide a oxygenase, chloroplast precursor, putative, expressed	1.02	down	1.00	up	16.91	up	1.00	down	1.01	up	1.09	up	ABA
OsAffx.25767.1.S1_s_a	LOC_Os03g59380	LTPL28 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	1.36	down	1.06	up	2.03	up	1.12	up	1.33	up	1.00	up	ABA
OsAffx.25809.1.S1_at	LOC_Os03g63580	phosphoesterase family protein, putative, expressed	1.01	down	1.00	up	20.33	up	1.00	up	1.00	down	1.01	up	ABA
OsAffx.25809.1.S1_x_a	LOC_Os03g63580	phosphoesterase family protein, putative, expressed	1.03	down	1.02	down	19.97	up	1.01	down	1.38	up	1.01	up	ABA
OsAffx.25830.1.S1_at	LOC_Os04g01980	receptor protein kinase, putative, expressed	1.06	down	1.00	up	1.84	down	1.10	up	1.02	up	2.56	up	JA
OsAffx.25840.1.S1_at	LOC_Os04g02560	expressed protein	4.48	up	1.42	up	1.28	down	1.10	up	1.18	up	1.11	down	IAA
OsAffx.25891.1.S1_at	LOC_Os04g06590	expressed protein	1.27	up	1.17	up	1.06	up	1.08	up	6.23	up	1.27	up	SA
OsAffx.2594.1.S1_at	LOC_Os02g13300	mitochondrial carrier protein, putative, expressed	1.31	up	1.02	up	5.41	up	1.14	down	1.94	up	1.33	up	ABA
OsAffx.25959.2.S1_at	LOC_Os04g10460	amidase, putative, expressed	1.19	down	1.19	down	2.19	down	1.61	down	1.14	down	1.77	up	ABA
OsAffx.25975.1.S1_at	LOC_Os04g11040	expressed protein	1.11	down	1.05	up	7.24	down	1.41	down	5.39	down	6.10	down	3
OsAffx.25978.1.S1_at	LOC_Os04g11120	expressed protein	1.42	down	1.08	down	8.74	down	1.53	down	1.90	down	2.55	down	2
OsAffx.26050.5.S1_at	LOC_Os08g18974	expressed protein	1.00	down	1.34	up	23.20	up	1.06	up	1.02	down	1.10	up	ABA
OsAffx.26103.1.S1_at	LOC_Os04g20070	tropinone reductase 2, putative, expressed	1.43	up	1.07	up	4.50	up	1.06	up	1.04	up	1.09	up	ABA
OsAffx.2611.1.S1_at	LOC_Os02g14910	bZIP transcription factor family protein, putative, expressed	1.13	down	1.16	up	2.45	down	1.22	down	1.32	down	1.46	down	ABA

OsAffx.2612.1.S1_at	LOC_Os02g14980	calcium-binding EF hand family protein, putative, expressed	**1.08**	down	**1.25**	down	**15.83**	up	**1.15**	up	**1.05**	up	**2.05**	up	2
OsAffx.26128.1.S1_at	LOC_Os04g24340	phytase, putative	**1.68**	down	**1.97**	up	**2.13**	down	**1.57**	down	**2.28**	down	**2.37**	up	4
OsAffx.2622.1.S1_at	LOC_Os02g15440	hypothetical protein	**1.25**	up	**3.26**	down	**3.09**	up	**1.20**	down	**2.14**	up	**1.74**	down	3
OsAffx.26295.2.S1_at	LOC_Os04g32830	expressed protein	**1.73**	down	**1.54**	down	**6.41**	down	**1.21**	up	**2.08**	down	**3.64**	down	3
OsAffx.26304.1.S1_x_a	LOC_Os04g33310	expressed protein	**1.09**	down	**1.37**	down	**3.19**	down	**1.08**	up	**1.56**	down	**1.06**	up	ABA
OsAffx.26317.1.S2_at	LOC_Os04g33920	LTPL102 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.51**	down	**1.63**	down	**68.61**	up	**1.28**	down	**1.36**	up	**1.23**	down	ABA
OsAffx.26343.1.S1_x_a	LOC_Os04g35490	expressed protein	**1.01**	down	**1.00**	up	**68.38**	up	**1.00**	up	**1.00**	down	**1.05**	up	ABA
OsAffx.26385.1.S1_at	LOC_Os04g39170	expressed protein	**1.06**	up	**1.03**	down	**6.60**	up	**1.02**	down	**1.20**	up	**1.01**	up	ABA
OsAffx.26423.1.S1_at	LOC_Os04g41970	endoglucanase, putative, expressed	**1.80**	down	**1.21**	down	**3.98**	down	**1.09**	down	**1.64**	down	**2.81**	up	2
OsAffx.26451.1.S1_at	LOC_Os04g44130	DEF12 - Defensin and Defensin-like DEFL family, expressed	**1.28**	down	**2.78**	down	**1.06**	down	**1.02**	down	**1.66**	down	**1.37**	down	BAP
OsAffx.26497.1.S1_at	LOC_Os04g47170	ATROPGEF7/ROPGEF7, putative, expressed	**1.30**	up	**1.11**	up	**2.67**	up	**1.20**	down	**1.13**	up	**1.13**	up	ABA
OsAffx.26509.1.S1_s_a	LOC_Os04g47770	cis-zeatin O-glucosyltransferase, putative, expressed	**1.19**	up	**1.09**	up	**2.69**	down	**1.42**	up	**1.21**	down	**1.21**	down	ABA
OsAffx.26540.1.S1_s_a	LOC_Os04g49550	RING-H2 finger protein ATL2A, putative, expressed	**1.00**	down	**1.69**	up	**1.47**	up	**1.23**	up	**1.13**	down	**2.65**	up	JA
OsAffx.26601.1.S1_x_a	LOC_Os04g54500	POLGAMMA2, putative, expressed	**1.35**	up	**1.15**	up	**2.50**	down	**1.10**	down	**1.38**	down	**1.08**	down	ABA
OsAffx.26635.1.S1_at	LOC_Os04g56570	heavy metal-associated domain containing protein, expressed	**1.03**	down	**1.02**	down	**18.65**	up	**1.05**	down	**1.05**	down	**1.08**	up	ABA
OsAffx.26636.1.S1_x_a	LOC_Os04g56580	inositol 1,3,4,5,6-pentakisphosphate 2-kinase, putative, expressed	**1.20**	up	**1.05**	up	**4.01**	up	**1.22**	up	**1.23**	up	**1.05**	up	ABA
OsAffx.26728.1.S1_at	LOC_Os05g04470	peroxidase precursor, putative, expressed	**1.80**	down	**1.82**	down	**8.10**	down	**1.60**	down	**2.72**	down	**1.98**	down	3
OsAffx.26738.1.S1_at	LOC_Os05g05040	expressed protein	**1.00**	down	**1.08**	up	**2.02**	down	**2.26**	down	**1.39**	down	**1.27**	up	2
OsAffx.26801.1.S1_x_a	LOC_Os05g09480	OsIAA16 - Auxin-responsive Aux/IAA gene family member, expressed	**2.35**	down	**1.32**	up	**6.67**	down	**1.38**	up	**2.03**	down	**3.02**	up	3
OsAffx.26826.1.S1_at	LOC_Os05g11210	lachrymatory factor synthase, putative, expressed	**1.87**	up	**5.46**	up	**26.76**	down	**1.24**	up	**2.42**	down	**2.23**	down	4
OsAffx.26937.3.S1_at	LOC_Os05g16930	protein kinase domain containing protein, expressed	**1.24**	down	**2.91**	down	**9.47**	down	**1.04**	down	**2.34**	up	**1.05**	down	3
OsAffx.26937.4.S1_x_a	LOC_Os05g17810	SHR5-receptor-like kinase, putative	**1.28**	down	**1.02**	up	**5.70**	down	**1.11**	up	**1.02**	up	**1.89**	up	ABA
OsAffx.26991.1.S1_at	LOC_Os05g23924	glycosyl hydrolase family 10 protein, putative, expressed	**1.22**	up	**1.12**	down	**2.98**	up	**2.70**	down	**1.94**	down	**2.09**	down	3
OsAffx.27033.1.S1_at	LOC_Os05g26940	CAMK_KIN1/SNF1/Nim1_like.23 - CAMK includes calcium/calmodulin depedent protein	**2.09**	down	**1.18**	up	**3.79**	up	**1.11**	down	**1.33**	up	**1.34**	up	2
OsAffx.27033.2.S1_s_a	LOC_Os05g26940	CAMK_KIN1/SNF1/Nim1_like.23 - CAMK includes calcium/calmodulin depedent protein	**1.16**	up	**1.36**	up	**3.51**	up	**1.13**	down	**1.11**	up	**1.24**	up	ABA
OsAffx.2707.1.S1_at	LOC_Os02g21300	transposon protein, putative, unclassified, expressed	**10.69**	up	**1.77**	up	**15.75**	up	**3.60**	up	**19.12**	up	**1.95**	up	4
OsAffx.27091.1.S1_at	LOC_Os05g30820	protein kinase, putative, expressed	**1.06**	up	**1.28**	down	**6.24**	down	**1.08**	down	**1.11**	down	**1.05**	up	ABA
OsAffx.27219.1.S1_at	LOC_Os05g38290	protein phosphatase 2C, putative, expressed	**2.51**	up	**1.58**	down	**73.05**	up	**1.88**	down	**2.83**	up	**1.94**	up	3
OsAffx.27222.1.S1_at	LOC_Os05g38350	glycerol-3-phosphate acyltransferase 8, putative, expressed	**1.25**	up	**1.23**	down	**5.64**	up	**1.11**	up	**1.44**	up	**1.04**	down	ABA
OsAffx.27222.1.S1_x_a	LOC_Os05g38350	glycerol-3-phosphate acyltransferase 8, putative, expressed	**1.28**	up	**1.12**	down	**5.68**	up	**1.16**	up	**1.55**	up	**1.15**	up	ABA
OsAffx.27244.1.S1_x_a	LOC_Os05g39850	MCM3 - Putative minichromosome maintenance MCM complex subunit 3, expressed	**1.31**	down	**1.18**	down	**5.64**	down	**1.08**	down	**2.85**	down	**1.84**	down	2
OsAffx.27267.1.S1_at	LOC_Os05g40960	Myb transcription factor, putative, expressed	**1.23**	down	**1.08**	up	**17.09**	down	**1.64**	down	**1.03**	down	**1.25**	up	ABA
OsAffx.27278.1.S1_x_a	LOC_Os05g41760	AP2 domain containing protein, expressed	**3.02**	up	**1.01**	up	**1.77**	up	**1.07**	down	**1.78**	up	**1.35**	up	IAA
OsAffx.27281.1.S1_at	AK240824	UDP-glucoronosyl/UDP-glucosyl transferase family protein	**1.18**	up	**1.07**	down	**4.45**	up	**1.57**	down	**2.33**	down	**1.07**	up	2
OsAffx.27319.2.S1_s_a	LOC_Os05g45380	hypothetical protein	**1.08**	down	**3.11**	down	**1.04**	down	**1.01**	down	**1.02**	down	**1.00**	up	BAP
OsAffx.27322.1.S1_s_a	LOC_Os05g45480	POEI45 - Pollen Ole e I allergen and extensin family protein precursor, expressed	**1.85**	down	**2.00**	down	**3.30**	down	**1.73**	down	**1.97**	down	**2.01**	down	4
OsAffx.27338.1.S1_s_a	LOC_Os05g46395	expressed protein	**1.19**	down	**1.19**	down	**2.92**	up	**1.01**	up	**1.31**	up	**1.01**	down	ABA
OsAffx.27339.1.S1_s_a	LOC_Os05g47830	expressed protein	**1.14**	down	**1.31**	up	**17.26**	up	**1.01**	up	**1.06**	down	**1.06**	down	ABA
OsAffx.27360.1.S1_s_a	LOC_Os05g48570	expressed protein	**1.15**	down	**1.06**	down	**3.86**	up	**1.30**	up	**1.25**	up	**1.03**	down	ABA
OsAffx.27370.1.S1_at	LOC_Os05g50940	conserved hypothetical protein	**1.74**	up	**2.77**	up	**1.11**	down	**1.48**	down	**1.11**	down	**1.22**	down	BAP
OsAffx.27398.1.S1_at	LOC_Os06g05000	early nodulin 93 ENOD93 protein, putative, expressed	**1.00**	up	**1.01**	up	**3.81**	up	**1.00**	up	**1.00**	down	**1.01**	up	ABA
OsAffx.27459.2.S1_s_a	LOC_Os06g05010	early nodulin 93 ENOD93 protein, putative, expressed	**1.30**	down	**1.36**	up	**3.22**	up	**1.24**	up	**3.02**	up	**1.35**	down	2
OsAffx.27459.3.S1_at	LOC_Os06g05010	early nodulin 93 ENOD93 protein, putative, expressed	**2.05**	down	**1.05**	up	**2.74**	down	**1.06**	down	**2.76**	up	**3.75**	down	4
OsAffx.27459.3.S1_x_a	LOC_Os09g39730	Core histone H2A	**2.38**	down	**1.10**	up	**2.31**	down	**1.22**	up	**3.17**	up	**2.74**	down	4
OsAffx.27508.10.S1_s_	LOC_Os10g36924	aquaporin protein, putative, expressed	**1.28**	up	**1.03**	down	**198.87**	up	**1.38**	up	**1.01**	up	**1.02**	up	ABA
OsAffx.27508.100.S1_s	LOC_Os07g38380	transmembrane protein 49, putative, expressed	**1.42**	down	**1.90**	down	**2.43**	down	**1.21**	up	**1.51**	up	**1.20**	up	ABA
OsAffx.27508.54.S1_s_	LOC_Os07g38380	transmembrane protein 49, putative, expressed	**1.05**	up	**1.06**	down	**3.13**	up	**1.02**	up	**1.10**	up	**1.07**	down	ABA
OsAffx.27513.1.S1_s_a	LOC_Os06g08640	transferase family protein, putative, expressed	**1.30**	down	**1.47**	down	**3.81**	down	**1.16**	up	**1.13**	down	**2.45**	up	2
OsAffx.27525.1.S1_at	LOC_Os06g09340	pectinesterase, putative, expressed	**1.12**	up	**1.05**	down	**2.89**	down	**1.07**	up	**1.43**	down	**1.00**	down	ABA
OsAffx.27555.1.S1_at	LOC_Os06g10580	cyclic nucleotide-gated ion channel, putative, expressed	**1.01**	down	**1.00**	up	**2.08**	down	**1.48**	up	**1.14**	up	**1.01**	up	ABA
OsAffx.27557.1.S1_at	9630	---	**7.14**	up	**1.00**	up	**1.53**	up	**1.00**	up	**1.01**	down	**1.11**	down	IAA
OsAffx.2760.1.S1_at	LOC_Os02g26470	expressed protein	**1.01**	down	**1.04**	up	**241.16**	up	**1.11**	down	**1.07**	down	**1.10**	down	ABA
OsAffx.27605.1.S1_s_a	LOC_Os06g13190	expressed protein	**1.60**	up	**1.01**	down	**1.07**	up	**1.17**	down	**3.15**	up	**1.05**	down	SA
OsAffx.27608.1.S1_at	LOC_Os06g13280	O-methyltransferase, putative	**1.89**	up	**1.22**	up	**4.60**	up	**1.11**	up	**1.90**	up	**2.50**	up	2
OsAffx.27633.1.S1_at	LOC_Os06g14280	cysteine-rich repeat secretory protein precursor, putative, expressed	**1.32**	down	**1.06**	down	**2.13**	down	**1.43**	down	**1.59**	down	**1.47**	down	ABA

OsAffx.27652.1.S1_x_a	LOC_Os06g15620	GASR7 - Gibberellin-regulated GASA	**1.91**	up	**1.10**	up	**7.54**	down	**1.24**	up	**1.09**	down	**1.47**	down	ABA
OsAffx.27660.1.S1_at	LOC_Os06g15910	potassium transporter, putative, expressed	**1.22**	up	**1.19**	down	**3.54**	up	**1.35**	down	**1.44**	up	**1.07**	down	ABA
OsAffx.27693.1.S1_at	LOC_Os06g18850	cadmium tolerance factor, putative, expressed	**1.07**	up	**1.28**	up	**8.03**	down	**1.48**	up	**1.73**	down	**1.67**	down	ABA
OsAffx.27718.1.S1_at	LOC_Os06g19740	expressed protein	**2.04**	down	**2.44**	up	**1.29**	down	**1.00**	up	**1.20**	down	**1.57**	up	2
OsAffx.27815.1.S1_s_a	LOC_Os06g24990	xylanase inhibitor protein 1 precursor, putative, expressed	**1.07**	down	**1.30**	up	**2.68**	up	**1.29**	down	**1.95**	up	**1.27**	up	ABA
OsAffx.27905.1.S1_at	LOC_Os06g32730	eukaryotic initiation factor iso-4F subunit p82-34, putative, expressed	**1.02**	up	**1.12**	down	**2.29**	up	**1.03**	up	**1.13**	down	**1.46**	down	ABA
OsAffx.27946.1.S1_at	LOC_Os06g35060	heavy metal-associated domain containing protein, expressed	**1.55**	up	**1.28**	up	**4.90**	down	**1.86**	up	**1.51**	down	**3.53**	down	2
OsAffx.27959.1.S1_x_a	LOC_Os06g36080	kinesin motor domain containing protein, expressed	**1.14**	up	**1.21**	down	**2.15**	up	**1.30**	up	**1.51**	up	**1.99**	up	ABA
OsAffx.28017.1.S1_at	LOC_Os06g39960	bZIP transcription factor domain containing protein, expressed	**1.16**	up	**1.23**	down	**4.61**	down	**1.63**	up	**1.80**	up	**2.65**	up	2
OsAffx.28093.1.S1_at	LOC_Os06g44040	DOMON domain containing protein, expressed	**1.35**	up	**1.13**	down	**3.28**	up	**1.23**	down	**1.38**	up	**1.36**	up	ABA
OsAffx.28099.1.S1_at	LOC_Os06g44410	histidine kinase, putative, expressed	**1.15**	down	**2.46**	down	**4.33**	down	**1.17**	down	**1.37**	down	**1.22**	down	2
OsAffx.28152.1.S1_s_a	LOC_Os06g47530	TKL_IRAK_DUF26-lh.6 - DUF26 kinases have homology to DUF26 containing loci, exp	**1.51**	up	**1.30**	down	**1.54**	up	**1.18**	up	**2.00**	up	**1.10**	up	SA
OsAffx.28161.1.S1_at	LOC_Os06g47850	zinc finger family protein, putative, expressed	**8.39**	up	**1.34**	up	**3.49**	up	**1.36**	up	**17.53**	up	**2.56**	up	4
OsAffx.28164.1.S1_at	LOC_Os06g48030	peroxidase precursor, putative, expressed	**1.05**	up	**1.82**	up	**4.58**	up	**1.25**	up	**1.11**	up	**1.51**	down	ABA
OsAffx.28187.1.S1_s_a	LOC_Os06g49390	NBS-LRR disease resistance protein, putative, expressed	**1.29**	down	**1.19**	up	**3.18**	down	**1.37**	up	**1.86**	down	**1.22**	down	ABA
OsAffx.28203.1.S1_at	LOC_Os06g50990	conserved hypothetical protein	**2.42**	up	**1.00**	up	**1.02**	down	**1.02**	down	**1.01**	down	**1.10**	up	IAA
OsAffx.28211.1.S1_at	LOC_Os06g51360	lysM domain containing protein, putative, expressed	**1.12**	up	**1.09**	up	**2.13**	up	**1.17**	up	**1.07**	up	**1.66**	up	ABA
OsAffx.2825.1.S1_x_at	LOC_Os02g32140	AP2 domain containing protein, expressed	**1.12**	down	**1.73**	up	**6.91**	up	**1.53**	up	**2.72**	up	**1.51**	up	2
OsAffx.28258.1.S1_at	LOC_Os07g04220	wound and phytochrome signaling involved receptor like kinase, putative, expressed	**1.07**	down	**1.25**	down	**2.87**	up	**1.13**	up	**1.68**	up	**1.16**	up	ABA
OsAffx.28335.1.S1_at	LOC_Os07g07790	LTPL75 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**2.34**	up	**1.53**	up	**4.97**	up	**1.03**	up	**1.33**	up	**2.23**	down	3
OsAffx.28337.1.S1_at	LOC_Os07g07860	LTPL76 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.83**	up	**1.04**	up	**6.42**	up	**1.04**	down	**1.35**	up	**1.19**	down	ABA
OsAffx.28364.1.S1_at	LOC_Os07g09520	expressed protein	**1.11**	down	**1.09**	down	**8.40**	down	**1.31**	down	**1.50**	down	**1.28**	up	ABA
OsAffx.28364.1.S1_x_a	LOC_Os07g09520	expressed protein	**1.27**	down	**1.45**	down	**5.97**	down	**1.14**	down	**1.69**	down	**1.25**	up	ABA
OsAffx.28379.1.S1_at	LOC_Os07g10230	glucosyltransferase, putative, expressed	**1.16**	down	**6.26**	up	**1.07**	down	**1.05**	down	**1.05**	down	**1.01**	down	BAP
OsAffx.28454.1.S1_s_a	LOC_Os07g15130	hypothetical protein	**1.02**	down	**1.06**	up	**8.06**	down	**1.15**	down	**1.59**	down	**1.57**	down	ABA
OsAffx.28664.1.S1_at	LOC_Os07g29810	disease resistant protein, identical, putative, expressed	**2.09**	up	**1.05**	down	**1.01**	down	**1.00**	up	**1.03**	down	**1.01**	up	IAA
OsAffx.28670.1.S1_s_a	LOC_Os07g30150	phosphoribosyl transferase, putative, expressed	**1.35**	down	**3.75**	up	**6.08**	down	**2.22**	up	**1.70**	down	**1.11**	up	3
OsAffx.28717.1.S1_at	LOC_Os07g32660	monocopper oxidase, putative, expressed	**1.09**	down	**1.43**	down	**2.37**	down	**1.06**	down	**1.77**	down	**2.15**	up	2
OsAffx.28727.1.S1_at	LOC_Os07g33320	expressed protein	**2.20**	up	**2.67**	down	**3.69**	up	**1.45**	down	**3.65**	up	**4.55**	down	5
OsAffx.2874.1.S1_at	LOC_Os02g35870	galactosyltransferase, putative, expressed	**1.24**	up	**1.13**	down	**2.51**	up	**1.46**	down	**1.30**	down	**1.01**	up	ABA
OsAffx.28754.2.S1_at	AK241373	receptor-like protein kinase 4, putative	**1.00**	up	**1.22**	down	**2.79**	up	**1.26**	down	**1.06**	up	**1.27**	down	ABA
OsAffx.28857.1.S1_at	LOC_Os07g41320	COBRA-like protein precursor, putative, expressed	**1.03**	up	**1.18**	up	**1.29**	down	**1.29**	down	**2.48**	down	**1.35**	down	SA
OsAffx.28867.2.S1_at	LOC_Os07g42070	DC1 domain-containing protein, putative, expressed	**17.36**	down	**1.22**	down	**29.83**	down	**1.71**	up	**7.18**	down	**7.70**	down	4
OsAffx.28880.1.S1_s_a	LOC_Os07g42910	cytochrome c oxidase subunit, putative, expressed	**1.09**	down	**1.02**	down	**5.38**	up	**1.32**	up	**1.07**	up	**1.38**	up	ABA
OsAffx.28888.1.S1_x_a	LOC_Os07g43450	conserved hypothetical protein	**1.15**	down	**1.02**	up	**3.68**	up	**1.11**	up	**1.02**	up	**1.04**	up	ABA
OsAffx.28901.3.S1_at	LOC_Os03g52880	BTBN9 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hyp	**1.02**	up	**1.08**	up	**2.18**	down	**1.07**	up	**1.05**	down	**1.17**	down	ABA
OsAffx.28906.1.S1_x_a	LOC_Os07g44850	gibberellin receptor GID1L2, putative, expressed	**1.00**	down	**1.00**	down	**5.37**	up	**1.01**	up	**1.05**	up	**1.04**	up	ABA
OsAffx.28929.1.S1_at	LOC_Os07g46220	SNARE associated Golgi protein, putative, expressed	**1.06**	up	**1.04**	down	**3.66**	up	**1.05**	down	**1.04**	down	**1.08**	up	ABA
OsAffx.28948.1.S1_at	LOC_Os07g47960	basic helix-loop-helix domain containing protein, expressed	**1.04**	up	**1.03**	up	**1.61**	up	**2.69**	down	**2.49**	down	**2.59**	down	3
OsAffx.28967.1.S1_x_a	LOC_Os07g08500	C-5 cytosine-specific DNA methylase, putative, expressed	**1.18**	down	**1.18**	down	**6.75**	down	**1.03**	down	**2.90**	down	**2.00**	down	3
OsAffx.2905.1.S1_at	LOC_Os02g38320	BTBZ3 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with TAZ zinc finger and	**1.17**	down	**1.06**	down	**1.45**	up	**1.03**	down	**1.06**	up	**5.32**	up	JA
OsAffx.29101.1.S1_at	LOC_Os08g08440	hypothetical protein	**1.17**	down	**1.02**	up	**2.85**	up	**1.00**	down	**1.34**	up	**1.00**	up	ABA
OsAffx.29133.1.S1_x_a	LOC_Os08g10330	SHR5-receptor-like kinase, putative, expressed	**1.03**	down	**1.30**	down	**3.59**	down	**1.18**	down	**1.55**	up	**1.62**	down	ABA
OsAffx.2917.1.S1_at	LOC_Os02g39620	ATOZI1, putative, expressed	**6.02**	down	**1.39**	down	**1.61**	down	**1.19**	up	**1.08**	down	**1.91**	down	IAA
OsAffx.2917.1.S1_s_at	LOC_Os02g39620	ATOZI1, putative, expressed	**3.09**	down	**1.18**	up	**2.47**	down	**1.01**	down	**1.39**	down	**3.48**	down	3
OsAffx.29230.1.S1_at	LOC_Os08g16030	expressed protein	**1.10**	up	**1.08**	down	**2.78**	down	**1.20**	up	**1.06**	up	**1.63**	up	ABA
OsAffx.29241.1.S1_s_a	LOC_Os08g16820	retrotransposon protein, putative, SINE subclass, expressed	**2.68**	up	**1.38**	up	**2.33**	down	**2.01**	down	**1.53**	down	**1.42**	down	3
OsAffx.2928.1.S1_at	LOC_Os02g40500	OsGrx_C2.1 - glutaredoxin subgroup I, expressed	**5.05**	up	**1.12**	down	**5.80**	up	**1.31**	up	**11.42**	up	**5.07**	up	4
OsAffx.29286.1.S1_at	LOC_Os08g20200	male sterility protein, putative, expressed	**1.00**	up	**1.01**	down	**33.36**	up	**1.14**	up	**1.21**	up	**1.16**	up	ABA
OsAffx.29494.1.S1_at	LOC_Os08g33670	no apical meristem protein, putative, expressed	**1.00**	down	**1.01**	down	**23.41**	up	**1.00**	up	**1.00**	down	**1.03**	up	ABA
OsAffx.2952.1.S1_at	LOC_Os02g43912	ceramide kinase-related, putative	**1.22**	up	**1.01**	up	**3.41**	up	**1.28**	up	**1.41**	up	**1.15**	up	ABA
OsAffx.29543.1.S1_x_a	LOC_Os08g35860	cytokinin dehydrogenase precursor, putative, expressed	**1.43**	up	**1.92**	up	**4.64**	up	**1.45**	up	**1.04**	up	**1.14**	down	ABA
OsAffx.29557.1.S1_at	9636	---	**1.01**	down	**1.10**	up	**2.99**	up	**1.04**	up	**1.05**	up	**1.10**	up	ABA
OsAffx.29571.1.S1_at	LOC_Os08g37432	MATE efflux family protein, putative, expressed	**1.21**	up	**1.49**	up	**1.45**	down	**1.52**	up	**3.50**	up	**2.50**	up	2
OsAffx.29578.1.S1_at	LOC_Os08g37970	MYB family transcription factor, putative, expressed	**2.60**	up	**1.07**	down	**1.01**	down	**1.05**	down	**1.00**	down	**1.00**	down	IAA

OsAffx.29599.2.S1_at	LOC_Os04g42820	hypothetical protein	**1.00**	down	**1.00**	up	**6.43**	up	**1.00**	up	**1.00**	up	**1.01**	up	ABA
OsAffx.29627.2.S1_at	LOC_Os08g41820	exo70 exocyst complex subunit domain containing protein, expressed	**1.44**	down	**1.82**	up	**4.78**	down	**1.88**	up	**1.18**	down	**1.00**	down	ABA
OsAffx.29632.1.S1_at	LOC_Os08g42390	glycerophosphoryl diester phosphodiesterase family protein, putative, expressed	**1.01**	down	**1.03**	down	**2.63**	down	**1.31**	up	**1.13**	up	**1.60**	up	ABA
OsAffx.29650.1.S1_at	LOC_Os08g43760	carrier, putative, expressed	**5.64**	up	**1.01**	up	**2.45**	up	**1.00**	down	**1.00**	up	**1.01**	down	2
OsAffx.2974.1.S1_s_at	LOC_Os02g45890	sulfotransferase domain containing protein, expressed	**10.18**	down	**2.30**	up	**61.91**	down	**1.15**	down	**20.91**	down	**2.77**	down	5
OsAffx.29871.1.S1_x_a	LOC_Os09g16330	pleiotropic drug resistance protein, putative, expressed	**3.13**	up	**1.33**	down	**1.98**	up	**1.23**	down	**6.06**	up	**1.45**	up	3
OsAffx.29875.1.S1_at	LOC_Os09g16520	cytochrome b5-like Heme/Steroid binding domain containing protein, expressed	**1.51**	down	**1.31**	down	**4.44**	down	**1.21**	down	**2.17**	down	**1.18**	down	2
OsAffx.29875.1.S1_s_a	LOC_Os09g16520	cytochrome b5-like Heme/Steroid binding domain containing protein, expressed	**1.21**	down	**1.17**	down	**4.53**	down	**1.18**	down	**2.25**	down	**1.62**	down	2
OsAffx.29955.1.S1_at	LOC_Os09g21120	armadillo/beta-catenin repeat family protein, putative, expressed	**1.10**	down	**1.09**	down	**27.23**	up	**1.01**	down	**1.01**	down	**1.01**	up	ABA
OsAffx.29958.1.S1_at	LOC_Os09g21180	homeobox associated leucine zipper, putative, expressed	**1.24**	up	**1.43**	up	**15.80**	up	**1.96**	down	**2.25**	up	**1.31**	up	3
OsAffx.29958.1.S1_x_a	LOC_Os09g21180	homeobox associated leucine zipper, putative, expressed	**1.67**	up	**1.70**	up	**17.02**	up	**1.87**	down	**2.21**	up	**1.25**	up	2
OsAffx.30020.1.A1_at	LOC_Os09g25740	expressed protein	**1.00**	up	**1.01**	up	**2.09**	up	**1.04**	down	**1.04**	down	**1.01**	down	ABA
OsAffx.30039.1.S1_at	LOC_Os09g26500	CXE carboxylesterase, putative, expressed	**1.02**	down	**1.01**	down	**2.00**	up	**1.72**	up	**2.65**	up	**1.06**	up	2
OsAffx.30042.1.S1_at	9637	---	**1.15**	down	**1.23**	down	**6.78**	up	**1.08**	up	**1.70**	up	**1.25**	up	ABA
OsAffx.30042.1.S1_x_a	LOC_Os09g26570	CAAX amino terminal protease family protein, putative, expressed	**1.11**	down	**1.46**	down	**10.57**	up	**1.07**	down	**1.38**	up	**1.05**	down	ABA
OsAffx.30049.1.S1_at	LOC_Os09g26920	OsSub57 - Putative Subtilisin homologue, expressed	**1.00**	up	**1.17**	down	**19.36**	up	**1.34**	down	**1.02**	down	**1.20**	down	ABA
OsAffx.30049.1.S1_x_a	LOC_Os09g26920	OsSub57 - Putative Subtilisin homologue, expressed	**1.06**	up	**1.00**	down	**16.69**	up	**1.09**	down	**1.09**	down	**1.08**	down	ABA
OsAffx.30069.1.S1_at	LOC_Os09g28910	carbonic anhydrase, chloroplast precursor, putative, expressed	**1.02**	down	**1.08**	up	**5.04**	up	**1.03**	down	**1.04**	down	**1.03**	up	ABA
OsAffx.30080.1.S1_at	LOC_Os09g29510	OsWAK80 - OsWAK receptor-like protein kinase, expressed	**1.19**	up	**1.17**	down	**1.37**	down	**3.93**	up	**1.82**	up	**6.23**	up	2
OsAffx.30127.1.S1_at	LOC_Os09g33650	expressed protein	**3.52**	down	**1.22**	up	**3.24**	down	**1.80**	down	**1.57**	down	**5.93**	up	3
OsAffx.30152.1.S1_s_a	LOC_Os09g36490	expressed protein	**1.20**	down	**1.03**	up	**1.03**	down	**1.05**	up	**2.34**	down	**1.02**	down	SA
OsAffx.30169.1.S1_at	LOC_Os09g37430	OsSAUR48 - Auxin-responsive SAUR gene family member	**10.70**	up	**1.62**	down	**1.02**	down	**1.01**	up	**1.00**	down	**1.02**	up	IAA
OsAffx.30176.1.S1_at	LOC_Os09g37710	NIN, putative, expressed	**1.05**	up	**2.68**	down	**2.14**	down	**1.73**	down	**1.09**	up	**1.19**	down	2
OsAffx.30183.1.S1_at	LOC_Os09g37930	expressed protein	**1.06**	up	**1.10**	down	**2.37**	up	**1.17**	up	**2.09**	up	**1.21**	up	2
OsAffx.30365.1.S1_at	LOC_Os10g09920	LTPL132 - Protease inhibitor/seed storage/LTP family protein precursor, putative, expre	**1.01**	down	**1.00**	up	**395.45**	up	**1.01**	up	**1.00**	down	**1.01**	up	ABA
OsAffx.30368.1.S1_at	LOC_Os10g10030	OsWAK111 - OsWAK receptor-like protein kinase, expressed	**1.01**	down	**1.00**	up	**19.46**	up	**1.00**	up	**1.01**	up	**1.02**	up	ABA
OsAffx.3043.1.S1_s_at	LOC_Os02g52190	helix-loop-helix DNA-binding protein, putative, expressed	**1.22**	down	**3.95**	up	**2.01**	up	**1.44**	up	**1.05**	down	**1.35**	down	2
OsAffx.30613.1.S1_x_a	LOC_Os02g14250	transposon protein, putative, unclassified	**1.52**	up	**2.59**	down	**5.83**	up	**1.05**	up	**1.46**	up	**1.13**	up	2
OsAffx.30613.3.S1_x_a	LOC_Os07g34120	transposon protein, putative, unclassified	**1.84**	up	**2.69**	down	**10.12**	up	**1.29**	up	**2.28**	up	**1.35**	up	3
OsAffx.30647.1.S1_x_a	LOC_Os10g32940	expressed protein	**1.72**	up	**2.93**	up	**1.11**	down	**1.18**	down	**1.91**	down	**1.62**	down	BAP
OsAffx.30689.1.S1_at	LOC_Os10g36390	monocopper oxidase, putative	**1.13**	up	**1.00**	up	**11.14**	down	**1.03**	down	**2.63**	down	**1.45**	down	2
OsAffx.3069.1.S1_at	LOC_Os02g54450	hypro1, putative, expressed	**1.60**	down	**1.58**	down	**4.79**	down	**2.17**	down	**3.42**	down	**4.23**	down	4
OsAffx.3071.1.S1_at	LOC_Os02g54520	MYB family transcription factor, putative, expressed	**1.15**	down	**1.12**	down	**4.84**	up	**1.13**	down	**1.15**	down	**1.15**	down	ABA
OsAffx.30714.1.S1_x_a	LOC_Os10g38800	leucine-rich repeat transmembrane protein kinase, putative, expressed	**1.19**	down	**1.23**	down	**2.55**	down	**1.08**	up	**1.02**	up	**1.01**	down	ABA
OsAffx.30751.1.S1_at	LOC_Os12g16350	enoyl-CoA hydratase/isomerase family protein, putative, expressed	**1.57**	up	**1.22**	up	**2.72**	up	**1.44**	down	**1.27**	up	**1.05**	up	ABA
OsAffx.30751.2.S1_at	LOC_Os10g42210	enoyl-CoA-hydratase, putative, expressed	**1.20**	down	**1.11**	down	**3.44**	up	**1.07**	down	**1.58**	up	**1.07**	up	ABA
OsAffx.30855.1.S1_x_a	LOC_Os11g07140	receptor kinase, putative, expressed	**1.33**	up	**1.27**	up	**2.13**	down	**1.39**	down	**1.85**	up	**1.46**	up	ABA
OsAffx.30930.1.S1_at	LOC_Os11g11530	ZmEBE-1 protein, putative, expressed	**1.01**	down	**1.02**	up	**2.86**	up	**1.00**	down	**1.03**	up	**1.14**	up	ABA
OsAffx.30969.1.S1_at	LOC_Os11g14050	leucine-rich repeat family protein, putative, expressed	**1.25**	down	**1.24**	down	**7.74**	down	**2.24**	down	**7.35**	down	**7.11**	down	4
OsAffx.31049.1.S1_at	LOC_Os11g18870	osFTL11 FT-Like11 homologous to Flowering Locus T gene; contains Pfam profile PF	**1.08**	down	**1.81**	up	**5.07**	up	**1.10**	down	**1.56**	up	**1.83**	up	ABA
OsAffx.31060.1.S1_s_a	LOC_Os11g19460	haloacid dehalogenase-like hydrolase family protein, putative, expressed	**1.11**	up	**1.09**	up	**2.65**	up	**1.17**	up	**1.22**	up	**1.15**	down	ABA
OsAffx.31123.1.S1_x_a	LOC_Os11g25030	mitochondrial 2-oxoglutarate/malate translocator, putative	**1.10**	up	**1.11**	down	**2.21**	down	**1.44**	down	**1.53**	down	**1.13**	down	ABA
OsAffx.31140.1.S1_at	LOC_Os11g26570	dehydrin, putative, expressed	**1.22**	down	**1.58**	down	**199.34**	up	**1.28**	down	**1.01**	up	**1.07**	up	ABA
OsAffx.3120.1.S1_at	LOC_Os03g03000	helix-loop-helix DNA-binding domain containing protein, expressed	**1.86**	down	**2.82**	down	**1.06**	down	**1.00**	down	**1.19**	up	**1.09**	up	BAP
OsAffx.31237.1.S1_at	LOC_Os11g31090	transferase family protein, putative, expressed	**2.22**	up	**1.46**	up	**5.67**	up	**1.33**	down	**1.77**	up	**1.55**	down	2
OsAffx.3129.1.S1_x_at	LOC_Os03g04470	expressed protein	**1.25**	up	**1.04**	up	**2.15**	down	**1.10**	down	**1.34**	down	**1.06**	down	ABA
OsAffx.31296.1.S1_at	LOC_Os11g34440	phospholipase A2, putative, expressed	**1.02**	up	**1.05**	up	**7.02**	up	**1.00**	down	**1.04**	up	**1.02**	up	ABA
OsAffx.31336.1.S1_at	LOC_Os11g36940	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	**1.11**	up	**1.13**	down	**2.68**	down	**1.13**	down	**1.15**	down	**1.36**	up	ABA
OsAffx.31339.1.S1_s_a	LOC_Os11g37080	h/ACA ribonucleoprotein complex subunit 1-like protein 1, putative, expressed	**1.02**	down	**1.13**	up	**2.01**	down	**1.20**	up	**1.34**	down	**1.18**	down	ABA
OsAffx.3135.1.S1_at	LOC_Os03g04900	MYB family transcription factor, putative, expressed	**1.38**	down	**1.52**	up	**38.67**	up	**1.51**	down	**1.55**	down	**1.45**	down	ABA
OsAffx.31356.1.S1_at	LOC_Os11g37880	stripe rust resistance protein Yr10, putative, expressed	**1.24**	down	**1.12**	down	**10.02**	up	**1.05**	down	**1.03**	down	**1.03**	up	ABA
OsAffx.31409.1.S1_s_a	LOC_Os03g19270	Universal stress domain protein containing protein	**1.56**	down	**1.11**	up	**38.66**	up	**1.81**	up	**2.84**	up	**1.14**	down	2
OsAffx.31420.1.S1_at	LOC_Os11g41150	nitrilase-associated protein, putative, expressed	**1.93**	down	**1.30**	up	**4.09**	down	**1.02**	down	**1.84**	down	**1.03**	up	ABA
OsAffx.31457.1.S1_at	LOC_Os11g43480	Leucine Rich Repeat family protein, expressed	**1.52**	up	**1.00**	down	**1.04**	down	**1.01**	up	**6.22**	up	**1.01**	up	SA
OsAffx.3147.1.S1_s_at	LOC_Os03g06250	retrotransposon protein, putative, unclassified, expressed	**1.07**	down	**1.17**	down	**4.36**	up	**1.04**	down	**1.02**	up	**1.12**	down	ABA

OsAffx.31531.1.S1_s_a	LOC_Os11g48060	laccase-22 precursor, putative, expressed	**1.56**	down	**1.23**	up	**5.39**	down	**1.72**	down	**5.78**	down	**3.73**	down	3
OsAffx.31567.1.S1_at	LOC_Os11g03880	D-mannose binding lectin family protein, expressed	**1.03**	down	**1.01**	up	**17.78**	up	**1.15**	up	**1.07**	down	**1.07**	down	ABA
OsAffx.31572.1.S1_at	LOC_Os11g04320	phosphoglycerate mutase, putative, expressed	**1.50**	up	**1.29**	up	**1.10**	up	**2.03**	down	**1.12**	down	**1.14**	down	ACC
OsAffx.31574.2.S1_at	LOC_Os12g04320	sulfotransferase domain containing protein, expressed	**13.07**	down	**1.77**	up	**54.13**	down	**1.17**	down	**9.54**	down	**8.12**	down	4
OsAffx.31633.1.S1_s_a	LOC_Os12g07480	TCP family transcription factor, putative, expressed	**2.00**	down	**1.19**	down	**1.14**	up	**1.25**	up	**1.12**	down	**1.08**	down	IAA
OsAffx.31649.1.S1_at	LOC_Os12g08700	expressed protein	**1.77**	up	**1.35**	down	**49.76**	up	**1.00**	down	**1.00**	up	**1.01**	up	ABA
OsAffx.31710.1.S1_x_a	LOC_Os12g12260	diacylglycerol kinase 1, putative, expressed	**1.65**	up	**1.08**	down	**2.67**	up	**1.24**	down	**1.06**	down	**1.37**	up	ABA
OsAffx.31974.1.S1_at	LOC_Os12g32200	expressed protein	**1.03**	down	**1.03**	down	**9.92**	up	**1.00**	up	**1.00**	down	**1.02**	up	ABA
OsAffx.31986.1.S1_at	LOC_Os12g32610	expressed protein	**1.36**	up	**1.33**	up	**18.85**	up	**1.15**	down	**1.14**	up	**1.06**	down	ABA
OsAffx.32171.3.S1_at	LOC_Os12g43490	thaumatin, putative, expressed	**1.17**	up	**1.31**	up	**5.24**	up	**1.15**	down	**1.08**	up	**1.03**	up	ABA
OsAffx.32172.1.S1_s_a	LOC_Os12g43580	expressed protein	**1.13**	up	**1.20**	up	**2.82**	up	**1.12**	up	**1.25**	up	**1.09**	down	ABA
OsAffx.32182.1.S1_at	LOC_Os12g43880	DNA binding protein, putative, expressed	**1.40**	up	**1.07**	down	**3.68**	up	**1.13**	up	**1.33**	up	**1.10**	down	ABA
OsAffx.32225.1.S1_x_a	LOC_Os01g57966	photosystem I assembly protein ycf3, putative	**1.07**	down	**1.21**	down	**1.04**	down	**1.14**	down	**2.63**	up	**1.93**	up	SA
OsAffx.32247.1.A1_at	LOC_Os12g34012	cytochrome c biosynthesis ccmC-like mitochondrial protein, putative	**1.03**	down	**1.41**	up	**2.19**	up	**1.72**	up	**1.34**	up	**1.19**	up	ABA
OsAffx.32297.1.A1_at	BA000029	---	**1.17**	down	**1.02**	down	**1.63**	up	**2.09**	up	**1.02**	up	**1.03**	up	ACC
OsAffx.32318.1.A1_at	AK242621	Oryza sativa Japonica Group cDNA, clone: J090019C07, full insert sequence.	**1.00**	down	**1.01**	up	**2.50**	up	**1.34**	up	**1.00**	up	**1.02**	up	ABA
OsAffx.3240.1.S1_s_at	LOC_Os03g14370	ACT domain containing protein, expressed	**1.86**	up	**1.12**	up	**3.23**	up	**1.03**	down	**1.27**	up	**1.74**	up	ABA
OsAffx.3268.1.S1_x_at	LOC_Os03g18360	BTBT1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with tetratricopeptide rep	**2.34**	up	**1.07**	down	**1.10**	up	**1.72**	up	**1.06**	up	**1.08**	up	IAA
OsAffx.3275.1.S1_at	LOC_Os03g19400	expressed protein	**1.15**	up	**1.23**	down	**3.88**	up	**1.25**	down	**1.29**	up	**1.21**	down	ABA
OsAffx.3427.1.S1_at	LOC_Os03g37960	acyl CoA binding protein, putative	**1.11**	up	**1.07**	up	**3.95**	down	**1.08**	down	**1.23**	up	**1.34**	up	ABA
OsAffx.3461.1.S1_at	LOC_Os03g40550	kinase, pfkB family, putative, expressed	**1.34**	up	**1.29**	up	**3.89**	down	**1.04**	down	**2.06**	down	**1.27**	down	2
OsAffx.3504.1.S1_at	LOC_Os03g43720	transporter family protein, putative, expressed	**1.22**	down	**1.48**	down	**13.67**	up	**1.01**	up	**1.01**	up	**1.02**	up	ABA
OsAffx.3504.1.S1_x_at	LOC_Os03g43720	transporter family protein, putative, expressed	**1.06**	up	**1.51**	down	**20.18**	up	**1.63**	up	**2.86**	up	**1.22**	up	2
OsAffx.3569.1.S1_at	LOC_Os03g50960	LTPL118 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.12**	up	**1.16**	down	**2.64**	up	**2.23**	down	**2.89**	up	**1.16**	up	3
OsAffx.3569.1.S1_x_at	LOC_Os03g50960	LTPL118 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	**1.20**	up	**1.18**	down	**2.74**	up	**2.14**	down	**3.02**	up	**1.18**	up	3
OsAffx.3602.1.S1_at	LOC_Os03g53390	expressed protein	**1.02**	up	**1.06**	down	**5.59**	up	**1.08**	up	**1.04**	up	**1.06**	up	ABA
OsAffx.3606.1.S1_s_at	AK105937	Oryza sativa Japonica Group cDNA clone:001-205-B08, full insert sequence.	**1.21**	down	**1.03**	down	**2.19**	up	**1.00**	down	**1.10**	up	**1.50**	up	ABA
OsAffx.3640.1.S1_at	LOC_Os03g58940	LTPL83 - Protease inhibitor/seed storage/LTP family protein precursor, putative, expres	**1.04**	down	**1.25**	down	**2.71**	down	**1.14**	down	**1.25**	down	**1.30**	up	ABA
OsAffx.3672.1.S1_at	LOC_Os03g62270	MATE efflux family protein, putative, expressed	**1.78**	up	**2.05**	up	**1.34**	down	**1.18**	up	**3.47**	down	**1.69**	down	2
OsAffx.3952.1.S1_s_at	LOC_Os04g30420	dehydrogenase, putative, expressed	**1.30**	up	**1.03**	up	**1.83**	up	**1.12**	down	**2.71**	up	**1.06**	up	SA
OsAffx.3967.1.S1_s_at	LOC_Os04g31520	RALFL21 - Rapid ALkalinization Factor RALF family protein precursor, expressed	**1.30**	down	**1.25**	down	**3.73**	down	**1.27**	down	**1.52**	down	**1.30**	down	ABA
OsAffx.3968.1.S1_at	LOC_Os04g31710	expressed protein	**1.00**	up	**1.00**	up	**62.50**	up	**1.01**	up	**1.00**	down	**1.02**	up	ABA
OsAffx.3994.1.S1_at	LOC_Os04g34250	serine/threonine-protein kinase receptor precursor, putative, expressed	**1.17**	up	**2.22**	down	**6.93**	up	**2.00**	down	**1.40**	up	**1.65**	up	3
OsAffx.4035.1.S1_x_at	LOC_Os04g40070	GRAM and C2 domains containing protein, putative, expressed	**1.04**	down	**1.03**	down	**49.26**	up	**1.01**	down	**1.02**	up	**1.01**	up	ABA
OsAffx.4107.1.S1_s_at	LOC_Os04g46350	homeobox associated leucine zipper, putative, expressed	**3.43**	up	**1.14**	down	**1.42**	up	**1.06**	up	**1.63**	up	**1.18**	down	IAA
OsAffx.4157.1.S1_x_at	LOC_Os04g52614	SHR5-receptor-like kinase, putative, expressed	**1.03**	down	**1.08**	down	**2.19**	down	**1.28**	up	**1.09**	up	**1.36**	up	ABA
OsAffx.4158.1.S1_at	LOC_Os04g52720	Cupin domain containing protein, expressed	**1.03**	down	**1.11**	up	**1.92**	down	**1.35**	up	**1.93**	down	**9.86**	up	JA
OsAffx.4159.1.S1_x_at	LOC_Os04g52730	NAD dependent epimerase/dehydratase family domain containing protein, expressed	**1.13**	up	**1.39**	down	**1.67**	up	**1.03**	up	**1.31**	up	**2.46**	up	JA
OsAffx.4161.1.S1_at	LOC_Os04g52900	ABC transporter family protein, putative, expressed	**1.60**	up	**1.13**	up	**1.25**	down	**1.08**	down	**2.11**	up	**1.30**	up	SA
OsAffx.4168.1.S1_s_at	LOC_Os04g53560	expressed protein	**1.53**	down	**2.74**	up	**30.99**	down	**1.12**	down	**7.92**	down	**1.25**	down	3
OsAffx.4180.1.S1_at	LOC_Os04g55100	expressed protein	**34.79**	up	**1.19**	down	**1.13**	down	**1.04**	down	**1.03**	down	**1.00**	up	IAA
OsAffx.4219.1.S1_at	LOC_Os05g01100	expressed protein	**1.19**	up	**1.03**	down	**3.34**	up	**1.13**	up	**1.02**	up	**1.03**	up	ABA
OsAffx.4250.1.S1_at	LOC_Os05g04440	peroxidase precursor, putative, expressed	**2.76**	down	**1.95**	down	**9.22**	down	**1.41**	down	**4.21**	down	**1.86**	down	3
OsAffx.4276.1.S1_s_at	LOC_Os05g08360	rRNA 2-O-methyltransferase fibrillarin 2, putative, expressed	**1.01**	up	**1.12**	up	**2.29**	down	**1.20**	up	**1.25**	down	**1.11**	down	ABA
OsAffx.4296.1.S1_at	LOC_Os05g10930	OsGrx_C15 - glutaredoxin subgroup III, expressed	**1.89**	up	**2.02**	down	**2.34**	up	**1.07**	up	**1.63**	up	**1.40**	up	3
OsAffx.4511.1.S1_at	LOC_Os05g33900	auxin-induced protein 5NG4, putative, expressed	**1.83**	up	**1.29**	down	**2.86**	up	**1.03**	up	**1.01**	up	**1.03**	up	ABA
OsAffx.4557.1.S1_s_at	LOC_Os05g39250	phosphatidylethanolamine-binding protein, putative, expressed	**1.19**	down	**1.21**	up	**85.66**	up	**1.59**	down	**1.20**	up	**1.03**	down	ABA
OsAffx.4567.1.S1_at	LOC_Os05g40080	OsWRKY54 - Superfamily of TFs having WRKY and zinc finger domains	**1.01**	down	**1.00**	up	**1.00**	up	**1.01**	up	**14.85**	up	**1.02**	up	SA
OsAffx.4639.1.S1_at	LOC_Os05g46610	myb-like DNA-binding domain containing protein, putative, expressed	**1.20**	down	**1.34**	up	**4.12**	down	**1.45**	down	**1.56**	down	**1.30**	up	ABA
OsAffx.4672.1.S1_at	LOC_Os05g49810	armadillo/beta-catenin-like repeat containing protein	**1.03**	down	**1.15**	down	**1.46**	up	**1.03**	down	**1.01**	up	**3.00**	up	JA
OsAffx.4676.1.S1_s_at	LOC_Os05g50450	hypothetical protein	**1.12**	down	**1.05**	down	**2.22**	up	**1.01**	up	**1.24**	up	**1.03**	up	ABA
OsAffx.4696.1.S1_at	LOC_Os06g02390	ADP-ribosylation factor 1, putative	**1.22**	down	**1.20**	down	**2.10**	down	**1.91**	down	**1.94**	down	**1.75**	down	ABA
OsAffx.4762.1.S1_at	LOC_Os06g08130	hypothetical protein	**14.28**	up	**1.00**	up	**1.04**	down	**1.01**	down	**1.01**	down	**1.06**	up	IAA
OsAffx.5019.1.S1_at	LOC_Os06g35630	reticuline oxidase-like protein precursor, putative, expressed	**1.52**	up	**2.29**	up	**1.19**	down	**1.52**	up	**1.97**	down	**2.43**	down	3
OsAffx.5050.1.S1_at	LOC_Os06g38750	proline-rich family protein, putative, expressed	**1.23**	down	**1.65**	up	**2.16**	down	**1.02**	up	**1.39**	down	**1.80**	down	ABA

OsAffx.5079.1.S1_at	LOC_Os06g41880	OsSub51 - Putative Subtilisin homologue, expressed	**3.67**	up	**1.04**	down	**1.02**	down	**1.01**	up	**1.03**	up	**1.02**	up	IAA
OsAffx.5098.1.S1_at	LOC_Os06g43950	expressed protein	**1.15**	up	**1.10**	up	**2.88**	up	**1.01**	up	**1.28**	up	**1.08**	up	ABA
OsAffx.5153.1.S1_at	CT832798	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA009A02, full insert sequence	**1.05**	up	**1.06**	down	**2.12**	up	**1.06**	up	**1.21**	up	**1.05**	up	ABA
OsAffx.5232.1.S1_s_at	LOC_Os07g06460	expressed protein	**1.43**	down	**1.00**	down	**1.40**	up	**1.57**	up	**3.14**	up	**2.07**	up	2
OsAffx.5257.1.S1_at	LOC_Os07g08970	uncharacterized protein ycf45, putative, expressed	**1.47**	up	**1.73**	down	**6.19**	up	**1.15**	up	**1.31**	up	**1.20**	up	ABA
OsAffx.5423.1.S1_at	LOC_Os07g23970	zinc finger, C3HC4 type domain containing protein, expressed	**1.06**	down	**1.16**	down	**2.12**	down	**1.20**	down	**1.27**	down	**1.26**	down	ABA
OsAffx.5522.1.S1_s_at	LOC_Os07g34110	integral membrane protein DUF6 containing protein, expressed	**2.09**	up	**1.47**	down	**5.92**	up	**1.15**	down	**1.86**	up	**1.54**	down	2
OsAffx.5607.1.S1_x_at	LOC_Os07g42280	von Willebrand factor type A domain containing protein, expressed	**1.07**	down	**1.11**	down	**3.40**	up	**1.09**	down	**1.78**	up	**1.13**	up	ABA
OsAffx.5699.1.S1_at	LOC_Os08g04470	U box protein 8, putative, expressed	**1.08**	up	**1.06**	up	**2.41**	up	**1.12**	up	**1.15**	up	**1.17**	up	ABA
OsAffx.5702.1.S1_s_at	LOC_Os08g04560	decarboxylase, putative, expressed	**1.24**	down	**1.03**	down	**2.45**	up	**1.30**	down	**1.83**	up	**1.55**	up	ABA
OsAffx.5729.1.S1_at	LOC_Os08g07070	expressed protein	**15.60**	up	**1.04**	down	**1.53**	down	**1.48**	down	**1.51**	down	**1.48**	down	IAA
OsAffx.5859.1.S1_x_at	LOC_Os08g17680	stromal cell-derived factor 2-like protein precursor, putative, expressed	**1.19**	down	**1.20**	up	**3.13**	down	**1.16**	up	**1.20**	down	**1.13**	up	ABA
OsAffx.6015.1.S1_at	LOC_Os08g33740	CSLA11 - cellulose synthase-like family A, expressed	**1.05**	down	**1.19**	down	**3.55**	down	**1.39**	down	**1.44**	down	**1.26**	up	ABA
OsAffx.6051.1.S1_at	LOC_Os08g37010	gibberellin receptor GID1L2, putative, expressed	**1.32**	down	**1.90**	up	**16.22**	up	**1.17**	up	**2.16**	down	**1.14**	down	2
OsAffx.6128.1.S1_at	LOC_Os08g43850	carrier, putative	**3.32**	up	**1.06**	up	**1.66**	down	**1.20**	down	**1.58**	down	**1.08**	down	IAA
OsAffx.6132.1.S1_s_at	LOC_Os08g44190	ZOS8-13 - C2H2 zinc finger protein, expressed	**1.42**	up	**1.50**	up	**3.31**	up	**2.50**	up	**3.38**	up	**1.44**	down	3
OsAffx.6250.1.S1_at	LOC_Os09g12400	hypothetical protein	**2.77**	down	**1.71**	down	**10.98**	down	**1.29**	down	**4.92**	down	**3.04**	down	4
OsAffx.6270.1.S1_at	LOC_Os09g14450	pollen signalling protein with adenylyl cyclase activity, putative, expressed	**2.37**	down	**1.59**	up	**1.85**	down	**2.01**	up	**1.17**	up	**1.12**	up	2
OsAffx.6292.1.S1_at	LOC_Os09g16090	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed	**1.69**	down	**1.25**	up	**17.31**	down	**1.25**	down	**2.15**	down	**4.22**	down	3
OsAffx.6325.1.S1_at	LOC_Os09g18450	flavonol synthase/flavanone 3-hydroxylase, putative, expressed	**1.74**	down	**1.88**	down	**5.69**	down	**1.50**	down	**1.92**	down	**1.25**	down	ABA
OsAffx.6397.1.S1_at	LOC_Os09g25690	retrotransposon protein, putative, unclassified	**1.03**	down	**1.11**	up	**39.43**	up	**1.27**	up	**1.53**	up	**1.14**	up	ABA
OsAffx.6404.1.S1_at	LOC_Os09g26170	MYB family transcription factor, putative, expressed	**1.82**	down	**2.21**	down	**11.99**	down	**1.22**	up	**1.18**	down	**1.07**	up	2
OsAffx.6406.1.S1_at	LOC_Os09g26490	alpha/beta hydrolase fold, putative	**1.36**	up	**1.05**	down	**8.24**	up	**1.20**	up	**1.85**	up	**1.58**	up	ABA
OsAffx.6408.1.S1_at	LOC_Os09g26610	OsSAUR38 - Auxin-responsive SAUR gene family member, expressed	**2.33**	down	**1.07**	down	**1.95**	up	**1.16**	down	**1.13**	up	**1.34**	down	IAA
OsAffx.6455.1.S1_at	LOC_Os09g30474	BPI/LBP family protein At3g20270 precursor, putative, expressed	**1.12**	up	**1.19**	down	**3.04**	up	**1.16**	up	**1.47**	up	**1.01**	up	ABA
OsAffx.6464.1.S1_at	LOC_Os09g31990	expressed protein	**12.36**	up	**1.00**	down	**1.07**	down	**1.03**	down	**16.45**	up	**1.04**	up	2
OsAffx.6497.1.S1_s_at	LOC_Os09g36850	expressed protein	**3.39**	up	**1.04**	up	**1.05**	down	**1.10**	up	**1.16**	up	**1.06**	up	IAA
OsAffx.6501.1.S1_x_at	LOC_Os09g37120	pyridoxal-dependent decarboxylase protein, putative, expressed	**1.12**	down	**1.76**	up	**7.06**	down	**1.09**	down	**2.78**	down	**1.59**	down	2
OsAffx.6505.1.S1_at	LOC_Os09g37440	OsSAUR49 - Auxin-responsive SAUR gene family member	**12.71**	up	**1.17**	down	**1.10**	down	**1.14**	up	**1.35**	up	**1.02**	up	IAA
OsAffx.6534.1.S1_at	LOC_Os09g39620	protein kinase family protein, putative, expressed	**1.83**	up	**1.82**	down	**2.96**	up	**1.31**	up	**3.31**	up	**1.76**	down	2
OsAffx.6703.1.S1_s_at	LOC_Os10g19925	conserved hypothetical protein	**1.01**	up	**1.00**	up	**1.12**	up	**1.02**	up	**17.44**	up	**1.03**	up	SA
OsAffx.6920.1.S1_at	LOC_Os10g39990	short-chain dehydrogenase/reductase SDR, putative	**1.00**	down	**1.01**	up	**6.51**	up	**1.01**	up	**1.01**	up	**1.02**	down	ABA
OsAffx.7025.1.S1_at	LOC_Os11g06770	ethylene-responsive transcription factor ERF110, putative, expressed	**1.64**	up	**1.54**	down	**3.69**	up	**1.11**	down	**10.28**	up	**1.71**	up	2
OsAffx.7132.1.S1_at	LOC_Os11g17380	protein kinase domain containing protein	**1.35**	down	**1.67**	down	**29.52**	down	**1.02**	down	**3.21**	down	**4.26**	down	3
OsAffx.7243.1.S1_s_at	LOC_Os11g29210	resistance-gene-interacting protein, putative, expressed	**1.26**	down	**1.22**	down	**8.54**	down	**1.52**	up	**1.68**	up	**1.27**	up	ABA
OsAffx.7265.1.S1_at	LOC_Os11g31380	no apical meristem protein, putative	**1.01**	down	**1.00**	up	**124.52**	up	**1.01**	up	**1.00**	down	**1.01**	up	ABA
OsAffx.7376.1.S1_at	LOC_Os11g41650	adenylyl-sulfate kinase, putative, expressed	**1.01**	down	**6.46**	down	**2.74**	up	**1.35**	up	**1.04**	up	**1.35**	down	2
OsAffx.7517.1.S1_x_at	LOC_Os12g07580	dirigent, putative, expressed	**1.20**	up	**1.05**	up	**2.50**	down	**1.46**	down	**1.46**	down	**1.08**	down	ABA
OsAffx.7625.1.S1_at	LOC_Os12g17860	retrotransposon protein, putative, Ty3-gypsy subclass	**1.01**	down	**1.00**	up	**1.02**	down	**1.01**	up	**21.93**	up	**1.02**	up	SA
OsAffx.7704.1.S1_at	LOC_Os12g26030	FACT complex subunit SPT16, putative, expressed	**1.17**	up	**1.58**	down	**2.33**	up	**1.70**	up	**1.61**	up	**1.60**	up	ABA
OsAffx.7733.1.S1_at	LOC_Os12g29330	no apical meristem protein, putative, expressed	**1.50**	up	**1.56**	up	**2.06**	up	**1.17**	up	**1.40**	up	**1.08**	up	ABA
OsAffx.7735.1.S1_at	LOC_Os12g29430	OsWAK125 - OsWAK receptor-like protein OsWAK-RLP, expressed	**1.12**	up	**1.04**	up	**1.02**	down	**1.00**	up	**1.00**	up	**8.07**	up	JA
OsAffx.7876.1.S1_s_at	LOC_Os12g43140	late embryogenesis abundant protein D-34, putative, expressed	**1.00**	down	**1.09**	up	**469.85**	up	**1.28**	up	**1.17**	up	**1.50**	up	ABA
OsAffx.8033.1.S1_at	LOC_Os10g33060	hcr2-5D, putative	**1.15**	down	**1.87**	down	**5.46**	up	**1.06**	down	**1.06**	up	**1.40**	down	ABA
OsAffx.9161.1.S1_at	LOC_Os01g41720	conserved hypothetical protein	**1.01**	down	**1.00**	up	**12.28**	up	**1.00**	up	**1.00**	up	**1.01**	up	ABA
OsAffx.9457.1.S1_at	LOC_Os01g60330	inactive receptor kinase At2g26730 precursor, putative, expressed	**1.03**	down	**1.12**	down	**2.28**	down	**1.28**	down	**1.60**	down	**1.20**	down	ABA
OsAffx.9523.1.S1_x_at	LOC_Os01g64820	POLA1 - Putative DNA polymerase alpha catalytic subunit, expressed	**1.43**	down	**1.24**	down	**3.73**	down	**1.05**	up	**2.07**	down	**1.45**	down	2
OsAffx.9698.1.S1_x_at	LOC_Os01g09260	cytokinin dehydrogenase precursor, putative, expressed	**1.03**	down	**12.22**	up	**1.05**	up	**1.39**	down	**1.48**	down	**1.48**	up	BAP
OsAffx.9719.1.S1_x_at	LOC_Os01g08380	transferase family protein, putative, expressed	**1.01**	up	**1.43**	up	**2.54**	down	**1.69**	up	**1.24**	up	**4.65**	up	2
OsAffx.9740.1.S1_s_at	LOC_Os01g73240	expressed protein	**1.18**	down	**1.14**	down	**2.66**	down	**1.65**	down	**2.19**	down	**1.81**	down	2
OsAffx.985.1.S1_x_at	LOC_Os01g59580	retrotransposon protein, putative, unclassified	**1.96**	down	**2.73**	up	**1.57**	down	**1.23**	down	**1.51**	down	**1.64**	down	BAP

Supplementary Table S2. Number of rice genes showing similar and opposite regulation by any two hormones is indicated.

	IAA	**BAP**	**ABA**	**ACC**	**SA**	**JA**
IAA	-	26/14	114/92	12/4	102/47	48/37
BAP	20	-	49/31	7/6	18/14	28/14
ABA	50	105	-	34/27	317/239	136/134
ACC	22	9	60	-	35/22	29/17
SA	15	58	53	23	-	124/95
JA	37	50	142	25	31	-

The number of rice genes showing similar regulation by any two hormones [up- (left) or down- (right) regulated by both hormones] are indicated on the upper (above the blank cells) side of the table. The number of rice genes showing opposite regulation by any two hormones (up-regulated by one hormone and down-regulated by other hormones) are indicated on the lower (below the blank cells) side of the table. IAA, auxin; BAP, cytokinin; ABA, abscisic acid; ACC, ethylene derivative; SA, salicylic acid; JA, jasmonic acid.

Supplementary Table S3. Primers sequences used for real-time PCR analysis.

Gene ID	**Primer sequence**
Os01g07030_F	GGTGGAGGGCATGGTGTACT
Os01g07030_R	CCATTGAGGCTATGCGTGTTC
Os01g18360_F	TCAACAAGTTCCTGGCCAGAA
Os01g18360_R	CCCGTCCTGGTCTTCATAGG
Os01g73200_F	TTCTTCAACGCAACCACCAA
Os01g73200_R	TCGATCATGCCCATCTTGAC
Os04g44280_F	AGGAGATCCCTGTGGTGATCAT
Os04g44280_R	TCCAAGCACCTGTTGATCCTT
Os04g44354_F	AGTTCATCAATTGCGCGTACAT
Os04g44354_R	TCTCGATGCAGTCACGTACGA
Os05g14370_F	CGGGAGCATACTGGATTGCT
Os05g14370_R	CCGACGTAGCGAGAATTCAGA
Os09g35870_F	TTCGTGAAGGTGAGCATGGA
Os09g35870_R	GGAGCAGTAGAACATGTCGTTGA
Os10g09920_F	GGTACATGCCCCATCAATGTG
Os10g09920_R	GGAACATTTAAGCTGAGCACGTT
Os10g34040_F	GGCTGTCGTCGACTACGAGAT
Os10g34040_R	CCGGTTGTACAGCTCCCAGTT
Os12g44290_F	AGATCAGGGATGCGTTTCATG
Os12g44290_R	GTCACGAGCCCGAAGATCAG

Supplementary Fig. S1. Validation of expression profiles of selected hormone-specific genes under different hormone conditions by real-time PCR analysis and comparison with microarray results. The expression under different hormone conditions has been represented in terms of fold change as compared to control condition. Error bars represent standard deviation. IAA, auxin; BAP, cytokinin; ABA, abscisic acid; ACC, ethylene derivative; SA, salicylic acid; JA, jasmonic acid.